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Life from information processing perspective

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Subcellular patterns of information processing

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Structural and functional features of the cell are determined by information stored in DNA. This information is represented by a limited set of genes, a genome. Each gene can be expressed individually to be fully converted into corresponding element of the cell structure or function. During gene expression, the information processing typically involves DNA transcription, RNA translation, and catalysis. This sequence of chemical reactions can be called a gene expression network, abbreviated GEN. Within the cell, GEN is an universal pattern of information processing. It is essentially four-dimensional. From this perspective, the cell can be considered as a highly regular composition of interacting GENs, a GENome. The opportunity to recognize an universal pattern of information processing in the sequence of well-known reactions has been completely overlooked. Here, I draw attention to this pattern and show that its implication yields a powerful conceptual framework suited very well to strongly integrate known subcellular phenomena and reveal their novel emergent features.

From the information processing perspective, all reactions within the cell fall into three categories: DNA transcription, RNA translation, and catalysis.

During DNA transcription, information is converted from DNA into RNA form. In this process, the DNA serves as a template for the synthesis of a linear heteromers of ribonucleotides. This is possible because any ribonucleotides are allowed to be attached to the deoxyribonucleotides by means of base pair. In general, the ribonucleotides differ very slightly from the deoxyribonucleotides. Their sugar, the ribose, is quite equal to the deoxyribose. Although there is no ribonucleotide with the thymine as a base, there is one with a uracil that resembles the thymine not only structurally but also functionally in the forming a complementary pair with the adenine. Consequently, the adenine-, guanine-, cytosine- or uracil-carrying ribonucleotide can attach only to the thymine-, cytosine-, guanine- or adenine-carrying deoxyribonucleotide respectively. This specificity plays a key role in DNA transcription, where one strand separates from another and exposes a particular sequence of deoxyribonucleotides serving as a template by guiding the synthesis of a linear heteromer of ribonucleotides which sequence is complementary to the deoxyribonucleotide sequence exposed. Thereafter this heteromer of ribonucleotides separates from the DNA strand as a single-stranded polyribonucleotide, a ribonucleic acid, abbreviated RNA. DNA transcription may occur in different regions of the DNA molecule at the same time and may be repeated in the same region many times yielding lots and lots of different RNA molecules as end products. All RNA molecules produced from the same region of DNA molecule are always identical. The DNA molecule persists DNA transcription and remains unexhausted.

During RNA translation, information is converted from RNA into polypeptide form. In this process, the RNA molecule serves as a template for the synthesis of a linear heteromers of amino acids, or amino acid chains. The RNA molecule to be translated, referred to as a messenger RNA, abbreviated mRNA, can be considered not only as a

sequence of a single ribonucleotides but also as a sequence of a ribonucleotide triplets. The maximal number of possible combinations of four single ribonucleotides in one triplet is $4^3 = 64$. Thus 64 triplets can be distinguished. Two triplets can link together by means of base pairing to form a triplet pair. Because of the base complementarity, the triplet pairs can be considered also as complementary in the sense that if one member of the triplet pair is specified the other is also specified. This triplet pair complementarity makes RNA translation possible. The certain amino acid attaches an adaptor RNA molecule, referred to as a transfer RNA, abbreviated tRNA, that contains one specific triplet providing this tRNA the potential to specifically recognize and attach the complementary triplet on mRNA. By orderly forthcoming attachment of tRNAs to mRNA by triplets pairing, corresponding amino acids come enough close together to be interconnected by means of a peptide bonds to form an amino acid chain, referred therefore to as a polypeptide chain or, more familiar, a polypeptide. Thus, the mRNA sequence can guide the synthesis of the polypeptide that is considered to be complementary to this mRNA in the sense that if the sequence of triplets on the mRNA is specified the sequence of amino acids on the polypeptide is specified as well. So, because the sequence of a single ribonucleotides predetermines the sequence of triplets on the mRNA, it predetermines also the sequence of a single amino acids on the polypeptide and, therefore, all polypeptides produced on the same mRNA must be identical. The combination of a single ribonucleotides in the triplet is usually called a codon, because it specifies amino acid, i.e. specific triplet codes for specific amino acid, and the set of 64 possible codons is therefore referred to as a triplet code. The triplet code itself is however termed degenerate because it contains redundancies in the sense that most amino acids are encoded by more than one codon. Moreover, any codons do not specify amino acids but constitute stop signals that terminates RNA translation. Thus, the set of peptidogenic amino acids in cellular world is restricted to just 20 member. The triplet code has been highly conserved during evolution. The meaning of each codon is the same in virtually all present-day cells. There are only few minor exceptions in which some few codons have deviate meanings. The universality of the triplet code provides a strong suggestion that the cellular world on the Earth evolved only once and all present-day cells are descendants of a single primordial cell. As for the way how the triplet code might be arisen, it remains still a theme of speculations. The RNA molecule persists RNA translation without to be exhausted.

During catalysis, information is converted from catalyst into metabolite form. In this process, the catalyst serves as a template for the reaction that otherwise could occur too slowly for cell to live. The catalyst does its job of catalysis by physically grappling with one or more substrate molecules and interacting with them to make or break chemical bonds. The catalyst is usually very specific for the chemical reaction it catalyzes, and the specificity lies in a sophisticated configuration of atoms at one or more active sites of catalyst. Only restricted set of substrate molecules can recognize this configuration and bind it. In catalysts, this binding causes a conformational shift that promotes the reaction in any way. Thereafter, the catalyst releases reaction products, acquires its original conformation and is available for catalysis anew. Thus, the catalyst persists catalysis without to be exhausted.

Generally, within the cell, the DNA serves as a template in the synthesis of RNAs by DNA transcription. DNA transcription reactions produce large numbers of various

RNAs most of them are mRNAs that serve as a templates in synthesis of a polypeptides by RNA translation. RNA translation reactions yield especially large numbers of different polypeptides most of them are building blocks for enzymes that serve as a catalysts providing the cell with opportunity to tame a bewildering variety of different chemical reactions occurring in molecular world, consolidate and even incorporate most of them into its own network. In this way, the information stored in DNA becomes expressed.

Thus, from the information processing perspective, the cell can be considered as a DNA expression network.

It is important to note that the information is stored in the DNA as a limited set of genes, a genome. Each gene can be expressed individually to be fully converted into corresponding element of the cell structure or function. For each gene, its own sequence of DNA transcription, RNA translation, and catalysis can be determined. This sequence of chemical reactions can be called a gene expression network, abbreviated GEN.

In some GENs, however, this sequence can be restricted. So, in any GENs, the end products are polypeptides functioning always as substrate molecules and never as catalysts. There are also GENs which end products are RNAs that never become translated into polypeptides, but function always at the level of RNA as substrate molecules. On the other hand, the sequence of reactions in some GEN extends if the products of DNA transcription or RNA translation undergo the post-transcriptional or post-translational processing respectively. This additional processing involves both folding to acquire mature three-dimensional conformation and modification of selected ribonucleotides or amino acid to modulate structural and functional properties of mature RNA or polypeptide molecule. Often, some ribonucleotide or amino acid sequences are to be removed from the primary RNA or polypeptide. Particularly, single primary RNA or polypeptide is to be cut up into separate molecules or, on the contrary, some primary RNAs or polypeptides are to be joined together to form single molecule. Generally, the same gene can undergo expression many times thus yielding a large amount of identical end products.

Despite of differences in details, it is obvious that the GEN is an universal pattern of information processing in the cell. It is essentially four-dimensional. Moreover, the spatio-temporal organization of the GEN is characterized by the strong directionality of the so called flow of information.

All elements of the GEN are the best known subcellular phenomena. The directionality of information flow is just the best known component of the so called central dogma of biology. Nevertheless, the opportunity to recognize an universal pattern in the directed sequence of well-known reactions has been completely overlooked. Perhaps, the central dogma of biology was too dogmatic just in solving the central problem of biology.

In turn, the GENs are arranged into the whole DNA expression network where each GEN can be considered as an "adaptor" subnetwork which recognizes a particular piece of information on the DNA and transfers it into a corresponding fragment of the whole cell network. GENs do not work in isolation but receive inputs from each other and

from environment. In each GEN, there are many control buttons that determine when, where, and how much of particular gene end product is synthesized. Just the astonishing harmony of the whole DNA expression network reflects the strong integrity of information stored in the cell genome. From this perspective, the cell can be considered as a highly regular composition of interacting GENs, a GENome.

In GENome, GENs interact to maintain each other. During information processing in particular GEN, it is just the job of other GENs to provide necessary elements for gene expression machinery. It is reasonable to distinguish three main parts of this machinery according to the sequence of information processing reactions in GEN.

The DNA transcription machinery is necessary to convert information from DNA into RNA form. The DNA serves as a template in this process. In the DNA molecule overall, both strands can be used as templates, but in any one gene only one strand is used and in the same gene it is always the same strand. To cite the gene, however, just the deoxyribonucleotides sequence on its non-template strand is conventionally used. In particular GEN, the DNA is represented by a corresponding gene. First of all, the DNA transcription machinery involves a pool of four different ribonucleotides with the triphosphate as a phosphate group. Further constituents of the DNA transcription machinery are numerous complex molecules of various nature that work to polymerize ribonucleotides on the template. A RNA polymerase serves to find an appropriate site on DNA, to bind the DNA at this site, to temporally separate the two strands in the adjacent region, and to begin generating of an RNA molecule on one of the separated strands. Then, the RNA polymerase moves along the DNA, maintaining growing fork to expose the template strand, and catalyzes the elongation of RNA molecule by addition of the incoming free ribonucleotide to the 3' growing point. When the RNA polymerase recognizes specific region on DNA which signals for termination of DNA transcription, both RNA polymerase and primary RNA molecule are released from DNA. A multitude of molecules assist the RNA polymerase to perform these tasks. In some GENs, the DNA transcription machinery additionally involves constituents for post-transcriptional processing of primary RNA. Spliceosome containing several kinds of polypeptides and RNAs cuts primary RNA to remove some ribonucleotide sequences, introns, and then rejoin adjacent regions, exons. Ribozymes are RNAs with an enzymatic activity restricted to cleaving primary RNAs at specific locations. Some constituents of the DNA transcription machinery are universal, others are gene-specific.

The RNA translation machinery is necessary to convert information from RNA into polypeptide form. The mRNA serves as template in this process. First of all, the RNA translation machinery involves a pool of 20 different amino acids. Further, numerous complex molecules function to enable the polymerization of amino acids on the template. One prominent part of the RNA translation machinery is a pool of tRNAs. In this pool, 30 to 40 different tRNAs can be identified in some cells and 50 to 100 - in other cells. Different tRNAs show very similar three-dimensional conformation. This reflects their functional similarity: all have to be chemically linked to a particular amino acid and to attach a corresponding codon on mRNA so that the amino acid can be added to a growing polypeptide chain. Mature tRNA molecule resembles cloverleaf folded into L-like shape with two arms. The end of one arm has a specific triplet of ribonucleotides, termed the anticodon, which enables the tRNA to be specifically

attached to complementary codon on the mRNA. The end of other arm is a free 3' terminus of the tRNA which can be linked to amino acid. Another prominent part of RNA translation machinery is a pool of 20 aminoacyl-tRNA synthetases. Each tRNA molecule can be recognized by one and only one of the 20 aminoacyl-tRNA synthetases. Likewise, each of these enzymes links one and only one of the 20 amino acids to a particular tRNA, forming an aminoacyl-tRNA. The most prominent part of RNA translation machinery is a ribosome, an association of any few specific ribosomal RNAs, abbreviated rRNAs, with more than 100 different polypeptides. In ribosome, a large and a small subunit are usually distinguished. Physically moving along an mRNA molecule, the ribosome binds and brings together various accessory molecules necessary for polypeptide synthesis and catalyzes the assembly of amino acids into polypeptide chain. In some GENs, the RNA translation machinery additionally involves constituents for post-translational processing of primary polypeptide. Some constituents of the RNA translation machinery are universal, others are mRNA-specific. Although the mRNA persists information processing by RNA translation, it degrades soon or later.

The catalysis machinery is necessary to convert information from enzyme into metabolite form. The catalyst serves as a template in this process. First of all, the catalysis machinery involves a particular pool of substrate molecules. This pool is usually catalyst-specific. Further constituents of the catalysis machinery are numerous complex molecules of various nature that assist the catalysis. Although the catalyst persists information processing by catalysis, it degrades soon or later.

Collectively, GENs in GENome work to replicate the complete DNA.

During DNA replication, information is reproduced. The DNA serves as a template in this process. The structure of DNA molecule immediately suggests how it may be replicated: its strands must be first separated and then each strand can serve as a template guiding the synthesis of complementary strand according to the strict rules of base pairing. The separation of strands exposes their deoxyribonucleotides and thus makes each of them available to be recognized and attached by free complementary deoxyribonucleotide in the cell matrix. By orderly forthcoming attachment, newly added deoxyribonucleotides transform each single strand into duplex identical with original. So, qualitatively, the DNA replication is relatively simple chemical reaction. But, quantitatively, it is very complex because of a large amount of DNA in the cell. Therefore, the DNA is usually replicated not as a whole but rather in fragments of various lengths which then are to be joined together.

In the cell, the DNA can contain more than one DNA molecule. Each DNA molecule can contain more than one region where the DNA replication can begin. Such regions are called replication origins. At each replication origin, the separation of strands resembles unzipping of a zipper with forming of two growing forks that move outward in opposite directions. Each growing fork is a zone where two strands expose their deoxyribonucleotides. While the new deoxyribonucleotides can be added exclusively at the 3' growing point, the restoring of the duplex can proceeds continuously only on the strand which is exposed in the 5'-to-3' direction. This part of the growing fork is called a leading strand. In contrast, the restoring of the duplex on the other strand for which the

5'-to-3' direction is away from the growing fork can occur only in short stretches, called Okazaki fragments that are later to be joined together. This part of the growing fork is called a lagging strand. While at each replication origin two growing forks are formed, the new synthesis proceeds bidirectional. The duplexes that are being restored by each replication origin elongate and eventually join each other. When the DNA replication is complete, each original DNA molecule is replaced by its two identical copies called daughter DNA molecules. While each of them is half old and half new, this type of replication is termed semiconservative. After replication, each couple of daughter DNA molecules usually undergoes processing that involves their packing and separation from one another.

In the cell, the DNA is never free but rather in association with a large number of diverse polypeptides. Such composition is called a chromatin. In the chromatin, most of the polypeptides serve to compact DNA sufficiently to fit it inside the cell. In distinct areas, the chromatin shows different degree of condensation. In areas with lowest degree of chromatin condensation, DNA fragments are present usually in so called B form. In this form the stacked base pairs are regularly spaced 0.34 nm apart the helix axis and the helix makes a complete turn every 3.4 nm with about 10 pairs per turn. On the outside of DNA molecule in B-form, the spaces between the intertwined strands form two helical grooves of different widths referred to as the major groove and the minor groove. Consequently, part of each base is accessible from outside the helix to both small and large molecules that bind to the DNA by contacting chemical groups within the grooves. These two binding surfaces of the DNA molecule are used by different DNA-binding molecules. In addition to the major B form of DNA, A form and Z form have been described. First of all, the DNA replication machinery involves a pool of four different deoxyribonucleotides. Also a pool of four different ribonucleotides is needed. In both pools, nucleotides contain always the triphosphate as a phosphate group. Further, numerous complex molecules function to enable the polymerization of deoxyribonucleotides on the template. A helicase unwinds and unzips the duplex to form growing fork. The local unwinding and unzipping produce the torsional stress leading to supercoiling of region adjacent to the fork. A topoisomerase removes this supercoil. On the exposed DNA strand, a specialized RNA polymerase, also called a DNA primase, forms a short RNA strand which serve then as a primer that can be elongated by a DNA polymerase, thereby restoring the duplex. The primer is needed while the DNA polymerase is unable to initiate replication but rather to carry out a deoxyribonucleotide addition only. At each DNA fragment, the primer is removed and replaced by growth of the deoxyribonucleotide strand from the neighboring DNA fragment. A DNA ligase joins the adjacent fragments. Combined with the ability to discriminate against incorporation of a mismatched deoxyribonucleotide, the proofreading activity of DNA polymerase is sufficient to reduce the error frequency of DNA replication significantly. Additionally, numerous molecules act to remove mismatched or damaged deoxyribonucleotides, further ensuring correct DNA replication and maintaining integrity of genome.

During DNA replication, each original DNA molecule will be ultimately replaced by a couple of daughter DNA molecules. Consequently, when the DNA replication is complete, the pool of free deoxyribonucleotides is exhausted, DNA replication machinery disappears, and chromatin polypeptides enrich the matrix. The post-

replicative packing of each DNA molecule by chromatin polypeptides results in structure referred to as a chromatid. Respectively, the packing of each couple of daughter DNA molecules produces a couple of two chromatids held together. This structure as a whole is referred to as a chromosome, its both constituents are called sister chromatids. Finally, each chromosome undergoes separation and sister chromatids segregate.

Whereas gene and genome are notions that refer to how information is stored in the cell, GEN and GENome refer to how the gene and genome function. The cells differ greatly in number and assortment of genes in genome and, subsequently, in number and assortment of GENs in GENome.

In some genomes, particular gene can be present in multiple copies which are either spread throughout the genome or arranged in tandem arrays. Often, some genes in the genome can be considered as a family of related genes. Such families can comprise from any few to 100 or even 1000 members which also can be either spread throughout the genome or arranged in tandem arrays. In the cell, the DNA can be not only monogenomic but also digenomic. Digenomic DNA contains two non-identical genomes. Both monogenomic and digenomic cells can exhibit high level of ploidy which refer to the number of genomes without distinguishing between identical and non-identical.

Practically, the cell suits the GENome to specific subset of sources of mass, impulse, and energy to produce their usable forms essential for the cell life. These sources label the start points of different metabolic pathways which refer to the routes of mass, impulse, and energy processing. Initially separated, these pathways become more and more intricately interwoven, but then divide anew into many branches which end points are marked by waste products. In contrast to sources of mass, impulse, and energy, the information source is appointed not in environment but rather in the cell itself and, more concretely, just in the DNA. In the cell, the same DNA, i.e. the same DNA molecule or the same set of DNA molecules, undergoes not only DNA expression but also DNA replication and provides in this way the cell with the key mechanism to couple these two phenomena into single one. If information encoded in the sequence of deoxyribonucleotides of DNA will be executed by DNA expression, the DNA will be reproduced by DNA replication. In other words, the DNA promotes its own reproduction by DNA replication through execution of its own information by DNA expression. As a result, the DNA not only persists information processing without to be exhausted but also becomes transformed into two identical copies of itself during the cell life history.

From the perspective of mass, impulse, and energy processing, bewildering large number of reaction types is recognized in cells. There is a great deal of convenience by their integration into subcellular patterns. In contrast, GEN and GENome seem to be a natural basis for this integration. As for the patterns, such as metabolic pathways, signaling cascades, regulatory motifs, functional modules, etc., they rather disclose some reciprocal relations between GENs. Taking into account the arrangement of chemical reactions into GENs provides the reverse engineering of these patterns with common platform.

Although differing greatly in the number and assortment of sources of mass, impulse, and energy, the cells are very similar in preparation carefully of the appropriate pools of such molecules as 4 ribonucleotides and 20 amino acids. Virtually each cell contains GENs that need these precursors to execute information stored in corresponding gene. Different cells are also similar in preparation carefully of the appropriate pool of 4 deoxyribonucleotides. Virtually in each cell, GENome needs these precursors to reproduce information stored in corresponding genome.

Spatio-temporally, the cell appears as a more or less quickly changing matrix composed of a bewildering number of chemicals participating on reactions involved in GENome. This matrix is mostly a heterogeneous water solution of a large array of mono- and polymolecules, but one prominent constituent is a tiny membrane composed of amphipathic molecules. Whereas one part of an amphipathic molecule is hydrophilic, i.e. water soluble, another part is hydrophobic, i.e. water insoluble. Placed in water, such molecules aggregate, arranging their hydrophobic portions as much in contact with one another as possible and their hydrophilic portions in contact with water. The most appropriate three-dimensional configuration of such aggregate is a bilayered membrane closed to form a vessel-like shape. In the cell, most of amphipathic molecules are in this configuration separating the matrix into an interior and an exterior part respectively. In the literature, only the interior part with the membrane is mentioned to be a cell, and the exterior part is referred to as an extracellular matrix. Here is preferred, though, to mention under the cell a whole matrix with the DNA as a key constituent. Other chemicals become constituents of the cell matrix not occasionally depending solely on the conditions in environment but rather regularly depending entirely on the information stored in the DNA. In this respect, the whole cell matrix can be considered as ultimate derivative of DNA.

Although sharing common structural and functional properties that have been conserved throughout evolution of the cellular world, the cells have evolved a variety of differences. In this respect, two large cell groups are usually distinguished: prokaryotic cells and eukaryotic cells.

The prokaryotic cells are commonly small entities with relatively simple spatio-temporal organization.

They have mostly only one DNA molecule, but any few cell types do have 2 or more. In the DNA, the number of deoxyribonucleotide pairs ranges from about 0.6 million to 5 millions, an amount sufficient to contain 1000 to 4000 genes. The genes are arranged close together with little intergenic space. Introns are extremely rare. The DNA is usually a ring-formed molecule. Although it is attached to the cell membrane, its largest part lies in the central region of the interior matrix and is arranged together with numerous polypeptides in a dense clump called nucleoid. The circular DNA molecule has usually only one replication origin. In addition, numerous accessory DNA molecules, called plasmids, are distributed in the interior matrix. They depend on cellular machinery to be replicated or expressed and can not survive at all outside of the cell. Plasmids carry some genes that, although not essential for cell life, are extremely

useful to the host in any situation. In prokaryotic cell, there is only one type of RNA polymerase which does the job of synthesis of all types of RNA molecule.

The cell membrane is commonly a single simply-shaped vessel that undergoes very slight changes in cell life history. Some cell types have however a second cell membrane which lies concentric to the first and subdivides the exterior matrix additionally. A sphere, a rod, or a spiral are the most abundant shapes of cell membrane-formed vessel which linear dimensions range from 1 to 10 μm. But, the diversity of shapes extends well beyond these basic types. In any few cell types, the cell membrane region associated with the DNA molecule can invaginate. In some other cell types, the cell membrane regions containing specialized sets of polypeptides are able not only to invaginate but also to pinch off completely, forming sealed vesicles which become suspended in the interior matrix. In cell types with two concentric cell membranes, sealed vesicles are constantly being discharged from outer cell membrane into environment and attack neighboring cells. In interior matrix, there are also numerous granular inclusions such as ribosomes and thylakoids. Thylakoids are flattened discs with light-sensitive pigment molecules.

In the exterior matrix, a rigid cell wall is commonly formed that is composed of complex assemblies of polypeptides and polysaccharides and is porous. In cell types with two concentric cell membranes, this wall is usually placed between them. The cell wall supports the cell to maintain its shape and provides it with additional mechanisms to protect key chemical reactions that occur preferentially in the interior matrix and at the cell membrane. Other prominent part of exterior matrix is a glycocalyx (capsule, gelatinous sheath or slime layer). Some prokaryotic cell types have flagella, which rotate like propellers to move cell through fluid medium. Fimbriae are short appendages that help cell attach to an appropriate surface.

The composition of metabolic pathways is relatively simple in prokaryotic cells, but, they show a broad variability in this respect. Some prokaryotic cells require only carbon dioxide as a carbon source. Certain prokaryotic cells use light as energy source. The others can oxidize various chemicals to obtain energy. Some prokaryotic cells can live only in the presence of oxygen, others only in the absence. Certain prokaryotic cells can live in the presence or absence of oxygen. Different metabolic pathways are often combined in the same cell and it can switch between them repeatedly. Some prokaryotic cells can also survive in environments that are considered as extremely hostile. They can inhabit extremely hot or cold habitats. They also can reside in extremely salt, acid, or alkaline surroundings.

The eukaryotic cells are generally much larger than prokaryotic cells and show relatively complex spatio-temporal organization.

They contain 1 to more than 50 long DNA molecules which are usually linear. On average, the DNA in a typical eukaryotic cell is about 1000 times greater in number of deoxyribonucleotide pairs than a DNA in a typical prokaryotic cell. Although a large amount of deoxyribonucleotide sequences in the DNA is non-coding, the average number of genes in a representative eukaryotic genome is still tenfold greater than in a

representative prokaryotic genome. The genes are distributed between different DNA molecules. Thus, each DNA molecule contains only the part of the genome.

The cell membrane is quite an elaborated system that changes significantly in cell life history.

In addition to intricately-shaped main cell vessel, which is 10 to 30 times larger in linear dimension and 1000 to 10,000 times greater in volume than a related vessel of typical prokaryotic cell, the cell membrane forms also an expanded set of various vesicles suspended in the interior matrix. Each vesicle has a lumen which content is considered to be topologically equivalent to the exterior matrix. The vesicles vary in dimensions and shape. Intensively communicating with one another, they compose an integral vesicular system.

The most prominent vesicle is a nuclear envelope. Its membrane makes up two concentric surfaces which lay close together with little space between them. Therefore, the nuclear envelope-forming vesicle looks like a double-membraned barrier subdividing the interior matrix into two functionally distinct compartments: a nucleus and a cytosol. The nucleus contains the DNA and is a principal site of DNA replication and DNA transcription. The eukaryotic cell has three different RNA polymerases, which specialize for synthesis of tRNAs, rRNAs, and mRNAs respectively. Sites where rRNAs join polypeptides to form ribosomes are called nucleoli. The cytosol is the site of RNA translation and of most of the cellular metabolism. The nuclear envelope is punctured at intervals by nuclear pores where membranes of two concentric surfaces fuse. The nuclear pores serve to actively transport molecules between nucleus and cytosol. The lumen of the nuclear envelope, referred to as a perinuclear space, continues into the labyrinthine lumen of the endoplasmic reticulum, a system of large flattened vesicles. The nuclear envelope and endoplasmic reticulum compose a part of vesicular system where molecules destined for secretion undergo processing.

Golgi apparatus, organized stacks of disc-like Golgi cisternae, is another part of vesicular system where molecules destined for secretion undergo sorting. Numerous small vesicles bud off from one area of vesicular system and fuse with another. In similar ways, the vesicular system interacts with the main cell vessel. Lysosomes are vesicles containing digestive enzymes. They fuse usually with vesicles containing food molecules. Vacuoles are vesicles to store water, sugars, salts, pigments, or toxins.

Most eukaryotic cell types also contain vesicles which are occupied by a bodies so resembling a prokaryotic cells that they are thought to originate from them. Indeed, there are numerous arguments to assume that the primordial eukaryotic host cell, which formed symbiotic association with any prokaryotic cells, assimilated them as so called mitochondria and plastids respectively. Although both mitochondria and plastids lost through time most of the genes originally presented in the genome of their precursors, they preserved however any part of their DNA and also the ability to self-double and self-divide. DNA of mitochondria and plastids is circular loop similar to prokaryotic DNA. As for the ways how the symbiotic form might be arisen, it is a matter of dispute. Whereas mitochondria can be found in most of eukaryotic cells, plastids are restricted to

any few cell types. Individual mitochondrion or plastid can contain many copies of its own DNA.

Ribosomes may be attached to endoplasmic reticulum on cytosol site or may lie free in cytosol. Sometimes, ribosomes combine into polyribosomes. Sites of endoplasmic reticulum with attached ribosomes are called rough endoplasmic reticulum. Primary polypeptides synthesized at ribosomes enter lumen of endoplasmic reticulum for post-translational processing. Mitochondria and plastids have also their own ribosomes to produce own polypeptides. These ribosomes resemble prokaryotic ribosomes.

Numerous polypeptides in the cell matrix are arranged into so called cytoskeleton giving the cell strength and rigidity, thereby helping to maintain cell shape. Other polypeptides are arranged into structures enabling both the movement of the cell as a whole and the movement of various structures within the cell matrix. The main cell vessel may have numerous short hair-like projections, cilia, that can move in an undulating fashion or few longer whip-like projections, flagella that move in whip-like fashion. Both cilia and flagella have similar construction, but differ from prokaryotic flagella.

In the exterior matrix of diverse eukaryotic cell types, more or less rigid cell wall is built. Also the glycocalyx is often present in exterior matrix. It may contain scales, spicules, spines, shells, sheaths, tests, thecae, or loricae which are often very complex structurally.

Eukaryotic cells show only a few variability according to the composition of metabolic pathways but it is usually very complex.

To describe a spatio-temporal organization of a single cell adequately, it is enough to outline how its spatial organization changes temporally.

While in the cell the DNA is produced only by DNA replication, it is reasonable to assume that the cell life history begins at the point where two newly produced sister cells halve the matrix inherited from the mother cell and each starts a self-dependent life. What the newborn cell has to do is just what its mother done: self-maintain as long as possible to self-double and then to self-divide. Because its DNA carries the same genome as the mother DNA, all abilities to fulfill this plan are inherited as well. To ensure that this plan will be fulfilled, all chemical reactions of the cell network must be well organized with respect to each other in space and time. This comprises also the precise logistics of a bewildering number of chemicals participating on these reactions and constituting the cell matrix.

In different cells, the spatio-temporal organization is differently complex.

In prokaryotic cells, the cell life history is short and simple.

In ideal environmental conditions, the prokaryotic cell needs only 30 minutes to self-double and to self-divide. Temporally, DNA expression and DNA replication seem to occur at the same time and proceed concurrently. Replication of single DNA molecule

begins at the single replication origin which is anchored to the cell membrane. Segregation of new DNA molecules appears to begin soon after starting of duplication of the replication origin, whereas the remainder of the DNA molecule awaits replication. Once DNA replication is complete, an assembly of new membrane and cell wall forms a septum, which eventually divides the cell in two. Because the origins of the two newly formed DNA molecules are anchored to different membrane sites, each daughter cell receives one DNA molecule. Some prokaryotic cells are capable to initiate the next round of DNA replication before the previous round is complete. This results in a cell with multiple bidirectional replication forks but only a single unduplicated terminus region. During this multifork replication, new replication origins soon after duplication undergo segregation in opposite directions.

In eukaryotic cells, the cell life history is much longer and more complex than in prokaryotic cells.

The duration of the cell life varies greatly from one cell type to another. Any few eukaryotic cells can grow and divide as quickly as prokaryotic cells, while the cell life of some other can last longer than a year. However, a typical eukaryotic cell needs usually 10 to 20 hours to self-double and to self-divide.

Temporally, the cell life history in an eukaryotic cell is traditionally divided into four major periods.

During the first period, G_1 phase, the newly born cell begins with DNA expression, cell matrix continuously grows in mass and volume, and organelles increase in number. The cell monitors conditions in its own matrix and in environment and, when the time is ripe, takes a decisive step that commits it to DNA replication. This period is considered to be a safety gap.

The second period, S phase, represents just the time of DNA replication. Polypeptides associated with DNA in chromatin are also produced. Those regions of chromatin that are least condensed and therefore most accessible to the replication machinery are replicated first, whereas the condensed chromatin tends to be replicated very late in S phase. Since eukaryotic DNA molecules are lineal, there is no place to produce the RNA primers needed to start the last Okazaki fragments at the very tips so that the strands become shorter after replication. To solve this end-replication problem, eukaryotic cells produce special enzyme, telomerase, which is able to restore the length of the strands. In contrast to prokaryotic cells, DNA expression and DNA replication in eukaryotic cells proceed concurrently only during a restricted period of cell life history.

The third period, G_2 phase, provides the next safety gap, allowing the cell to ensure that DNA replication is complete before it plunges into cell division.

During the fourth period, M phase, the cell division occurs. In a comparatively short M phase, the contents of cell matrix, which were doubled by activities of the preceding three periods, collectively called interphase, are to be exactly segregated into two daughter cells.

In process of cell division, two subprocesses are usually distinguished: mitosis and a cytokinesis.

The mitosis, also called karyokinesis, refers to the segregation of the reduplicated DNA, the cytokinesis is a division of the cell matrix as a whole. The mitosis is often considered as a culmination of the cell life history. With minor variations, the events in mitosis follow the same sequence in all eukaryotic cell types. Although they unfold continuously, the mitosis is conventionally divided into five subperiods.

During the first subperiod, prophase, the cell prepares itself for mitosis. In the nucleus, the chromatin rearranges to condense into chromosomes, each comprising two identical chromatids linked together at a multiple points along their length. In the cytosol, the cytoskeleton rearranges to build a specialized machinery, a spindle apparatus, which is able to capture chromosomes and segregate sister chromatids from one another.

During the second subperiod, prometaphase, the nuclear envelope breaks up into multiple small vesicles and chromosomes are released in the cytosol and captured by the spindle apparatus.

During the third subperiod, metaphase, the cell seems to pause until all chromosomes are aligned appropriately at the middle plane between the two poles of the spindle, poised for segregation.

During the forth subperiod, anaphase, the sister chromatids on each chromosome abruptly split apart and are pulled by the spindle apparatus to its opposite poles. Meanwhile, the cell itself stretches out and the spindle apparatus pushes its poles apart and elongates. Whereas the pulling moves the chromatids to segregate them into two equal subsets, one at each pole of the spindle, the pushing increases the distance between these subsets.

The fifth subperiod, telophase, is marked by a disappearance of the spindle apparatus and by a coalescence of small vesicles to form a nuclear envelope around each subset of chromatids establishing thus the two daughter nuclei. In each newly formed nucleus, the chromatin begins to decondense.

Thus, in contrast to prokaryotic cells, segregation of new DNA molecules in eukaryotic cells is temporally separated from DNA duplication.

The cytokinesis accompanies the mitosis, beginning usually in anaphase, continuing in telophase, but finishing later as the mitosis is complete. Just the cytokinesis, by which the cell is divided into two daughter cells, is traditionally viewed as the end of the M phase and the cell life history.

In each period or subperiod, the cell is in a specific stage. So, the cell life history can be considered as a sequence of these stages. The transition of the cell into each sequential stage is a precisely regulated process, overseen by numerous genes whose job is to ensure that this sequence is carried out correctly. There are numerous critical checkpoints, at which the transition into a particular stage of the cell life history can be

arrested and delayed, if the cell is hindered by unfavorable conditions to complete previous events without errors or even damaged by any agent. Arrests and delays at critical checkpoints provide time for cell to correct errors and repair damages. The critical checkpoints are points at which the cell life history may be regulated by extracellular signals.

Duration of each period or subperiod respectively varies considerably in different cells.

In some cells, there is no G_1 and G_2 phase and DNA replication and cell division occur very rapidly so that both S and M phase are very short. In contrast, other cells exit G_1 phase to enter a phase of replicative quiescence, a G_0 phase, where they become arrested unless called on to leave replicative quiescence by an appropriate extracellular signal. If they acquire no signal to do so, they may even cease S, G_2, and M phases altogether and proceed into the replicative senescence. During G_0 phase, metabolic activity of the cell may vary significantly.

During its life history, the cell often changes drastically structural and functional characteristics.

For example, the cell can alternate between the motile and sessile life styles or change repeatedly between the locomotion by means of pseudopodia and swimming by means of flagella. It can also alternate between the active and passive life style or even become a dormant spore or cyst for a long period of time.

The cell may divide either symmetrically producing two identical daughter cells or asymmetrically producing two non-identical daughter cells.

The asymmetric cell division involves unequal segregation of the cell fate determinants between the two daughter cells during cytokinesis. These determinants may specify cell fate either directly through intrinsic metabolic pathways or indirectly through interaction with extrinsic determinants but, in each case, the cell fate specification is always achieved by differential DNA expression. The DNA expression may be made differential at each reaction of the DNA expression network in many ways.

Generally, the life history of the single cell begins with one cell but ends with two.

The ability of the DNA molecule to be produced not only casually with a sequence depended mainly on chance but also causally with a sequence predetermined by a prototype make this molecule unique and suit it well for its specific role in origin and evolution of the cellular world.

Whereas in the molecular world the DNA molecule was merely a side-product of evolution and the DNA replication occurred to some extent occasionally and seldom, exactly the DNA molecule became the key substance and the DNA replication - the key reaction that both made the origin of the cellular world just possible. In molecular world on the early Earth, the same substance might be occasionally involved in more than one chemical reaction. As a result, a special network could evolve in which so coupled reactions promote each other. Likewise, the DNA was one time involved in a

sophisticated network of intimately interconnected chemical reactions and so promoted to successfully transform the DNA replication from an occasional event into a highly persistent one. As for the way by which this network might originate, it is still a matter of dispute. Most important, while involving the DNA replication, this network, once originating billions years ago, persists until now by progressive self-propagation and self-diversification.

Moreover, while progressively self-propagating and self-diversifying since its origin, this network tirelessly develops itself to only one super-network that is so huge that it is impossible to imagine and describe its spatio-temporal organization realistically. Temporally, this super-network stretches itself out through approximately 3 or 4 billions years. Spatially, first as small as a single mycoplasma, it is since billions of years as large as the whole biosphere of the Earth. The present-day biosphere is merely a visible top of iceberg in ocean of time. The ancient part of this gigantic life pattern leaves very scarce traces. In the known universe, it is the most complex structure that just represents a whole cellular world, and one part of the super-network, the cell, is often considered as an atom of the cellular word in the sense to be their smallest entity. As for the other respects, this "a-tom" is in reality a true auto-tom: the self-division is its essential feature. A self-dividing cell creates a bewildering diversity of life patterns in the cellular world.

In conclusion, the proposed conceptual framework based on notions of GEN and GENome seems to be suited very well to strongly integrate known subcellular phenomena and reveal their novel emergent features. Whereas gene and genome are notions that refer to how information is stored in the cell, GEN and GENome refer to how the gene and genome work. During information processing in particular GEN, it is just the job of other GENs to provide necessary elements for gene expression machinery. Collectively, GENs in GENome work to replicate the complete DNA so that the life history of the single cell begins with one cell but ends with two. Practically, the cell suits the GENome to specific subset of sources of mass, impulse, and energy to produce their usable forms essential for the cell life. Spatio-temporally, the cell appears as a more or less quickly changing matrix composed of a bewildering number of chemicals participating on reactions involved in GENome.

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Supercellular patterns of information processing

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The ability to produce two identical copies of itself to be replaced by them is the most universal functional feature of each single cell. Just this feature suggests the mechanism of formation and the nature of an universal life pattern: the progressive cell propagation produces what can be called a cell progression. At the base of the cell progression, one cell grows and divides giving rise to two daughter cells. These newly formed cells themselves grow and divide producing four daughter cells which then give rise to eight cells and so on. In growing cell progression, the number of progeny cells redoubles after each round of cell divisions. The cell progression is an universal life pattern in principle. It is essentially a four-dimensional pattern of information processing. The implication of the well-known feature of the single cell to recognize an universal life pattern has been overlooked completely. Here, I draw attention to this implication and show that it yields a powerful conceptual framework suited very well to strongly integrate known life phenomena and to reveal their novel emergent features.

The whole cellular world is only one cell progression which arose from one single primordial cell and has 3 or 4 billions years of uninterrupted history. It can be called a general cell progression. The present-day biosphere is merely a tiny slice from it, a visible top of iceberg in ocean of time. The ancient part of this gigantic life pattern leaves very scarce traces. In the known universe, it is the most complex structure. The ultimate goal of biology is to understand its spatio-temporal organization as completely as possible.

Although all cells of the general cell progression should be theoretically identical to each other genetically, this is not the case in the nature. Rather, the general cell progression consists of numerous cell subprogressions which can be distinguished from each other just by different DNAs. In the general cell progression, DNA undergoes not only a multiplication but also a diversification. Each cell subprogression which is specified by a particular individual DNA can be referred to as an individual cell progression. The general cell progression can be considered as a growing composition of an increasing number of individual cell progressions.

Generally, the life history of an individual cell progression begins with a founder cell. In the founder cell, the DNA can be either monogenomic or digenomic. Digenomic DNA contains two non-identical genomes. Both monogenomic and digenomic cells can exhibit high level of ploidy which refer to the number of genomes without distinguishing between identical and non-identical.

If founder cell is monogenomic, the life history of the individual cell progression is simple.

Monogenomic DNA remains the same in all its cells beginning with founder cell. All members of such cell progression are genetically identical with one another and with the founder cell: each cell is considered to be a clone of the founder cell.

If in any cell the DNA will be significantly altered in any way, this cell becomes a new founder cell giving rise to a new individual cell progression.

One way to alter the monogenomic DNA is a sequence mutation which arises either spontaneously or as a result of exposure to mutagenic agents in environment. While sequence mutation is only the way to produce variants of the same gene, called alleles, it is considered as an ultimate source of gene diversification. Weather a mutation is good, neutral, or harmful depends on how it affects survival of the individual cell progression.

The other way to alter the monogenomic DNA is a sequence transfer that can be either intragenomic or intergenomic. There are a large number of extraordinarily specialized mechanisms of sequence transfer. Some mechanisms require more or less extensive sequence homology, the others do not.

If founder cell is digenomic, the life history of the individual cell progression becomes more complex.

The digenomic founder cell, a zygote, is a product of syngamy of two monogenomic cells, gametes. By syngamy, gametes first unify physically their complete matrices and then combine their complete DNAs. Both DNAs are usually homologous in the sense that, although differing in deoxyribonucleotides sequences, they show the same genome composition. Consequently, the zygote receives one allele of the gene from each gamete and contains two alleles of the same gene. If both its alleles are alike, the gene is homozygous. If its alleles are different, the gene is heterozygous. When the gene is heterozygous, one allele may be dominant and the other recessive since only one allele of the same gene can be expressed in digenomic cell. Only eukaryotic cells are able to form completely digenomic founder cell. The digenomic cell can be either in monokaryotic or in dikaryotic state.

Commonly, newly formed zygote progressively propagates producing cell subprogression which cells remain all digenomic. This digenomic cell subprogression can be called a zygotic cell progression.

Soon or later, any cells of zygotic cell progression deviate from normal sequence of stages in cell life history. First signs of such deviation occur during prophase, where homologous chromosomes recognize each other and become physically paired along their length. So, the two couples of chromatids are juxtaposed making a bundle of four, called a tetrad. At each tetrad, a remarkable process occurs: paired non-sister chromatids exchange homologous fragments of DNA through breakage and reunion of their arms at points called crossovers. During prometaphase, tetrads are released in the cytosol and captured by the spindle apparatus. During metaphase, they are aligned appropriately at the middle plane between the two poles of the spindle. During anaphase, homologous chromosomes are segregated by spindle apparatus, whereas sister chromatids of each chromosome remain joined together. Because of recombination the sister chromatids are strongly speaking not identical but rather different. Additionally, while the spindle apparatus segregates chromosomes randomly to either of a two poles, the distribution of

homologous chromosomes between two nuclei is also random. After cell division is complete, the cell is replaced by two cells which do not need to double their DNA and immediately undergo cell division to segregate sister chromatids. The series of these two cell divisions is collectively called meiosis. Meiosis replaces one digenomic cell, a meiocyte, by four monogenomic cells, unlucky designated tetrads. Genomes of tetrads differ not only from each other but also from two genomes of the meiocyte. Totally, a zygotic cell progression can produce 4*N* different genomes, where *N* is a number of cells that undergo meiosis, a meiocytes. The meiosis is the main source of DNA diversification in eukaryotic cells.

Each tetrad progressively propagates and so the zygotic cell progression branches into a multitude of monogenomic cell subprogressions which can be called tetradic cell progressions.

Thus, if the founder cell is digenomic, the individual cell progression contains one zygotic cell progression and 4*N* tetradic cell progressions.

In tetradic cell progressions, any monogenomic cells soon or later become gametes which can take part on syngamy to form new zygotes. Usually, gametes forming a zygote originate from different individual cell progressions. Alternatively, zygote can be formed by autogamy if gametes originate from the same individual cell progression or even from the same meiocyte. Very often, gametes exhibit female-male dimorphism. The female gamete, an egg, is usually non-motile and is said to be fertilized by a motile male gamete, a sperm. The same individual cell progression can produce either both gamete types, eggs and sperm, or only one of both gamete types, eggs or sperm.

In one extreme case, the zygote does not propagate but immediately undergo meiosis which products then propagate progressively. In this case, individual cell progression only consists of a zygote and of four tetradic cell progressions. The number of tetradic cell progressions can be reduced even to two if the zygote does not replicate DNA but immediately segregates non-sister chromatids randomly to either of a two daughter cells.

In other extreme case, the zygote progressively propagates, but tetrads do not. They immediately become gametes and take part in production of new zygotes and thus leave individual cell progression that therefore does not branch into tetradic cell progressions.

In an individual cell progression, not all cells necessarily have an equal chance of surviving and propagation. Many of them may die away. Immortality must be considered as a feature of an individual cell progression, not of a single cell. However, the immortality is rather a potential feature: despite the ability to persist forever by progressive cell propagation, no one individual cell progression becomes really immortal.

Thus, an individual cell progression is a primary source of genome multiplication and diversification.

Within the general cell progression, one individual cell progression gives rise to many new individual cell progressions which in turn give rise to the next generation of individual cell progressions and so on. A pool of homologous genomes arises. In this pool, genome variants are produced rather randomly without any confident expectation on future needs. However, some of them can make their individual cell progressions better suited to given environmental conditions. These individual cell progressions are more likely to survive and to produce next generation of new individual cell progressions than others. Changes in genome that can pass through more than one generation of individual cell progressions making them better suited to particular environment are called adaptations. Because the environment is always in changing, there is no one perfectly-adapted genome in pool. When previous adaptations are no longer suitable to new environmental conditions, extinction of such genomes from the pool occurs. Thus, genomes obey natural selection by changes in environment. Natural selection is made tougher by a constant struggle for limited resources of mass, impulse, and energy. Only the fittest survive a struggle for existence.

Some changes in genome can make it no more homologous to other genomes in pool. A new genome pool and, consequently, a new type of individual cell progressions arise. However, there is a great deal of convenience by definition of boundaries between different pools of genomes.

The genome multiplication and genome diversification seems to be the ultimate aim in the life history of an individual cell progression. Just these both events ensures the continuity of life from one generation of individual cell progressions to the next and so secures the immortality of the general cell progression and so the immortality of the Life on the Earth.

Thus, the genome multiplication and diversification provide row material for evolution of types of individual cell progressions.

Different individual cell progressions display broad variability according to the temporal organization.

Within some individual cell progressions, all cells divide symmetrically so that two sister cells are always identical in their potential. If any cell differentiates in any direction of specialization, it retains the ability to de-differentiate or even to re-differentiate in other direction.

Within other individual cell progressions, some cells divide asymmetrically so that two sister cells are not always identical in their potential and may adopt distinct fates. Asymmetric cell division is a source of the cell diversification within the same individual cell progression. Although genetically identical, two sister cells produced by asymmetric cell division give rise to the cell subprogressions which differ from one another by differential DNA expression. Therefore, they can be called differential cell progressions. An individual cell progression can contain a large number of differential cell progressions which sometimes may be in complex interrelation to each other since asymmetric cell division can occur also within a differential cell progression itself.

Within some individual cell progressions, asymmetric cell divisions occur occasionally so that the cell diversification is rather a random.

Within other individual cell progressions, asymmetric cell divisions occur rather regularly so that the cell diversification is an established process during which the cell potential usually decreases sequentially. The progressive propagation of the initially totipotent founder cell produces a number of pluripotent cells. The totipotentiality of the founder cell is usually owed to an unique set of the call fate determinants which becomes simply exhausted even if cells divide symmetrically. After a critical number of pluripotent cells is reached, they may divide either symmetrically or asymmetrically. Each asymmetric division produces one pluripotent cell and one multipotent cell. In turn, after a critical number of multipotent cells is reached, they also may divide either symmetrically or asymmetrically. The sequential diminishing of the cell potential ends with production of unipotent cells which fate is usually a division arrest and a terminal differentiation. A terminally differentiated cell can not de-differentiate. On the contrary, non-terminally differentiated cells may alternatively de-differentiate and even re-differentiate into other direction of specialization. In each newly formed founder cell, the totipotentiality is restored.

Asymmetric cell division is associated with either symmetric or asymmetric kinetics of cell propagation. Cell progression generally tends to grow exponentially when the kinetics of cell propagation is symmetric. On the contrary, the asymmetric kinetics of cell propagation can pose a fundamental barrier to exponential growth.

Asymmetric cell division associated with asymmetric kinetics of cell propagation is generally appreciated as an essential property of the so called stem cell. Stem cell divides very rarely. If it divides, only one daughter cell inherits stem cell property. On the contrary, the other daughter cell becomes a non-stem cell but propagates rather quickly giving rise to a large number of progeny cells. So, the stem cell gives rise to a differential cell progression that consists of a stem cell lineage and a number of differential cell subprogressions each of which has a non-stem daughter cell at the base. Whereas the potential to divide seems to remain unlimited throughout the whole stem cell lineage, the propagation of each non-stem daughter cell is accompanied by a sequential restriction of the division capacity down to the division arrest, terminal differentiation, and death. Thus, each non-stem cell gives rise to the differential cell subprogression with a limited number of progeny cells.

The differential cell progression with a stem cell at the base can be called an asymmetric cell progression and the differential cell subprogressions within it can be called limited cell progressions.

An asymmetric cell progression is a steady state system.

At the base of this system, the asymmetric division of the first stem cell yields the second stem cell and the first non-stem cell. The newly formed second stem cell remains inactive for a long period of time during which the first non-stem cell progressively propagates producing the first limited cell progression. Within a limited cell progression, the cells first propagate at the fastest rate producing a growing number

of so called transit amplifying cells. After a critical number of division rounds is reached, the cells become committed to undergo differentiation into one or more directions of specialization. Differentiating cells propagate at the lower rate and, when a critical number of division rounds is reached, they become mature specialized cells which do not divide and become exhausted by performing their special functions. At certain critical point of the history of the first limited cell progression, the second stem cell divides producing the third stem cell and the second non-stem cell so that the exhausted first limited cell progression becomes replaced by the newly formed second limited cell progression. Since the potential to divide remains unlimited throughout the stem cell lineage, the asymmetric cell progression produces unlimited number of limited cell progressions which replace each other in consecutive order. So, an asymmetric cell progression can maintain near a constant number of cells.

Different individual cell progressions display broad variability according to the spatial organization too.

Within some individual cell progressions, the cells will be rather randomly dispersed in space and each cell seems to become autonomous in behavior.

Just the individual cell progressions with this type of cell arrangement are poorly studied while most attention usually was paid solely the single cell. This type of cell arrangement allows different individual cell progressions to superpose each other in space.

Within other individual cell progressions, the cells will remain in an association, a cell colony, held together in any way.

In the individual cell progressions with this type of cell arrangement, the founder cell first gives rise to primary cell colony which body plan is usually a filamentous chain, a hypha, or a globular body, a sphaera. By further cell propagation, an initial primary cell colony usually clones itself giving rise to a number of primary cell colonies respectively. Within a growing individual cell progression, these primary cell colonies may be either dispersed in space or held together in association forming a secondary cell colony of any kind and size and for any period of time under specific environmental circumstances. In turn, an initial secondary cell colony can give rise to a number of secondary cell colonies. Within a growing individual cell progression, also the secondary cell colonies may be either dispersed in space or held together in larger cell association. So, different individual cell progression can superpose each other even at the level of the secondary cell colony.

Generally, the cell association has advantageous ability to carry out activities with a complexity not possible by single cell.

Within an association, many cells come together to collectively respond to environmental conditions. This collective respond is usually more effective than by a single cell.

Some cell associations are continuously growing systems, the others are rather steady state systems which cell number is balanced in any ways.

The balance between cell propagation and cell elimination may be secured by DNA-orchestrated set of homeostatic mechanisms so that the cell association becomes able to maintain near a constant number of cells. This ability seems to be advantageous since some cell associations evolve homeostatic mechanisms which even involve a programmed cell death, the cell apoptosis, eliminating not only damaged cells but also superfluous healthy cells.

Different cell associations show a significant variation of degree of integration and coordination among cells.

Within an association, the cells will either remain similar or become different.

Progressive cell propagation may be accompanied by cell differentiation creating the diversity of specialized cells. The number of specialization directions can range from 1 to more than 200. Specifically designed to perform different functions, the cells may collectively respond to brighter spectrum of environmental conditions. This differential collective respond is usually more effective than by an association of similar cells.

Within an association, the cell differentiation will be either a random or an established process.

Progressive cell propagation may be accompanied by the establishment of an amount of differential cell progressions that may be asymmetric cell progressions. As a result, the cell association can contain a number of regions each of which is occupied by particular asymmetric cell progression. Within such region, stem cell is usually located in especially carefully protected area, a stem cell niche. If the stem cell divides, one daughter cell is retained as a stem cell but the other becomes non-stem cell and must leave the stem cell niche to enter an area occupied by limited cell progressions. Since limited cell progressions replace each other in consecutive order, near constant number of cells can be maintained within their area. The newly formed non-stem cell first enters a section occupied by a pool of transit amplifying cells and proceeds through a number of division rounds at the fastest rate providing a renewal of this pool. The transit amplifying cells are regularly committed to enter the next section occupied by a pool of differentiating cells which propagate at the lower rate. Finally, the differentiating cells are regularly committed to enter a section occupied by a pool of mature specialized cells which become inevitably exhausted by performing their functions.

Thus spatially, each region occupied by an asymmetric cell progression consists of two areas: a stem cell niche with one stem cell and an area occupied by limited cell progressions. In turn, the area occupied by limited cell progressions consists of three sections: a section occupied by a pool of transit amplifying cells, a section occupied by a pool of differentiating cells, and a section occupied by a pool of mature specialized cells.

The cells of an asymmetric cell progression put together a well-proportioned unit. This unit is a very stable dynamic system being able to exist eternally owing to the very fine co-ordination of the whole hierarchy of the cell propagation, cell elimination, and cell differentiation events. Using inflow of negative entropy from environment this unit can maintain sufficiently high level of hierarchy organization, so ensuring endless self-renewal. Since the asymmetric cell progression is potentially immortal, the cell association establishing a superposition of asymmetric cell progressions is therefore potentially immortal as well and can persist forever maintaining near a constant number of cells.

Stem cell lineage plays a key role in this hierarchy. It is namely the source of preservation of genetic fidelity and the source of self-renewal of the whole asymmetric cell progression. Stem cells remain undifferentiated while simultaneously producing highly specialized cells. The splitting of the stem cell progeny into two separate cell groups that drastically differ in division frequency and division number is assumed as a consequence of a selective pressure in evolution of cell association types to avoid the negative results of mutations. On the one hand, this splitting allows to reduce the division frequency of just those cells that reside permanently in cell association and so ensures the protection against accumulation of mutations. The division of these cells is very rare and is protected so sufficiently that they may divide unlimited number of times. On the other hand, the splitting allows to reduce the number of cell division rounds in the group of intensively proliferating cells and therefore to minimize the rate of malformation arising out of deleterious mutations. Also non-deleterious mutations in intensively proliferating cells do not accumulate since this progeny of the stem cell soon or later leaves the cell association. So, the splitting provides asymmetric cell progression with the property to exist beyond the number of cell divisions that leads to a significant risk in deleterious mutation.

Stem cells that acquire a mutation or are damaged by injury are to be culled from the cell association and therefore either undergo apoptosis or become directly a transit amplifying cells so that these asymmetric cell progressions soon or later become completely exhausted. In cell association, the number of asymmetric cell progressions is however maintained since each stem cell, if necessary, can alternate from asymmetric to symmetric cell division which results into two stem cells as well. While cell association can maintain stem cells as reservoirs for genetic fidelity, deleterious mutation spectrum could still arise.

The evolution brought into being an extensive diversity of cell associations with asymmetric cell progressions and their combinations.

Thus, some individual cell progression may have very regular spatio-temporal organization.

In conclusion, the proposed conceptual framework strongly integrates known life phenomena each of which can be described as a particular four-dimensional pattern of information processing within the related four-dimensional whole. This is advantageous while revealing novel emergent features and thus providing more insights into understanding of these phenomena. The whole cellular world is only one cell

progression which arose from one single primordial cell and has 3 or 4 billions years of uninterrupted history. This general cell progression can be considered as a growing composition of an increasing number of individual cell progressions each of which is specified by a particular individual DNA. Individual cell progressions are ultimate sources of genome multiplication and diversification. Different individual cell progressions display a broad variability in spatio-temporal organization which mostly depends upon whether the cells divide symmetrically or asymmetrically, whether the asymmetric cell divisions occur occasionally or regularly, whether the asymmetric cell division is associated with symmetric or asymmetric kinetics of the cell propagation, whether the cells will be rather randomly dispersed in space to become autonomous in behavior or remain in an association to form cell colony (primary, secondary, etc.), whether the cell association grows continuously or is a steady state system. The most regular spatio-temporal organization of an individual cell progression involves establishment of numbers of asymmetric cell subprogressions each of which has a stem cell at the base.

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Diversity of individual cell progressions in biosphere

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The present-day biosphere is merely a tiny slice from the general cell progression, a visible top of iceberg in ocean of time. However, although the number of individual cell progressions in this tiny slice represents only a small fraction of the whole, it is enormous. Much work is needed to describe and systematize this diversity completely. Here, I review the diversity of individual cell progressions with special focus of formation of cell associations. Animal individual cells progressions are reviewed in more details. To describe the formation of animal cell associations, a notion of a closed and orientable surface is used. In contrast to abstract mathematical surface, the real biological surface is made up not by dimensionless points but by three-dimensional matrix with embedded cells. So, it is actually a closed and orientable wall, since there is a distance between its two sides. The thickness of the wall may have regional differences in magnitude. Additionally, the two sides of the wall can be differently designated according to their orientation to interior or exterior of the cell association. To avoid confusion, one must be aware that the wall is not a boundary of the cell association but just its body. The complexity of animal cell association enhances gradually at different phylogenetic and ontogenetic stages. Vertebrata display the most sophisticated spatio-temporal organization of the wall.

Researchers are keenly interested in the proper identification of the diverse forms involved in their researches and the systematics is usually considered as the most practical tool in each scientific discipline. Therefore, while researchers deal with individual objects, scientific texts deal rather with groups of individuals sharing certain similarities. In systematics, closely related individuals are usually grouped into the same species, species - into the genus, genera - into the family, families - into the order, orders - into the class, and classes - into the phylum.

Historically, the principal objects of research and systematization in biology were originally individual living things for which the concept of an organism has been introduced and appropriate principles of systematization have been elaborated. When the multicellular nature of known organisms has been revealed by a microscope and numerous unicellular organisms have been discovered, the organism concept became very heterogeneous while ranging from the single cell to multicellular composition. The development of reliable systematization principles for unicellular organisms as for multicellular organisms met a number of difficult problems which remain unresolved. As a consequence, numerous controversial systems of life arise, but no one is adopted in biology for now.

In systematics, the main cause for all problems is that the multicellular organism is not an universal life pattern. There are also cells that do not associate with each other during progressive cell propagation. In contrast to multicellular organism, the individual cell progression is an universal life pattern and is therefore better suited to be used as a principal supercellular object of research and systematization in biology. It is essentially a four-dimensional pattern of information processing at the supercellular level of life

organization. Different individual cell progressions display a broad variability in spatio-temporal organization which mostly depends upon whether the cells divide symmetrically or asymmetrically, whether the asymmetric cell divisions occur occasionally or regularly, whether the asymmetric cell division is associated with symmetric or asymmetric kinetics of the cell propagation, whether the cells will be rather randomly dispersed in space to become autonomous in behavior or remain in an association to form cell colony (primary, secondary, etc.), whether the cell association grows continuously or is a steady state system, and so on.

Once originated on the Earth, the first cell founded the first individual cell progression which in turn gave rise to the general cell progression. The life history of the general cell progression involves the evolution of individual cell progressions creating their phylogenetic diversity. Evolution of individual cell progressions in turn involves the evolution of cells creating their diversity too. It is reasonable to distinguish between the phylogenetic and ontogenetic cell diversity. Whereas the phylogenetic cell diversity is a result of the genome multiplication and diversification during life history of the general cell progression, the ontogenetic cell diversity is a result of differential DNA expression during life history of some individual cell progressions.

It must be noted that the present-day biosphere is merely a tiny slice from the general cell progression, a visible top of iceberg in ocean of time. However, although the number of individual cell progressions in this tiny slice represents only a small fraction of the whole, it is enormous. Much work is needed to describe and systematize this diversity completely.

Since the evolution of individual cell progressions intrinsically involves the evolution of cells, it is reasonable first to review the phylogenetic cell diversity.

Phylogenetic cell diversity and separate system of cell types

The origin of the first cell, the evolution of the cell types during the Life history on the Earth, and the phylogenetic relations between different cell types within the present-day biosphere remain the matter of speculations and hot debates (see, for example, Bapteste E and Brochier C 2004, Brown JR and Doolittle WF 1997, Cavalier-Smith T 1998, 2001, 2002a, 2002b, Deamer DW 1997, Emelyanov VV 2003, Gupta RS 1998, Margulis L 1996, Martin W and Russell MJ 2003, Woese CR 1998, 2000, 2002, Woese CR *et al* 2000).

The phylogenetic cell diversity can be summarized as a compact system of cell types (Table 1). To avoid confusion, an independent hierarchy of taxonomic categories is used in this system: individuals are grouped into the same shoot, shoots - into the sprig, sprigs - into the twig, and twigs - into the branch.

Table 1. System of phylogenetic cell types

- Branch 1. Bacteria
  - Twig 1. Unibacteria
    - Sprig 1. Posibacteria
      - Shoot 1. Actinobacteria (5 orders of individual cell progressions)
      - Shoot 2. Dictyoglomi (1 species of individual cell progressions)
      - Shoot 3. Firmicutes (3 classes of individual cell progressions)
      - Shoot 4. Thermotogae (7 genera of individual cell progressions)
    - Sprig 2. Archaebacteria
      - Shoot 1. Crenarchaeota (5 orders of individual cell progressions)
      - Shoot 2. Euryarchaeota (8 classes of individual cell progressions)
  - Twig 2. Negibacteria
    - Sprig 1. Eobacteria
      - Shoot 1. Chloroflexi (6 orders of individual cell progressions)
      - Shoot 2. Deinococci (2 families of individual cell progressions)
    - Sprig 2. Glycobacteria
      - Shoot 1. Acidobacteria (2 families of individual cell progressions)
      - Shoot 2. Aquificae (2 families of individual cell progressions)
      - Shoot 3. Bacteroidetes (3 orders of individual cell progressions)
      - Shoot 4. Chlamydiae (5 families of individual cell progressions)
      - Shoot 5. Chlorobi (5 genera of individual cell progressions)
      - Shoot 6. Chrysiogenetes (1 species of individual cell progressions)
      - Shoot 7. Cyanobacteria (7 orders of individual cell progressions)
      - Shoot 8. Deferribacteres (5 genera of individual cell progressions)
      - Shoot 9. Fibrobacteres (3 species of individual cell progressions)
      - Shoot 10. Fusobacteria (7 genera of individual cell progressions)
      - Shoot 11. Gemmatimonadetes (1 species of individual cell progressions)
      - Shoot 12. Lentisphaerae (2 genera of individual cell progressions)
      - Shoot 13. Nitrospirae (4 genera of individual cell progressions)
      - Shoot 14. Planctomycetes (6 genera of individual cell progressions)
      - Shoot 15. Proteobacteria (5 classes of individual cell progressions)
      - Shoot 16. Spirochaetes (3 families of individual cell progressions)
      - Shoot 17. Thermodesulfobacteria (3 genera of individual cell progressions)
      - Shoot 18. Verrucomicrobia (2 orders of individual cell progressions)
- Branch 2. Karyota
  - Twig 1. Unikonta
    - Sprig 1. Amoebozoa
      - Shoot 1. Acanthamoebida (2 genera of individual cell progressions)
      - Shoot 2. Entamoebida (2 genera of individual cell progressions)
      - Shoot 3. Lobosea (2 orders of individual cell progressions)
      - Shoot 4. Mycetozoa (5 to 8 orders of individual cell progressions)
      - Shoot 5. Pelobionta (2 families of individual cell progressions)
    - Sprig 2. Opisthokonta
      - Shoot 1. Animalia (21 to 38 phyla of individual cell progressions)
      - Shoot 2. Choanoflagellata (3 families of individual cell progressions)
      - Shoot 3. Fungi (4 to 5 phyla of individual cell progressions)
      - Shoot 4. Microsporidia (20 to 22 families of individual cell progressions)
      - Shoot 5. Nucleariida (2 genera of individual cell progressions)
  - Twig 2. Bikonta
    - Sprig 1. Cabozoa
      - Subsprig 1. Rhizaria
        - Shoot 1. Acantharea (3 orders of individual cell progressions)
        - Shoot 2. Athalamea (2 genera of individual cell progressions)
        - Shoot 3. Cercozoa (3 to 9 orders of individual cell progressions)
        - Shoot 4. Foraminifera (6 to 8 orders of individual cell progressions)
        - Shoot 5. Haplosporidia (4 genera of individual cell progressions)

Shoot 6. Paramyxea (2 genera of individual cell progressions)
Shoot 7. Plasmodiophorida (7 genera of individual cell progressions)
Shoot 8. Polycystinea (6 families of individual cell progressions)
Subsprig 2. Excavata
Shoot 1. Diplomonadida (2 families of individual cell progressions)
Shoot 2. Euglenozoa (7 to 9 orders of individual cell progressions)
Shoot 3. Heterolobosea (2 orders of individual cell progressions)
Shoot 4. Jakobidae (3 genera of individual cell progressions)
Shoot 5. Malawimonadida (2 species of individual cell progressions)
Shoot 6. Oxymonadida (3 families of individual cell progressions)
Shoot 7. Parabasalida (3 orders of individual cell progressions)
Sprig 2. Corticata
Subsprig 1. Alveolata
Shoot 1. Apicomplexa (5 to 9 orders of individual cell progressions)
Shoot 2. Ciliophora (9 classes of individual cell progressions)
Shoot 3. Dinoflagellata (11 to 13 orders of individual cell progressions)
Shoot 4. Ellobiopsida (2 species of individual cell progressions)
Shoot 5. Perkinsea (2 genera of individual cell progressions)
Subsprig 2. Plantae
Shoot 1. Glaucophyta (5 families of individual cell progressions)
Shoot 2. Rhodophyta (2 classes of individual cell progressions)
Shoot 3. Viridiplantae (3 phyla of individual cell progressions)
Subsprig 3. Chromista
Shoot 1. Actinophryida (2 genera of individual cell progressions)
Shoot 2. Bacillariophyta (3 classes of individual cell progressions)
Shoot 3. Bicosoecida (5 genera of individual cell progressions)
Shoot 4. Blastocystis (6 species of individual cell progressions)
Shoot 5. Bolidophyta (2 species of individual cell progressions)
Shoot 6. Centroheliozoa (3 families of individual cell progressions)
Shoot 7. Chrysomerophyta (1 species of individual cell progressions)
Shoot 8. Chrysophyta (6 to 9 orders of individual cell progressions)
Shoot 9. Cryptophyta (2 to 4 families of individual cell progressions)
Shoot 10. Developayella (1 species of individual cell progressions)
Shoot 11. Dictyochophyta (2 orders of individual cell progressions)
Shoot 12. Eustigmatophyta (5 genera of individual cell progressions)
Shoot 13. Haptophyta (4 to 5 orders of individual cell progressions)
Shoot 14. Hyphochytriomyceta (2 species of individual cell progressions)
Shoot 15. Labyrinthulida (2 families of individual cell progressions)
Shoot 16. Oikomonada (1 species of individual cell progressions)
Shoot 17. Oomyceta (6 to 8 orders of individual cell progressions)
Shoot 18. Opalinida (4 genera of individual cell progressions)
Shoot 19. Pelagophyta (7 genera of individual cell progressions)
Shoot 20. Phaeophyta (11 to 14 orders of individual cell progressions)
Shoot 21. Phaeothamniophyta (2 orders of individual cell progressions)
Shoot 22. Pinguiophyta (4 genera of individual cell progressions)
Shoot 23. Placididea (2 genera of individual cell progressions)
Shoot 24. Raphidophyta (5 genera of individual cell progressions)
Shoot 25. Xanthophyta (4 orders of individual cell progressions)
Bikonta incertae sedes:
Shoot Apusomonadida (2 genera of individual cell progressions)

Differences between prokaryotic and eukaryotic cells with respect to spatio-temporal organization, as first defined in the 1930s by Chatton and more fully developed in the 1960s by Stanier and Van Niel, are of so profound importance and significance that systematists still prefer to claim the prokaryota-eukaryota dichotomy as the most basic in cellular world (Cavalier-Smith T 1998, Margulis L *et al* 2000, Vellai T and Vida G 1999). So, cells are usually grouped into two major taxa: Bacteria (unnecessary synonym: Prokaryota) and Karyota (unnecessary synonym Eukaryota). In system of cell types, these taxa can be ranked as branches. Which branch emerges first, Bacteria or Karyota, is unclear (Bapteste E and Brochier C 2004). Whether the first cell was a bacterium or a karyote is also not clear (Bapteste E and Brochier C 2004).

Differences between bacterial cells with a single cell membrane and cells with two concentric cell membranes are usually weighed higher than others if one wishes to divide Bacteria into separate groups (Cavalier-Smith T 1998, 2002a, Gupta RS 1998, 2000). Therefore, bacterial cells are sometimes grouped into taxa Unibacteria (synonym Monodermata) and Negibacteria (synonym Didermata) which can be ranked as twigs in separate system of cell types. Which bacterial twig emerges first, Unibacteria or Negibacteria, is unclear.

Among Unibacteria, differences in cell membrane composition give reason to recognize two large groups: Posibacteria and Archaebacteria (Cavalier-Smith T 1998, 2002a). These taxa can be ranked as sprigs in separate system of cell types. Posibacteria usually exhibit Gram-positive staining which suggest the name of the taxon. Archaebacteria are unique with regard to the composition of the cell membrane which is built rather by isoprenoid ether lipids than by acyl ester lipids. They are also unusual in metabolism (Schäfer G *et al* 1999). Some are known to be able to produce methane. The others are sulfate reducers. Many Archaebacteria live in extreme environments. Some prefer habitats like geysers whose temperature exceeds that of boiling water or like black smokers with very salty, acid, or alkaline hot water. Others prefer cold habitats like glaciers. These extreme hostile conditions are unusual today but may have been prevalent on the early Earth. The question whether the earliest bacterium was a posibacterium, an archaebacterium or a common ancestor from which they both evolved independently is unclear at present. Posibacteria and Negibacteria are sometimes joined in a clade Eubacteria. On the contrary, Archaebacteria and Karyota are joined in a clade Neomura. Posibacteria involve four taxa which can be ranked as shoots in separate system of cell types, Archaebacteria - only two.

Negibacteria are characterized by secondary cell membrane and, therefore, mostly exhibit Gram-negative staining which suggest the name of the taxon (Cavalier-Smith T 1998, 2002a). Differences in the composition of the outer cell membrane allow to divide Negibacteria into two separate groups: Eobacteria and Glycobacteria. These taxa can be ranked as sprigs in separate system of cell types. In Eobacteria, both leaflets of the outer cell membrane are built by phospholipids. In Glycobacteria, the outer leaflet of the outer cell membrane is built rather by lipopolysaccharides. Since lipopolysaccharide synthesis is immensely more complex than phospholipid synthesis and is unlikely to evolve first, it is suggested that Eobacteria are more ancestral (Cavalier-Smith T 1998, 2002a). Eobacteria involve two taxa which can be ranked as shoots in separate system of cell types. Glycobacteria are more diverse and contains 18 shoots some of which tend to

group with each other (for example, Bacteroidetes and Chlorobi, Chlamydiae, Lentisphaerae and Verrucomicrobia, Fibrobacteres and Acidobacteria).

At current stage, the knowledge of bacterial cell diversity in the biosphere is likely still incomplete and the list of bacterial cell types tends to lengthen (Curtis TP *et al* 2002, Hugenholtz P *et al* 1998, Rosselló-Mora R and Amann R 2001, Ward BB 2002, Whitman WB *et al* 1998, Zinder SH and Dworkin M 2001). Therefore, the system of bacterial cell types may change drastically in future.

Among Karyota, the fundamental difference between ancestrally uniciliate and biciliate cells gives reason to distinguish two large groups: Unikonta and Bikonta (Cavalier-Smith T 2002b, 2003). It is argued that the common ancestor of Unikonta probably had only a single centriole and cilium per kinetid. In some bicentriolar Unikonta, the anterior cilium remains anterior in successive cell generations and does not transform into a posterior one. On the contrary, a major shared derived character of all Bikonta is just a ciliary transformation in which the anterior cilium and its associated roots are always the first formed but, in the next cell generations, they undergo often marked changes in structure and function to become a corresponding posterior organelles. Taxa Unikonta and Bikonta can be ranked as twigs in separate system of cell types. Which karyotic twig emerges first is unclear.

Among Unikonta, two large groups can be recognized: Amoebozoa and Opisthokonta (Cavalier-Smith T 2002b, 2003). These taxa can be ranked as sprigs in separate system of cell types. Amoebozoa ancestrally had an anterior cilium. On the contrary, Opisthokonta ancestrally had a single posterior cilium with a bicentriolar kinetid. This contrasting ciliary orientation may reflect a primary divergence in feeding mode of the first karyotes. It suggests that Amoebozoa and Bikonta may be sister clades, jointly called Anterokonta. Amoebozoa involve five taxa which can be ranked as shoots in separate system of cell types, Opisthokonta - also five.

Bikonta also may be divided into two large groups: Cabozoa and Corticata (Cavalier-Smith T 2002b, 2003). In contrast to Cabozoa, Corticata have a relatively rigid cell cortex, often supported by microtubules, some of which originate as ciliary roots made of distinctive bands of aggregated microtubules, but lack evenly radiating single microtubules resembling aster. Cabozoa involve 15 taxa which can be ranked as shoots in separate system of cell types. Among Cabozoa, two subsprigs, Rhizaria (8 shoots) and Excavata (7 shoots) can be recognized. Corticata are more diverse and contains 33 shoots which may be grouped in three subsprigs: Alveolata (5 shoots), Plantae (3 shoots), and Chromista (25 shoots). The position of one bikont shoot, Apusomonadida, is unclear.

Although extremely successful due to the number of individual cell progression species, Animalia, Fungi, and Viridiplantae represent not more than only three of 59 karyotic cell types with a rank of a shoot.

In comparison with Bacteria, the knowledge of karyotic cell diversity in the biosphere is more complete, although many cell types are still poorly studied. Moreover, as last two decades show, Karyota seem to be much less diverse in terms of spatio-temporal

organization of the cells than previously thought and the list of their cell types rather shortens than lengthens (Cavalier-Smith T 1998, 2002b, 2003, Corlis JO 2002, Patterson DJ 1999, Taylor FJR 2003). Therefore, the future research will undoubtedly change the system of karyotic cell types as well.

Diversity of individual cell progressions and formation of cell associations

Since the spatio-temporal organization of individual cell progressions is much more variable than that of cells, it is not surprisingly that the diversity of individual cell progression types is enormous. This diversity depends greatly on the phylogenetic cell type (Table 1).

Here, the diversity of individual cell progressions is reviewed with special focus on formation of cell associations. Therefore, more attention is paid to phylogenetic cell types by which the formation of cell association takes place during the life history of individual cell progressions.

A. Bacteria

In Bacteria, most individual cell progressions are characterized by dispersion of cells in environment.

However, it is now recognized that dispersed bacterial cells are often found in close association with surfaces and interfaces forming loose aggregates known as biofilms (Branda S *et al* 2005, Crespi BJ 2001, Davey ME and O'Toole GA 2000). In the nature, the biofilm usually houses a mixture of cells belonging to different individual cell progression species. Single-species biofilms are rather artificial products created for research purposes. The biofilms are as diverse as their constituent cells. The biofilm offers its member cells several benefits. Its formation and maintenance critically depends upon production of substances for exterior matrices of cells (Branda S *et al* 2005). Under different environmental conditions, the very same substances play different roles within biofilm.

Some dispersed bacterial cells have a relatively constant habitat, but others are subjected to environmental conditions that frequently change and the cell must alternate between two or many structural and functional states (Dworkin M 2001).

Additionally, in some bacterial individual cell progressions with disperse cell arrangement, cells can closely aggregate into simplest temporary cell associations.

This modus is characteristic for proteobacterial order Myxococcales which dispersed cells live in the soil and feed on other bacteria (Dao DN *et al* 2000, Dworkin M 2001, Raven PH *et al* 1999, Zinder SH and Dworkin M 2001). In superposition of different growing individual cell progressions, the cells usually stay together in loose associations in which the digestive enzymes secreted by individual cells are pooled, thus increasing the efficiency of feeding. When nutrients are exhausted, further cell propagation is ceased and cells glide toward any aggregation centers producing numerous mounds of cells. In each mound, cells join tightly into a fruiting body, within

which any cells differentiate into spores. A fruiting body is a chimerical association containing cells from different individual cell progressions. It can contain more or less elaborate stalk. The majority of the cells die in the process of forming fruiting bodies. Also in fruiting body, only spores survive and become dispersed in environment. When the conditions are more favorable, the spore germinates to continue expansion of individual cell progression. The same individual cell progression repeatedly takes part in formation of the fruiting bodies.

Numerous bacterial individual cell progressions are characterized by formation of cell associations (Dworkin M 2001, Zinder SH and Dworkin M 2001). Bacterial primary cell colony may be formed as a cell pair, rosette, hypha, flat square, cuboid packet, clump, or sphaera. Secondary cell colony ranges from simple branching colony of hyphae to the three-dimensional mycelium.

Cell associations in form of a multinucleoid plasmodium are also known.

Unibacteria: Posibacteria: Thermotogae

In variety of Thermotogae, the progressive cell propagation is accompanied by the formation of cell pairs, hyphae, and sphaerae (Huber R and Hannig M 2003). In genus *Thermosipho*, the hypha can contain up to 12 cells surrounded by a sheath. In genus *Fervidobacterium*, the primary cell colony is either a short hypha, a small sphaera of up to 7 cells, or a large irregular aggregate of up to 50 cells.

Unibacteria: Posibacteria: Firmicutes

In variety of genera (*Bacillus*, *Clostridium*, *Desulfotomaculum*, *Sporolactobacillus*, *Sporosarcina*, *Thermoactinomyces*, etc.), the cell can change from symmetric to asymmetric cell division if conditions become hostile (Angert ER 2005, Dworkin M 2001, Errington J 2003, Zinder SH and Dworkin M 2001). During asymmetric cell division, both chromatids adopt a novel configuration stretching from the one pole of the cell to the other. The cell division machinery assembles at both poles of the cell, but cytokinesis occurs at only one pole. A portion of one chromatid is first trapped by the division septum and becomes then packaged into the smaller cell, a forespore. Daughter cells remain attached to each other forming a cell pair. The larger daughter cell, unlucky designated as mother cell, then fully encloses the forespore which differentiates into an endospore. Since the matrix of the larger cell takes part on endospore formation, the endospore has two concentric cell membranes. This condition can be a prerequisite of a negibacterial cell type origin. If the maturation of the endospore is complete, the remnant matrix of the larger cell eventually lyses and dies. The endospore is extraordinarily resistant to most external extremes (temperature, desiccation, chemical agents, radiation, physical disruption, etc.) and can remain metabolically quiescent for a considerable period of time.

In genera *Anaerobacter*, *Epulopiscium*, and *Metabacterium* (Angert ER 2005, Angert ER *et al* 1996, Angert ER and Losick RM 1998), the cell undergoes asymmetric cell division first after it contains three or more chromatids. Then, it divides at both poles so that two smaller cells a formed. They both become engulfed by the larger cell within

which they propagate progressively producing multiple forespores. In *Anaerobacter* and *Metabacterium*, all forespores become mature endospores within the "mother" cell before they become released. In *Epulopiscium*, the forespores remain rather active than dormant when they become released.

In genus *Arthromitus* (Angert ER 2005), the progressive cell propagation results in formation of a long hypha attached to host ileum. Each cell within the hypha is able to undergo asymmetric cell division if environmental conditions become unfavorable. The smaller cell usually divides ones producing two identical cells which either are immediately released or become encased in a common spore coat.

In genera *Streptococcus* and *Lactobacillus*, cells are held together in hyphae (Zinder SH and Dworkin M 2001).

In genus *Sarcina*, the progressive propagation of coccoid cells results in formation of cuboid packets which in turn are held together forming a long packet chains (Zinder SH and Dworkin M 2001).

Unibacteria: Posibacteria: Actinobacteria

In Actinobacteria (Angert ER 2005, Dworkin M 2001, Raven PH *et al* 1999, Wösten HAB and Willey JM 2000), when the founder cell progressively propagates, the progeny cells remain tightly associated in a primary cell colony, forming a short hypha which then branches giving rise to a growing secondary cell colony where hyphae become more and more intricately interwoven. In genus *Streptomyces*, the secondary cell colony is distinguished by a marked tendency toward radial spreading and branching and resembles the fungal mycelium. It either penetrates into the substrate or travels along its surface. After a number of hours of substrate growth, the colony begins to develop vertically forming aerial hyphae. When conditions in environment become unfavorable, any cells in aerial hyphae differentiate into spores, which can survive even in extremely hostile conditions. Whereas other cells of the colony die rather by apoptosis, the spores are dispersed in environment. Each spore monitors its environment and, if conditions are favorable, germinates and propagates forming new primary and secondary cell colony respectively. So, spores contribute to distribution of the individual cell progression in the environment. In colony, each cell can become a new founder cell.

Negibacteria: Eobacteria: Deinococci

In Deinococcaceae (Murray RGE 1999), the cells may be held together in pairs and in tetrads.

In genus *Thermus* (Williams RAD and Da Costa MS 1999), the cells are held together in short or long hyphae. Unusual rotund forms of the primary cell colony are sometimes seen in liquid cultures. The "aggregation" type, for example, consists of several cells bound together by the external layer of the cell envelope. This layer encloses not only the cells but also a large intercellular space. A "vesicular" type is seen as developing from an extended bleb on the surface of a single cell.

Negibacteria: Eobacteria: Chloroflexi

In Chloroflexi (Hanada S and Pierson BK 2002), the cells are mostly held together in a hypha with gliding motility. In genus *Chloronema*, the hyphae are often spirally twisted and thickly sheathed. In genus *Oscillochloris*, the hypha may be surrounded by a thin layer of slime.

Negibacteria: Glycobacteria: Aquificae

In genera such as *Aquifex*, *Hydrogenobacter*, *Hydrogenobaculum*, *Hydrogenothermus*, *Thermocrinis*, the cells may be held together in cell pairs (Huber R and Eder W 2002). Additionally, large aggregates, containing up to about 100 cells, may be formed in genera *Aquifex*, *Hydrogenothermus*, and *Thermocrinis*. Within a permanent flow of medium under exposure to air, the *in vitro* colony of the genus *Thermocrinis* grows in streamer-like cell masses predominantly composed of long hyphae.

Negibacteria: Glycobacteria: Bacteroidetes

In genus *Flexibacter* (Dworkin M 2001), the rod-shaped cell grows and undergoes progressive cell propagation producing long, threadlike hyphae. The hyphae then fragments into shorter hyphae which continue to grow and fragment. Alternatively, the hyphae can fragment into rod-shaped cells.

Negibacteria: Glycobacteria: Chlorobi

In Chlorobi (Overmann J 2000), the cells may divide by binary and ternary fission. In genus *Chloroherpeton*, the cell is a long filament, highly flexible, and motile by gliding. In genus *Chlorobium*, long chains of almost spherical cells may be formed in growing *in vitro* culture during stationary phase. Strains with vibrioid morphology can form coils of C-shaped cells. In genus *Pelodictyon*, ternary fission leads to the formation of large three-dimensional nets.

Negibacteria: Glycobacteria: Planctomycetes

In Planctomycetes (Ward N *et al* 2004), rosettes or aggregates are formed by many spherical cells joined together at the distal tips of their stalks. In genus *Isosphaera*, the cell colony is a hypha that moves by gliding.

Negibacteria: Glycobacteria: Cyanobacteria

In Cyanobacteria, the formation of cell associations is abundant (Dworkin M 2001, Meeks JC and Elhai J 2002, Raven PH *et al* 1999, Van den Hoek C *et al* 1995).

In some orders, the typical primary body plan is a hypha. In orders Oscillatoriales and Stigonematales, hypha is rather a long chain with equal diameter throughout the whole length. In order Nostocales, the hypha may be either a short trichome tapered from one end to other as in family Rivulariaceae or a long chain as much as a meter in length as

in family Nostocaceae. In the hypha, cells often show signs of differentiation. In nostocaceal genus *Anabaena*, for instance, cells take on a distinctive character at regular intervals along the hypha and become able to incorporate atmospheric nitrogen into organic molecules. These few specialized cells are more larger than other cells in a hypha and have an especially thickened cell wall to maintain anaerobic conditions, since nitrogen fixation can not occur in the presence of the oxygen. They perform nitrogen fixation for their neighbors and share the products with them. Generally, the hypha may break into fragments which separate and develop into new hyphae. Additionally, some cells in the hypha can differentiate into spores, called akinetes, which survive unfavorable environmental conditions and give rise to new hyphae contributing to the distribution of the individual cell progression in the environment (Moore D *et al* 2004). Hyphae may be dispersed in space or held together in a secondary cell colony within a thin gelatinous matrix.

In order Pleurocapsales (Angert ER 2005, Dworkin M 2001, Montejano G and León-Tejera H 2002), the cell termed a baeocyte is initially phototactic and motile by gliding until it becomes covered by a thick, fibrous sheath. At this point, the baeocyte tends to become attached to any surface and then undergoes progressive DNA replication increasing in size. In some species of genus *Dermocarpa*, the size increase is as much as 1000-fold. When the maximum size has been reached, this bacterial multinucleoid plasmodium undergoes multiple fissions within the fibrous sheath which then ruptures, releasing the numerous small baeocytes. In genus *Dermocarpella*, the growing plasmodium becomes rather ovoid and pyriform and undergoes asymmetric binary fission. The smaller portion remains attached to its original site and continues growth. The larger portion undergoes subsequent divisions to form the baeocytes. In genus *Pleurocapsa*, the growing initial plasmodium gives rise to the branching colony of plasmodia attached to each other. Each plasmodium can undergo multiple divisions to produce baeocytes.

In order Chroococcales, the primary cell colony may be either an irregular lump or a more or less accurate sphaera.

Cyanobacterial hyphae and sphaerae can control their position in the water column to obtain the optimum amount of light and nutrients.

Negibacteria: Glycobacteria: Proteobacteria

In variety of genera, the cells may be held together in cell pair, rosette, or hypha (Angert ER 2005, Dworkin M 2001, Hanson RS and Hanson TE 1996, Yurkov VV and Beatty JT 1998, Zinder SH and Dworkin M 2001).

In genus *Caulobacter* (Dworkin M 2001, Zinder SH and Dworkin M 2001), the free-swimming, non-growing, flagellate cell attaches to the substratum, takes off the flagellum, and changes to the stalked sessile stage. It then grows and divides asymmetrically producing two cells attached to each other. The bottom daughter cell, unlucky designated as mother cell, remains stalked and sessile. It will then grow to be replaced by the next cell pair. The top daughter cell produces flagellum, detaches from its sister, and become free-swimming and non-growing. It will then attach to the

substratum to transform into new stalked cell, thus contributing to the distribution of individual cell progression in space. Many stalked cells may be held together in a cell colony in form of a rosette.

In genus *Bdellovibrio* (Angert ER 2005, Dworkin M 2001), the free-swimming, non-growing, flagellate cell attaches to any negibacterial prey cell and penetrates its outer membrane by rapid rotation. It sheds the flagellum and enters the periplasm of the prey cell. It then grows but does not divide so that a long curved multinucleoid plasmodium is formed. Once the prey cell cytoplasm is consumed, the plasmodium ceases growth and fragments into flagellate cells. These cells then lyse the prey cell and swim off, each ready for the next encounter with a new susceptible host cell.

In genus *Rhodomicrobium* (Dworkin M 2001), the free-swimming, non-growing, flagellate cell sheds its flagellum, becomes a sessile, stalked cell, and begins to propagate progressively in the presence of optimal environmental conditions. The progeny cells remain in connection to each other forming a branching colony of hyphae. Alternatively, the colony produces both the free-swimming, non-growing, flagellate cells and spores.

Growing *in vitro* colonies of the genus *Escherichia* exhibit a complex structure with some areas undergoing cell death and reproduction being limited to a small number of cells at the colony edge (Crespi BJ 2001).

Unibacteria: Archaebacteria: Crenarchaeota

In variety of genera, cell association occurs in form of cell pair, short hypha, or grape-like aggregate (Huber H and Stetter KO 2002). In genus *Pyrodictium*, cell association grows as a three-dimensional network of cells and extracellular hollow tubules, cannulae, which interconnect the cells. In liquid cultures, the network forms flakes of up to 10 mm in diameter, visible by the naked eye, or tiny white balls about 1 mm in size.

Unibacteria: Archaebacteria: Euryarchaeota

In variety of genera, cell association occurs in form a cell pair, tetrad, cluster, aggregate, or hypha (Bertoldo C and Antranikian G 2003, Bonin AS and Boone DR 2004, Garcia JL *et al* 2001, Whitman WB *et al* 1999, Whitman WB and Jeanthon C 2002). Hyphae differ in length.

These examples surely testify to the ability of Bacteria to exploit intercellular interactions and communication to facilitate their adaptation to changing environmental parameters.

B. Karyota

In Karyota, numerous individual cell progressions are characterized by dispersion of cells in environment.

Likewise, in some karyotic individual cell progressions with disperse cell arrangement, cells can aggregate into simplest temporary associations as well.

One example are individual cell progressions of the mycetozoal order Dictyosteliida (Cavender JC 1990, Dao DN *et al* 2000, Raven PH *et al* 1999). Two monogenomic cells fuse and build a giant zygote which digests all the other monogenomic cells adjacent to it. When it has eaten all of them, it encysts itself in a thick wall and undergoes meiosis. Tetrads progressively propagate producing four tetradic cell progressions and then monogenomic cells are liberated from the cyst. Free monogenomic cells propagate further to continue expansion of the individual cell progression which superposes with others. When food supply is exhausted, tens of thousands of cells from different individual cell progressions join together to form moving streams of cells that converge at a central point. Here they pile atop one another to produce a conical mound called a tight aggregate. Subsequently, a tip arises at the top of this mound, and the tight aggregate bends over to produce the migrating slug with the tip of the front. The slug, also called a grex or a pseudoplasmodium, is usually 2 to 4 mm long and is encased in a slimy sheath. Moving with its anterior tip slightly raised, it migrates to leave dark and moist environment. When reaching an illuminated area, the slug ceases migration and transforms into fruiting body composed of a tubular stalk and a spore case. Within fruiting body, cells differentiate either into stalk cells or into spore cells. Whereas the spore cells disperse in environment where they can propagate further after a period of dormancy, the stalk cells inevitably die. After germination, spore can take part in growth of the individual cell progression. The same individual cell progression repeatedly takes part in formation of the fruiting bodies.

With some differences in how it occurs, this pattern of transitory cell association appears also among the heteroloboseal order Acrasida (Blanton RL 1990). In this respect, the karyotic Dictyosteliida and Acrasida resemble bacterial Myxococcales. Long treated together as cellular slime molds, Dictyosteliida and Acrasida are now recognized to be quite unrelated to each other. Although very similar, their patterns of temporal cell association seem to evolve separately.

In contrast to Bacteria, there are much more karyotic individual cell progressions which are characterized by association of the cells.

Although hypha and sphaera remain typical body plan of the primary cell colony also in Karyota, they are often more complex as in Bacteria. Some Karyota also appear to be very much better at organized division of labor in cell association. Also in Karyota, hyphae and sphaerae can form secondary cell colonies. However, karyotic secondary cell colonies are usually much more sophisticated as in Bacteria. Some colonies sustain growth perpetually, others generally have a determinate period of growth after which they maintain steady state mass.

Hyphae and sphaerae often have plasmodial character. The nuclei flow freely in plasmodium. According to the mode of formation, two types of plasmodia are usually distinguished: a coencyte and a syncytium. A coencyte is formed if karyokinesis is not accompanied by cytokinesis during progressive cell propagation. On the contrary, a syncytium is formed if some uninucleate cells fuse together.

Unikonta: Amoebozoa: Entamoebida

In few species of genus *Entamoeba*, immature cyst contains 1, 2, or 4 nuclei. When mature, cyst contains 8 or even 16 nuclei.

Unikonta: Amoebozoa: Lobosea

Lobosea (Goodkov AV *et al* 1999, Smirnov AV and Goodkov AV 1999) are actually plasmodia that move by means of so-called amoeboid movement and do not have constant body form. The locomotive form is the most representative characteristic. The diversity of locomotive forms is broad, but not unlimited.

In genus *Chaos* of the order Euamoebida, there are from two to several hundred nuclei per plasmodium. The plasmodium body is polypodal with strong tendency to adopt elongated form in continuous rapid locomotion. The ability to cyst formation has been reported for *Chaos illinoisense* only.

In order Leptomyxida, multinucleate plasmodia with 8 to several hundred nuclei are common. Within the plasmodium, nuclei propagate simultaneously. When fully extended, the plasmodium may be 3 mm or more in length. Cysts produced by local condensation of cytoplasm are also multinucleate. Two plasmodia merge to form a chimerical plasmodium.

In genus *Phreatamoeba*, the flattened plasmodium with a single broad pseudopodium bearing numerous subpseudopodia contains up to 40 nuclei. Plasmodia range in size from 11 to 160 mm and vary in shape from elongated to laterally expanded. Their form is irregular and changes continuously but slowly. Nuclei propagation is usually synchronous, although asynchronous propagation does occur rarely. Plasmodium fragmentation occurs independently from nuclei propagation. Cysts are spherical. By budding, the plasmodium produces flagellate uninucleate cells which swim away. The flagellate cell may also crawl across a substratum by means of temporary pseudopodia.

Unikonta: Amoebozoa: Mycetozoa

In Myxogastria (Frederick L 1990, Novozhilov YK *et al* 2000, Raven PH *et al* 1999, Sujatha A *et al* 2005), the zygote gives rise to a multinucleate plasmodium. Nuclei flow freely in the plasmodium and divide synchronously about once every 24 hours. The plasmodium creeps along and phagocytizes decaying material. Different plasmodia usually fuse to build a chimerical plasmodium which swells by further growth and becomes increasingly meshed. Cytoplasm exhibits conspicuous streaming. The plasmodium may become very large, with millions of nuclei, but ultimately, when conditions are adverse, it forms a series of small bumps, each of which becomes a fruiting body. Within the sporangium of the fruiting body, the digenomic nuclei may either become a digenomic spores or undergo meiosis. If the meiosis occurs, tetrads become immediately isolated into spores which are to be released and dispersed in environment. Inside the spore, the cell differentiates either into an amoebae-like cell or into a flagellated cell. Under favorable conditions, spore germinates and liberates

mature cell. Free-living cell can repeatedly transdifferentiate, but only cells of the same differentiation type can fuse to form new zygote.

Unikonta: Amoebozoa: Pelobionta

In genus *Pelomyxa* (Whatley JM and Chapman-Andresen C 1990), more than a dozen of species have been described in the past, but most of them seem either to represent different stages of the life history of the same species *Pelomyxa polustris* or to be color variants of these stages resulting from the type of food. The life history begins with a small binucleate amoeboid cell. Its nuclei are large. The cell grows to a plasmodium which can contain up to 1000 or more nuclei. In plasmodium, nuclei propagate simultaneously and synchronously. While a mitotic apparatus is lacking, the nucleus simply pinches apart into two nuclei by division. During the active feeding and growth phase, the plasmodium obtains an elongated and ovoid shape and a well-developed posterior, villous uroid. Later, during the stationary phase, the plasmodium becomes spheroidal and lacks an uroid. It can either revert directly to the active stage or undergo plasmotomy to produce cysts. Cysts with two or three envelops are also multinucleate. Large plasmodia are fragile and often fragment by binary or multiple division. In early spring, the plasmotomy gives rise to small binucleate amoeboid cells.

Bikonta: Cabozoa: (Rhizaria): Acantharea

In most Acantharea (Febvre J 1990), the biflagellate cell develops usually into an uninucleate amoeboid which then propagate without cytokinesis producing a multinucleate plasmodium. The plasmodium may alternate between amoeboid and radiolarian forms. A radiolarian has an elaborate mineralized skeleton composed of long spines which are distributed very regularly. The production of biflagellate cells may take place in an oval cyst after complete remodeling of plasmodium. These cells are then shed, but their fate remains unknown.

In genus *Haliommatidium*, the single nucleus does not divide during feeding and growth phase, but increases in size by progressive polyploidization. During encystment, depolyploidization occurs, abruptly restoring nuclei to a more normal size. This progressive karyokinesis is followed by fragmentation of the cytoplasm. After a series of transformation, oval flagellate cells are shed.

Bikonta: Cabozoa: (Rhizaria): Cercozoa

In Chlorarachniophyceae (Hibberd DJ 1990, Van den Hoek C *et al* 1995), naked amoeboid uninucleate cells are united via filopodia into net-like plasmodium. Each cell can transform itself into coccoid resting stage or produce uniflagellate zoospore. It has been suggested that resting stages appear to be able to give rise directly to the amoeboid cells and also to zoospores via tetrads. Ultimately, the zoospores appear to give rise directly to amoeboid cells.

In cercomonadid genus *Cercomonas* (Mylnikov AP and Karpov SA 2004, Van den Hoek C *et al* 1995), the progressive cell propagation can be accompanied by the production of more or less flattened plasmodium with set of flagella and contractile

vacuoles. Plasmodium is usually of coencytic origin, but syncytial origin is possible too. The number of nuclei in a plasmodium may reach 100 or more. The mature plasmodium produces extensions, fragments, and disintegrates into uninucleate biflagellate cells which can propagate further. The single cell can alternate between actively swimming stage and slightly moving trophic (amoeboid) stage. It can also encyst.

In genus *Massisteria*, the plasmodium stage is present, but cysts are not known.

In genus *Spongomonas*, biflagellate cells are embedded in common gelatinous matrix. The cell association is usually a sphaera but, sometimes, it extremely elongates into a thread-shaped mass which tends to be intricately curved. Flagella protrude to the outside of the cell association giving it a bristly appearance.

In genera *Cladomonas* and *Rhipidodendron*, biflagellate cells are embedded in a fan-shaped gelatinous matrix built of dichotomously branching gelatinous tubes which are united laterally and sometimes fuse lengthwise. In the matrix, each tube contains a single cell at its anterior end.

In desmothoracid genus *Clathrulina*, stalked cells surrounded by homogenous chitinous envelope with numerous regularly arranged openings may be associated.

In Phaeodarea (Cachon J *et al* 1990), the karyokinesis and cytokinesis are delayed so that the progressive DNA multiplication leads to the formation of an uninucleate plasmodium. Up to 2000 chromosomes may be present in the single nucleus. The plasmodium may possess an internal silica skeleton with tubular spines. Later, the plasmodium undergoes reductional karyokinesis producing hundreds of multinucleate plasmodia each of which develops two flagella.

Bikonta: Cabozoa: (Rhizaria): Foraminifera

In genus *Patellina*, the zygote propagates without cytokinesis until it becomes a plasmodium with four digenomic nuclei which then undergo meiosis. When meiosis is complete, cytokinesis occurs and all the tetrads are released from the common test. They live independently, but, soon or later, two or more cells of two mating types aggregate. In the aggregate, cells propagate without cytokinesis until they become plasmodia each with four monogenomic nuclei. Then, the plasmodia leave their tests, round out, and cytokinesis takes place producing monogenomic cells of two mating types. Whereas most of them pair and fuse to form zygotes, remaining monokaryotic cells will be later digested by zygotes which become released and live independently.

In genus *Rotaliella* (Lee JJ 1990), the zygote gives rise to a plasmodium with four digenomic nuclei. Whereas three of these nuclei remain condensed and later undergo meiosis producing twelve tetrads, the fourth nucleus does not. Instead of this, it swells, forms nucleolus, becomes active but later will die. When released from the test, tetrads live independently. After a period of growth, each tetrad propagates without cytokinesis and becomes a plasmodium with many monogenomic nuclei. When the cytokinesis occurs, monogenomic cells remain in a common test. They pair and fuse to form zygotes which become released.

In genus *Sorites*, the digenomic plasmodium contains hundreds of nuclei. Some of them become active somatic nuclei. In mature digenomic plasmodium, all nuclei undergo meiosis at the same time but tetrads from the somatic nuclei then degenerate.

In genus *Rosalina*, the digenomic plasmodium matures and produces many tetrads which then are released. Each tetrad develops its own shell and growth to monogenomic plasmodium. Mature monogenomic plasmodium undergoes cytokinesis leading to formation of gametes. In some species, gametes are flagellate and swim before fusing to form zygotes.

Generally, the plasmodium is usually surrounded by an elaborated calcareous or agglutinated test which in turn is surrounded by a network of reticulate pseudopodia. The digenomic plasmodium is usually much larger in overall size then the corresponding multinucleate plasmodium.

In genus *Syringammina* (Tendal ØS 1990), there is a plasmodium enclosed by a branched tube system made of a transparent, cement-like organic substance. Besides numerous nuclei, the cytoplasm contains huge numbers of barite crystals, granullae. The test of plasmodium consists of foreign material held together by cement-like substance. There are reasons to suppose that plasmodium is heterokaryotic with a differentiation between somatic and generative nuclei.

Bikonta: Cabozoa: (Rhizaria): Haplosporidia

Haplosporidia are symbiotrophs in invertebrate animals (Perkins FO 1990). Their life history is poorly studied. Prior to sporulation, the symbiotroph exists in host as an unwalled multinucleate plasmodium and contains haplosporosomes as the only unusual organelle. Karyokinesis occurs within a persistent nuclear envelope. Sporulation is first seen by deposition of a thin wall around the plasmodium which then becomes a sporont. Further nuclear multiplication and increase in plasmodium size is followed by multiple and irregular subdivision into uninucleate sporoblasts. It has been suggested that meiosis may occur prior to sporoblasts formation. Pairs of sporoblasts then fuse to form binucleate sporoblasts followed by karyogamy. Zygotes undergo a complex series of events to become spores. Upon degeneration of host tissue, these spores are liberated into the aqueous environment of the host. Their fate is unknown.

Bikonta: Cabozoa: (Rhizaria): Paramyxea

Paramyxea are parasites of marine invertebrate animals (Desportes I and Perkins FO 1990). The young primary cell is amoeboid. It develops between the host cells and continuously enlarges. The first karyokinesis produces two unequal nuclei. The smaller nucleus becomes surrounded by a thin layer of cytoplasm and divides to produce two equal nuclei. These nuclei then undergo propagation producing a plasmodium with a variable number of small nuclei. Propagation is accompanied by sporulation which is characterized by formation of propagules. The propagule consists of several spores enclosed inside one another that arise by a process of internal cleavage. At this stage, the plasmodium can be considered as a sporont. With increased number of nuclei, there

is increased differentiation of sporonts. In mature sporonts, some nuclei may be products of meiosis.

Bikonta: Cabozoa: (Rhizaria): Plasmodiophorida

Plasmodiophorida are symbiotrophs of plants, fungi, etc. (Dylewski DP 1990). The biflagellate cell infects the host cell and develops into the spherical multinucleate plasmodium. At the cessation of nuclei propagation, cleavage by furrowing occurs correlated closely with the meiosis. The karyogamy has also been claimed to occur. The cleavage results in production of spores which develops in biflagellate cells infecting new hosts.

Bikonta: Cabozoa: (Rhizaria): Polycystinea

In Polycystinea (Cachon J *et al* 1990), the karyokinesis and cytokinesis are delayed so that the progressive DNA multiplication leads to the formation of an uninucleate plasmodium. During this growth phase, the nucleus increases progressively in size becoming huge in some genera (for example, *Thalassicolla*). The plasmodium is characterized by regularly perforated internal silica skeleton with radial axopods emerging among fine, ramified pseudopods. Later, the plasmodium undergoes division by binary fission, multiple fission, or budding. Division of the nucleus differs from typical mitosis in several respects. Multiple fission is thought to involve depolyploidization, since the number of chromosomes decreases at each successive division until small biflagellate spores are formed, each only with few chromosomes. Spores are formed inside the original central capsule. They may be released directly into the surrounding water after the capsule bursts. The capsule formation may be also associated with the development of the special polycystarian stage. Triggered by an unknown cause, the capsule flattens, widens, and lengthens into long tubes that give rise to small capsules from which the spores are then liberated.

In genus *Collozoum*, for example, there are large associations of shelled plasmodia which are held together by a gelatinous matrix.

Bikonta: Cabozoa: (Excavata): Diplomonadida

In order *Giardia* (Adam RD 2001, Svärd SG *et al* 2003, Vickerman K 1990a, Yu LZ *et al* 2002), the trophozoite is a plasmodium which contains two digenomic nuclei. The trophozoite can be considered a bizygote. Within the plasmodium, nuclei replicate synchronously and the fundamental task of the cytokinesis is to make sure that the nuclei are distributed to the daughter plasmodia accurately. Upon induction of encystation, the trophozoite quickly becomes rounded and both nuclei replicate. Late in encystation, the karyokinesis occurs and four nuclei replicate, generating plasmodium with four digenomic nuclei each of which is tetraploid. If released from the cyst, the plasmodium becomes an excyzoite which undergoes twice the cytokinesis and four trophozoites are formed. The cytokinesis in the excyzoite is reminiscent of meiosis and syngamy. However, whether it is an ancestral or derivative form of them is still not clear.

Bikonta: Cabozoa: (Excavata): Euglenozoa

Euglenozoa can give rise to very dense population, causing water blooms (Van den Hoek C *et al* 1995). Cells loss their flagella, surround themselves in a thick envelope of mucilage, and cover the surface of the water with a floating skin (for example, euglenid genus *Euglena*).

In genus *Colacium* (Walne PL and Kivic PA 1990), cell association is made up of two to eight stalked cells enclosed in mucilaginous envelopes. Cells may redevelop flagella, swim away from colony, settle elsewhere eventually on their anterior ends, and secrete new stalks to form new colonies.

In genus *Cephalothamnium* of the order Kinetoplastida (Vickerman K 1990b), cells are clustered at the end of a common secreted stalk which is attached to the copepod host. Flagellated cells are attached to the stalk by their posterior ends.

Bikonta: Cabozoa: (Excavata): Oxymonadida

In some Oxymonadida, cell associations in form of a multinucleate plasmodium may occur.

Bikonta: Cabozoa: (Excavata): Parabasalida

In Calonymphyda (Dolan MF *et al* 2000, Dyer BD 1990b), nuclei propagation leads to formation of a plasmodium. In plasmodium, the number of parabasal bodies, axostyles, and cilia seems to be multiplied in proportion to the number of nuclei. In genus *Metacoronymph*, for example, the plasmodium may contain as many as 1000 nuclei. The plasmodium frequently divides symmetrically or asymmetrically producing smaller plasmodia.

Bikonta: Corticata: (Alveolata): Apicomplexa

Apicomplexa are parasites of animals (Vivier E and Desportes I 1990).

In class Gregarinia, the spherical mature gamontocyst contains numerous spindle-shaped young sporocysts each of which is occupied by a zygote. The zygote immediately undergoes meiosis and tetrads then divide one time so that the mature sporocyst contains eight sporozoites. When released from the gamontocyst, each sporocyst can infect a new host and liberate sporozoites. If the single sporozoite enters a host cell, it propagates producing many merozoites. Some of the merozoites transform into gamonts. Two gamonts pair, join together, and become surrounded by a common cyst wall forming a young gamontocyst within which both gamonts propagate without cytokinesis producing two multinucleate plasmodia. In each plasmodium, nuclei travel to the periphery where the cytokinesis occurs producing numerous gametes. The remainders of plasmodia perish. Within the common gamontocyst, gametes pair and fuse to produce zygotes each of which become surrounded by separate cyst wall forming new sporocyst.

Bikonta: Corticata: (Alveolata): Ciliophora

Traditionally, Ciliophora are treated as a single-celled (Dovgal IV 2002, Fokin SI *et al* 2001, Lynn DH and Small EB 1990, Orias E 1998). But actually, they are motile multinucleate plasmodia. The plasmodium typically has a large number of characteristic cilia which are arranged in longitudinal rows or spirals. Coordinated beating of cilia provides motility to plasmodium. Cilia often fuse to form structures specialized for feeding or locomotion. Food enters through gullet and passes in specialized vacuoles. Waste products empty via cytoproct. Plasmodium usually releases tough but flexible outer pellicle.

In genus *Paramecium*, for instance, the zygote progressively propagates without cytokinesis producing a plasmodium with four digenomic nuclei. Cytokinesis yields two dikaryotic plasmodia. In each of them, one nucleus differentiates into a large macronucleus which swells, forms nucleolus, and makes the plasmodium metabolically active. The other nucleus undergoes mitosis to form two digenomic nuclei, micronuclei, which remain condensed and inactive. The trikaryotic plasmodium can move as a whole by numerous cilia. It contains some differently specialized regions. Plasmodium can divides by transverse fission. It can also encyst to disperse in environment. When the time is ripe, micronuclei undergo meiosis to produce monogenomic nuclei, of which all but one degenerate. The macronucleus degenerates too. Remaining monogenomic nucleus divides once more to produce two nuclei. One of them remains stationary but the other becomes migratory. The nuclei pair and fuse to form a new digenomic nucleus and the cell becomes a zygote. Often, the production of the stationary and migratory nuclei is accompanied by conjugation of two trikaryotic plasmodia whereby they form a cytoplasmic bridge and can exchange the migratory nuclei. Each migratory nucleus crosses the cytoplasmic bridge, pairs and fuses with a stationary nucleus of the conjugation partner. Both plasmodia become zygotes which then separate from each other.

In *Tetrahymena vorax*, the plasmodium alternates between two forms: microstome and macrostome. The microstome feeds on bacteria. Depletion of the bacterial population can stimulate the microstome to differentiate into a macrostome which begins ingesting other ciliates or even its siblings. The presence of appropriate bacteria population stimulates the macrostome to dedifferentiate back to the microstome. In a cyst, the plasmodium can undergo progressive division yielding several offspring cells called tomites.

In Karyorelictea, the plasmodium contains two to many macronuclei.

In any genera (*Oxytricha*, *Euplotes*, *Blepharisma*, etc.), two plasmodia may become united by their dorsal regions forming the so called doublet. It is usually interpreted as the result of an abortive transverse fission, since the doublet undergoes a series of transformations necessary for return to the normal singlets. However, the doublets appear repeatedly and the successive series of their transformations is always the same, suggesting that the doublet stage is not simply an error of nature but rather an adaptation. In contrast to creeping singlets, the doublets of *Oxytricha bifaria* can swim and search for possible new spaces to colonize (Banchetti R and Erra F 2003).

In some genera, zygote produces a stalked sessile plasmodium. By conjugation, one partner is usually resorbed by other. In any few genera such as *Carchesium*, *Zoothamnium* (Song W *et al* 2002), the zygote produces a stalked plasmodium which gives rise to a branched colony of plasmodia with a common contractile stalk. In this sessile colony, plasmodia are small microzooids some of them can however differentiate into a large macrozooids which are then released to form new colonies. The number of plasmodia in the colony may be over 100. Zygotes can be produced both by autogamy and conjugation.

In genus *Stephanopogon*, the plasmodium contains 2-16 nuclei. However, it is unclear whether *Stephanopogon* belongs to Ciliophora (Corlis JO 1990b).

Bikonta: Corticata: (Alveolata): Dinoflagellata

Traditionally, Dinoflagellata are treated as a single-celled (Raven PH *et al* 1999, Taylor FJR 1990, Van den Hoek C *et al* 1995). But what is thought to be a single cell contains up to 100 typical DNA amounts and may be actually a plasmodium with unique "multinucleate" dinokaryon. In dinokaryon, the chromatin is permanently condensed during all stages of plasmodium life history. If the dinokaryon divides, its envelope remains intact during all stages of division and the entirely extranuclear spindle apparatus must pass through tunnels in envelope to attach chromosomes. After dinokaryon division is complete, the plasmodium immediately undergoes cytokinesis yielding two schizonts.

The zygote is a digenomic plasmodium with a chimerical dinokaryon. It may be either biflagellate and motile or non-flagellated and non-motile. The non-motile zygote is thick-walled, remains dormant during winter, and undergoes meiosis first during germination. Meiosis products are monogenomic plasmodia which then propagate producing many schizonts. At an unknown trigger, schizonts may become gametes which pair and fuse to form new zygotes.

In genus *Pheopolykrikos* of order Gymnodiniales, the schizont grows to a plasmodium bearing many dinokarya and several sets of flagella and flagellar furrows. This large plasmodium then fragments into dinospores each of which contains only one dinokaryon.

In genus *Gloeodinium* of order Phytodiniales, the non-motile schizonts are united into colony by thick, stratified sheaths of mucilage.

In few genera such as *Dinoclonium*, *Dinothrix*, and *Haplozoon*, schizonts remain in a filamentous colony, if they do not separate after dividing. The colony can even branch.

Bikonta: Corticata: (Chromista): Actinophryida

In genus *Actinosphaerium* (Febvre-Chevalier C 1990, Mikrjukov KA and Patterson DJ 2001), the zygote progressively propagates without cytokinesis until it becomes a spherical multinucleate plasmodium with numerous slender retractile pseudopodia

arranged radially. Soon or later, the plasmodium retracts all pseudopodia and releases a gelatinous envelope. After some nuclei disappear, the plasmodium undergoes cytokinesis to form a number of digenomic cells. Within the envelope, each digenomic cell becomes surrounded by separate cell wall and divides one time so that each cyst contains two digenomic cells. Each digenomic cell undergoes meiosis during which all but one monogenomic nucleus degenerate and the cell becomes a gamete. Within each cyst, both gametes fuse to form a new zygote.

In genus *Actinophrys*, the zygote sometimes gives rise to a sphaera-like cell association which however disintegrates later. Dispersed in environment, free living cells frequently alternate between various cell body forms accompanied by dramatic change in behavior so that these forms have been for a long time treated as a tens of different species scattered within a dozen of distinct genera. Some of these cell body forms are actually multinucleate plasmodia producing resting spores. Soon or later, the free living cell settles and encysts. Within the cyst, the binary fission produces two cells which undergo meiosis. After each meiotic division, one offspring nucleus degenerates so that the cyst contains only two tetrads. One tetrad differentiates into male gamete with pseudopodia oriented towards the other tetrad which becomes a female gamete. Fertilization results in an encysted zygote (Febvre-Chevalier C 1990).

Bikonta: Corticata: (Chromista): Bacillariophyta

In genus *Stephanopyxis* (Van den Hoek C *et al* 1995), the zygote gives rise to the cell colony. As soon as the cell colony consists of 8, 16, or 32 cells, it breaks. The division type is unique: one daughter cell is the same size as the mother cell while the other is smaller. It is shorter and narrower by about twice the thickness of the girdle. Thus, the average cell size decreases with each successive round of cell division. When the cells have decreased in size to between 0.4 and 0.2 of their original, maximum diameter, they become meiocytes and will undergo meiosis to form gametes if environmental conditions are suitable. Some cells, however, continue to divide until their progeny cells become too small and die. Smaller meiocytes usually produce male gametes, and larger meiocytes usually produce female gametes. The zygote swells and its expansion is accompanied by a concomitant growth of the zygote wall. At this stage, the zygote is called an auxospore. After karyokinesis, one of the daughter nuclei degenerate, the other moves across to the other side of the auxospore and performs a second karyokinesis, after which the new initial fristule is formed.

In some genera such as *Chaetoceros*, *Melosira*, *Rhizosolenia*, *Skeletonema*, etc., the usual primary body plan is a hypha of indefinite length (Round FE and Crawford RM 1990). There is however no evidence of cell interaction in hypha. Cells remain equivalent to each other and each cell can give rise to new hypha.

In genus *Licmophora*, for example, bilateral-symmetric cells form branching primary cell colony (Raven PH *et al* 1999, Round FE and Crawford RM 1990).

Cell aggregates which are formed when Bacillariophyta bloom are a primary source of marine snow (Thornton DCO 2002).

Bikonta: Corticata: (Chromista): Bicosoecida

Bicosoecida are poorly studied and little is known about their life history. But some of them are known that cells live in loose association (Dyer BD 1990a).

Bikonta: Corticata: (Chromista): Centroheliozoa

In genus *Raphidiophrys,* cells are often held together by cytoplasmic processes. Each cell has a thick gelatinous coat with minute spines.

Bikonta: Corticata: (Chromista): Chrysophyta

In variety of genera (Kristiansen J 1990, Raven PH *et al* 1999, Van den Hoek C *et al* 1995), cell associations occur during the life history of individual cell progression.

In genus *Hydrurus*, cells are loosely arranged in a gelatinous matrix. The hypha-like primary cell colony with apical growth may be up to 30 cm long. By branching and fragmentation of hyphae or by formation of flagellated spores, hyphae of the same individual cell progression become dispersed in environment.

In genus *Cyclonexis*, wheel-like primary cell colony is composed of 10 to 20 wedge-shaped cells. Young cell colony is funnel-shaped.

Genus *Dinobryon* is known for bush-like colonies of hyphae. The zygote forms typical cyst. Tetrad propagates forming a colony. In colony, each cell is surrounded by a vase-shaped case, a lorica, drawn out at its base. The lorica may be hyaline or cellulose. The elongated cell body is attached to the base of the lorica with its attenuated posterior tip. In colony, daughter cells remain attached to the inner margin of aperture of parent loricae and there secrete new loricae. Each cell can become a spherical cyst. Male and female colonies are similar. Also gametes are similar.

In genera *Monas* and *Ochromonas*, sphaera contains 20 to 50 biflagellate cells.

In genus *Uroglena,* sphaera is composed of ovoid cells arranged on periphery of a gelatinous mass. In sphaera, cells may be connected with one another by gelatinous processes running inward and meeting at a point. The sphaera divides by bipartition. Cysts are spherical.

In genus *Chrysocapsa*, primary cell colony is a sphaera. Within sphaera, cells are distributed rather without order. They are embedded in a mucilage envelope.

In genus *Chrysosphaera*, the sphaera is regular.

In genus *Synura,* the zygote forms a cyst enclosed in a siliceous wall. The germination of the cyst is accompanied by meiosis. Flagellate tetrads propagate and each forms a spherical or ellipsoidal colony. In this sphaera, ovoid cells held together by a gelatinous matrix are arranged radially. The sphaera is covered by tile-shaped siliceous scales having minute spines. Each cell can become a spherical cyst. The sphaera can also

fragment. Sphaerae of the same individual cell progression are dispersed in space. Male and female sphaerae are similar. Male gametes swim to female sphaerae and fertilize eggs.

Genus *Anthophysa* form colonies of sphaerae. In this secondary cell colony, sphaerae occur at tips of bush-shaped gelatinous matrix.

Bikonta: Corticata: (Chromista): Cryptophyta

Cryptophyta are usually motile biflagellate cells which continue to swim even during the division. In some species, however, non-motile cells tend to form colonies invested in multiple mucilaginous sheaths (Gillott M 1990).

Bikonta: Corticata: (Chromista): Dictyochophyta

In genus *Ciliophrys* (Febvre-Chevalier C 1990), cell propagation results in a rather irregular cell association containing sometimes over 100 cells. Cells are first spherical with extremely fine radiating pseudopodia, but some cells can become flagellated and swim away. Two or more cells often fuse together to form a multinucleate plasmodium. Also the plasmodium can produce one or more flagellated cells which are capable of pulling the whole mass slowly as they swim.

Bikonta: Corticata: (Chromista): Haptophyta

In genus *Pleurochrysis* (Green JC *et al* 1990, Van den Hoek C *et al* 1995), the zygotic cell progression is dispersed in space, but tetradic cell progressions consists of branching hyphae which clone themselves by production of zooids. Some zooids can become gametes.

In genus *Isochrysis* (Green JC *et al* 1990, Van den Hoek C *et al* 1995), young cells are non-motile, hemispherical, and form cuboidal masses. Older cells are spherical and surrounded by concentric layers of mucilage. Sometimes, the mucilage is secreted only on one side. In this case, a branched stalk can be built up, consisting of curved transverse layers. For a long period, this type of cell colony has been even treated as a separate species named *Chrysotila*.

In some Haptophyta (Green JC *et al* 1990, Raven PH *et al* 1999, Van den Hoek C *et al* 1995), there is a bloom-forming stage. In genus *Phaeocystis*, for example, it develops in mid-April or in May in the North Sea. The cells first form small spherical colonies. In the sphaera, cells are held together by a gelatinous matrix. Each initial primary sphaera gives rise to large lobed secondary colony. Numerous secondary colonies aggregate forming massive blooms. Storms often whip blooms into soapy foams.

Bikonta: Corticata: (Chromista): Hyphochytriomyceta

In Hyphochytriomyceta (Fuller MS 1990), when the flagellate cell stops swimming, it rounds and encysts. In genus *Rhizidiomyces*, the spore germination followed by progressive nucleus propagation results in development of a growing spherical

plasmodium with rhizoids. In genus *Hyphochytrium*, the spore germination includes emergence of the germ tube. The nucleus moves to the tip of the tube and propagates progressively. Concomitant with an increasing diameter of the germ tube, a swollen area develops. Tubes extend from the swollen area. Nuclei move into these tubes followed by a swelling of their tips. Thus, the polycentric habit of the hyphae colony is established and maintained.

Bikonta: Corticata: (Chromista): Labyrinthulida

Traditionally, Labyrinthulida have been grouped with the slime molds, but are now recognized to be distinct from them. It has also been discovered that they have an organelle, a bothrosome, that is capable of secreting ectoplasm outside their cells (Porter D 1990). Ectoplasm projections expand to form a network over which the cell can travel. The Labyrinthulida appear to be unique in this ability. The ectoplasmic network absorbs nutrients and attaches the cell to surfaces.

In genus *Labyrinthula*, spindle-shaped trophic cell progressively propagates producing cells that form colony which can increases indefinitely within the common ectoplasmic network. Cells exhibit gliding motility within the network. Enlarged cells undergo meiosis and release biflagellate zoospores.

In genus *Labyrinthuloides*, trophic cell progressively propagates to produce cells that separate from each other or may be held together within the parent wall to form a spherical colony, a sorus. The ectoplasmic network does not surround the developing sorus, but emanates from the basal side. Within the sorus, spores are produced and, when released, move apart by gliding on their individual ectoplasmic networks.

In genus *Thraustochytrium*, trophic cell grows by enlargement and progressive nuclear division to spherical multinucleate plasmodium. Progressive cleavage of the plasmodium produces spores which are released by dissolution of plasmodium wall. The spores develop into biflagellate zoospores.

In genus *Schizochytrium*, trophic cell divides by two successive divisions to form cluster of four cells. Each cell propagates producing a sorus releasing several biflagellate zoospores.

Bikonta: Corticata: (Chromista): Oomyceta

In most Oomyceta (Dick MW 1990, Raven PH *et al* 1999), large colonies of hyphae are formed during the life history of individual cell progression. For example, in genus *Saprolegnia*, the zygotes become free first after long period of dormancy. Each free zygote germinates and progressively propagates forming a short hypha with a tube-like spore case, a sporangium, at the tip. Released spores are free-swimming biflagellate cells which first migrate before they encyst. If time is ripe, the spore germinates and propagates building a hypha that increasingly branches forming a large bush-like colony of hyphae. Hyphae release cellulose wall. In the colony, sporangia are built at tips of hyphae and release numerous spores for further distribution of the individual cell progression in space. Secondary cell colonies of different individual cell progressions

usually superpose each other. At some hyphae, specialized sporangia, oogonia and antheridia, are built. In oogonia, cells undergo meiosis and tetrads immediately differentiate into large eggs. In antheridia, cells undergo meiosis without cytokinesis and become plasmodia each with four monogenomic nuclei. Coming together with an oogonium, the antheridium forms tubes through which monogenomic nuclei can enter oogonium and fertilize eggs. Newly formed zygotes become thick-walled oospores.

Bikonta: Corticata: (Chromista): Opalinida

Opalinida are symbionts in the posterior end of digestive tract of vertebrate hosts (Corlis JO 1990a). In genus *Opalina*, the zygote encysts and leaves the host gut with feces. The new host is usually a tadpole approaching a metamorphosis. In the new host, the zygocyst gives rise to a rounded multinucleate plasmodium with many rows of cilia. This feeding stage, a trophont, grows to large flattened plasmodium with flexible, leaf-like body which often exhibits a shape resembling a scalene triangle. In response to changes in host preceding its breeding season, the plasmodium begins a series of divisions without intervening growth, a palintomy. Small plasmodia transform into infective cysts which leaves the host gut to be ingested by newly hatched tadpoles. In their guts, plasmodia excyst and undergo division with meiosis producing micro- and macrogametes bearing many flagella. The gametes fuse, the digenomic zygotes round up and transform into zygocysts.

Bikonta: Corticata: (Chromista): Pelagophyta

In genus *Chrysonephos* (Boddy S *et al* 1999), the cell association occurs in form of a hypha provided with an external wall consisting of microfibrills. Hyphae are embedded in a mucilaginous envelope which favors their aggregation. Inside the hypha, the cells may differentiate into flagellate zoospores.

Bikonta: Corticata: (Chromista): Phaeophyta

Phaeophyta dwell almost exclusively in marine or coastal environment. There are only a few rare freshwater brown algae.

Most individual cell progression species of Phaeophyta form large colonies of hyphae (Clayton MN 1990, Raven PH *et al* 1999, Van den Hoek C *et al* 1995). The complexity of the colonies varies enormously from macroscopic branched hyphae to foliose plants many meters long.

In genus *Laminaria*, for example, the zygote propagates forming a multicellular sporophyte. The sporophyte body develops from an initial hypha to a massive three-dimensional colony of tightly connected hyphae, a kelp. The kelp is covered by a gelatinous sheath and consists of a root-like holdfast attached to the firm substrate, a stem-like stalk, a stipe, and numerous leaf-like blades branching from the stipe. In kelp, cellular connections occur not only between cells of a particular hypha but also between cells of neighboring hyphae. In cortical regions, hyphae fuse and filamentous organization of the secondary cell colony is not more evident. Hyphae also show signs of differentiation. At the surface of the kelp, some hyphae develop into sporangia where

cells undergo meiosis. Tetrads differentiate into zoospores, free-swimming biflagellate cells. After a period of migration, each zoospore gives rise to a multicellular gametophyte which develops from an initial hypha to a small bush-like colony of hyphae. Although all zoospores look similar, the gametophyte becomes either a female or a male. In gametophyte, cells at the tips of hyphae differentiate into gametes. Female gametophyte produces large eggs, male gametophyte - free-swimming sperm. If sperm fertilize eggs and zygotes propagate, new sporophytes overgrowth the maternal gametophyte.

In some genera, sporophyte and gametophyte are quite similar in appearance to each other. But mostly, the sporophyte is much larger as the gametophyte.

Genus *Fucus* has no free-living gametophyte at all. The zygote is floating. Upon landing in an acceptable habitat, zygote will develop into kelp which tips often contain gas bladders and conceptacles which have either oogonia or antheridia producing eggs and sperm respectively.

In some genera, kelps are especially huge. For example, in genera *Nereocystis* or *Macrocystis*, kelp is of about 50-100 m long and grows in deeper water anchored to the bottom by their holdfasts. Kelps of genus *Sargassum* sometimes break off from their holdfasts and form floating masses. They stay afloat by producing gas-filled bladders which act like buoys.

Bikonta: Corticata: (Chromista): Xanthophyta

In Xanthophyta (Van den Hoek C *et al* 1995), formation of cell associations during life history of individual cell progressions is abundant.

In order Tribonematales, cells form a long hypha. Cell body is cylindrical or fusiform swelled at the center. Cell wall consists of two parts overlapping at the midregion. Individual cell progression grows either by fragmentation of hyphae or by production of some kind of spores. Spores may be flagellated and free-swimming zoospores, or they may be non-flagellated aplanospores.

In order Vaucheriales (Gavrilova OV and Rudanova EE 1999, Gavrilova OV *et al* 2000), the zygote forms a cyst with a thick wall and becomes a hypnozygote. After germination, the zygote produces a tubular hypha which is a multinucleate plasmodium with no internal partitioning into cells. Hyphae branch irregularly. The hypha clone itself by fragmentation or by either aplanospores or zoospores. Round aplanospores are formed at the tip of sporangium. After maturation, a deep green aplanospore, which demonstrates dense packing of nuclei and chloroplasts, is released from the sporangium. The amount of nuclei in mature aplanospore is about 2000. All nuclei are involved in the process of karyokinesis. All nuclei divide simultaneously. Individual mitotic stages coincide in time. Mitotic spindle is completely closed. Nuclear envelope remains intact until the late telophase. The germination of aplanospore occurs without a lag period immediately after release from the sporangium. The duration of germination time varies. At the end of germination, all nuclei and chloroplasts migrate from the aplanospore towards the vegetative branch. Vegetative thallome is formed as a result of

the aplanospore germination. Thallome consists of the branching tubular filaments with no septae. The thallome exhibits tip, or apical, growth. A site of expansion in tip-growing cells is associated with dome-shaped apex of the filament, which results in characteristic tubular morphology. Apical growth is characterized by the highly determined localization and movement of organelles, as well as by polarization of the synthesis and secretion of cell wall precursors. Meiosis takes place immediately before the formation of gametes. Each antheridium produces numerous spermatozoids. On the contrary, the ripe oogonium contains only one single egg ready for fertilization.

In order Botryidiales, the multinucleate plasmodium is usually a sphaera with numerous branching extensions which function as rhizoids to anchor in soil. The plasmodium can divide up into a large number of zooids, which are liberated from the plasmodium when the environment is flooded with water. If the plasmodium begins to dry, it retracts into the rhizoids and form thick-walled resting spores. The spore germinates with production of zooid.

In order Mischococcales, elongate cylindrical plasmodia are often bent and are attached by a short stalk (for example, genus *Ophiocytium*). The uppermost part of the plasmodium wall opens like a lid to liberate the spores. The emerging spores often settle on the rim of the parent plasmodium wall and there grow up into new plasmodia.

Bikonta: Corticata: (Plantae): Glaucophyta

Glaucophyta are rare in nature (Kies L and Kremer BP 1990). In some species, cells tend to form colonies (for example, *Gloeochaete wittrockiana*). In other species, karyokinesis produces multinucleate plasmodium which divides by infurrowing of the plasma membrane (for example, *Glaucocystis nostochinearum*).

Bikonta: Corticata: (Plantae): Rhodophyta

In Rhodophyta (Gabrielson PW *et al* 1990, Raven PH *et al* 1999, Van den Hoek C *et al* 1995), formation of cell associations during life history of individual cell progressions is abundant.

Class Bangiophyceae

In order Porphyridiales, individual cells are embedded in a common mass of mucilage forming either a spherical (genus *Porphyridium*) or filamentous (genus *Chroodactylon*) colony. Gametes and zygote are unknown.

In genus *Erythrotrichia* of order Erythropeltidales, the zygote grows into an upright, unbranched filamentous cell colony, a sporophyte, which is anchored to the substratum by short rhizoids. The upper cell acts as a spore which escapes the colony and then gives rise directly to a new colony, thus effecting the distribution of individual cell progression in space. Mature sporophyte produces meispores. Each meiospore grows into tiny filamentous gametophyte with three cells. The apical cell of this dwarf gametophyte swells, cuts off a male gamete, and become an oogonium. In other Erythropeltidales, the cell colony is either a tiny blade or a disc.

In the only known species of order Rhodochaetales, *Rhodochaete parvula*, the zygote develops into single digenomic carpospore which is released from the maternal gametophyte and gives rise to a digenomic multicellular sporophyte. The sporophyte grows as a branched colony of hyphae. Young sporophyte can clone itself by production of digenomic spores. Mature sporophyte develops meiosporangia within which monogenomic meiospores are produced. Each meiospore grows into a multicellular gametophyte which looks alike the sporophyte. In mature gametophyte, the female gametangium is almost indistinguishable from surrounding cells and differentiates into egg. Tiny male gametangia are cut off from other cells by curved lateral walls and produces male gametes. They however are not flagellated and, if released from the gametophyte, are rather carried by water currents to find and fertilize eggs.

In genus *Porphyra* of order Bangiales, the zygote propagates within the maternal oogonium producing a number of 4, 8, 16, or 32 digenomic carpospores. At this stage, the maternal oogonium is called a carpogonium. Carpospores are usually released by the breaking of the carpogonium wall. Each carpospore gives rise to a branched colony of hyphae, a sporophyte, which for a long period of time has been treated as a separate genus *Conchocelis*. The sporophyte produces a special type of sporangia, a conchosporangia, within which the cells differentiate into digenomic conchospores. During conchospore germination, meiosis takes place and tetrads become arranged in a row in the four-celled, uniseriate germling which subsequently gives rise to single multicellular leaf-like gametophyte. The leaf is almost always one cell thick. It is irregularly folded. Its base is anchored to the substratum by rhizoids. Young gametophyte can clone itself by production of spores along the upper margin of the sheet. Mature gametophyte usually develops both male and female gametangia, but some completely male gametophytes do occur. The female gametangium resembles surrounding cells and differentiates into an egg. The spermatangium, on the contrary, changes producing a new wall layer and progressively propagates producing up to 128 tiny male gametes. They however are not flagellated and, if released from the male gametophyte, are rather carried by water currents to find and fertilize eggs. After fertilization, zygotes are still retained on the maternal gametophyte and develop into the carpogonia.

Class Florideophyceae

Generally, the zygote propagates producing a multicellular carposporophyte which develops from an initial hypha to the bush-like colony of hyphae. The carposporophyte produces carpospores, releases them and die. After germination, each carpospore develops into a multicellular tetrasporophyte which produces tetrasporangia where cells undergo meiosis with subsequent differentiation of tetrads into tetraspores. Each tetraspore develops into a multicellular gametophyte of either female or male types. Both the tetrasporophyte and gametophyte can clone itself by digenomic and monogenomic spores respectively. Female gametophyte produces carpogonia with eggs that are retained on the gametophyte. Sperm are not flagellated and, if released from the male gametophyte, are rather carried by water currents to find and fertilize eggs. After fertilization, zygotes are still retained on the maternal gametophyte and develop into the carposporophytes.

In some Rhodophyta, cell associations are coralline, secreting a hard shell of calcium carbonate crystals around themselves.

Bikonta: Corticata: (Plantae): Viridiplantae

Phylum Chlorophyta (green algae)

Class Chlorophyceae

Numerous individual cell progression species of Chlorophyceae are characterized by association of the cells (Melkonian M 1990, Raven PH *et al* 1999, Van den Hoek C *et al* 1995). However, the zygote does not propagate but often serves as a resting spore which remains dormant during a period of potentially damaging environmental changes such as desiccation. After germination, it immediately undergoes meiosis. Each tetrad then produces cell association by progressive propagation. There is a wide variety of shapes and forms of cell associations, including hyphae and sphaerae.

In order Oedogoniales (Raven PH *et al* 1999, Van den Hoek C *et al* 1995), the zygote undergoes meiosis which is preceded by a period of dormancy. The meiosis produces four meiospores. Two meiospores give rise to relatively broad female hyphae, the other two to thinner male hyphae. Hyphae clone themselves by production of zoospores. The zoospore swims around before attaching itself to the substratum and growing into a new hypha. Female hypha can form large swollen cells which give rise to oogonium mother cell, while the male hypha produces small discoid sporangia arranged in stacks. Each male sporangium forms a male spore which become released, swims and, if attracted to any female hypha, attaches itself to it. The same female hypha attracts many male spores which then stimulate the oogonium mother cells to develop oogonia. Then, each male spore develops into dwarf antheridium which produces two flagellate male gametes. The newly formed zygotes remain enclosed within the oogonia for a long time.

In order Chlorosarcinales (Van den Hoek C *et al* 1995), the colony is a more or less cubical group or packet of cells.

Order Sphaeropleales

In order Sphaeropleales (Van den Hoek C *et al* 1995), the zygote becomes a hypnozygote which then gives rise to a filamentous colony consisting of elongate, cylindrical multinucleate hyphae. Each hypha contains a number of ring-like accumulations of cytoplasm separated by large vacuoles. Each ring harbors several nuclei. The colony can fragment by dissociation of hyphae. Gametes are produced within the hyphae. The hypha produces either a many small biflagellate male gametes or a smaller number of eggs. Fertilization and hypnozygote formation occur within the female hypha.

In genus *Hydrodictyon* (Raven PH *et al* 1999, Van den Hoek C *et al* 1995), the zygote develops into a spherical resting stage, the hypnozygote. After a period of dormancy, the hypnozygote germinates, undergoes meiosis, and releases four biflagellate

zoospores. Each zoospore forms an irregularly shaped multinucleate plasmodium bearing pointed projections. This stage is called a polyeder. The contents of the polyeder divide up into zooids which are then discharged into a vesicle. When the vesicle is extruded from the polyeder, the zooids order themselves into a more or less spherical net-like colony. Within this initial colony, each cell in turn becomes a multinucleate cylindrical plasmodium which may contain up to 20000 small biflagellate zooids. The zooids exhibit only a few transient, convulsive movements and soon become associated laterally to produce a young daughter net-like colony which is then liberated through the disintegration and dispersion of the mother plasmodium wall and matures to the large colony of cylindrical plasmodia. The zooid can also be liberated individually. In this case, it swims around freely, then comes to rest, loses its flagella, and transforms into hypnospore. The germination of hypnospore results in the zoospore which then gives rise to the polyeder and so on. Soon or late, the formation of biflagellate gametes is triggered which immediately undergo syngamy to form new zygotes.

In genus *Pediastrum* (Van den Hoek C *et al* 1995), the zygote gives rise to hypnozygote from which zoospores emerge on germination. Each zoospore gives rise to the polyeder which in turn produces the initial colony. This colony is circular, flat and radially organized. It is usually one cell thick. The cells around the colony margin bear born-like projections. Each of these cells becomes a multinucleate plasmodium which produces biflagellate zooids. These are always discharged together into a vesicle which is then extruded from the mother plasmodium.

In order Chaetophorales (Raven PH *et al* 1999, Van den Hoek C *et al* 1995), elongated, cylindrical cells form a hypha (for example, genus *Uronema*). Primary hypha can gives rise to a branched (for example, genera *Stigeoclonium*, *Draparnaldia*) or solid (for example, genus *Schizomeris*) colony of hyphae. Each cell can produce a quadriflagellate zoospore.

Order Chlamidomonadales

In family Volvocaceae (Desnitski AG 2000, Kirk DL 2003, Kirk DL and Nishii I 2001, Nozaki H and Krienitz L 2001), usual form of the cell associations in tetradic cell progression is a sphaera (Raven PH *et al* 1999, Van den Hoek C *et al* 1995). In sphaera, cells are connected by fine cytoplasmic bridges, plasmodesmata, which may be important in coordinating the development and behavior of the cell association. Sphaerae are usually of precise geometric shape.

In genus *Gonium*, for example, the cell association is a concave sphaera made of 4 to 32 cells. Their flagella beat independently, but since they are all oriented in the same direction, they are able to propel the sphaera through the water. However, cells remain equivalent to each other. In genus *Pandorina*, the sphaera consists of 8, 16, or 32 cells attaching closely to each other in a gelatinous matrix. The sphaera of genus *Eudorina* contains 16 to 32 cells, of genus *Pleodorina* - 64 to 128 cells.

Most elaborated is the sphaera of genus *Volvox*. The cells live in temporally shallow ponds that fill with spring rains but dry out in the heart of the summer. Just shortly

before the pond dries up, zygotes are produced. For a long time, they remain however dormant to survive the heat and drought of late summer and the cold of winter. When rain fills the pond in spring, each zygote breaks dormancy and immediately undergoes meiosis. Each tetrad progressively propagates, whereas cells remain associated in a hollow sphaera. In sphaera, the cells are connected by plasmodesmata and are also imprisoned in a rigid honeycomb of chambers walled with cellulose. Within the sphaera, there is some division of labor among cells. Most cells are small and biflagellate. The beating of flagella is coordinated to propel the body along like a rolling ball. Any few cells differentiate into large gonidia which are usually confined to one end of the sphaera, where they give rise to new miniature sphaerae. New sphaerae are initially sheltered inside the large parent, while their cells are oriented with flagella interiorly and they must therefore turn themselves right side out. If this is done, they are released from the parent sphaera and swim away. Thereafter, the cells of parent sphaera commit suicide, whereas juvenile sphaerae grow, mature, and produce the next generation of juvenile sphaerae. This event repeats many times until the pond is about to dry up. Gonidia undergo modified pattern of specialization and differentiate into eggs or sperm. The sperm are to be released and swim up to non-motile eggs. After fertilization, large number of new zygotes is produced. Thus, a particular individual cell progression lives only one year.

Interestingly, in genus *Chlamidomonas* (Van den Hoek C *et al* 1995), the sphaera is formed only if free-living monogenomic cells become gametes and are ready for syngamy. When these cells are brought together, a very characteristic phenomenon occurs, a clumping. The gametes unite into groups very quickly. Each clump begins with association of two cells of different mating types via their flagella. Other gametes also attach themselves to this pair producing a clump.

Class Ulvophycea

In Ulvophycea (Floyd GL and O'Kelly CJ 1990, Raven PH *et al* 1999, Van den Hoek C *et al* 1995), the zygote usually propagate forming a sporophyte.

In order Dasycladales (Floyd GL and O'Kelly CJ 1990, Raven PH *et al* 1999, Van den Hoek C *et al* 1995), the zygote germinates immediately and grows into the uninucleate plasmodium. For instance, in genus *Acetabularia* (Dumais J *et al* 2000, Mandoli DF 1998), the plasmodium consists of three parts: a root-like rhizoid, a tiny stalk, and a flattened umbrella-like cap. In young sporophyte, the nucleus resides within the rhizoid and expands enormously developing into the giant nucleus. In mature sporophyte, the giant nucleus gradually decreases in size and undergoes meiosis. Subsequent rounds of karyokinesis lead to production of up to 20000 tiny nuclei which are transported to the cap by cytoplasmic streaming and become concentrated in the rays, gametangia. Cleavage of the gametangia produces cysts, each with a single monogenomic nucleus. The contents of the sporophyte are almost wholly used up during formation of cysts so that it subsequently disappears. The cyst usually requires a period of dormancy before it germinates. In the meantime, it becomes a multinucleate plasmodium. Upon germination, the cyst content divides up into numerous biflagellate gametes which then become set free through an opening in the cyst wall.

In order Cladophorales (Floyd GL and O'Kelly CJ 1990, Raven PH *et al* 1999, Shepherd VA *et al* 2004, Van den Hoek C *et al* 1995), the sporophyte is first a multinucleate plasmodium which then gives rise to a bush-like colony of plasmodia. In mature sporophyte, each plasmodium can swell somewhat and its content divides into monogenomic quadriflagellate meiospores which then exit through a pore at the upper end of the plasmodium. Each meiospore develops into gametophyte. Sporophyte and gametophyte look alike and can be distinguished only by the size of the cell or by nucleus. Also their development follows essentially identical pathways. Gametophytes produce biflagellate gametes of both mating types which are similar to each other in appearance.

In order Caulerpales (Van den Hoek C *et al* 1995), the zygote attaches itself to the substratum and grows slowly into a tiny branched plasmodium which initially contains one single enormous nucleus. This nucleus then divides many times to give a large number of small nuclei. The plasmodium subsequently can cleave up into multiflagellate, multinucleate zoospores. Probably, the meiosis takes place during this process, since about half of the zoospores grow into male gametophytes and half into female gametophytes. The sporophyte may itself bud off gametophytes directly. Gametophytes are also plasmodia. They can have a bubble-like (for example, genus *Derbesia*), bush-like (for example, genus *Bryopsis*), or leaf-like (for example, genus *Caulerpa*) appearance. Mature gametophytes develop gametangia producing biflagellate gametes. Male and female gametes look differently.

In order Ulotrichales (Van den Hoek C *et al* 1995), the quadriflagellate zygote swims down, attaches itself to the substratum, and becomes immobile. It germinates only short-day conditions, when it swells up into the large stalked cell. Its contents divide up to give 4-16 quadriflagellate zoospores. During this process, the meiosis probably occurs. Each zoospore swims down, attaches itself to the substratum, and gives rise to an unbranched hypha. All cells in the hypha are able to divide. The hypha clone itself by production of quadriflagellate zoospores. From 2 to 16 zoospores are produced per cell. They are initially discharged into the vesicle and then released from the parent cell. In long days, the hyphae produce biflagellate gametes which are smaller than the zoospores. The same hypha produces gametes of the same mating type. Gametes fuse to form quadriflagellate zygotes.

In order Acrosiphoniales (Van den Hoek C *et al* 1995), the zygote develops into the large stalked cell within which the meiosis occurs and quadriflagellate zoospores are produced. Each zoospore gives rise to the multinucleate hypha which then produces either unbranched (for example, order *Urospora*) or branched (for example, genus *Acrosiphonia*) hyphae colony attached to the substratum by several rhizoids. Each hypha can divide its content into many quadriflagellate zoospores each of which gives rise to new colony of multinucleate hyphae. Male hyphae produce male gametes which are smaller than female gametes produced by female hyphae. Gametes are biflagellate.

Order Ulvales

In genus *Monostroma* (Van den Hoek C *et al* 1995), the zygote develops into the large stalked cell which then bores into the calcareous shell of cirripeds and takes on an

irregular outline with a number of protrusions. In this condition, it spends a summer. Germination of the zygote produces quadriflagellate zoospores which are released through a discharge tube. Each meiospore attaches itself to the substratum and grows to form first a discoid and then a hollow spherical cell colony. This colony ruptures at its upper end and becomes sac-shaped. The sac splits and gives rise to a leaf-like gametophyte, only one layer of cells thick. The leaf grows up to 20 cm high and is irregularly undulate and folded. The female gametophyte produces rather larger gametes than the male gametophyte. In both cases, gametes are biflagellate.

In genus *Ulva* (Dion P *et al* 1998, Malta EJ *et al* 1999, Raven PH *et al* 1999, Van den Hoek C *et al* 1995), the zygote germinates immediately and gives rise to the massive three-dimensional colony of tightly connected hyphae which is called a sea lettuce because of its leafy appearance. This leafy sporophyte is two cells thick but can be a meter long. It can be free-floating or attached to the substratum. Cells in the marginal part of the sporophyte undergo meiosis producing a numbers of quadriflagellate meiospores. Half of the meiospores grow into male gametophytes, while the other half grow into male gametophytes. Mating type determination occurs during meiosis. Gametophytes are similar to the sporophyte in development and appearance. Gametophyte produces biflagellate gametes of two types.

Class Trebouxiophyceae

In order Prasiolales (Van den Hoek C *et al* 1995), the zygote is first binucleate. It is uniflagellate and can swim around for some time. After a few days, a karyogamy occurs within the zygote which then comes to rest, germinates, and gives rise to a leaf-like colony of hyphae. The leaf is only one cell thick. The sporophyte clone itself by digenomic aplanospores. Regions of the sporophyte, where the formation of aplanospores occurs, become two- or four-layered. In mature sporophyte, meiosis takes place in the upper parts. Tetrads progressively propagate producing gametophytes which remain attached to the sporophyte. Half of the gametophytes are male, the other half is female. The mature gametophyte completely consists of gametes which generally become discharged together in large numbers, simultaneously. The male gametes are small motile biflagellate cells, while the female gametes are large and non-motile. If any male gametes touch egg, it becomes absorbed so that a uniflagellate, binucleate zygote is produced.

Phylum Streptophyta

Class Zygnemophyceae

In order Zygnematales (Graham LE *et al* 2000, Hoshaw RW *et al* 1990, Raven PH *et al* 1999, Van den Hoek C *et al* 1995), almost all individual cell progression species live in freshwater environment making up the filamentous periphyton growing on and around the larger aquatic plants. The zygote of genus *Spirogyra*, for example, is a resting spore which withstands winter and undergoes meiosis only in spring. Each tetrad produces a hypha which cells divide in one plane producing end-to-end chain of cells. The hypha can be anchored to objects in the water by a rhizoid cell. The hyphae usually fragment to distribute the tetradic cell progression in space. The gametes are non-motile. To

produce new zygote, two hyphae of different mating types line up beside one another aligning neighboring cells which then produce conjugation tubes. The cells from one hypha can move over into the other hypha or, alternatively, cells from both hyphae can move into the conjugation tube. In either case, the cells of two mating types meet and fuse together producing zygotes which then develops into resting spores.

In order Desmidiales (Hoshaw RW *et al* 1990, Raven PH *et al* 1999), only few individual cell progression species form cell associations. Like Zygnematales, their zygotes are resting spores, their tetradic cell progression grows as long hyphae, and their zygotes are produced by conjugation.

Class Chlorokybophyceae

In Chlorokybophyceae (Graham LE *et al* 2000, Van den Hoek C *et al* 1995), cells are grouped into more or less cubical packet and are embedded in a common gelatinous matrix. Many packets in turn form a large mucilaginous colony. Within the colony, biflagellate zoospores are formed.

Class Klebsormidiophyceae

In Klebsormidiophyceae (Graham LE *et al* 2000, Van den Hoek C *et al* 1995), cell propagation leads to formation of a non-branching hypha which dissociates easily into fragments containing one to a few cells. Each cell is able to transform into a biflagellate zoospore which can swim away and develop into a new hypha after settling. Formation of gametes and their fusion to zygote have not been documented.

Class Charophyceae

In order Charales (stoneworts and brittleworts) (Graham LE *et al* 2000, Raven PH *et al* 1999, Van den Hoek C *et al* 1995), the mature zygote sinks into the sediments and becomes dormant for a short or long period of time. During germination, meiosis takes places producing a quadrinucleate cell which then divides into a small outer uninucleate cell and a larger inner trinucleate cell. All three nuclei of the inner cell subsequently degenerate. The outer cell gives rise to a multicellular gametophyte which develops to a colony of hyphae. It consists of a series of so called "giant cells" up to several centimeters in length with branches coming off at nodes composed of smaller cells. The gametophyte is anchored in mud or silt by translucent rhizoid cell. Growth occurs at the apex. Oogonia and antheridia grow at the nodes. Oogonium is oblong and consists of a central cell surrounded by five tubular, spiraling cells. A crown of smaller cells sits atop these cells where they come together. Antheridium is spherical. Mature male gametes are biflagellate.

In order Coleochaetales (Graham LE *et al* 2000, Raven PH *et al* 1999, Van den Hoek C *et al* 1995), the zygote undergoes meiosis after a period of dormancy. Tetrads propagate to produce 8 to 32 cells which then become biflagellate zoospores. When released, the zoospores swim away and each begins life as a multicellular gametophyte. It is a tiny discoid or a cushion-like colony of hyphae. Gametophyte can produce free-swimming biflagellate zoospores which leave the parent colony to begin new colonies. Colonies

may be found in freshwater habitat either growing on larger aquatic plants or attached to rocks or soil. In each gametophyte, cells can differentiate either into a large non-motile eggs in oogonia or into smaller free-swimming biflagellate sperm in antheridia. Each antheridium produces only one single sperm which becomes surrounded by other cells. Newly formed zygotes are usually retained on the maternal sporophyte. The surrounding cells propagate to produce a layer of sterile tissue which envelops the zygote and may provide nourishment until zoospores swim away.

Phylum Cormophyta (land plants)

Cormophyta are also called Embryophyta, since the young sporophyte begins its development within the tissue of its parent gametophyte.

In Marchantiophyta (liverworts) (Graham LE *et al* 2000, Raven PH *et al* 1999), the zygote develops into a multicellular sporophyte which is a massive three-dimensional colony of tightly connected hyphae. This colony is composed of foot, short stalk, and capsule. Monogenomic spores produced within the capsule are disseminated by wind. After germination, each spore develops into a multicellular gametophyte which is much larger than a sporophyte. It is flat and lobed. The three-dimensional growth is highly organized. Cell differentiation produces a variety of specialized cell types. The lower surface of the gametophyte bears numerous rhizoids, hair-like projections, which anchor it and absorb nutrients from the soil. On the smooth upper surface of the gametophyte, there are gemmae caps or archegonia and antheridia. Gemmae caps contain spores to distribute tetradic cell progression in space. Archegonia are umbrella-headed stalks where eggs are produced. Antheridia are disk-headed stalks where flagellated sperm are produced. Sperm swim to the vicinity of the eggs in a continuous film of water and fertilize those producing zygotes.

In Bryophyta (mosses) (Gilbert SF 2000, Raven PH *et al* 1999), the zygote progressively propagates producing a multicellular sporophyte which is a massive three-dimensional colony of tightly connected hyphae. The colony consists of a foot, a stalk, and a capsule. Meiosis within the capsule yields monogenomic spores of two distinct types: female or male. They are released and eventually germinate, each progressively propagating to form either female or male multicellular gametophyte. Also in Bryophyta, the gametophyte, rather than the sporophyte, is the more conspicuous. Development of a gametophyte begins with an initial hypha which first gives rise to a colony of hyphae, a protonema, anchored to soil by rhizoid. Three days of favorable growing conditions produce upright shoots covered with leafy structures. The development of the gametophyte illustrates the transition from a filamentous to a highly organized three-dimensional growth type. The gametophyte can fragment to distribute tetradic cell progression in space. The shoots bear archegonia or antheridia at their tips. Female gametophyte develops archegonia where any cells differentiate into eggs. Male gametophyte develops antheridia where any cells differentiate into flagellated sperm which however need external water to reach eggs. If chemically attracted to the entrance into an archegonium, sperm fertilize the eggs to produce new zygotes. The embryonic sporophyte develops within the archegonium, and the mature sporophyte stays attached to the mother gametophyte. At first, the sporophyte is green and photosynthetic. At

maturity, it is brown, not more photosynthetic, and is nourished by mother gametophyte.

In Pteridophyta (ferns) (Gilbert SF 2000, Raven PH *et al* 1999), the zygote progressively propagates producing a massive three-dimensional colony of tightly connected hyphae. Young sporophyte develops a root-bearing rhizome from which fronds project. Fronds are variable in size and shape. Nearly all fronds first appear as a fiddlehead which unrolls as it grows. Fronds are secondarily subdivided into leaflets. They may have evolved by uneven branching. The sporophyte ranges in size from low-growing moos-like forms to tall trees. Sporophyte develops vascular tissue to conduct water and minerals up from the soil and to transport organic nutrients from one part to another. Within sporangia located in sori on underside of leaflets, meiosis yields tetrads differentiating into spores. They are released and disperse mostly by wind. After germination, each spore progressively propagates to form a multicellular gametophyte which grows and develops both archegonia and antheridia. Flagellated sperm use water to swim from antheridia to archegonia and to fertilize eggs. The embryonic sporophyte develops within the archegonium, and the mature sporophyte stays attached to the mother gametophyte. It remains photosynthetic and soon outgrows the space.

In gymnosperm Spermatophyta (seed ferns, cycads, conifers and others) (Gilbert SF 2000, Raven PH *et al* 1999), the sporophyte develops roots, stem, and leaves. Roots anchor a sporophyte in soil and give support. Numerous root hairs absorb water and minerals from the soil. Stem forms main axis, along with lateral branches, produces leaves and arrays them to be exposed to as much sun light as possible. Leaves are adapted to maximize photosynthetic activity. Leaves that bear sporangia are called sporophylls. They are arranged on cones. The sporophyte produces cones of two types: female seed cones and male pollen cones. Each scale of a seed cone has two ovules surrounded by an integument and with one opening at one end. In sporangium within the ovule, the cell undergoes meiosis producing four tetrads which directly differentiate into female spores. One female spore develops into a multicellular female gametophyte with 2 to 6 archegonia, each containing a single large egg. Each scale of pollen cone has two or more sporangia on underside. Within the sporangium, each cell undergoes meiosis and produces four tetrads which immediately differentiate into male spores. Each male spore develops into an immature male gametophyte, a pollen grain, consisting of two or three cells. Thus, gametophytes are diminutive, reduced to a mere few cells. Pollen grains remain on the sporophyte for only a short time. They are released and carried by wind to female seed cones where they land and germinate. After germination, the pollen grain matures to produce male gametes and to develop a pollen tube that grows into the female gametophyte. Pollen tube growth is quite slow, up to a year. After fertilization, ovule matures and becomes a seed composed of embryo, reserve food, and coat. Seed cone opens to release seeds. Under appropriate conditions, seed germinates and produce young sporophyte.

In angiosperm Spermatophyta (flowering plants) (Gilbert SF 2000, Raven PH *et al* 1999), the sporophyte develops roots, stem, and leaves. Once the sporophyte becomes mature, it initiates the development of flowers. The flower contains highly modified leaves arranged in rings. The first ring becomes green sepals which enclose the flower before it opens. The second ring becomes large and colorful petals. Sepals and petals are

sterile. The third ring becomes a pollen-producing stamens. Stamen is a slender stalk with an anther at the tip. Anther is a modified sporophyll and contains male sporangia where cells undergo meiosis and tetrads differentiate into male spores. Each male spore develops into a mature male gametophyte, a pollen grain. The pollen grain contains of three cells two of which are sperm. The fourth ring of leaves within the flower becomes carpels which fuse to form a pistil. Carpel is a modified sporophyll and consists of the stigma, the style, and the ovary. The ovary contains one or more ovules attached by a placenta to the ovary wall. The ovule has one or two outer layers of cells, integuments, which enclose the female sporangium where the cell undergoes meiosis and tetrads differentiate into female spores. The largest of these spores undergoes three mitotic divisions to produce a female gametophyte which is a seven-celled embryo sac with eight nuclei. The cell with two nuclei is called a central cell. One of uninucleate cells is the egg. If released, pollen grains can be transferred to the carpels by various agencies such as wind, water, or animals. After any pollen grain lands on the stigma of the carpel, it takes up water and the pollen tube emerges. The pollen tube grows down, passes between cells of stigma and style, enters the ovule through opening and discharges both sperm. One sperm fertilizes the egg to produce zygote which propagates forming an embryo and a suspensor. The suspensor anchors embryo and transfers nutrients to it from the sporophyte. Another sperm unites with central cell to form digenomic triploid cell which gives rise to the endosperm (Berger F 2003, Olsen OA 2001). The endosperm develops into nutritive tissue. The ovule develops into seed, the ovary develops into a fruit. Different kinds of fruit employ different kinds of dispersal mechanisms for dissemination of seeds. Under favorable conditions, seed germinates to produce young sporophyte.

Unikonta: Opisthokonta: Fungi

Most Fungi form cell associations (Raven PH *et al* 1999). Typical form of the primary cell colony is a hypha which is actually a tube-shaped plasmodium enclosed by a rigid chitinous wall. Some hyphae have cross walls, septa, with pores which allow cytoplasm and organelles to pass freely. Fungal hyphae are microscopic, but the radially-expanding secondary cell colony, a mycelium, can be very large rivaling the mass of the largest plants and animals. Fungi are non-motile. They move to a food source by growing toward it. Fungal growth is mainly confined to the tips of the hyphae. Some mycelia can grow up to a kilometer a day. When one of the hyphae contacts a food supply, the entire secondary cell colony mobilizes and relocates resources to exploit the new food. If all food is depleted, production of spores is triggered. Another form of distribution of the individual cell progression in space is fragmentation of a mycelium. Colonies of different individual cell progressions superpose each other and communicate chemically via pheromones especially prior to mating.

Phylum Chytridiomycota

Chytridiomycota are poorly studied. Some are known to have zygotic meiosis. Some are unicellular, some produce solitary hyphae, and others produce mycelia. They have flagellated gametes. In genus *Allomyces* (Barr DJS 1990, Raven PH *et al* 1999), for example, the zygote propagates and produces the digenomic sporophyte. The sporophyte grows by branching and clones itself by production of digenomic zoospores.

Each mature sporophyte develops sporangia which become released and after a period of dormancy produce monogenomic zoospores by meiosis. After germination, each monogenomic zoospore produces gametophyte. The mature gametophyte produces gametes of both types, male and female. By syngamy, gametes produce biflagellate zygote which, however, losses both flagellae and begins to propagate.

Phylum Zygomycota

A zygospore is a chimerical plasmodium containing a number of monogenomic nuclei of two mating types (Raven PH *et al* 1999). It has a period of dormancy before nuclei pair and fuse. Then, digenomic nuclei immediately undergo meiosis and zygospore germinates. Germination involves development of one or more sporangiophores with sporangia at their tips. Sporangia release monogenomic spores each of them gives rise to its own mycelium. With little cellular differentiation among mycelium, hyphae specialize for various functions. Stolons are horizontal hyphae that exist on the surface of the food. Rhizoids are hyphae that grow into the food and carry out digestion. Sporangiophores are stalks that bear sporangia where spores are produced. If released, spores are dispersed by air current and give rise to new mycelia contributing to distribution of the tetradic cell progression in space. Sometimes, two hyphae of different mating types are chemically attracted and grow toward each other. Ends of hyphae swell as nuclei enter. Cross walls without pores develop behind each end, forming multinucleate gametangia. Both gametangia merge into a single chimerical plasmodium which develops a thick wall forming a zygospore. The zygospore remains attached between both parental hyphae during period of dormancy.

Phylum Ascomycota

If a plasmodial ascogonium receives nuclei from a plasmodial antheridium through a cytoplasmic bridge, it becomes a single chimerical plasmodium containing numerous nuclei of two mating types (Borkovich KA *et al* 2004, Coppin E *et al* 1997, Kronstad JW and Staben C 1997, Raven PH *et al* 1999, Saupe SJ 2000). Within this plasmodium, nuclei of two mating types pair but do not fuse. They exist side-by-side and propagate synchronously. Plasmodium develops a compact colony of chimerical plasmodial hyphae surrounded by an ascocarp. Walled-off tips of some hyphae become large dikaryotic cells. After its monogenomic nuclei fuse, the cell becomes a meiocyte where the digenomic nucleus undergoes meiosis and each tetrad then undergoes one mitotic division. The cell becomes an ascus, a finger-shaped plasmodium containing eight monogenomic nuclei. Within ascus, each nucleus becomes surrounded by a separate cell wall and differentiates into an ascospore. Ascus swells and bursts, expelling ascospores. At the time they are released, the thick-walled ascospores are resistant to adverse environments. Given the right conditions, the ascospore germinates and develops a mycelium. In mycelium, some aerial hyphae can differentiate into conidiophores which tips contain conidiospores. Conidiospores contribute to distribution of the tetradic cell progression in space. If two hyphae of different mating types are attracted to each other, they differentiate into an ascogonium and an antheridium respectively and form a cytoplasmic bridge through which all the nuclei of the antheridium enter the ascogonium.

In subphylum Saccharomycotina (yeast), cells are usually dispersed in space, but, in response to nitrogen limitation and abundant fermentable carbon source, cells of the zygotic cell progression can undergo transition to filamentous growth (Lengeler KB *et al* 2000, Wittenberg C and La Valle R 2003). The filamentous growth represents a dramatic change in the normal pattern of cell growth in which the cells become elongated, switch to unipolar budding pattern, remain physically attached to each other, and invade the growth substrate. Related transition to filamentous growth occurs also in tetradic cell progressions but rather in nutrient-rich environment. In the tetradic cell progression, cells essentially represent gametes that are short-lived in nature. An elaborate pattern of axial budding has evolved in these cells and is thought to promote rapid mating. Thus, while the role of transition to filamentous growth in zygotic cell progression may be to forage for nutrients, the role in tetradic cell progression may be to forage for mating partners.

Phylum Basidiomycota

A dikaryotic zygote gives rise to a mycelium. In hyphae, septa separate dikaryotic regions from each other (Casselton LA and Olesnicky NS 1998, Hibbett DS and Binder M 2001, Kronstad JW and Staben C 1997, Kües U 2000, Raven PH *et al* 1999). In apical region of the hypha, nuclei propagate synchronously whereby one of the nuclei divides in the main axis of the hypha, while the other divides into a hyphal branch, a clamp. Septa are formed across each of the mitotic spindles so that the new subapical region and the clamp become monokaryotic. If the apex of the backward growing clamp fuses with the new subapical region, dikaryotic condition is reestablished. The mycelium continues its existence for years, perhaps even hundreds of years. Production of conidiospores is rare. Conidiospores may be released either passively or forcibly. Also fragmentation of the mycelium can take place. Occasionally, the mycelium develops one or more basidiocarps. Basidiocarp is a fruiting body such as mushroom or puffball composed of tightly packed hyphae whose walled-off ends become club-like basidia. If walled-off by a complete septum, the end of the hypha becomes a large cell where both nuclei fuse and digenomic nucleus undergoes meiosis. The cell becomes a basidium by forming four projections each of which obtains its own monogenomic nucleus and develops into a basidiospore. Also basidiospores may be released either passively or forcibly. After germination, each basidiospore forms its own mycelium. Monogenomic mycelium is short-living. If two hyphae of different mating types are attracted to each other, their apical regions fuse together producing a dikaryotic zygote. Rapidly growing new dikaryotic mycelium remains attached to parental monokaryotic mycelia.

Unikonta: Opisthokonta: Microsporidia

Microsporidia are parasites which hosts are representative of almost all invertebrate animal phyla (Canning EU 1990). Karyokinesis often produces a spherical or filamentous plasmodium. Nuclei may be isolated or paired in a dikaryon arrangement. The nuclear envelope remains intact during karyokinesis. Plasmodium may divide by simultaneous fission into smaller multinucleate plasmodia or dikaryotic cells. The plasmodium development culminates in karyogamy producing digenomic nuclei which immediately undergo meiosis. Monogenomic nuclei propagate until the plasmodium

becomes a sporont producing spores. Spores are highly characteristic with a polar tube which is everted in the hatching process and allows the passage of the sporoplasm through it so that the host cell is infected by inoculation.

Unikonta: Opisthokonta: Nucleariida

In Nucleariida, multinucleate plasmodium, with sharply pointed fine radiating pseudopodia, actively moves varying in form and shape. Sometimes, it becomes a spherical. Number of nuclei per plasmodium ranges from 4 to 80. Nuclear envelope remains intact by karyokinesis.

Unikonta: Opisthokonta: Choanoflagellata

Although considered the closest relatives of Animalia, Choanoflagellata are not yet thoroughly studied (Buck KR 1990, Maldonado M 2004, Nielsen C 2001). It is even not known whether they are monogenomic or digenomic. The cell typically has a funnel-shaped contractile collar of cilia surrounding a single flagellum. Often, cells remain in hypha-like or sphaera-like association and show a limited degree of differentiation. In hypha-like association, cells are usually clustered at end of a simple or branching stalk. Sphaera-like associations, such as of genus *Sphaeroeca*, have collars on the outer side of the sphaera, but others, such as of genus *Diaphanoeca*, have collars facing the interior of the sphaera. Of special note is a sphaera of genus *Proterospongia*, which external cells are typically flagellated and ciliated, but internal cells are non-motile. *Proterospongia* may be the direct ancestors of Porifera.

Unikonta: Opisthokonta: Animalia

The evolution of individual cell progressions of Animalia clearly involved the development of considerable diversification of cells within the cell association.

In Animalia (Gilbert SF 2000, Nielsen C 2001), the zygote propagates by cleavage so that the cells become more and more smaller. Then, the cell association grows and develops in a large variety of ways, forming an initial body with a species-specific primary body plan. This initial body usually clones itself giving rise to an expanding population of primary cell colonies that often remain attached to each other, forming a larger cell association with a species-specific secondary body plan. The secondary cell colony may show differentiation of primary cell colonies. Soon or later, the onset of meiosis is triggered. The tetrads may propagate forming an association of monogenomic cells, but this case is extremely rare. Mostly, the tetrads do not propagate but differentiate into eggs or sperm. The egg usually develops only from one of the tetrads, while the other three become polar bodies and rather degenerate.

Each primary cell colony may frequently change from a free-swimming stage to a sessile stage. In addition to the settlement, this change may include more or less dramatic transformation of the primary body plan. The cloning and formation of secondary cell colony may occur from both the free-swimming stage and sessile stage. In some species, the free-swimming stage is restricted to the initial primary cell colony which soon or later settles and irreversibly transforms into the sessile stage.

Similarly, each secondary cell colony may frequently change from a free-swimming stage to a sessile stage and this change may include more or less dramatic transformation of the secondary body plan.

Generally, most specialized cells can de-differentiate into primordial cells or even re-differentiate into other cell types.

Formation of animal body plans

While the morphological diversity of animal cell associations seems to be overwhelming, the underlying body plans are nevertheless governed by rather few general principles.

The primary body plan is always a sphaera or its derivative. The sphaera which can be topologically described as the simplest closed surface, with two sides and no boundary lines, can give rise to more complex closed surface such as solenoid or even to a system of solenoids, some embedded in another.

The secondary body plan is a series of primary body plans. However, the serial arrangement may become not more evident.

In contrast to the abstract mathematical surface, the real biological surface is made up not by dimensionless points but by three-dimensional matrix with embedded cells. So, although the biological surface, like the mathematical surface, is with two sides and no boundary lines, it is actually a wall, since there is a distance between its two sides so that these two sides enclose a space with a volume. In other words, whereas a mathematical surface has no thickness, the biological surface does have. The thickness of the wall may have regional differences in magnitude. Additionally, the two sides of the wall can be differently designated according to their orientation to interior or exterior of the body.

Thus, it is very important to recognize that the description of the animal body plan can be generally given in terms of a closed and orientable wall, without boundary lines and with two distinguishable sides. That side of the wall which is oriented into the exterior of the body is here designated as an outside, and that which is oriented in the interior of the body is an inside. One must be aware that the space, which seems to be the interior of the body at the first glance, is actually the exterior.

Within the wall, some cells may become polarized cells arranged in cell layers. Some cell layers may be described as the closed surfaces, but their local orientation may greatly deviate from the direction of the wall orientation, giving rise to the internal complexity of the wall. Additionally, other cell layers may not be described as closed surfaces at all. So, the underlying principles of surface topology remain valid only at the wall level but not at the level of separate cell layers.

The complexity of the primary and secondary body plan enhances gradually at different ontogenetic and phylogenetic stages, providing insight into the most basic directions of animal evolution.

A. Sphaera as a primary body plan

In early part of animal phylogenesis, the primary body plan corresponds to the three sphaera types: a morula, blastula, and gastrula.

Similar to many other Karyota, ancestral Animalia were able to form a small spherical cell association, the morula, within which the ciliated cells were held together by a semi-fluid extracellular matrix. The morula was without polarity and rolled throughout the water. In extant animal phyla, the morula is retained only as a transitory stage during development of the initial primary cell colony.

The next sphaera derivative, the blastula, evolved when the outermost cells came into close contact to each other forming junctions between cells so that the innermost compartment of the wall was isolated more or less completely from the exterior. This division of the wall into an innermost and outermost compartment had the advantage of a regulated interior, providing the cell association with a higher degree of independence from environment. The blastula then evolved a preferred direction of swimming, establishing an anterior-posterior polarity of the body which was associated with a division of labor between cells of the outermost compartment of the wall. At the anterior pole, the cells with longer cilia formed the most ancestral sensory organ, the apical organ. Around the posterior pole, the more advanced blastula evolved a ring of compound cilia to enhance the power of swimming. This ring, usually called the archaeotroch, was also capable to capture larger food particles and transfer them to the leeward side at the posterior pole where the cells lost the cilia at all. Although distinct parts may be distinguished in the blastula wall, it remains an integumental.

The gastrula came into existence when the wall of the blastula posteriorly to the archaeotroch bent inwards, forming a sac with more or less expanded cavity, the archenteron, which then functioned as a primitive gastral space. The archenteron offered the possibility of the retaining, absorbing, and digesting larger food particles, enhancing thus the food uptake. Although the archenteron formation is achieved by drastic change of a local curvature of the wall, it remains uninterrupted. However, in contrast to the morula and blastula, two main regions of the wall, the integumental wall and gastral wall, are to be distinguished in the gastrula.

In Porifera (Amano S and Hori I 1996, 2001, Bavestrello G *et al* 2002, 2003, Bonasoro F *et al* 2001, Boury-Esnault N *et al* 2003, Degnan BM *et al* 2005, Gallissian MF and Vacelet J 1992, Hill MS and Hill AL 2002, Leys SP 1999, 2003, Leys SP and Degnan BM 2001, 2002, Manconi R and Pronzato R 1991, Nielsen C 1998, 2001, Reiswig HM and Miller TL 1998, Uriz MJ *et al* 2001, Woollacott RM 1993), the cleavage usually leads to direct formation of the blastula with the anterior-posterior polarity. The innermost compartment of the wall is filled by semi-fluid matrix with loosely arranged cells. In some species, it is completely cell-free. In the outermost compartment, the cells are arranged in an epithelium-like layer and become apically ciliated, except the

posterior pole. Sometimes, cilia are first oriented into the cell-free interior and the blastula must turn inside out through an opening between cells. The blastula is a free-swimming stage of the initial primary cell colony. It swims by beating of cilia, but soon or later settles with anterior pole against the substratum and irreversibly transforms into a sac-shaped sessile stage, a sponge, with an expanded cavity, the atrium, which opens upward. The margin of the atrial opening is a boundary between two distinct parts of the integumental wall, the feeding wall and atrial wall, which attach each other by their inside surfaces so closely that the double-walled nature of the sac is not more evident. In the sponge wall, the innermost compartment is filled by the primordial cells, archaeocytes, which produce the semi-fluid matrix, a mesohyl, and spicules. Sometimes, archaeocytes must differentiate into more specialized sclerocytes to be able to produce spicules. Archaeocytes also differentiate into flattened cells, a pinacocytes, some of them contain contractile fibers. Pinacocytes arrange into a non-sealed epithelium-like bilayer, composing the outermost compartment of the feeding wall, and into a monolayer, forming numerous water canals running through both walls. Further, archaeocytes differentiate into characteristic cells, the choanocytes, with a funnel- or tube-shaped collar of long villi surrounding a longer cilium. Choanocytes are usually arranged into well-defined epithelium-like layer, composing the outermost compartment of the atrial wall. The undulating movement of the cilium propels water away from the cell body, thus inducing water current between villi into the collar. The water currents induced by all choanocytes create flow of water through canals. The water enters canals through numerous pores in the feeding wall and leaves through numerous pores in the atrial wall and then through atrial opening. Food particles are captured both by pinacocytes and by choanocytes. They engulf food particles from the water, digest them in vacuoles, or pass them to archaeocytes which transport nutrients from cell to cell. The wall of the sponge is loosely organized. The cell junctions occur only occasionally between the archaeocytes, when some of them arrange together to produce spicules, for example. At the sessile stage, the initial primary cell colony clone itself by fission or budding, giving rise to an expanding sessile secondary cell colony, respectively. Very often, the formation of secondary cell colony proceeds without any sign of fission or budding so that the initial sponge develops into a growing massive sponge colony of a sycon or leucon type, with an intricate net of common water canals and numerous choanocyte chambers. In any cases, special resting stages, gemmulae, contribute to distribution of individual cell progression in space. Gemmulae can survive extremely unfavorable conditions that cause the rest of the sponge colony to die. Archaeocytes and choanocytes can undergo meiosis producing gametes. Eggs and sperm are produced at different times. Eggs develop either from archaeocytes or from choanocytes which lose their collars and move into the matrix. Sperm develop from choanocytes only. In the sponge colony, the whole choanocyte chamber can become transformed into sperm which is shed into the chamber lumen and expelled from the colony through common water canals. When single sperm enters another sponge, it becomes trapped by an archaeocyte and transported to an egg in the matrix to form a zygote. Development of new initial primary cell colonies takes place inside the maternal sponge in almost all Porifera species.

In Cnidaria (Ball EE *et al* 2002, Barneah O *et al* 2002, Blackstone NW *et al* 2004, Cartwright P 2003, Dahan M and Benayahua Y 1998, Davy SK and Turner JR 2003, Freeman G 2005, Gröger H and Schmid V 2001, Gutiérrez-Rodríguez C and Lasker HR

2004, Isomura N *et al* 2003, Kossevitch IA *et al* 2001, Lasker HR *et al* 2003, Martin VJ 2000, Nielsen C 1998, 2001, Weis VM *et al* 2002, Yamashita K *et al* 2003), the cleavage usually leads to the formation of the blastula which then elongates and becomes a flat, pear-shaped planula. Cells are held together by semi-fluid extracellular matrix. The innermost compartment of the wall may contain loosely arranged cells or may be completely cell-free. In the outermost compartment, cells are apically ciliated. At the anterior pole, cells develop longer cilia and become sensory, forming an apical organ. The planula is the free-swimming stage of the initial primary cell colony. At the posterior pole, the wall often bends inwards to form the more or less expanded archenteron, making the planula planktotrophic. The planula usually settles with the anterior pole, attaches to the substratum, and becomes a flat primordial disk. All specialized cells become rather absorbed and ingested by primordial cells which propagate and begin to produce a gelatinous to almost cartilaginous, hyaline matrix, the mesoglea. The primordial disk expands in a variety of ways. The lover side develops into a pedal disk. At the upper side, a circular fold of the wall usually stretches upwards forming a sac-shaped polyp with an expanded cavity which then functions as a new gastral space. A ring of tentacles with extensions of the gastral space surrounds the sac opening. The next circular fold extends from the sac opening into the gastral space. Longitudinal folds, mesenteries, may extend radially. Although the relation of the new gastral space to the archenteron is uncertain, the two main regions of the polyp wall, the integumental wall and gastral wall, may be clearly distinguished. Their innermost compartments fuse to a thin sheath which, however, may locally swell and even contain cells. Cells of the outermost compartment are anchored to the basement membrane and form an uninterrupted sealed layer within which the primordial interstitial cells differentiate mostly into the tall cells, a myoepitheliocytes, containing muscle fibers at the base. The fibers interconnect longitudinally in the integumental wall and circularly in the gastral wall. Thus, there are two antagonistic muscle layers in the polyp. Numerous sensory, nervous, secretory and other specialized cells are scattered between myoepitheliocytes. Most characteristic are however cnidocytes. A cnidocyte contains nematocyst, a fluid-filled capsule with a long spirally coiled hollow thread. When the trigger of the cnidocyte is touched, the nematocyst is discharged. Some threads trap pray or predator, some have spines to penetrate and inject paralyzing toxins. Nervous cells interconnect to form a neural plexus which transmits impulses in several directions at once, resulting in multiple firing of nematocysts in body parts not directly stimulated. Both nerve and muscle fibers enable polyp for directional movement. The polyp can contract or extend. Tentacles can extend to grasp pray. In the gastral wall, cells secrete digestive juices. In the integumental wall, cells can secrete an external cuticle. Although sedentary, polyp is not completely sessile in most species. Some can glide from place to place on the pedal disc. Others can crawl on the side of the body or even walk on the tentacles. By fission or budding, the initial polyp gives rise to a growing number of polyps which often remain attached to each other and form an expanding secondary cell colony. In some species, the colony of polyps may be enclosed in a hard, chitinous covering. In the colony, polyps may differ structurally and functionally. Primordial cells can undergo meiosis producing gametes. Both eggs and sperm are usually shed freely in the water. In some species, polyp fragmentation can bring forth specialized free-swimming stages, medusae, which then produce and disperse gametes. In any species, the free-swimming planula develops direct into the medusa. The medusae are able to clone themselves too.

In Ctenophora (Henry JQ and Martindale MQ 2004, Nielsen C 1998, 2001, Sullivan LJ and Gifford DJ 2004), the cleavage leads to the formation of a blastula which then becomes a very delicate sac-shaped free-swimming body with an expanded archenteron and a pair of tentacles. Thus, two main regions of the wall, the integumental wall and gastral wall, may be clearly distinguished. The spacious innermost compartment of the wall, contains predominantly a gelatinous hyaline matrix, a mesoglea, and a few smooth muscle cells and mesenchymal cells. The smooth muscle cells are very large and branched. In the outermost compartment of the wall, the cells are arranged in an epithelium. Between both compartments, there is a conspicuous basement membrane. Externally, the body typically looks as a spherical or ovoid, but may become extremely flattened in the tentacular plane. In the integumental wall, the epithelium is first monolayered but, later, it becomes separated in an external layer of ciliated cells, with sensory and secretory cells scattered between them, and an internal layer of nerve and muscle cells. A dome-shaped cap with specialized sensory cells protrudes from the anterior pole. In some species, however, these sensory cells are situated rather in a small anterior cavity. Below the anterior cap or cavity, there is usually a concentration of nerve cells in the integumental epithelium. The integumental wall may form folds or lappets. Eight meridional rows of large fused cilia, a comb plates, are the only locomotory organs of the body so that the typically weakly swimming of the body is largely at the mercy of the prevailing water currents. The presence of combs is just the most distinctive feature of the phylum, giving its name. The tentacles are cylindrical and often have numerous side branches. The tentacles are muscular and can be retracted into the sheaths. The tentacular epithelium bears very characteristic cells, a colloblasts, which are formed continuously from undifferentiated interstitial cells of the basement growth zone. Apically, the colloblast has numerous granules which release sticky mucus substance by contact with a prey. The opening of the archenteron is a narrow slit which leads through a large flattened pharynx into a rather small stomach. The pharyngeal plane is transverse to the tentacular plane, establishing the so called biradial symmetry of the body. A narrow aboral extension of the stomach leads to a pair of canals with an extremely precise branching pattern so that, in addition to the main aboral canal, there are usually a pair of transverse canals, two pharyngeal canals, two tentacular canals, and eight meridional canals along comb plates. The gastral epithelium is composed of both ciliated and phagocytic cells. Digestion begins extracellularly but is completed always intracellularly. The free-swimming body grows continuously. In few species, it settles and becomes sessile. The cloning and formation of secondary cell colony have never been observed. However, Ctenophora are known as having a substantial capacity for regeneration. They are able to regenerate lost part: once used to capture prey, a tentacle is usually lost and subsequently regenerated. They may regenerate the whole body even from a small fragment. Gametes are produced in meridional canals and shed through numerous tiny pores in the comb plates. Each body usually produces both eggs and sperm, but in separate canals. The egg is usually connected with three clusters of nurse cells through intercellular bridges.

B. Sphaera-in-sphaera as a primary body plan

The opening of the archenteron may close partially or completely forming a solenoid or sphaera-in-sphaera, respectively. Since the solenoid formation may be achieved by the

partial closure of the archenteron and by transitory interruption of the wall, the solenoid at the first glance seems to be more ancestral primary body plan than the sphaera-in-sphaera. But, in the ontogenesis of many extant animal phyla, rather the sphaera-in-sphaera formation precedes the solenoid formation. It may even precede the gastrula formation as the ontogenesis of some Cnidaria shows. Additionally, one of the most basal animal phyla, Placozoa, possibly retained the sphaera-in-sphaera as a primary body plan. Taken together, these facts suggest that the sphaera-in-sphaera may be more ancestral primary body plan than the solenoid.

The phylum Placozoa comprises only one known individual cell progression species, *Trichoplax adhaerens*, which life history has never been studied in any natural habitat and is known very fragmentary (Ender A and Schierwater B 2003, Maruyama YK 2004, Thiemann M and Ruthmann A 1991). Zygote formation and propagation were not observed. The best known stage, kept alive in various laboratories, is a sphaera which is so extremely flattened that it looks as a double-walled disk creeping on substratum in warm water. Therefore, two main regions of the wall, the lower wall and upper wall, are usually distinguished. Their inside surfaces attach each other so closely that the double-walled nature of the disk is not more evident. The innermost compartment of the wall is filled by a gelatinous matrix with a meshwork of star-shaped fibre cell. The fibre cells are tetraploid, contain actin filaments, and are therefore responsible for the sometimes quite rapid changes of the body shape. In the outermost compartment of the wall, the ciliated cells are arranged in an epithelium-like layer. At the lower wall facing substratum, the ciliated cells are rather tall cells between which some secretory cells are scattered. At the upper wall, the layer contains flat ciliated cells and spectacular cells with inclusions originating from degenerating cells. The body clones itself by fission, by budding, or by formation of secondary free-swimming stages, the swarmers. The swarmer consists of two concentric walls surrounding a central lumen and is therefore a sphaera-in-sphaera. When the swarmer settles, it opens at one side and stretches out so that the lower and upper walls become established by inner and outer walls respectively. Meiosis was not observed. Eggs seem to be formed in the lower wall and become surrounded by fibre cells which function as nurse cells. In culture, eggs form fertilization membrane and start to divide, but the progeny cells soon disappear.

C. Solenoid as a primary body plan

The blastula may transform into either gastrula or sphaera-in-sphaera which both can convert into each other and both can give rise to the solenoid. So, there is a variety of ontogenetic ways of solenoid formation which phylogenetic interrelationships remain unclear. If the gastrula is a preceding stage, the solenoid may be formed either by a partial closure of the archenteron opening leaving two openings or by the formation of an additional invagination which then fuses with archenteron to produce the second opening. If the sphaera-in-sphaera is a preceding stage, the solenoid formation requires the establishment of two new openings.

The tube between two openings of the solenoid functions as a gastral tube, the gut, which lumen represents the exterior in relation to the body. It may extend and branch in complex ways without affecting the solenoidal topology of the wall. The food particles pass the gut lumen only in one direction from one opening, the mouth, to the other, the

anus. The origin of different gut regions depend greatly on the way by which the solenoid is formed and varies between the most phyla.

In addition to the anterior-posterior polarity, the solenoid developed a dorsal-ventral polarity and became bilateral symmetric. However, one must be aware that the anterior-posterior axis may deviate from the ancestral orientation depending on the way of solenoid formation.

Generally, the innermost compartment of the wall remains filled predominantly by the semi-fluid matrix with only few cells. Some of these cells arrange in a pair of branched canals which open into a posterior cavity, the cloaca. The branches terminate with specialized cells which function as a protonephridia. The outermost compartment of the wall remains predominantly the myoepithelium. Numerous sensory, nervous, secretory and other specialized cells are mostly scattered between myoepitheliocytes, but may form local concentrations as well. Both compartments of the wall are usually separated by a basement membrane. The two main regions of the wall, the integumental wall and gastral wall, become more elaborated and develop a variety of specialized regions. The apical organ usually persists, but its location depends greatly on the way of solenoid formation. Numerous ciliary bands are formed, but their relation to the archaeotroch is not clear.

A large number of extant animal phyla retained the solenoid as a primary body plan of the initial body.

In Rotifera (Birky CW 2004, Fontaneto D *et al* 2003, Gilbert JJ 2003, Gomez A and Carvalho GR 2000, Nielsen C 2001, Schröder T 2003, Serra M *et al* 2004, Wallace RL 2002, Welch DBM and Meselson MS 2001, Welch JLM *et al* 2004), the initial free-swimming body is solenoid-shaped. The innermost compartment of the wall contains predominantly semi-fluid matrix but also a pair of branched canals which open into the cloaca. The branches terminate with specialized cells, the flame cells, functioning as a protonephridia. The outermost compartment of the wall is the myoepithelium which becomes plasmodial in many regions. The integumental wall develops a variety of structures such as ciliary rings, ridges, pits, papillae, and bristles. The wheel-shaped anterior region with one or more ciliary discs, a corona, becomes the most distinctive feature of the phylum, giving its name. Cuticular plates encircle the body forming a protective lorica. The posterior aspect of the body typically narrows forming a retractile foot. Food particles captured by the corona are transported through the ciliated buccal tube to the muscular pharynx, a mastax, which contains hard chitinous jaws and chews ceaselessly. The particles are crushed and manipulated before being passed into the ciliated oesophagus, where the preliminary digestion occurs, and then into the stomach which may be either cellular with cilia or plasmodial without cilia. There is usually a pair of gastric glands, but some few species have four gland pairs and one unpaired elongated gland. Short ciliated intestinal tube opens into the cloaca. As a species-specific number of cells or nuclei is reached, the cell division becomes restricted to the highly determined subset of the cells within the innermost compartment of the wall and is used by the initial body to clone itself, developing an expanding population of new bodies. The life span of the body is usually around 1 to 2 weeks. In some species, bodies of homogenous or heterogeneous age remain in a free-swimming secondary cell

colony embedded in a common gelatinous matrix. Both the solitary and colonial bodies may settle down and become sessile, attaching to the substratum by foot. Sessile bodies actively sway from side to side and contract frequently. The population continues to expand until deteriorating conditions stimulate the onset of the meiosis within the subset of dividing cells, producing tetrads. Some of them are actually eggs and wait to be fertilized, but other tetrads propagate and each develops into a monogenomic dwarf male with vestigial, non-feeding gut. In the male, most cells differentiate into sperm and oversized copulatory organ. Fertilization produces a dormant zygote which is highly resistant and may remain quiescent for months or years. In most species, however, the meiosis, male development, and fertilization have never been observed, since the population survives unfavorable condition rather by cryptobiosis and may remain in this stage for months, years, or even a century. The recovery requires 10 minutes to several hours. Thus, some Rotifera species retain the most ancestral type of the life history of the individual cell progression, being able to form cell associations not only within the zygotic cell progression but also within the tetradic cell progressions.

In Cycliophora (Kristensen RM 2002, Obst M and Funch P 2003), which comprise only one known individual cell progression species, *Symbion pandora*, the free-swimming stage of the initial body, a chordoid, is solenoid-shaped. In the wall, the thin innermost region is filled with semi-fluid matrix and is cell-free. The outermost compartment is a myoepithelium. The chordoid usually settles on the bristle surrounding mouth of the lobster, becomes eventually attached to it, and transforms into a sessile feeding stage of the initial body. From the attachment disc, a short stalk develops. At the stalk, there is a main trunk with a U-shaped gut which mouth and anus lie close to each other and are directed upwards. Around the mouth, a circular fold expands into a bell-shaped buccal funnel with a ciliated margin. The gut has well-defined oesophagus, stomach and rectum regions. The buccal funnel and gut continually degenerate and are replaced by internal budding. The sessile body clones itself: a special stage, a pandora, with a miniature sessile body is continuously produced in special brood chamber, escapes and immediately attaches nearby so a large population of feeding stages arises. Triggered by the imminent molting of the lobster host, the body of either male or female type is developed by internal budding. The significantly smaller male body is a simple sac without buccal funnel and gut. It breaks free, matures to produce two stores of sperm and two copulatory organs, and then attaches to the sessile body which is in the process of producing a female body. In the female body, only one tetrad differentiates into the egg. After its single egg is fertilized, the female body eventually breaks free and settles nearby. The zygote develops into the chordoid within a female body which progressively degenerates allowing the chordoid to escape and swim to new host.

In Micrognathozoa (Kristensen RM 2002, Kristensen RM and Funch P 2000, Sorensen MV 2003), which comprise only one known individual cell progression species, *Limnognathia maerski*, the initial free-swimming body is solenoid-shaped, but the gut has only a temporary anus of interdigitating integumental and gastral cells. The innermost compartment of the wall is filled by semi-fluid matrix with few muscle cells and contains two pairs of protonephridia. The outermost compartment is a mono- or multiciliated epithelium. At the dorsal and lateral side of the body, the integumental myoepitheliocytes produce intracellular skeletal plates. At the ventral side, cells bear compound cilia and are the chief locomotory organ. Pharyngeal cells secrete cuticular

jaws which are similar to those of Rotifera. The cloning, meiosis, fertilization, and development have not been observed, but there are numerous indices that Micrognathozoa may be similar to Rotifera also in this respect.

In Gnathostomulida (Herlyn H and Ehlers U 1997, Nielsen C 2001), the gut is blind, but some species have a temporary, periodically functional, anus of interdigitating integumental and gastral cells. The innermost compartment of the wall contains muscle cells. There are also 2-5 pairs of protonephridia. The outermost compartment is a monociliated epithelium. Pharynx is equipped by cuticular jaws similar to those of Rotifera and Micrognathozoa. During the body life history, the onset of meiosis is triggered many times so that the juvenile stages alternate with adult stages, reliving periods of maturity over and over again. The body produces gametes of both types but in separate regions. Fertilization occurs internally with production of a single large zygote which then breaks directly through integumental wall to escape from the body. Remarkably, the cleavage exhibits a spiral pattern.

In Kamptozoa (Entoprocta) (Nielsen C 1998, 2001, 2002a, Wasson K 1998), the free-swimming stage of the initial body, a trochophore, is solenoid-shaped. The innermost compartment of the wall is filled by semi-fluid matrix with a few cells arranged in a pair of branching canals. Each canal usually has three branches terminated with a multiciliated cells functioning as a protonephridia. The outermost compartment is a ciliated myoepithelium. The body is named a trochophore for the wheel-like appearance of the two main bands of compound cilia: a large prototroch which girdles the body around the middle and a smaller metatroch which is just below the mouth and parallel to the prototroch. In most species, the trochophore has a large retractable frontal organ with concentrations of sensory, nervous, and secretory cells. Between both openings of the U-shaped gut, there can be also a foot with three pairs of sacs filled by an adhesive secretion. The trochophore usually swims only few hours before it settles and, when it is ready to settle, it usually creeps on the substratum on the foot and tests it with the frontal organ. When a suitable spot has been found, the trochophore settles on the foot which sacs turn inside out and give off their content. The hyposphere is retracted so that it envelopes the body completely forming a closed atrium. The body becomes attached to the substratum with the ring-shaped zone. Most of the trochophore organs disappear, but the gut persists and rotates about 180°. The depressed ventral side with the mouth above the anus becomes surrounded by tentacle buds. Then, the atrium opens exposing short tentacles. The body stretches upwards. The region attached to the substratum develops into a shorter or longer cylindrical stalk carrying the main trunk. Tentacles carry characteristic bands of cells with longer cilia. There are numerous lateral concentrations of sensory cells. At the bottom of the atrium, nervous cells concentrate into a dumbbell-shaped ganglion which connects with a fine nervous net of the body. Within the innermost compartment of the wall, the cells reestablish a new pair of branching protonephridial canals which open at the bottom of the atrium. The sessile body secretes a thin chitinous cuticle which is however quite thick at the stiff portion of the stalk. The initial body clones itself giving rise to an expanding secondary cell colony. At maturity, additional paired canals develop in the innermost compartment of the wall and open at the bottom of the atrium. Each canal usually connected with one or two sacs within which gametes are produced. Eggs are retained, sperm is shed.

Fertilized eggs become attached exteriorly to the atrium surface where developing trochophores are retained for a period. The cleavage is spiral.

In Priapulida (Lemburg C 1998, Nielsen C 2001), the initial free-swimming body is a solenoid-shaped. From exterior, it looks as an elongated cylinder which anterior part becomes a large introvert, carrying many rings of specialized spines. In some species, there are tentacles around the mouth. The spacious innermost compartment of the wall is filled by semi-fluid matrix and contains muscle cells, erythrocytes and amoebocytes. There is also a pair of canals with numerous protonephridial branches. Canals open lateral to the anus. The outermost compartment of the wall is a myoepithelium. The integumental epithelium secretes a chitinous cuticle and spines. The pharynx contains circles of cuticular teeth. The free-swimming initial body may develop caudal appendages to anchor the sediment. The growth is accompanied by periodic molting. Adult stages show a male-female dimorphism, producing either eggs or sperm. Gametes are produced in the innermost compartment of the wall and shed through common protonephridial canals.

In Kinorhyncha (Neuhaus B and Higgins RP 2002, Nielsen C 2001), the initial free-swimming body is solenoid-shaped. From exterior, it looks as an elongated cylinder tapering towards the posterior end. The anterior part of the body is an introvert with a retractable mouth cone. Small stylets surround the mouth. The median part of the introvert carries many rings of specialized spines. The mouth cone can be retracted inside the introvert which in turn can be retracted into the trunk. The innermost compartment of the wall contains muscles and amoebocytes. A pair of protonephridia is present. The outermost compartment of the wall is an epithelium which may be plasmodial. The integumental epithelium secretes cuticle and spines and the growth involves a number of molts during which time a characteristic segmental arrangement of cuticular plates, spines, and muscles is acquired. There is usually a male-female dimorphism of adult stages. Gametes are produced in the innermost compartment of the wall and shed through paired pores situated on the terminal segment.

In Loricifera (Heiner I and Kristensen RM 2005, Kristensen RM 2002, Nielsen C 2001), the initial free-swimming body is solenoid-shaped. Its anterior part houses an introvert with a mouth surrounded by stylets. A specialized system of hardened cuticular plates and spines, a lorica, surrounding the body, gives the phylum its name. There is a varying number of molts. The adult stages show a male-female dimorphism.

In Nematoda (Hodgkin J 2002, Nielsen C 2001), the blastula develops the archenteron with an elongated opening. The lateral opening lips become pressed together and fuse, living a large mouth. Later, the small anus is formed, and the body becomes solenoid-shaped and starts to curve. The innermost compartment of the wall contains muscle cells and a few excretory cells. The outermost region contains epithelial or myoepithelial cells and a few sensory, nervous, and secretory cells. Some regions of the wall become plasmodial. The epithelium secretes a thick elastic collagenous cuticle which surrounds the body and also lines the buccal cavity, pharynx, and rectum. The cuticle hardens and must be molted four times to permit growth. As a species-specific number of cells or nuclei is reached, the cell division becomes restricted to the highly determined subset of the cells within the innermost compartment of the wall and is used

by the initial body to clone itself, developing an expanding population of new bodies. The body is able to save itself by cryptobiosis, when its environment becomes hostile. If meiosis is triggered, it occurs within a subset of dividing cells. The body first produces sperm and then turns to production of eggs. Fertilization is internal with copulation.

In Nematomorpha (Bohall PJ *et al* 1997, Nielsen C 2001, Schmidt-Rhaesa A 2002), the nematode-like solenoid-shaped body externally looks as an extremely elongated slender cylinder. It is specialized for parasitic lifestyle. The nutrient uptake occurs through integumental wall and the rudimentary intestine is involved in the food storage only. Some species lack the mouth, and the pharynx is without lumen. The body is surrounded by cuticle which must be molted several times to permit growth. The adult stage is non-feeding. It leaves the host, produces and lays gametes, and dies.

In Gastrotricha (Nielsen C 2001, Weiss MJ 2001), the initial free-swimming body is solenoid-shaped. It is elongated and flattened. The innermost compartment of the wall contains a pair of branching canals. Most branches are terminated by specialized cells, solenocytes, functioning as protonephridia. The outermost compartment of the wall is myoepithelial and mostly plasmodial. The integumental wall is covered by scales and bristles or by cilia which are often grouped in bands and stripes. The adhesive tubules project from the surface of the body, providing short-term attachment to the substratum. The gut is roughly triangular in cross-section. The food is sucked into the mouth by pumping pharynx which in some species has a pair of pores which vent excess water. The cloning is by release of thin-shelled digenomic cells giving rise to rapidly expanding population of free-swimming bodies. If the meiosis is triggered, the body may produce gametes of both types but not at the same time. Fertilization is internal with copulation. The zygote is thick-shelled and dormant. It can remain viable and survives for a long period of time in hostile environment.

D. Solenoid-in-solenoid as a primary body plan

There is a variety of ways to transform the solenoid into the solenoid-in-solenoid. The more or less spacious lumen of the internal solenoid, a coelom, which is topologically equivalent to the exterior of the body is filled by fluid. The internal solenoid is usually coiled around the gut, occupying space between the integumental and gastral walls. The wall thus becomes divided into three main regions: the integumental wall, the gastral wall, and the coelomic wall. The portion of the coelomic wall which attached to the integumental wall is usually called a parietal wall, while that which attaches the gastral wall is called a visceral wall. The coelomic wall becomes a principal place of gamete production. The single internal solenoid tends to divide so that more than one internal solenoid is present. However, more typically, a number of paired or unpaired bladders develops in space between the integumental and gastral wall and then gives rise to the internal solenoid-like bladder associations.

In Bryozoa (Ectoprocta) (Bayer MM and Todd CD 1997, Hageman SJ 2003, Hughes RN *et al* 2004, Nielsen C 1998, 2001, 2002a, 2002b, Temkin MH and Bortolami SB 2004, Wendt DE and Woollacott RM 1999), the free-swimming stage of the initial body, a cyphonautes, has a well-developed gut and is planktotrophic. The integumental wall at the posterior pole develops a half-circular fold which extends anterior-

posteriorly, surrounding an expanded vestibule. The U-shaped ridge of ciliated cells divides the vestibule into an anterior inhalant and a posterior exhalant chamber. The body soon becomes laterally compressed. The integumental epithelium of the episphere usually secretes two triangular valves. The epithelium of the exhalant chamber develops a large, complicated adhesive sac. The cyphonautes can spend weeks in the plankton, but whether it can clone itself has not been reported. But, when the time is ripe, the cyphonautes creeps on the substratum, explores it and, when a suitable spot has been found, the sac with adhesive secretion turns inside out giving off its content and the cyphonautes becomes attached to the substratum. After settling, the sac expands over the substratum and the cyphonautes becomes dorso-ventrally compressed by muscle contraction. The shells are released and the episphere expands over the upper side of the body and fuses with the sac border so enclosing all specialized cells which then degenerate. The body becomes a primordial disk which then expands in a variety of patterns to give rise to a sessile stage of the body, a cystid. Cells arrange into two concentric monolayers separated by a common basement membrane. At the upper side, a polyp-like bud, a polypide, develops. First, two invaginations grow and fuse forming an U-shaped gut so that both monolayers become solenoid-shaped. The internal solenoid is coiled around the new gut. Both arms of the gut are directed upwards, the mouth and anus lie close to each other. Then, a ridge with a circle of tentacles, a lophophore, develops around the mouth. The lophophore usually develops two lateral extensions which run in the direction of the anus so that the tentacle crown becomes horseshoe-shaped. The lumen of the interior solenoid, the coelom, expands and sends extensions into tentacles. Thus, three main regions of the wall, the integumental wall, gastral wall, and coelomic wall, may be clearly distinguished. The innermost compartment of the wall is reduced. The outermost compartment is the myoepithelium. Numerous sensory, nervous, secretory and other specialized cells are scattered between myoepitheliocytes. At the posterior side of the mouth, nervous cells concentrate into a ganglion with lateral extensions following the lophophore base. The ganglion connects with a fine nervous net. Tentacles carry characteristic bands of cells with longer cilia. Myoepitheliocytes of the oesophagus can shorten or widen thereby contracting or expanding the oesophagus space. There is often a gizzard with teeth at the entrance into the stomach. Waste products accumulate in the cells of the stomach, the whole polypide degenerates, and the cystid forms periodically a new polypide. The coelom is crossed by muscular folds by which the polypide can be retracted into the cystid which then closes. Whereas the cystid has a sometimes quite thick chitinous cuticle with calcified layers, the polypide cuticle is rather thin. The initial sessile body clones itself by budding so that a large secondary cell colony arises which often shows a specialization of bodies. There are a large numbers of budding patterns and colony forms. The colony largely dies off in winter and regenerates in the following summer. Masses of cells surrounded by chitinous cuticle can remain dormant for some time, withstand unfavorable conditions, and then germinate to regenerate colony. In visceral coelomic wall, primordial cells can undergo meiosis producing gametes which then float in the coelomic fluid. Eggs can be shed into the water but are mostly retained in special chambers. Sperm are usually shed through transitory pores at the tips of the tentacles. Free-swimming sperm can be captured by tentacles and fertilize the eggs. The new cyphonautes develops mainly in a brood chamber in one of a bewildering variety of ways.

In Phoronida (Bartolomaeus T 2001, Nielsen C 1998, 2001, 2002a, Santagata S 2002, 2004), the developing free-swimming stage of the initial body, the actinotrocha, is first solenoid-shaped. Then, some cells enter the space between the integumental and gastral walls and arrange anterior-posteriorly into a series of three bladders which wound into internal solenoids around the gut. The lumina of these solenoids are referred to as a protocoel, mesocoel, and metacoel, respectively. The metacoel communicates with the exterior through pores. When tentacles develop, narrow extensions of the mesocoel enter them. Bands of longer and more closely set cilia develop along the lateral faces of the tentacles and become feeding and locomotory organ of the actinotrocha. Later, a band of large compound cilia develops around the anus and functions as the main locomotory organ. Just anterior to the anus, the median invagination of the integumental wall develops into a pair of protonephridial canals each with several branches equipped by solenocytes. The common part of the protonephridial canals soon disappears. The protonephridial pores are situated near the pores of the metacoel. In the advanced actinotrocha, solenocytes form clusters and drain the innermost compartment of the wall. Gradually, the actinotrocha develops a complicated nervous plexus with an additional sensory organ which is protruded when the actinotrocha is testing the substrate for settling. If the actinotrocha is about to be ready for settling, a long tubular invagination of the ventral part of the integumental wall, a metasomal sac, develops and occupies much of the space around the gut. At settling, the actinotrocha rapidly transforms. The metasomal sac everts, pulling the gut into an U-shaped. Contractions in the body bring the mouth and anus close to each other and make them both directed upwards. The body stretches up, both arms of the gut extremely elongate and run close to each other. Most cilia and tentacles are either resorbed or cast off and then ingested by the developing sessile body. The main part of the protocoel is lost but it persists, though as a small uncharacteristic lumen. The mesocoel sends extension in new tentacles which grow from small frontal knobs at the base of old tentacles forming usually a horseshoe-shaped row of tentacles, a lophophore. The lophophore bears from ten to several hundreds of tentacles. The arms of the lophophore can be spirally coiled. The metacoelic wall forms numerous mesenteries which suspend the gut. A well-defined plexus of blood canals develop within the gastral and metacoelic wall. Two or three longitudinal blood canals run along the gut which is surrounded by a blood chambers, the lacunae. In tentacles, small blind blood canals are formed in folds of the frontal side of the mesocoelic wall. The terminal protonephridial canals breaks off and become resorbed and ingested, the canals now end blindly. At a later stage, mesocoelic epithelium forms a pair of large funnels which gain connection with the protonephridial ducts to form metanephridial canals. The integumental wall produces cylindrical chitinous tube covered by mud or sand. The initial sessile body clones itself by budding, forming a small secondary cell colony. Gametes are produced within the visceral metacoelic wall near the stomach region. Eggs are usually retained in the mesocoelic extensions in the tentacles. The sperm becomes enclosed in elaborate spermatophores which are shed through metanephridial canals and float in the water. If they are engulfed by lophophores of another specimen, most sperm enter the mesocoel to fertilize eggs.

In Brachiopoda (Lüter C 2000, Nielsen C 1998, 2001, 2002a), the developing free-swimming stage of the initial body is first gastrula-shaped. Then, some cells enter the space between the integumental and gastral walls laterally to the gastral cavity and

arrange anterior-posteriorly into a series of coelomic bladders, three or four on each side. The gastral cavity finally closes. Dorsally to each coelomic pair, the integumental epithelium forms a pair of thickenings with bundles of chaetae. Whether the free-swimming stage can clone itself has not been reported. At settling, the body attaches with the posterior pole, where the stalk develops. The mouth and anus break through, and the gut elaborates. The horseshoe-shaped lophophore develops and becomes intricately coiled and wound. Within the innermost compartment of the wall, some cells secrete hyaline matrix and spicules. Two shell valves become secreted from special areas of dorsal integumental wall. These areas expand to an upper and a lower mantle fold and valves soon enclose completely the whole body and the lophophore. Special muscles open and close the valves. Valves are usually unequal in size. The stalk protrudes through slit between the posterior edges of the valves. The first pair of coelomic bladders disappears. The second pair develops extensions to the lophophore. The third pair becomes a spacious body coelom which sends elaborate extensions into the mantle folds and into the stalk. The fourth pair has not been followed through the transformation. Neural concentration, blood and metanephridial canals become more or less developed. The juvenile sessile stage grows and matures to become an adult sessile stage. Gametes are produced within the wall of the body coelom. There is usually a male-female dimorphism at maturity. Eggs can be spawned free or retained in the lophophore. The sperm is usually shed through the metanephridial canals.

In Sipunculida (Nielsen C 1998, 2001), the cleavage is spiral and the free-swimming stage of the initial body is first a trochophore which then develops a pair of coelomic bladders. Later, the bladders fuse completely surrounding the gut and tentacles develop from the rim of the mouth. In most species, the trochophore develop additional structures and becomes a pelagosphaera which usually has an extended ciliated lower lip with a buccal organ and a lip gland and a retractile terminal organ with sensory and secretory cells. The coelom sends extensions in the tentacles, and a pair of metanephridial canals is developed. The pelagosphaera is a very long-living free-swimming stage, up to one year, and is adapted for long range dispersal by currents, but whether it can clone itself has not been reported. It usually does not settle, but transforms into a free-living juvenile stage which then grows and matures to become a free-living adult stage. The coelom extremely expands and develops numerous canals extending into the integumental wall. Its anterior part with extensions in the tentacles becomes pinched off. The gut becomes U-shaped and forms twisted loops suspended in the posterior part of the coelom. The slender anterior part of the body, the introvert, can be retracted by longitudinal muscular folds of the coelomic wall and everted by contraction of circular muscles. The mouth is terminal to the introvert, the anus is situated at the base of introvert. Metanephridia also become suspended in the coelom. Nephridiopores are situated near the anus. Small cell complexes, the urns, regularly detach from the coelomic epithelium and swim around in the coelomic fluid. They trap and remove particulate debris, and secrete mucus in response to pathogens. Frequently, they travel to the metanephridial funnels and drop collected waste products for excretion. The integumental wall secretes a stiff and very tough cuticle. The free-living body is able to regenerate lost parts of its tentacles, introvert, trunk, or gut. In some few species, it is also able to clone itself by breaking into a large anterior portion and a smaller posterior portion, each capable of regrowing the missing part. Gametes are produced in the visceral coelomic wall and released into the coelom where they mature.

Ripe eggs and sperm are selectively collected in metanephridial canals and shed into see.

In Annelida (Fischer A and Fischer U 1995, Giangrande A 1997, Gibson GD and Smith HL 2004, Halanych KM *et al* 2002, Henderson SY and Strathmann RR 2000, Hansen B 1993, Hardege JD and Bartels-Hardege HD 1995, Licciano M *et al* 2002, Müller MCM *et al* 2003, Nicolaidou A 2003, Nielsen C 1998, 2001, Pernet B 2000, 2001, 2003, Quast B and Bartolomaeus T 2001, Shankland M and Seaver EC 2000, Walters LJ *et al* 1997), the cleavage is spiral and the initial free-swimming body is a primitive trochophore which usually does not settle but, when the time is ripe, undergoes a cloning by internal budding which involves a rapid addition of new segments, forming a free-living secondary cell colony. The gut stretches out so that the colony becomes a segmented worm with a common gastral tube. In each segment, a gut is surrounded by a pair of coelomic bladders. Thus, three main regions of the wall, the integumental wall, gastral wall, and coelomic wall, may be clearly distinguished. The innermost compartment of the wall contains muscle layers, a plexus of blood canals, and paired protonephridial canals which open into the corresponding coeloms. The outermost compartment is a layer of ciliated epithelium, but many cells are actually myoepitheliocytes. At each segment, the integumental wall develops a variety of paired structures such as appendages, ganglia, and metanephridia. Appendages which are thought to be a homologues of the lophophore develop into branched parapodia. Some branches may function as gills. In some species, the appendages at the first segment rather form a ring of tentacles around the mouth. In any other species, they develop into two bundles of numerous slender feather-like gills. Transverse and paired longitudinal nerves connect paired ganglia into a closed nervous system. Metanephridia are shown to be a modified protonephridial canals. The integumental epithelium secretes a collagenous cuticle. Some cells secrete chitinous bristles, chaetae that project from the body. Additionally, the worm may secrete and inhabit a calcareous tube attached to firm substrata. The integumental muscle layers are usually circular. The gut may have a pair of lateral branching diverticula in each segment. The coelomic epithelium produces a fluid in which many cells float. In coelomic epithelium, some cells become chlorogogen. In the coelomic wall, muscle layers are longitudinal and arranged in bundles which usually are very thick in the parietal coelomic wall. In some species, segments show signs of differentiation. Some segments may even fuse to form specialized regions. Budding or fragmentation leads to formation of new free-living secondary cell colonies. Budding can occurs at each segment. Also gametes can be produced in each segment in the visceral coelomic wall, but in some species the gamete production is restricted to few segments. Gametes are usually released into coelom for maturation and storage and then exit via metanephridial canal.

In Mollusca (Chaparro OR *et al* 2002, Eyster LS 1995, Fishera GR and Dimock RV 2002, Gibson GD 2003, Gros O *et al* 1997, Hickman CS 1995, Hohenlohe PA 2002, Kay MC and Emlet RB 2002, Nielsen C 1998, 2001, Page LR 2000, Reynolds PD 2002, Ruthensteiner B *et al* 2001, Von Boletzky S 2003, Zardus JD 2002, Zardus JD and Morse MP 1998), the cleavage is spiral and the free-swimming body, a veliger, has essentially the same topology as the trochophore, but usually develops additional structures such as shells, velar lobes, and foot. It transforms without settling, forming a free-living juvenile stage which then grows and matures to become a free-living adult

stage. A large area of dorsal integumental wall forms a fleshy mantle which usually expands in folds covering the body laterally and enclosing more or less spacious mantle cavity. The mantle may secrete calcareous spicules or one or more calcareous shells. The form of the shell is highly variable. The postoral area of the ventral integumental wall forms the foot. The ciliated gills, the ctenidia, are thought to be a homologues of the lophophore. The gut is usually U-shaped. In the floor of the buccal cavity, the specialized gland secretes a rasp-like band of thickened, toothed chitinous cuticle, a radula. In the stomach, mineral particles move from the stomach lumen into intestine, whereas food particles move into extremely expanded diverticula for absorption and intracellular digestion. There are two or even more pairs of coeloms and metanephridial canals which likely are rudiments of additional segments, suggesting that ancestral Mollusca were able to form secondary cell colony by internal budding but this ability became rudimentary later. Gametes are produced in the coelomic wall and usually exit via metanephridial canals into the mantle cavity.

In Nemertea (Henry JQ and Martindale MQ 1996, Jondelius U *et al* 2004, Maslakova SA *et al* 2004, Nielsen C 1998, 2001, Senz W 1997, Turbeville JM 2002), the cleavage is spiral but the gastrula rather develops into a helmet-shaped free-swimming stage of the initial body, a pilidium, sometimes with ear-flap-like lateral lobes on each side. Without to reach the trochophore stage, the pilidium immediately starts to form the secondary cell colony by internal budding, producing a long worm with a poorly established segmentation pattern. In some species, the pilidium even reaches the stage with unpaired and paired bladders which however do not develop an internal solenoid but undergo rather an aberrant development, forming the so called embryonic disks. The worm has a straight gut with a number of pairs of lateral branching diverticula. Above the mouth, there is a long tubular proboscis which may be retracted into a spacious unpaired coelom and may be everted for the capture of the prey or for defense. When everted, it may be lost and the regeneration of a new proboscis is very rapid. Branches of paired protonephridial canals are arranged serially along the worm body. The worm is extremely fragile, and usually disintegrates into fragments which then rapidly regenerate the whole worm body. In space between the integumental and gastral wall, small bladders are arranged serially along the body on either side. At maturity, these bladders swell due to gamete production. Gametes are released through tiny canals in the integumental wall.

In Platyhelminthes (D'Souza TG *et al* 2004, Hoshi M *et al* 2003, Nielsen C 1998, 2001), the cleavage is spiral and the developing initial body begins to form a trochophore and even develops a pair of protonephridial canals and a set of projecting lobes with ciliary bands at margins. But later, it enlarges axially at the expense of these lobes, which shrink and gradually disappear, and becomes a free-living body that is dorso-ventrally flattened to varying degrees and anterior-posteriorly elongated. The body has no gut, but some species develop a branched gastral cavity which may be a homologue of the digestive diverticula. The body clones itself by fission and a large population of bodies is formed. In parasitic species, the initial body is able to form secondary cell colony by adding of new segments so that a long segmented worm is formed which is extremely fragile and disintegrates into fragments. Gametes are formed in the innermost compartment of the wall within which a very complex system of specialized sacs, canals, and copulatory organs develops. The fertilization is always internal.

In Arthropoda (Akam M 2000, Guerao G *et al* 2004, Møller OS *et al* 2004, Nielsen C 2001, Olmstead AW and LeBlanc GA 2001, Vieira RRR and Rieger PJ 2004, Vogt G *et al* 2004, Zrzavy J and Stys P 1997), the initial solenoid-shaped body usually undergoes cloning by internal budding, forming a free-living secondary cell colony which is a linear series of repeating segments with a common gut. Segmentation usually manifests itself both externally and internally. However, the signs of segmentation may be eliminated during later development. Whereas all segments ancestrally were similar in structure and function, they mostly differentiate in modern species. Similar segments are usually organized in specialized regions, the tagmata. Primitively, each segment bears a pair of appendages which are thought to be homologues of the lophophore. There is however a tendency to lose appendages from some segments. In addition to a flexible cuticle, an appendage is covered by a linear series of hard circular articles. Specialized muscles within the wall of the appendage may move the articles separately. Appendages may be frequently branched. There is a variety of specialized appendages adapted for reception, feeding, food manipulation, respiration, locomotion, and copulation. Just the ability to modify endlessly the basic appendage form is a key to the overwhelming success of Arthropoda due to the number of individual cell progression species. Each segment has a pair of small coelomic bladders associated with a pair of metanephridial canals, but most of coeloms soon obliterate or coalesce with the spacious innermost compartment of the wall which is unlucky called a haemocoel, since it is filled by blood and contains a plexus of blood canals. Only few metanephridial canals persist in marine species. In terrestrial species, the excretion occurs through tubular diverticula of the gut, the Malpighian tubules. Generally, since the cuticle hardens and must be molted to permit growth, the juvenile secondary cell colony passes through a series of intermediate stages, instars, until reaching the adult size and the ability to initiate meiosis. Gametes are produced in the wall of the few remaining coeloms and shed through their modified metanephridial canals. Fertilization may occur both externally and internally. There is a large variety of developmental patterns.

For example, in crustacean Arthropoda such as Cirripedia (Harvey R *et al* 2003, Watanabe H *et al* 2004), the hatching stage is a free-swimming nauplius which is actually a secondary cell colony. The only signs of segmentation are three pairs of appendages which are used in swimming and feeding. Subsequent molts transform the nauplius into a cypris with a bivalved mantle, the carapace, and more segments with or without appendages. The cypris swims for a week or two in the plankton and then settles with a preoral region to the substratum. It moves over the substratum using first appendages and, when it finds a suitable side, secretes an adhesive to attach itself permanently and become a sessile colony. The preoral region may form a flexible muscular stalk. The setose appendages become oriented upwards and are used to filter particulate food or capture prey. The carapace encloses the mantle cavity and the body. Within the carapace, the calcareous valves grow with the body but do not molt, whereas the rest of the exoskeleton does.

In other Arthropoda, the development may deviate greatly from ancestral pattern and contain instars differing from each other dramatically.

In Onychophora (Bartolomaeus T and Ruhberg H 1999, Mayer G *et al* 2004, Nielsen C 2001), the archenteron of the gastrula becomes compressed, but a new wide opening, called mouth-anus, soon opens in the same area. At the posterior region of the anus, a pair of compact cell bands emerges in the space between the integumental and gastral walls, grow forwards along the sides of mouth-anus, and form a row of coelomic bladders on each side. The lateral lips of mouth-anus fuse creating a solenoid-shaped body. Each coelomic bladder divides into a dorsal and ventral part. Each ventral bladder differentiates into the metanephridial canal with a thick-walled funnel and a thin-walled sacculus. Most dorsal bladders collapse and their walls become incorporated into the innermost compartments of the integumental and gastral walls. Remaining dorsal bladders fuse and become a place of gamete production. Gametes are shed through modified metanephridial canals. The body is clearly a free-living secondary cell colony. There are numerous indices that Onychophora must be seen as a specialized, terrestrial offshoot from the early aquatic Panarthropoda.

In Tardigrada (Hohberg K and Greven H 2005, Nelson DR 2002, Nielsen C 2001, Suzuki AC 2003), the development of the primary body plan is poorly studied. The formation of a solenoid-shaped body with four pairs of coelomic bladders in space between integumental and gastral walls has been reported. But, the origin of the coelomic walls is uncertain and their fate has not been documented. The segmented body is rather a free-living secondary cell colony. Since Tardigrada retain such ancestral features as the constancy of cell number in some regions and the ability to go into cryptobiosis, they must be seen as a very early offshoot of Panarthropoda.

In Chaetognatha (Nielsen C 2001), the blastula develops the archenteron with two primordial cells situated at the bottom. They soon detach from the wall, move into the archenteron, and divide once. The antero-lateral parts of the archenteron wall form a pair of folds which grow towards the archenteron opening carrying primordial cells at the tips. The anterior part of the archenteron thus becomes divided into one median and two lateral sacs. As the archenteron opening closes, sacs become bladders. But a new opening breaks through from an anterior invagination to the median sac. The anterior parts of the lateral bladders become pinched off. The body elongates and curves, and all cavities and lumina disappear. The gastral cavity becomes flat and its wall is bordered by the lateral masses, which meet along the midline at the posterior end of the body. The newly hatched initial body is completely compact, but the gastral cavity and two pairs of coeloms soon become re-established. Whereas the anterior coelomic bladders fuse together, the posterior bladders form a median mesenterium and become quite thin-walled laterally. Finally, each posterior bladder develops a transverse fold which divides lateral part of the coelom into an anterior and a posterior cavity, each with one of the primordial cells. The anus breaks through at the level of transverse folds and the body becomes a modified solenoid-in-solenoid. The innermost compartment of the wall consists of muscles. The outermost compartment of the integumental wall is mostly a multilayered epithelium which consists of an outer layer of polygonal cells covering two or more layers of interdigitating cells. The epithelium secretes cuticle, teeth, and spines. It rests on a basement membrane which extensions form fins. The mouth opens into a pharynx, which leads to a tubular intestine and further to a shot rectum. In some species, anterior part of the intestine has a pair of diverticula. The outermost compartment of the coelomic wall is a myoepithelium. Each primordial cell enters the

space between the integumental and coelomic walls and gives rise to an elongate mass within which the gametogenesis occurs at the maturity: eggs in the anterior masses, sperm in posterior masses, respectively. The eggs are stored in paired canals which open at the level of the anus and function as seminal receptacle. Sperm are shed into the coelom where they mature.

In Echinodermata (Byrne M *et al* 2003, Chen BY and Chen CP 1992, Chia FS *et al* 1993, Emlet RB 1995, Gosselin P and Jangoux M 1998, Hart MW 2002, Henry JJ *et al* 1991, Komatsu M *et al* 2000, Lacalli TC 2000, Lacalli TC and West JE 2000, McEdward LR and Janies DA 1997, Nakano H *et al* 2002, 2003, 2004, Nielsen C 1998, 2001, Selvakumaraswamy P and Byrne M 2000, Sumida PYG *et al* 2001, Tominaga H *et al* 2004), the blastula develops an expanded archenteron. Three pairs of coelomic bladders are pinched off from the gastral wall into the space between the integumental and gastral walls. The secondary invagination of the integumental wall fuses with the archenteron to form the gut. The early free-swimming stage, a dipleurula, later develops in any direction of specialization depending on species. The late free-swimming stage swims, but soon or later settles to bottom, and undergoes remarkable transformation, converting it into the juvenile stage. The transformation is characterized by changing of one coelomic compartment into an unique system consisting of a perioesophageal ring and five radial canals, establishing pentameric symmetry. The pentamery which in itself is secondary can be recognized in all juvenile and adult stages of Echinodermata, but the free-swimming stage is always bilateral symmetric. Among Echinodermata, Crinoidea (sea lilies and feather stars) retain the most ancestral appearance of the juvenile and adult stages: the late free-swimming stage transforms into a sessile stage that possess a stalk in sea lilies, the oral surface with a mouth at center is oriented upward, the branched arms encircle the mouth, the gut is U-shaped so that the anus is also oral but displaced to periphery. The free-swimming stages of some few species of Asteroidea (sea stars) (Bosch I *et al* 1989, Knott KE *et al* 2003, Vickery MS *et al* 2002) and Ophiuroidea (brittle stars) (Balser EJ 1998) are known to be able to clone themselves by budding, usually from the posterior part of the body, in some cases producing feeding stages and in other cases producing pre-feeding stages that then complete early development and form feeding stages. Recently, the spontaneous cloning of free-swimming stages has been detected in Holothuroidea (sea cucumbers) and Echinoidea (sea urchins and sand dollars) too (Eaves AA and Palmer AR 2003). The cloning of free-swimming stages may be therefore an ancient ability of Echinodermata. Adult stages of Echinodermata are known to possess considerable regenerative capacities as well as the ability to clone themselves by fission or budding (Thorndyke MC *et al* 2001, Wilkie IC 2001).

In Pterobranchia (Lester SM 1988, Mayer G and Bartolomaeus T 2003, Nielsen C 2001), the elongated free-swimming stage of the initial body has two pairs of flattened bladders laterally to the gut. The lumina of these bladders are referred to as the mesocoel and metacoel. After a short period of free-swimming, the initial body starts to test the substratum creeping on the ventral side. Then, it settles with the ventral depression and secretes a thin surrounding cuticle. All organs disappear and the transformation involves the development of the sessile stage rather from a compact mass of cells. At the upper side, a collar consisting of one to nine pairs of the feather-shaped tentacles is developed. In the interior, a compact mass of cells arrange into a

bladder which becomes a globular stomach and a narrow rectum. An invagination from the ventral integumental wall develops between tentacles and fuses with stomach. The new gut is U-shaped, the anus is situated a short distance behind the ring of tentacles. After a few days, the cuticle breaks open and the sessile stage starts feeding and growth. The lower side stretches into a narrow stalk. The upper side, the proboscis, becomes a flat shield with a narrow neck used in creeping and secreting the tube. In the proboscis, there is an impaired protocoel which opens to the exterior through a pair of dorsal canals. A pair of collar mesocoels surrounding the pharynx send extensions into the tentacles. The mesocoels communicate with the exterior through a pair of dorsal canals which open postero-laterally. The major part of the gut is suspended in mesenteria formed by the median walls of the paired metacoelic bladders. The metacoels extend into the stalk region where the septum between them can be lacking. Thus, three main regions of the wall, the integumental wall, gastral wall, and coelomic wall, may be clearly distinguished. The innermost compartment of the wall contains muscle layers and a plexus of blood canals and lacunae. One blood canal near the protocoel has specialized cells, podocytes, and is believed to be a site for filtration of primary urine. The outermost compartment of the wall is a monolayered myoepithelium. A dorsal extension of the pharynx, a stomochord, runs anteriorly between the pharynx and protocoel. The stomochord consists of vacuolated cells and is either compact or has a lumen. The pharynx has a pair of gill slits. The tube material contains keratin and collagen. The secondary cell colony is sometimes quite extensive aggregations of tubes housing solitary sessile stages with lively cloning themselves by budding. However, the bodies are not completely sessile. They can move around in the tubes and may even leave the aggregation and start to build a new one if conditions become too hostile. Gametes develop within the metacoelic wall. They are shed directly into the exterior through short canals. Fertilized eggs are usually deposited in the tubes where the early development takes place.

In Enteropneusta (Cameron CB 2002a, 2002b, Nezlin LP and Yushin VV 2004, Nielsen C 1998, 2001, Ruppert EE *et al* 1999, Tagawa K *et al* 2001, Urata M and Yamaguchi M 2004), the early free-swimming stage, a tornaria, has unpaired protocoelic bladder and paired mesocoelic and metacoelic bladders which origin varies between species. The tornaria usually swims for several months, increasing in size, but whether it can clone itself has not been reported. The innermost compartment of the wall becomes spacious and is filled by a gelatinous matrix. In full-grown tornaria, the wall of the buccal cavity forms a narrow dorsal invagination, a stomochord. The pharynx develops two or three pairs of gill pockets. At transformation, the pharynx extremely stretches anterior-posteriorly so that the hindgut becomes pulled backwards. The gill pockets become situated in the anterior part of the metacoelic region of the body where the gill slits break through. Additional gill slits develop in a series behind the first few. The newly formed gill slits are oval, but soon become U-shaped due to the development of a dorsal outgrowth, the tongue bar. The number of gill slits increases with growth to near 200 in some species. Each slit opens laterally into an atrium which in turn opens to the exterior via the pore so that two rows of pores are seen on the dorsal integumental wall. The metacoelic wall finally grows around the atria and forms the musculature. The strengthened basement membrane develops between the cell layers. The oesophageal wall forms folds restricting the lumen. Posterior to the oesophagus, the gut forms numerous paired diverticula within which the phagocytosis and intracellular digestion

occurs. The anus is terminal. The protocoelic wall develops a thick layers of muscles so that the most anterior part of the body becomes an almost spherical to elongate conical proboscis. There is a small canal connecting the protocoel with the exterior. One of the blood canals within the protocoelic wall contains podocytes. The proboscis is supported by the strengthened basement membrane of the dorsal buccal wall and stomochord. A pair of canals connects paired mesocoel with the exterior, opening in invaginations of the integumental wall which develop in association with the atria of the first gills. Dorsal to buccal cavity, the integumental wall develops an unpaired bladder, a collar cord, by regular infolding in some species or through delamination in others. The lumen of the collar cord usually obliterates partly or completely, and persists in a few species only. Lateral to each row of atria, a row of small bladders develops in space between the integumental and metacoelic walls, forming rounded ridges or flat wings. At maturity, these bladders swell due to the gamete production and bulge into the metacoel. Gametes are shed through tiny canals in the integumental wall. Fertilization usually occurs externally.

In Tunicata (Urochordata) (Chadwick-Furman NE and Weissman IL 2003, Jeffery WR and Swalla BJ 1992, Lacalli TC 1999, Manni L *et al* 2004, McHenry MJ and Patek SN 2004, Nielsen C 2001, Satoh N 1994, Tarjuelo I and Turon X 2004, Young CM and Vazquez E 1995), the gastrula has an elongated archenteron. A longitudinal strip of the gastral wall then becomes internalized. Some cells of this strip interdigitate to form a median row of disk-shaped cells, a urochord, which becomes surrounded by a basement membrane. Near the urochord, a strip of the integumental wall folds forming an elongated neural cavity which expands encompassing the opening of the archenteron. Then, the longitudinal lips of the neural cavity gradually fuse together so that a neuro-gastral lumen becomes internalized. The body begins to curve, the neural lumen separates from the gastral one and elongates. The body now consists of a globular trunk and a slim tail which becomes very pronounced and encircles the trunk. The rather voluminous gut may have a lumen, but has neither mouth nor anus. The anterior part of the neural tube becomes divided longitudinally with the left part separated from the main neural tube. Three frontal adhesive papillae are the attachment organs used in settling. They contain sensory and secretory cells. Just behind the adhesive papillae, a shallow dorsal invagination develops into an oral siphon. In the pharynx, a ventral longitudinal groove develops into an endostyle. Pair of integumental invaginations fuses dorsally forming an atrium with a median anal siphon. Between the atrium and pharynx, two or three gill openings break through on each side. The tail contains the posterior part of the main neural tube, the urochord, and two lateral bands of muscle cells which are arranged in 2 or 4 rows. The posterior part of the neural tube becomes a spinal cord consisting of four longitudinal rows of cells innervating muscle cells. The urochord becomes a stack of coin-shaped cells and is surrounded by a strengthened basement membrane. A matrix lenses secreted between urochordal cells fuse into a central rod. The urochordal cells become more and more flat and arrange into the monolayered bladder with a rod in the lumen. The only trace of the original gut is a row of cells along the ventral side of the urochord. The tail wall secretes a thin tunic with a cellulose-like tunicin. The tadpole-like body hatches, swims for a short period, then settles and transforms into a barrel-shaped sessile stage of the initial body. At settling, the body attaches by adhesive papillae, the cuticle is shed, and the tail becomes retracted. The cellular material of the tail and of the main neural tube becomes resorbed. The separate

left part of the neural tube persists and becomes a cerebral ganglion. The gut rotates so that the oral siphon finally points away from the substratum. In the innermost compartment of the wall, primordial cells secrete a semi-fluid matrix and the body swells. The pharynx expands into a spacious branchial basket with a high number of gill slits. The water is sacked in through the mouth which forms an incurrent siphon. The food particles are caught by a fine mucous filter net secreted continuously by the cells of the endostyle and transported to the oesophagus. The filtered water passes through gill slits into the both lateral atria and out through middorsal excurrent siphon. A narrow oesophagus leads into a stomach with various digestive diverticula and glands. An intestine opens in the left atrium. Extensions from the endostyle can form two epicardial bladders with more or less expanded lumina which are interpreted as a mesocoel. There is a plexus of blood canals and lacunae surrounded by basement membrane without cellular covering. Only around a large lacuna situated ventral to the posterior part of the pharynx, cells arrange into a pericardial chamber which develops into a heart with circular musculature. The heartbeat and the direction of blood flow reverse periodically. Blood canals traverse the pharyngeal wall between the gill slits. In blood, primordial cells, usually called haemoblasts, give rise to all blood cells such as lymphocytes, leukocytes, vacuolated cells, pigment cells, and nephrocytes. Nephrocytes accumulate waste products and transport them to the special regions of the tunic. The thick tunic is secreted by integumental wall which sends extensions with blood canals in it. The budding can take place not only in the sessile stage but also precociously in the free-swimming stage. The buds develop through a large number of different types. The budding usually gives rise to the growing secondary cell colony. Also special dormant stages contribute to distribution of the individual cell progression in space. In secondary cell colony, bodies of three consecutive generations are connected to each other by a stalk and have a common plexus of blood canals. Circulating haemoblasts can undergo meiosis and the developing eggs move through plexus of blood canals from older to younger bodies as they grow and mature. Some circulating haemoblasts can concentrate in the interior of any bodies. They usually form one or more compact cell masses in space between the integumental and atrial walls on either side. When the cell mass receives an egg derived from the preceding generation, part of this cell mass differentiates into an egg envelop, forming an egg follicle and a follicle stalk, whereas the remainder differentiates to produce sperm. When the cell mass receives no egg, it differentiates as a whole to produce sperm. Gametes are usually shed from the atrial siphons. The fertilization and the rapid development usually take place in seawater, but sometimes also in special brood chambers situated in the atrium.

In Cephalochordata (Gemballa S *et al* 2003, Holland LZ 2002, Holland PWH 2000, Nielsen C 2001), the gastrula elongates during the archenteron formation. The archenteron opening narrows, the dorsal side of the gastrula becomes flattened, the dorso-median gastral wall thickens, and the overlaying integumental wall forms the so called neural plate which becomes overgrown by a pair of lateral folds. Posteriorly these folds continue around the archenteron opening. The folds soon fuse leaving an anterior opening so that the neuro-gastral canal is formed. However, a neural cord with a narrow cavity, a neurocoel, soon separates from the archenteron. One medio-dorsal longitudinal plate of the archenteron wall folds up forming the notochord, and two lateral longitudinal plates form grooves within which the segmentation begins. Each groove breaks up into a row of bladders which are the first signs of the secondary body plan.

The bladders differentiate first at the anterior end, and new bladders become added anterior-posteriorly. The developing anterior bladders have a lumen which arises as a small diverticulum in open connection with the archenteron, while the following bladders are more compact. By the time two pair of bladders have formed, the body hatches and swims by movement of cilia, continuing the formation and differentiation of bladders. At the stage of about 7-8 pairs, the left anterior diverticulum remains small but the right becomes larger so that the bladders at the right side become situated a little more posteriorly than those of the left side and the bladders of the two sides alternate. Each bladder divides into a dorsal and ventral bladder. Whereas dorsal bladders, a somites, retain separate lumina, the ventral bladders soon fuse to a pair of longitudinal bladders which in turn fuse together to one coelomic bladder surrounding the gut except mid-dorsally. The median part of each somite becomes a thick muscular wall which extends dorsally around the neural bladder and ventrally around the coelomic bladder, giving rise to the myomere of that body segment. Another part of the somite remains a thin wall which lateral portion attaches to the integumental wall, forming with the muscular wall a cavity called a myocoel, and medial portion develops extension with a sclerocoel, separating the muscular wall from the notochord. At the stage of about 17 somites, an invagination forms on the left side of the anterior integumental wall and fuses with the archenteron wall. Just behind the newly formed mouth, the pre-oral pit, a pit of Hatschek, is formed. At the same time, the first gill slit breaks through on the right side near the ventral midline well behind the mouth. Additional gill slits develop in a series behind the first fill slit. This series slowly moves to the left side, while a new series of gill slits develops on the right side. The gill slits soon become U-shaped by the development of tongue bars. Each vertical slit becomes divided into a row of gill pores by the development of transverse synapticles. The system becomes supported by a skeleton formed by a thickened basement membrane. The gill slits divide the coelom into a number of narrow spaces. Much later, a pair of longitudinal dorso-lateral integumental folds grow outward above the gill slits, flex downward covering the branchial basket, and finally fuse at the ventral midline leaving only a posterior atrial opening, some distance in front of the anus, creating thus the atrium. These folds contain coelomic compartments which are originally parts of the coelom. The cilia of the gill pores create the water current which enter the spacious pharynx through the large mouth and buccal cavity, passes through the gill pores to the atrium and leaves through the atrial opening. The mouth is surrounded by a ring of slender tentacle-like cirri. The buccal cavity has a series of ciliated grooves making up the so called wheel organ. The buccal cavity is separated from the pharynx by a transverse muscular velum with an aperture of adjustable diameter in the center. Along the pharynx, there is a ciliated ventral endostyle, producing mucus with iodine, and a dorsal groove. Captured food particles are transported posteriorly to the oesophagus and then to the intestine with an anterior digestive diverticulum and a short rectum. A row of nephridial canals is found on each side in the branchial region. Each canal opens in the atrium at the base of the tongue bar. The nephridium is a cell of unique art, the cyrtopodocyte, consisting of one part forming a usual podocytic lining of a blood canal and another part which resembles a protonephridial solenocyte. At the dorsal region of the body, there is a longitudinal series of small bladders know as a fin boxes. The septa between adjacent boxes represent the fin rays. The neural cord is surrounded by a cells arranged in sheath. The notochord is composed of large, vacuolated, disk-like myoepitheliocytes arranged in a stiff longitudinal column which is surrounded by a thick sheath of cells. In space

between the integumental and atrial walls, there are two mid-lateral rows of small bladders. At maturity, these bladders swell due to the gamete production and bulge into the atrium. There is a male-female dimorphism. Gametes are shed into the atrium through ruptures. Fertilization usually occurs externally.

In Vertebrata (Gilbert SF 2000, Shimeld SM and Holland PWH 2000), the ontogenesis is usually complicated through large amounts of yolk or by species-specific extraembryonic structures so that the stages of the primary and secondary body plan formation are hard to discern. The ontogenesis resembles that of Cephalochordata, but has many important differences. The neurocoel of Cephalochordata is not closed and is actually a dorsal atrium with an anterior opening. On the contrary, the neurocoel of Vertebrata is closed and just the anterior portion of the neural bladder becomes the brain. The spacious ventral atrium of Cephalochordata is completely developed and connects with pharyngeal lumen through gill slits. On the contrary, the ventral atrium of Vertebrata is vestigial and presented merely by a pair of narrow posterior ducts. The lateral portions of the integumental wall do not contribute to the formation of the ventral atrium as in Cephalochordata but develop into the so called neural crest and placodes. Just the neural crest and placodes contribute to the formation of many structures considered to be novelties of Vertebrata, including the branchial skeleton, cranium, and numerous cranial ganglia.

When the secondary body plan of Vertebrata is established, the wall generally involves:

poorly segmented integumental wall,
poorly segmented gastral wall arranged as a common gut,
segmented chordal wall arranged as a chain of compact chordal bladders,
poorly segmented atrial wall arranged as a pair of atrial ducts,
poorly segmented neural wall arranged as an elongated neural bladder,
poorly segmented coelomic wall arranged as a coelomic bladder,
poorly segmented meningeal wall arranged as a meningeal bladder,
segmented somitic wall arranged as paired chains of compact somitic bladders,
segmented germinal wall arranged as paired chains of compact germinal bladders.

Generally, Vertebrata display the most sophisticated spatio-temporal organization of the wall. In some Vertebrata, the wall integrity is maintained by complex interactions between asymmetric cell progressions of different types.

Conclusions

In contrast to multicellular organism, the individual cell progression is an universal life pattern and is therefore better suited to be used as a principal supercellular object of research and systematization in biology.

The present-day biosphere is merely a tiny slice from the general cell progression, a visible top of iceberg in ocean of time. However, although the number of individual cell progressions in this tiny slice represents only a small fraction of the whole, it is enormous. Much work is needed to describe and systematize this diversity completely.

The evolution of individual cell progressions intrinsically involves the evolution of cells which phylogenetic diversity in biosphere can be summarized in a compact system of cell types.

The spatio-temporal organization of individual cell progressions is much more variable than that of cells. Therefore, it is not surprisingly that the diversity of individual cell progression types is enormous. This diversity depends greatly on the phylogenetic cell type. Above, the diversity of individual cell progressions was reviewed with special focus on formation of cell associations. Therefore, more attention was paid to phylogenetic cell types by which the formation of cell association takes place during the life history of individual cell progressions.

Animal individual cells progressions were reviewed in more details. To describe the formation of animal cell associations, a notion of a closed and orientable surface was used. In contrast to abstract mathematical surface, the real biological surface is made up not by dimensionless points but by three-dimensional matrix with embedded cells. So, it is actually a closed and orientable wall, since there is a distance between its two sides. The thickness of the wall may have regional differences in magnitude. Additionally, the two sides of the wall can be differently designated according to their orientation to interior or exterior of the cell association. To avoid confusion, one must be aware that the wall is not a boundary of the cell association but just its body.

The complexity of animal cell association enhances gradually at different phylogenetic and ontogenetic stages. Vertebrata display the most sophisticated spatio-temporal organization of the wall.

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Diversity of asymmetric cell progressions in Mammalia

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It is reasonable to distinguish between phylogenetic and ontogenetic cell diversity. Whereas the phylogenetic cell diversity is a result of the genome multiplication and diversification during life history of the general cell progression, the ontogenetic cell diversity is a result of differential genome expression during life history of some individual cell progressions. Here, I review the ontogenetic cell diversity in mammalian individual cell progression in relation to the diversity of asymmetric cell (sub)progressions with special focus on pattern of their interactions within mammalian wall. To describe this pattern, Mammalian Wall Formula is proposed. Regional differences in composition of mammalian wall from the perspective of Mammalian Wall Formula are reviewed in more details.

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Complete hierarchy of universal life patterns

Nikita Tirjatkin

Life is extraordinarily complex. Multilevelness is the key characteristic of its complexity: living world is actually a hierarchically organized system of systems. An important attribute of the hierarchy is the gradual integration of systems from the bottom level to the apex. To determine particular level in biological hierarchy, it is necessary to know a corresponding universal life pattern which variability underlies the diversity of systems at this level. However, just in this respect, our knowledge is woefully incomplete. Here, I show that the investigation of living world from the information processing perspective allows recognizing the complete hierarchy of universal life patterns.

Complexity of the living world continues to be in focus of debates (Cohen IR and Harel D 2007, Coveney PV and Fowler PW 2005, Csete ME and Doyle JC 2002, Emmeche C 1997, Gilbert SF and Sarkar S 2000, Grizzi F and Chiriva-Internati M 2005, Mikulecky DC 1996, Van de Vijver G *et al* 2003, Weiss JN *et al* 2003) substantiating the need for the systems approach that would combine analysis with synthesis in scientific research. In current biology, the methodology of empirical and theoretical investigation is experiencing the Renaissance of the systems approach due to the recent progress in data processing (Andrianantoandro E *et al* 2006, Barrett CL *et al* 2006, Drubin DA *et al* 2007, Heinemann M and Panke S 2006, Ideker T *et al* 2001, Kitano H 2002, Mesarovic MD *et al* 2004, Westerhoff HV and Palsson BO 2004, Wolkenhauer O 2001).

Multilevelness is the key characteristic of life complexity: living world is actually a hierarchically organized system of systems (Andrianantoandro E *et al* 2006, Emmeche C 1997, Grizzi F and Chiriva-Internati M 2005, Mesarovic MD *et al* 2004, Valentine JW 2003, Van de Vijver G *et al* 2003, Zylstra U 1992). An important attribute of the hierarchy is the gradual integration of systems from the bottom level to the apex so that upper levels are said to emerge out of the lower levels. To determine particular level in biological hierarchy, it is necessary to know a corresponding universal life pattern which variability would underlie the diversity of systems at this level. However, just in this respect, our knowledge is woefully incomplete. The only universal life pattern recognized is the cell (Mazzarello P 1999). All other known life patterns are doubtlessly specific. Recently, the list of familiar subcellular and supercellular (supracellular) life patterns such as organelle, tissue, organ, organism, etc. has been significantly extended through various structural and functional units referred to as modules, motifs, etc. (Alm E and Arkin AP 2003, Alon U 2003, Csete ME and Doyle JC 2002, De Silva E and Stumpf MPH 2005, Huang S 2004, Oltvai ZN and Barabási AL 2002). However, no one of them can be accepted as universal life pattern. Therefore, the presentation of their hierarchy as “life’s complexity pyramid” (Oltvai ZN and Barabási AL 2002) is an overestimation of their significance.

Thus, the biological hierarchy composed completely of universal life patterns lacks. This big gap in biology foundation hampers progress within the “era of biology” significantly.

Meanwhile, the investigation of life from information processing perspective allows recognition in living world of many new life patterns (Tirjatkin N 2005a, 2005b, 2005c, 2007). Some of them seem to be universal. Here, I show their significance discussing some particular and general aspects of life complexity and life diversity. Aspects which are internal to biology are discussed first. Then, the discussion is extended to aspects which intrinsically connect biology with closely-related disciplines. Finally, concluding discussion closes the theme.

Intradisciplinary aspects of life complexity and life diversity

Subcellularly, the information processing involves two tightly coupled reactions: genome expression and genome replication. During genome expression, information is converted first from DNA into RNA (transcriptome) form by DNA transcription, then from RNA into polypeptide (proteome) form by RNA translation, and finally from polypeptide into metabolite (metabolome) form by catalysis. It is important to note that the genome is a limited set of genes and each gene is usually expressed separately to be fully converted into the corresponding element of the cell structure or function. For each gene, its own sequence of DNA transcription, RNA translation, and catalysis can be determined. This directed sequence of chemical reactions is the most basic universal life pattern which can be called a gene expression network, abbreviated GEN. Its variability is virtually unlimited. Additionally, in some GENs, the obligatory sequence of chemical reactions can be restricted or extended. So, in many GENs, end products are polypeptides functioning always as substrate molecules and never as catalysts. In many other GENs, end products are RNAs that never become translated into polypeptides, but function always at the level of RNA as substrate molecules. On the other hand, in many GENs, products of DNA transcription or RNA translation undergo post-transcriptional or post-translational processing respectively. The cell itself can be considered as a highly regular composition of interacting GENs which can be called GENome. Whereas gene and genome are notions that refer to how information is stored in the cell, GEN and GENome refer to how the gene and genome work. During information processing in particular GEN, it is just the job of other GENs to provide necessary elements for gene expression machinery. Collectively, GENs in GENome work to replicate the complete genome so that the life history of the single cell begins with one cell but ends with two. In particular cell, the GENome is suited to specific subset of sources of mass, impulse (momentum), and energy to produce their usable forms essential for the cell life. Thus, subcellularly, all chemical reactions are organized highly regular: first into GENs and then into GENome.

Supercellularly, the information processing involves other two important reactions: genome multiplication and genome diversification. Mechanism of genome multiplication is always the same: the genome replication by genome expression. On the contrary, mechanisms of genome diversification differ greatly ranging from the spontaneous sequence mutation to the highly regulated sequence transfer. Progressive genome replication is usually associated with progressive cell propagation producing a sequence: one cell, two cells, four cells, eight cells, and so on. This sequence can be called cell (GENome) progression. The whole cellular world is only one cell progression which arose from one single primordial cell and has 3 or 4 billions years of uninterrupted history. It can be called general cell progression. The present-day

biosphere is merely a tiny slice from it, a visible top of iceberg in ocean of time. The ancient part of this gigantic life pattern leaves very scarce traces. Although all cells of the general cell progression should be theoretically identical to each other genetically, this is not the case in the nature: genome diversification produces cell progressions each of which is specified by a particular individual genome and can be called individual cell progression. Respectively, the general cell progression can be considered as a growing composition of an increasing number of individual cell progressions. Individual cell progression is universal life pattern with virtually unlimited variability. Spatiotemporal organization of a particular individual cell progression mostly depends upon whether the cells divide symmetrically or asymmetrically, whether the asymmetric cell divisions occur occasionally or regularly, whether the asymmetric cell division is associated with symmetric or asymmetric kinetics of the cell propagation, whether the cells will be rather randomly dispersed in space to become autonomous in behaviour or remain in an association to form cell colony (primary, secondary, etc.), whether the cell association grows continuously or is a steady state system, and so on. Thus, supercellularly, chemical reactions are organized highly regular too: first into individual cell progressions and then into the general cell progression.

So, from information processing perspective, all chemical reactions in living world fall into three categories: DNA transcription, RNA translation, and catalysis. They are organized in strong hierarchy of life patterns: GENs, cells (GENomes), individual cell progressions, and the general cell progression (Table 1).

Table 1. Complete hierarchy of universal life patterns

Level	Spatiotemporal pattern
4	general cell progression
3	individual cell progression
2	GENome
1	GEN

The general cell progression occupies the apex of the hierarchy. Most likely, it is unique and merits its own name (for example, Zoe). Other three life patterns in this hierarchy are doubtlessly universal. Their innumerable variations underlie the life diversity.

Management of life diversity is of crucial importance for many purposes in biology and beyond (Mayr E and Bock WJ 2002). On the one hand, individual living things are to be differentiated from each other: they must be specified and compared. As a result, types, sorts, kinds, etc. of individual living things can be recognized. On the other hand, individual living things are to be integrated with each other: they must be classified and systematized. As a result, abstract groups, sets, collections, etc. of individual living things can be recognized. Processes of specification, comparison, classification, and systematisation are so intimately interwoven that they are hard to discern clearly.

To manage life diversity, Carl Linnaeus arranged abstract groups of individual living things (taxa) within taxonomic hierarchy where each level is indicated by taxonomic category (rank). It is important to note that the Linnaean taxonomic hierarchy is not only an abstract system of systems but also formal system of systems. It is abstract since

taxa are abstract groups by definition whereas taxonomic categories are not concrete patterns but mere abstract indicators of levels. It is formal since formal rules prescribe even how names of taxa have to be formed while the number of levels in hierarchy is arbitrary. There is great deal of convenience by arrangement of taxa within the Linnaean taxonomic hierarchy. In the past 250 years since publishing of the tenth editions of *Systema Naturae* by Linnaeus, his taxonomic hierarchy has been considerably elaborated and some new categories and an extensive variety of supercategories, subcategories, infracategories, etc. have been proposed. Table 2 shows most familiar categories prevailing in modern interpretations of the Linnaean taxonomic hierarchy.

Table 2. Linnaean taxonomic hierarchy

Level	Category
7	kingdom
6	phylum
5	class
4	order
3	family
2	genus
1	species

In his theory of descent with modification, Charles Darwin provided an explanation of the origin of species. Suggesting their common descent, this theory substantiates the possibility and necessity for conversion of the Linnaean taxonomic hierarchy into genealogy. The term “phylogeny” coined by Ernst Haeckel corresponds quite strictly to the theory of common descent: phylogeny is equivalent to the taxonomic genealogy. Phylogeny may be presented in form of a tree-like drawing (dendrogram) usually referred to as the Tree of Life. The Tree of Life is often assumed to be better suited to manage life diversity than the Linnaean taxonomic hierarchy. Therefore, there are tremendous attempts to reconstruct phylogeny as precisely as possible. Recent progress in data processing contributes significantly to this endeavour. Diverse schools compete in this field of research delivering stuff for hot debates at all epistemological levels (Hull DL 2001a, Mayr E and Bock WJ 2002). Unfortunately, results obtained are rather contradictory than compatible and the success is not yet in sight (Brummitt RK 2002, Doolittle WF and Bapteste E 2007, Simonson AB *et al* 2005). Ironically, the Linnaean taxonomic hierarchy becomes rather supplemented than replaced and continues to be in use (Brummitt RK 2002, Dayrat B 2005, Schuh RT 2003). How ever that may be, it must be noted that even if the conversion of the Linnaean taxonomic hierarchy into genealogy would succeed successfully, resulting taxonomic genealogy would remain formal abstract system of systems.

It is true that taxonomic genealogy reflects real process of common descent. But, this in no way justifies treating taxa of taxonomic genealogy as concrete groups of individual living things. Taxa are actually formal abstract groups and must be treated as such in both the taxonomic hierarchy and taxonomic genealogy. It is also true that individual living things may integrate into concrete groups, sets, collections, etc. such as population, community, society, etc., but taxa do not belong to them. Unfortunately,

abstract and concrete groups of individual living things are often mixed producing rather distorting picture of the living world.

Originally, the principal objects of research in biology were individual living things for which the concept of an organism has been introduced. When the multicellular nature of known organisms has been revealed by a microscope and numerous unicellular organisms have been discovered (Mazzarello P 1999), the organism concept became very heterogeneous while ranging from the single cell to multicellular composition. Multicellular organism in turn is very heterogeneous concept while ranging from loose cell associations to tight cell associations which differ vastly in form and display great variability in degree of organization (Tirjatkin N 2005c). As a result, an organism is treated very differently in distinct biological disciplines. For example, in developmental biology, morphology, and physiology, an organism is a multicellular composition which is viewed as a system while cells are viewed as subsystems. In microbiology, on the contrary, an organism is a cell which is viewed as a system while the multicellular composition is viewed as supersystem. In general biology, evolutionary biology, and ecology, an organism is both the cell and multicellular composition. Dealing with life complexity, systemics tends to discern the cell and organism concepts restricting the later to the multicellular composition. Dealing with life diversity, systematics adopts heterogeneous concept of organism. The role of the organism concept in the conceptual and theoretical framework of biology continues to be in focus of debates (El-Hani CN and Emmeche C 2000, Greene HW 2005, Gutmann M and Neumann-Held E 2000, Perlman RL 2000, Ruiz-Mirazo K *et al* 2000, Van Speybroeck L 2000, Wagner GP and Laubichler MD 2000).

On the one side, there is an intuition of organism as an individual in the living world. However, individuality in the living world is always relative changing from level to level in the hierarchy of life patterns. On the other side, there is an intuition of individual in the living world as an organised entity. However, degree of organization in the living world is always relative changing not only from level to level in the hierarchy of life patterns but also at each level from poorly organized to highly organized entities. There is no clear criterion to decide to what level in the hierarchy of life patterns or to what degree of organization the concept of organism can be applied. Criteria such as self-organization, self-maintenance, self-regulation, etc. belong to the most unclear ones.

Under these considerations, in systemics, an organism can not be saved not only as universal life pattern but even as specific life pattern. Subsequently, in systematics, it can not be saved as an individual living thing. According to complete hierarchy of universal life patterns (Table 1), individual living things are GENs, cells (GENomes), individual cell progressions, and the general cell progression. While the general cell progression is most likely unique, three other types of individual living things are enormously variable. Therefore, it is reasonable to have at least three taxonomic hierarchies (or genealogies): first for GENs, second for cells (GENomes), and third for individual cell progressions. It is important to note that, in addition to abstract taxonomic genealogies, such individual living things as GENs, cells (GENomes), and individual cell progressions also arrange in concrete genealogy and that this concrete genealogy is just the general cell progression. According to the nature of universal life

patterns in hierarchy (Table 1), this concrete genealogy is one single genealogy of individual cell progressions at lower resolution, one single genealogy of cells (GENomes) at middle resolution, but a multiple N_1-fold genealogy of GENs at higher resolution where N_1 is a number of genes in genome (or GENs in GENome) of the primordial cell from which the general cell progression arose. Both abstract and concrete genealogies may be presented in form of a tree-like drawing (dendrogram). Some individual cell progressions may produce cell associations in form of true trees.

Particular and general aspects of life complexity and life diversity discussed above are internal to biology. However, the living world is a part of the whole world and in turn itself involves human world as a part. Therefore it is reasonable to examine here some interdisciplinary aspects of life complexity and life diversity.

Interdisciplinary aspects of life complexity and life diversity

The living world is mere a tiny part of the entire world. An explicit knowledge of how does hierarchical organization of the living world correspond to the hierarchical organization of the entire world would be advantageous.

The entire world (Universe) is considered to be material in the sense that it comprises only one single thing: a matter. The matter is simply defined as that which exists. To exist is the general feature of the matter. The entire world is also considered to be complex in the sense that it comprises a multitude of different material objects being in specific relations to each other. To be material is a feature which makes all the material objects similar and therefore undistinguishable. On the contrary, specific relations of material objects to each other can be used to recognize differences between them. Relations are however of various degree of specificity. Some of them are of principal significance and must be shortly introduced here.

There is a specific relation between two material objects which is called a distance. If defined to each other by distances only, material objects constitute that which is referred to as a space. If any distance is chosen to be a standard quantity of space, other distances can be measured by it provided any appropriate instrument can be constructed for this task. The space is of course abstraction while ignoring all the relations of material objects to each other except distances. Nevertheless, it remains material while referring to at least one type of relations of material objects to each other. In addition to distance with its length, the space concept contains a large number of notions derived from distance notion. Whereas some of them such as a field with its area or a room with its volume remain material, others such as point, line, or surface do not. While natural space is too cumbersome to establish a spatial reference frame for scientific purposes, various artificial spaces are invented. Most familiar is the so called Euclidean space which is imagined as a homogenous and isotropic continuum of points. The homogeneity means the equivalence between all the points in space or invariability in spatial translocation. The isotropy means the equivalence between all the directions in space or invariability in spatial rotation. Thus, the Euclidean space is multidimensional and multidirectional. In Euclidean space, various spatial reference frames can be established. Most popular is the so called Cartesian reference frame consisting of three plane surfaces perpendicular to each other. In Cartesian reference frame, the

specification of the position of a particular point is reduced to the measure of the lengths of the three perpendiculars dropped from this point to those surfaces. A particular material object can be thus defined by position of all the points involved in the space amount which is occupied by this object. These points can be used to determine all the spatial characteristics such as size, shape, volume etc. One specific point can be chosen to represent position of the object in the space. In chosen spatial reference frame, each given material object can be described by unique set of spatial characteristics.

There is also another specific relation between two material objects which is called an event. In contrast to distance, event is a complex relation. However, events are recognized to build sequences of events and all sequences are recognized to build a bundle of sequences which are all oriented in the same direction. Some sequences of events can be used as the so called temporal reference frames. In this respect, most useful are sequences of cyclic events in which moments correspond to periods with their duration just in similar way as points correspond to distances with their length in spatial reference frame. Therefore, the period is usually considered as amount of what is called a time. If any period is chosen to be a standard quantity of time, other periods can be measured by it provided any appropriate instrument can be constructed for this purpose. A particular material object can be thus defined by "position" of all the moments involved in time amount which is "occupied" by this object. These moments can be then used to determine all the temporal characteristics. In temporal reference frame, each given material object can be described by unique set of temporal characteristics.

Further, events are recognized to hide a subordinate relation between two material objects which is called an interaction. In turn, interaction is also a complex relation which hides a sophisticated hierarchy of successive subordinate relations. Each of these relations becomes more and more specific and can be responsible only for limited number of events in the entire world. Consequently, a bewildering hierarchy of notions is developed to describe interactions between material objects. This hierarchy is yet not completely understood. Some notions are well defined, other on the contrary are not. Moreover, some well defined notions are often used very inaccurately. Therefore, misleading sentences are very abundant in the scientific literature. For example, while the well defined notion of energy is used sometimes too freely, such senseless statements as "The Universe is composed of two things: matter and energy" can be found even in textbooks. This statement ignores that energy is merely one of the all specific notions characterizing matter and is invented solely to describe some particular aspects of interaction between material objects. In addition to spatial and temporal reference frames, other reference frames can be established to take into consideration particular aspects of interaction between material objects. Different reference frames are often unified into single one for scientific purposes. Unification is usually based on invention of space-like abstractions. For example, Euclidean space and time are often unified into the so called Minkowski space. One of the more general types of space-like abstractions is the Hilbert space in which more general reference frames can be established. Although all these space-like abstractions are hard to imagine, they are very useful scientific tools.

Generally, material objects are said to exist and interact in space and in time. Both space and time seem to be infinite, but distances and periods accessible for scientific

investigation by modern instruments are limited. Using scientific methods, researchers try to recognize spatiotemporal patterns of interactions between material objects in accessible distances and periods. But, there is a great deal of convenience by introduction of spatial and temporal reference frames, by definition of boundaries of a given material object in space and in time, and so on. How material objects are distributed in space: discretely or continuously? How does the distribution of material objects in space change with time: discretely or continuously? These and many other questions remain a matter of hot debates. Respectively, numerous assumptions underlie the scientific investigation of the entire world and a large numbers of models are developed to describe it.

Table 3 summarizes current knowledge on hierarchical organization of the entire world (Ellis GFR 2002, Haubold H and Mathai AM 1998). This knowledge is rather implicit. The hierarchy is incomplete. There is no one spatiotemporal pattern which universality would be unquestionable. Therefore, the determination of levels of the hierarchy is restricted to labelling by numbers whereas labelling with plus or minus reflects common schema of investigating the entire world from the focal level (designated here as level 0) in two directions: up to the largest scale (numbers with plus) and down to the smallest scale (numbers with minus). The largest scale corresponds with the entire world. But, how large is this scale is not clear. It is also unclear how many levels must be there in hierarchy.

Table 3. Hierarchical organization of the entire world

Level	Spatiotemporal patterns
…	entire world
…	…
…	…
+2	group of galaxies, cluster of galaxies, supercluster of galaxies, …
+1	cluster of stars, galaxy
0	body (asteroid, comet, moon, planet, star), star system
-1	compound subatomic particle, atom, molecule
-2	…, “fundamental” particle
…	…

Actually, it is assumed that the entire world is an extremely complex network composed of huge numbers of “fundamental” interactions continuously creating an enormously complex matrix composed of bewildering numbers of different “fundamental” particles involved in these interactions. It is also assumed that “fundamental” particles fall into two categories: ordinary particles and virtual particles. Ordinary particles do not directly interact with each other but rather exchange virtual particles which are thus the mediators of “fundamental” interactions. Four types of “fundamental” interactions – gravitation, electromagnetism, weak interaction, and strong interaction – recognized at present are believed to be different aspects of a single “fundamental” interaction. There are numerous theories about this believe but no one with decisive confirmation. Further investigations can dramatically change our knowledge on “fundamental” interactions and corresponding “fundamental” particles.

Here is no place to discuss how “fundamental” particles integrate to form all the spatiotemporal patterns at higher levels of the hierarchy. For purposes of this article, it is enough to focus attention just to the focal level and examine the diversity of corresponding spatiotemporal patterns to find such tiny celestial body as the planet named Earth. Planets are abundant but not ubiquitous. Not all star systems bear planets. The Solar System only by chance involves some of them inclusive Earth which seems to be unique in owing tiny space where its lithosphere, hydrosphere, and atmosphere come together. This space referred to as ecosphere consists of non-living (abiotic) and living (biotic) components being in tight interconnections. Living component usually referred to as biosphere represents the known living world. Whether there are other planets or other celestial bodies bearing their own living worlds is unknown. It is important to note that the non-living and living components are undistinguishable from the perspective of mass, impulse, and energy processing. The difference becomes apparent only from the perspective of information processing: life originates by coupling of genome replication to genome expression and develops by continuous genome multiplication and genome diversification.

Thus, the known living world is not more than the Earth-specific spatiotemporal pattern restricted to the biosphere. Therefore, the universality of recognized life patterns (Table 1) is relative.

Unfortunately, the terms “ecosphere” and “biosphere” have had somewhat competing histories (Huggett RJ 1999) so that they continue to be used interchangeably. It would be advantageous to cease this practice to avoid confusions. Respectively, ecological hierarchies describing complexity of the ecosphere have to be clearly separated from biological hierarchies describing complexity of the biosphere.

Strongly speaking, there are two types of ecological systems. If attention is attracted to the abiotic component, the ecosystem is treated as a geosystem-like system (geoecosystem) and the biotic component is viewed as contributing to the mass, impulse, and energy processing within the lithosphere, hydrosphere, and atmosphere. On the contrary, if attention is attracted to the biotic component, the ecosystem is treated as a biosystem-like system (bioecosystem) and the abiotic component is viewed as an environment for biotic component. Respectively, it is reasonable to distinguish between two types of ecological hierarchies: geoecological hierarchy and bioecological hierarchy. Describing hierarchical relations between geoecosystems, geoecological hierarchy is a further quantification of the ecosphere into a series of Earth-specific spatiotemporal patterns involving corresponding fragments of the biosphere. On the contrary, describing hierarchical relations between bioecosystems, bioecological hierarchy involves life patterns extended through corresponding fragments of the ecosphere. Unfortunately, just mixed ecological hierarchies are currently in use. They rather hinder than help to understand complexity of the ecosphere.

Quantification of the ecosphere into a series of Earth-specific spatiotemporal patterns is not easy. The ecosphere seems to bear an extremely heterogeneous collection of patterns with an enormous variety of interconnections. Really good idea on how to fit all these patterns into one single geoecological hierarchy lacks. Actually, spatial

thinking prevails (Gustafson EJ 1998, Olson DM *et al* 2001, Platt T and Sathyendranath S 1999, Urban DL *et al* 1987, Wu J and David JL 2002) and the ecosphere is simply quantified by gradual fragmentation of its area from global to local (Table 4). However, even such oversimplified version of the geoecological hierarchy is far from to be elaborated completely: there is even no agreement on how to name spatial categories determining its levels.

Table 4. Geoecological hierarchy

Level	Area (km^2)	Spatial category
8		ecosphere
7	$>10^5$	ecozone
6	10^4-10^5	ecoprovince
5	10^3-10^4	ecosection
4	10^2-10^3	ecodistrict
3	10^1-10^2	-
2	10^0-10^1	-
1	$<10^0$	ecosite

Extension of life patterns through corresponding fragments of the ecosphere is not easy too. The ecosphere seems to bear an extremely heterogeneous collection of interactions between individual living things and their environments. Furthermore, environment of an individual living thing may contain not only abiotic but also biotic components. Therefore, bioecological hierarchy always contains somewhat ambiguous patterns. Under such circumstances, dealing for the most part with specific life patterns does not contribute to clarity. On the contrary, an explicit recognition of the complete hierarchy of universal life patterns (Table 1) may eliminate some ambiguities from bioecological hierarchy (Table 5).

Table 5. Bioecological hierarchy

Level	Spatiotemporal pattern
4	general cell progression + its environment = ecosphere
3	individual cell progression + its environment
2	GENome + its environment
1	GEN + its environment

Thus, there is a great deal of convenience both by the quantification of the ecosphere into a series of Earth-specific spatiotemporal patterns and by the extending of life patterns through corresponding fragments of the ecosphere.

After origin of the Life on the Earth, history of the Earth is inseparable from the history of the living world: it is obvious that the geosystems and biosystems coevolve and the geoecosystems and bioecosystems emerge at the interface of this coevolution. To explain origin of species, Charles Darwin proposed an elaborated theory which he interchangeably called either the theory of descent with modification or the theory of Natural Selection. Whereas the first name referred to the correct explanandum, the second name referred to the correct explanans. Thus, from the beginning, this theory

was more than a theory of evolution of living things. Indeed, in the past 150 years since publishing of the first editions of *On the 0rigin of Species* by Darwin, his theory has been considerably extended and tends to become a theory of coevolution of geosystems and biosystems and of emergence of geoecosystems and bioecosystems at the interface of this coevolution. Respectively, the most important aspect of ecological hierarchies is that, if combined with taxonomic hierarchies embracing diversity of corresponding spatiotemporal patterns, they would reflect evolutionary relations between history of the Earth and history of the living world.

On the one side, the origin of the Life on the Earth so fundamentally altered the mass, impulse, and energy processing within the lithosphere, hydrosphere, and atmosphere that corresponding geosystems acquired a variety of additional structural and functional features that could only exist due to biotic influences (Dietrich LEP *et al* 2006, Dietrich W and Perron JT 2006, Kasting JF and Siefert JL 2002). For example, the presence of life converts some rock-forming processes into soil-forming processes so that the term "pedosphere" is usually applied to affected part of the lithosphere. Large biogenic fluxes of gases maintain atmosphere of the Erath in an extreme state of disequilibrium in which highly reactive gases such as methane and oxygen coexist many order of magnitude from photochemical steady state. Respectively, whilst geosystems and biosystems coevolved, geoecosystems emerged at the interface of this coevolution as the result of processes caused by biosystems. Taking into account profound contribution of geoecosystems to the evolution of geosystems (Lieberman BS 2005, Naylor LA 2005), it would be advantageous to restore four-dimensionality of Earth-specific patterns in geoecological hierarchy (Table 4).

On the other side, limited sources of mass, impulse, and energy within the lithosphere, hydrosphere, and atmosphere of the Earth make the living world so sensitive to changes in environment that the information processing in corresponding biosystems acquired a variety of additional structural and functional features that only exist owing to environmental influences (Kampfner RR 1998, Marijuán PC 2002). These range from simple signalling pathways to complex communication networks and from primitive responses to sophisticated conscious behaviours. Respectively, whilst biosystems and geosystems coevolve, bioecosystems emerge at the interface of this coevolution as the result of processes caused by geosystems. Taking into account profound contribution of bioecosystems to the evolution of biosystems (Bock WJ 2003, Johnson MTJ and Stinchcombe JR 2007, Ricklefs RE 2007), it would be advantageous to preserve four-dimensionality of universal life patterns by converting biological hierarchy (Table 1) into bioecological hierarchy (Table 5).

Similar to the living world (biosphere), the ecosphere is not more than Earth-specific spatiotemporal pattern. Therefore, neither the levels of biological hierarchy nor the levels of ecological hierarchies could be used to multiply the number of levels above and below of focal level in Table 3. Unfortunately, such misuse comes about very often producing rather distorted picture of the entire world.

The human world is mere a tiny part of the living world. Strongly speaking, it is specific life pattern with the highest degree of organization. However, there is strong intuition of the human world as being more than the specific life pattern.

Actually, it is assumed that the human world is an extremely complex network composed of huge numbers of “fundamental” interactions continuously creating an enormously complex matrix composed of large numbers of different individuals involved in these interactions. However, there is no agreement on what “fundamental” interactions would underlie hierarchical organization of the human world. There is also no agreement on how the hierarchical organization of the human world would look. Instead, there are large numbers of hierarchies describing different specific fragments of the human world. The most famous is the control hierarchy from which the notion of the hierarchy originates.

Maybe, investigation of the living world neither from mass, impulse, and energy processing perspective nor from information processing perspective is enough for understanding of its complexity. There is however no idea from what perspective this can be done.

Human world is the most prominent part of the biosphere usually designated as anthroposphere. In human world, communication networks are the most complex and conscious behaviours are the most sophisticated. As human activities become more evolved, corresponding part of the ecosphere (sometimes referred to as technosphere) becomes more prominent too. The technosphere is that part of the ecosphere which is not only used but also modified or even made by humans. An intangible but the most influential part of the technosphere is the noosphere – the sphere of collective human thought increasingly dominated by science.

All scientific activities fall into two categories: research and development. Research activities aim to obtain that knowledge on all the material objects in the entire world which makes able to discern between the useless objects and useful ones and between the harmful objects and harmless ones. Development activities aim to obtain that knowledge on all the material objects in the entire world which makes able to convert the useless objects into useful ones and the harmful objects into harmless ones. On the one side, science evolves by continuous exchange of facts and ideas between research and development. On the other side, it also evolves by interaction with other parts of the noosphere and technosphere. This evolution is accompanied by simultaneous differentiation of science in growing number of disciplines and their integration.

Dealing with the most general scientific inquiries, philosophy aims to clear relations between the subjective and objective, between the potential and actual, and between the phenomenal and essential. It also aims to clear how the essential and phenomenal relate to the actual and potential and how the actual and potential relate to the objective and subjective. However, philosophers seem to be doomed to provide only subjective criteria in order to determine the “correct” epistemology and the “correct” ontology. Therefore, philosophical discussions easily become vicious circles affecting the practice of philosophy in particular and of science in general. Indeed, although dealing with more specific scientific inquiries, other scientific disciplines are far from to be in better position than philosophy. They too are doomed to provide only subjective knowledge even if they often claim to answer “objectively” on many questions. The rightness of that “objective” answers may be every time questioned. At all, how can science be ever

right when philosophy is always wrong? Philosophers are aware on the failure of philosophy in the past (Searle JR 1999) but take it of course philosophically to look optimistically on the future of philosophy in particular and of science in general. Ironically, recent developments in the technosphere and ecosphere suggest rather pessimistic scenarios for the future of the anthroposphere in particular and of biosphere in general. It is not unlikely that neither science nor noosphere have time to become competent enough to be able to preserve the Life on the Earth from destruction by human activities.

To finish discussion on interdisciplinary aspects of life complexity and life diversity, it is reasonable to clearly discern two types of relation between the entire world, living world, and human world.

It is obvious that the human world is involved in the living world which in turn is involved in the entire world. This extensional relation (Table 6) is hierarchical.

Table 6. Extensional relation between the entire world, living world, and human world

entire world			
non-living world		living world	
non-artificial world	artificial world	non-human world	human world

It is also obvious that the human world evolved from the living world which in turn evolved from the entire world. This intensional relation recognized by the number of authors (Table 7) is evolutionary (developmental, progressive) but not hierarchical. Unfortunately, since the term “level” is used to describe this relation too, it is usually interpreted as hierarchy with the human world at the apex. Such erroneous interpretation not only produces an extremely distorting picture of the entire world but also makes the term “hierarchy” controversial. Because this controversy is too often ignored or overlooked in discussions about complexity-related issues (supervenience, emergence, causation, etc.), their results unavoidably become misleading.

Table 7. Intensional relation between the entire world, living world, and human world

World	Author			
	H. Spencer	C. L. Morgan	E. Husserl	N. Hartmann
human world	superorganic	mind	society consciousness	spiritual mental
living world	organic	life	nature	organic
entire world	inorganic	matter		physical

Concluding discussion

Hierarchical view has always been fundamental to understanding complexity and diversity in biology and ecology. However, although most researchers agree that the biosphere and ecosphere are hierarchically organized systems of systems, there are disagreements in how their hierarchical organization might look.

On the one side, discussions on how to apply the hierarchy concept in biology and ecology revealed some general types of hierarchies. Marjorie Grene attracted attention to differences between control hierarchies and taxonomic hierarchies (Grene M 1969, 1987). Ernst Mayr distinguished between constitutive hierarchies and aggregative hierarchies but also between inclusive hierarchies and exclusive hierarchies (Mayr E 1982). James Valentine pointed out the difference between simple and cumulative hierarchies (Valentine JW 2003, Valentine JW and May CL 1996). Stanley Salthe proposed to distinguish between specification hierarchies and scalar hierarchies (Salthe SN 1985, 1991, 1993, 2002).

On the other side, the application of hierarchy concept in biology and ecology resulted in a variety of hierarchies differing greatly in numbers of levels and in choice of patterns to determine these levels. As a rule, biological and ecological patterns have been combined in the same hierarchy (Tables 8, 9, and 10).

Table 8. Hierarchy examples (authors are biologists)

Authors		
Wright S 1964	Bonner IT 1969	Miller JG and Miller JL 1990
world biota	Universe	supranational system
local biota	galaxy	society
species	star (system)	community
deme	planet	organization
multicellular organism	Earth's surface	group
organ	community	organism
cell	population	organ
macromolecule	organism	cell
molecule	organ	
	tissue	
	cell	
	macromolecule	
	molecule	
	atom	
	elementary particle	

Table 9. Hierarchy examples (authors are ecologists)

Authors		
Odum EP 1959	Odum EP 1991	Odum HT and Odum EC 2000
biosphere	biosphere	cosmos
ecosystem	biogeographical region	landscape geology
community	biome	society (economics)
population	landscape	ecosystem
organism	ecosystem	microbe
organ system	living community	chemical reaction
organ	population	
tissue	organism	
cell		
protoplasm		

Table 10. Most familiar (conventional) hierarchies

In biology (Campbell NA *et al* 2003)	In ecology (Allen TFH and Hoekstra TW 1990)
ecosystem	biosphere
community	biome
population	landscape
organism	ecosystem
organ system	community
organ	population
tissue	organism
cell	cell
molecule	

Genetic studies have always been associated with distinction between genotype and phenotype. After the structure of DNA molecule has been deciphered by James Watson and Francis Crick, rapid development in molecular genetics literally obliged the distinction between genotype and phenotype to become incorporated into hierarchical view in biology and ecology. Indeed, James Valentine (Valentine JW 1969, 1973, Valentine JW and May CL 1996) soon recognized "genetic" hierarchy underlying biological and ecological hierarchies (Table 11). Within "genetic" hierarchy, genes form the basic unit, aggregated at the genomic level. The genome is associated with an organism. The subsequent pattern of aggregation depends upon the hierarchy of interest. If it is a taxonomic hierarchy, the genomes are aggregated into gene pools associated with species, these into genera, these into family, and so forth. If it is an ecological hierarchy, the genomes are aggregated into gene pools associated with populations, these into communities, these into bioprovinces, and so forth.

Table 11. "Genetic" hierarchy (Valentine JW and May CL 1996)

Hierarchy		
taxonomic	genetic	ecological
order	collection of collected gene pool collections	realm
family	collection of gene pool collections	bioprovince
genus	collection of gene pools	community
species	gene pool	population
organism	genome(s)	organism
	gene	

After the replicator concept has been set out and the distinction between replicators and vehicles has been appointed (Dawkins R 1976, 1982), David Hull introduced distinction between replicators, interactors, and lineages (Hull DL 1980, 1988). He argued that the appropriate levels in biological hierarchy would be not genes, organisms, and species but just replicators, interactors, and lineages (Hull DL 1989, 2001b). Instead, Niles Eldredge and Stanley Salthe proposed to distinguish between "genealogical" hierarchy and "ecological" hierarchy (Eldredge N 1985, 2008, Eldredge N and Grene M 1992, Eldredge N and Salthe SN 1984, Salthe SN 1985, 1993, Vrba ES and Eldredge N 1984). Whereas "genealogical" hierarchy is viewed as hierarchy of replicators and refers to information transfer, "ecological" hierarchy is viewed as hierarchy of interactors and

refers to “matter-energy” transfer. Table 12 shows patterns included in an early version of “genealogical” and “ecological” hierarchy (Eldredge N and Salthe SN 1984).

Table 12. “Genealogical” and “ecological” hierarchy (Eldredge N and Salthe SN 1984)

Hierarchy	
genealogical	ecological
(special case: all life)	entire biosphere
monophyletic taxon	biotic region
species	local ecosystem
deme	population
organism	organism
gene	cell
codon	enzyme

Of course, the literature offers much more examples of hierarchies in biology and ecology than presented in Tables 8 to 12. Known biological and ecological hierarchies can be criticized for many reasons pointing out numerous particular errors. Here, the criticism focuses not on any particular error but on one common shortcoming: all these hierarchies employ only one universal life pattern – the cell – if any. All other patterns employed are doubtlessly specific. Strongly speaking, this shortcoming degrades all these hierarchies to simple lists of levels which have to do only with some selected specific fragments of such hierarchically organized systems of systems as biosphere and ecosphere.

By contrast, proposed biological hierarchy (Table 1) employs those patterns of information processing in living world (Tirjatkin N 2005a, 2005b, 2005c) which seem to be universal. Indeed, it has been recognized that from information processing perspective, all chemical reactions in living world fall into three categories: DNA transcription, RNA translation, and catalysis. It has been also recognized that these reactions arrange in strong hierarchy of life patterns: GENs, cells (GENomes), individual cell progressions, and the general cell progression. This arrangement is undistinguishable from the perspective of mass, impulse, and energy processing. The general cell progression occupies the apex of this hierarchy representing the whole living world (biosphere). Other three life patterns in this hierarchy are doubtlessly universal. They are innumerably variable and this variability underlies the diversity of biosystems at corresponding levels.

Proposed biological hierarchy (Table 1) is complete in the sense that the life patterns employed are necessary and sufficient for understanding of hierarchical organization of the living world (biosphere) as uniform system of biosystems. Extension of life patterns through corresponding fragments of the ecosphere would convert biological hierarchy (Table 1) into bioecological hierarchy (Table 5) which would be complete in the sense that resulted patterns would be necessary and sufficient for understanding of hierarchical organization of the ecosphere as uniform system of bioecosystems. However, they would be insufficient for understanding of hierarchical organization of the ecosphere as uniform system of geoecosystems.

Explicit recognition of the complete hierarchy of universal life patterns makes the understanding of life complexity amazingly easy. Living world – an extremely complex network composed of huge numbers of different chemical reactions continuously creating an enormously complex matrix composed of bewildering numbers of different chemicals involved in these reactions – becomes at once comprehensible as soon as one becomes familiar with how such basic chemical reactions as DNA transcription, RNA translation, and catalysis arrange in strong hierarchy of such life patterns as GENs, cells (GENomes), individual cell progressions, and the general cell progression.

If combined with taxonomic hierarchies embracing diversity of corresponding life patterns, the complete hierarchy of universal life patterns provides basic reference frame for secure orientation within living world. Additionally, this basic reference frame is suited very well for ordering of innumerable specific life patterns: they either disclose specific reciprocal relations between some GENs within any cells (GENomes), between some cells within any individual cell progressions, or between some individual cell progressions within the general cell progression or disclose specific reciprocal relations between some universal life patterns and environment. In addition to conventional specific life patterns, many important specific patterns of information processing in living world have been recognized (Tirjatkin N 2005a, 2005b, 2005c, 2007).

Explicit recognition of the complete hierarchy of universal life patterns provides also an appropriate conceptual framework suited very well to give rise just to that theoretical framework for which development Sidney Brenner called at the very end of the second millennium (Brenner S 1999). If we ask, however, what we have to know about GENs, GENomes, individual cell progressions, and the general cell progression, we must state that the living world remains *terra incognita* for us and much work is needed to develop an appropriate theoretical framework which would describe life in all reasonable details.

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Patterns of information processing in living world

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Life is extraordinarily complex: it is an extremely complex network composed of huge numbers of different chemical reactions continuously creating an enormously complex matrix composed of bewildering numbers of different chemicals involved in these reactions. Additionally, awfully large numbers of interactions between non-living and living worlds contribute to life complexity. Although our knowledge on the diversity of chemical reactions and chemicals in living world grows progressively, our understanding of how they integrate to generate life-relevant structures and functions is still far away from being complete. Here, I show that the investigation of life from information processing perspective allows recognition in living world of complete hierarchy of universal life patterns and many important specific life patterns making the understanding of life complexity amazingly easy.

Traditionally, chemical reactions are considered as steps of mass, impulse (momentum), and energy processing. From this perspective, their integration in living world is usually described in terms of networks composed of pathways which refer to routes of mass, impulse, and energy transfer. Different sources in environment label start points of these pathways. Initially separated, pathways usually become more and more intricately interwoven, but then divide anew into many branches whose end points are marked by waste products. Although many patterns have been discovered within such networks, they do not make the understanding of life complexity easier. At all, it becomes increasingly apparent that the investigation of life from the perspective of mass, impulse, and energy processing is not enough for understanding of how chemical reactions in living world integrate to generate life-relevant structures and functions.

Alternatively, chemical reactions may also be considered as steps of information processing. From this perspective, their integration in living world may be described in terms of networks composed of pathways which refer to routes of information transfer. It is important to note that information processing is not restricted to any limited subset of chemical reactions – as usually assumed – but absolutely all the reactions are involved in it. Although information concept remains in focus of hot debates in philosophy of sciences in general (for review see, for example, Capurro R and Hjørland B 2003) and in philosophy of biology in particular (Adami C 2004, Barbieri M 2003, Emmeche C 1999, Godfrey-Smith P 2000, Griffiths PE 2001, Jablonka E 2002, Manson NC 2006, Sarkar S 1996, 2000, Smith JM 1999, 2000, Sterelny K 2000, Winnie JA 2000), it continues to be an indispensable concept in modern sciences. Moreover, it actually becomes a central concept in the conceptual framework of contemporary biology. At all, it becomes increasingly apparent that information processing must be treated as a major theme in living world and biology must be viewed as an informational science (Auffray C *et al* 2003, Ideker T *et al* 2001). The reason for this is that, in contrast to sources of mass, impulse, and energy, the information source is appointed not in environment but rather in the living world itself and, more concretely, in the DNA molecules. Information stored in DNA molecules is just what makes living world autonomous from the environment even if the dependence on sources of mass,

impulse, and energy makes it sensitive to changes in environment. This suggests that the investigation of life from the information processing perspective may also contribute to the understanding of life complexity as well.

Indeed, investigation of life from information processing perspective allows recognition in living world of complete hierarchy of universal life patterns and many important specific life patterns (Tirjatkin N 2005a, 2005b, 2005c, 2007, 2008) making the understanding of life complexity amazingly easy.

Complete hierarchy of universal life patterns

Multilevelness is the key characteristic of life complexity: living world is actually a hierarchically organized system of systems (Andrianantoandro E *et al* 2006, Emmeche C 1997, Grizzi F and Chiriva-Internati M 2005, Mesarovic MD *et al* 2004, Valentine JW 2003, Van de Vijver G *et al* 2003, Zylstra U 1992). An important attribute of the hierarchy is the gradual integration of systems from the bottom level to the apex so that upper levels are said to emerge out of the lower levels. To determine particular level in biological hierarchy, it is necessary to know a corresponding universal life pattern which variability would underlie the diversity of systems at this level. However, just in this respect, our knowledge is woefully incomplete. The only universal life pattern recognized is the cell (Mazzarello P 1999). All other known life patterns are doubtlessly specific. Recently, the list of familiar subcellular and supercellular (supracellular) life patterns such as organelle, tissue, organ, organism, etc. has been significantly extended through various structural and functional units referred to as modules, motifs, etc. (Alm E and Arkin AP 2003, Alon U 2003, Csete ME and Doyle JC 2002, De Silva E and Stumpf MPH 2005, Huang S 2004, Oltvai ZN and Barabási AL 2002). However, no one of them can be accepted as universal life pattern. Therefore, the presentation of their hierarchy as “life’s complexity pyramid” (Oltvai ZN and Barabási AL 2002) is an overestimation of their significance. Thus, the biological hierarchy composed completely of universal life patterns lacks. This big gap in biology foundation hampers progress within the “era of biology” significantly.

Meanwhile, the investigation of life from information processing perspective allows recognition in living world of many new life patterns (Tirjatkin N 2005a, 2005b, 2005c, 2007). Some of them seem to be universal (Tirjatkin N 2008).

Subcellularly, the information processing involves two tightly coupled reactions: genome expression and genome replication. During genome expression, information is converted first from DNA into RNA (transcriptome) form by DNA transcription, then from RNA into polypeptide (proteome) form by RNA translation, and finally from polypeptide into metabolite (metabolome) form by catalysis. It is important to note that the genome is a limited set of genes and each gene is usually expressed separately to be fully converted into the corresponding element of the cell structure or function. For each gene, its own sequence of DNA transcription, RNA translation, and catalysis can be determined. This directed sequence of chemical reactions is the most basic universal life pattern which can be called a gene expression network, abbreviated GEN. Its variability is virtually unlimited. Additionally, in some GENs, the obligatory sequence of chemical reactions can be restricted or extended. So, in many GENs, end products are

polypeptides functioning always as substrate molecules and never as catalysts. In many other GENs, end products are RNAs that never become translated into polypeptides, but function always at the level of RNA as substrate molecules. On the other hand, in many GENs, products of DNA transcription or RNA translation undergo post-transcriptional or post-translational processing respectively. The cell itself can be considered as a highly regular composition of interacting GENs which can be called GENome. Whereas gene and genome are notions that refer to how information is stored in the cell, GEN and GENome refer to how the gene and genome work. During information processing in particular GEN, it is just the job of other GENs to provide necessary elements for gene expression machinery. Collectively, GENs in GENome work to replicate the complete genome so that the life history of the single cell begins with one cell but ends with two. In particular cell, the GENome is suited to specific subset of sources of mass, impulse (momentum), and energy to produce their usable forms essential for the cell life. Thus, subcellularly, all chemical reactions are organized highly regular: first into GENs and then into GENome.

Supercellularly, the information processing involves other two important reactions: genome multiplication and genome diversification. Mechanism of genome multiplication is always the same: the genome replication by genome expression. On the contrary, mechanisms of genome diversification differ greatly ranging from the spontaneous sequence mutation to the highly regulated sequence transfer. Progressive genome replication is usually associated with progressive cell propagation producing a sequence: one cell, two cells, four cells, eight cells, and so on. This sequence can be called cell (GENome) progression. The whole cellular world is only one cell progression which arose from one single primordial cell and has 3 or 4 billions years of uninterrupted history. It can be called general cell progression. The present-day biosphere is merely a tiny slice from it, a visible top of iceberg in ocean of time. The ancient part of this gigantic life pattern leaves very scarce traces. Although all cells of the general cell progression should be theoretically identical to each other genetically, this is not the case in the nature: genome diversification produces cell progressions each of which is specified by a particular individual genome and can be called individual cell progression. Respectively, the general cell progression can be considered as a growing composition of an increasing number of individual cell progressions. Individual cell progression is universal life pattern with virtually unlimited variability. Spatiotemporal organization of a particular individual cell progression mostly depends upon whether the cells divide symmetrically or asymmetrically, whether the asymmetric cell divisions occur occasionally or regularly, whether the asymmetric cell division is associated with symmetric or asymmetric kinetics of the cell propagation, whether the cells will be rather randomly dispersed in space to become autonomous in behaviour or remain in an association to form cell colony (primary, secondary, etc.), whether the cell association grows continuously or is a steady state system, and so on. Thus, supercellularly, chemical reactions are organized highly regular too: first into individual cell progressions and then into the general cell progression.

So, from information processing perspective, all chemical reactions in living world fall into three categories: DNA transcription, RNA translation, and catalysis. They are organized in strong hierarchy of life patterns: GENs, cells (GENomes), individual cell progressions, and the general cell progression. The general cell progression occupies the

apex of the hierarchy. Most likely, it is unique and merits its own name (for example, Zoe). Other three life patterns in this hierarchy are doubtlessly universal. Their innumerable variations underlie the life diversity.

Diversity of individual cell progressions in biosphere

The present-day biosphere is merely a tiny slice from the general cell progression, a visible top of iceberg in ocean of time. However, although the number of individual cell progressions in this tiny slice represents only a small fraction of the whole, it is enormous. Much work is needed to describe and systematize this diversity completely. Review of the diversity of individual cell progressions with special focus on formation of cell associations (Tirjatkin N 2005c) can be summarized as follows.

Within some individual cell progressions, the cells will be rather randomly dispersed in space and each cell seems to become autonomous in behaviour. Just the individual cell progressions with this type of cell arrangement are poorly studied while most attention usually was paid solely the single cell. This type of cell arrangement allows different individual cell progressions to superpose each other in space. Additionally, in some individual cell progressions with dispersed cell arrangement, cells can closely aggregate into simplest temporary cell associations. Within other individual cell progressions, the cells will remain in an association, a cell colony, held together in any way. In the individual cell progressions with this type of cell arrangement, the founder cell first gives rise to primary cell colony which body plan is usually a filamentous chain, a hypha, or a globular body, a sphaera. By further cell propagation, an initial primary cell colony usually clones itself giving rise to a number of primary cell colonies respectively. Within a growing individual cell progression, these primary cell colonies may be either dispersed in space or held together in association forming a secondary cell colony of any kind and size and for any period of time under specific environmental circumstances. In turn, an initial secondary cell colony can give rise to a number of secondary cell colonies. Within a growing individual cell progression, also the secondary cell colonies may be either dispersed in space or held together in larger cell association. So, different individual cell progression can superpose each other even at the level of the secondary cell colony. Generally, the cell association has advantageous ability to carry out activities with a complexity not possible by single cell. Within an association, many cells come together to collectively respond to environmental conditions. This collective respond is usually more effective than by a single cell. Some cell associations are continuously growing systems, the others are rather steady state systems whose cell number is balanced in any ways. Different cell associations show a significant variation of degree of integration and coordination among cells. Within an association, the cells will either remain similar or become different. Progressive cell propagation may be accompanied by cell differentiation creating the diversity of specialized cells.

As in most Karyota, life history of an animal individual cell progression begins at the moment of fertilization when two of the most specialized monogenomic cells, the egg and the sperm, combine to produce the most specialized digenomic cell, the zygote. The zygote propagates by cleavage so that the cells become smaller and smaller. Then, the cell association grows and develops in a large variety of ways, forming an initial body

with a species-specific primary body plan. This initial body usually clones itself giving rise to an expanding population of primary cell colonies that often remain attached to each other, forming a larger cell association with a species-specific secondary body plan. The secondary cell colony may show differentiation of primary cell colonies. Soon or later, the onset of meiosis is triggered. The tetrads may propagate forming an association of monogenomic cells, but this case is extremely rare. Mostly, the tetrads do not propagate but differentiate into eggs or sperm. The egg usually develops only from one of the tetrads, while the other three become polar bodies and rather degenerate. Each primary cell colony may frequently change from a free-swimming stage to a sessile stage. In addition to the settlement, this change may include more or less dramatic transformation of the primary body plan. The cloning and formation of secondary cell colony may occur from both the free-swimming stage and sessile stage. In some species, the free-swimming stage is restricted to the initial primary cell colony which soon or later settles and irreversibly transforms into the sessile stage. Similarly, each secondary cell colony may frequently change from a free-swimming stage to a sessile stage and this change may include more or less dramatic transformation of the secondary body plan.

While the morphological diversity of animal cell associations seems to be overwhelming, the underlying body plans are nevertheless governed by rather few general principles. The primary body plan is always a sphaera or its derivative. The sphaera which can be topologically described as the simplest closed surface, with two sides and no boundary lines, can give rise to more complex closed surface such as solenoid or even to a system of solenoids, some embedded in another. The secondary body plan is a series of primary body plans. However, the serial arrangement may become not more evident. In contrast to the abstract mathematical surface, the real biological surface is made up not by dimensionless points but by three-dimensional matrix with embedded cells. So, although the biological surface, like the mathematical surface, is with two sides and no boundary lines, it is actually a wall, since there is a distance between its two sides so that these two sides enclose a space with a volume. In other words, whereas a mathematical surface has no thickness, the biological surface does have. The thickness of the wall may have regional differences in magnitude. Additionally, the two sides of the wall can be differently designated according to their orientation to interior or exterior of the body. Thus, it is very important to recognize that the description of the animal body plan can be generally given in terms of a closed and orientable wall, without boundary lines and with two distinguishable sides. That side of the wall which is oriented into the exterior of the body is here designated as an outside, and that which is oriented in the interior of the body is an inside. One must be aware that the space, which seems to be the interior of the body at the first glance, is actually the exterior. Within the wall, some cells may become polarized cells arranged in cell layers. Some cell layers may be described as the closed surfaces, but their local orientation may greatly deviate from the direction of the wall orientation, giving rise to the internal complexity of the wall. Additionally, other cell layers may not be described as closed surfaces at all. So, the underlying principles of surface topology remain valid only at the wall level but not at the level of separate cell layers. The complexity of the primary and secondary body plan enhances gradually at different ontogenetic and phylogenetic stages, providing insight into the most basic directions of animal evolution. According to primary body plan, four major phylogenetic groups can be

distinguished in Animalia. First, there are 3 phyla with sphaera as a primary body plan: Porifera, Cnidaria, and Ctenophora. Second, there is at least one phylum with sphaera-in-sphaera as a primary body plan: Placozoa. Third, there are 11 phyla with solenoid as a primary body plan: Rotifera, Cycliophora, Micrognathozoa, Gnathostomulida, Kamptozoa, Priapulida, Kinorhyncha, Loricifera, Nematoda, Nematomorpha, and Gastrotricha. Fourth, there are 18 phyla with solenoid-in-solenoid as a primary body plan: Bryozoa, Phoronida, Brachiopoda, Sipunculida, Annelida, Mollusca, Nemertea, Platyhelminthes, Arthropoda, Onychophora, Tardigrada, Chaetognatha, Echinodermata, Pterobranchia, Enteropneusta, Tunicata, Cephalochordata, and Vertebrata.

When the secondary body plan is established in Vertebrata, the wall generally involves poorly segmented integumental wall, poorly segmented gastral wall arranged as a common gut, segmented chordal wall arranged as a chain of compact chordal bladders, poorly segmented atrial wall arranged as a pair of atrial ducts, poorly segmented neural wall arranged as an elongated neural bladder, poorly segmented coelomic wall arranged as a coelomic bladder, poorly segmented meningeal wall arranged as a meningeal bladder, segmented somitic wall arranged as paired chains of compact somitic bladders, segmented germinal wall arranged as paired chains of compact germinal bladders.

Diversity of asymmetric cell progressions in Mammalia

It is reasonable to distinguish between phylogenetic and ontogenetic cell diversity. Whereas the phylogenetic cell diversity is a result of the genome multiplication and diversification during life history of the general cell progression, the ontogenetic cell diversity is a result of differential genome expression during life history of some individual cell progressions.

Most regular spatio-temporal pattern of differential genome expression during life history of an individual cell progression is associated with the establishment of asymmetric cell (sub)progressions (Tirjatkin N 2005b). Each asymmetric cell (sub)progression has a stem cell at the base and is therefore characterized by asymmetric kinetics of cell propagation (not to be confused with asymmetric cell division). Stem cells divide very rarely. If stem cell divides, only one daughter cell inherits stem cell property. On the contrary, the other daughter cell becomes a non-stem (bud) cell but propagates rather quickly giving rise to a large number of progeny cells. So, an asymmetric cell (sub)progression consists of a stem cell lineage and a number of cell (subsub)progressions each of which has a bud cell at the base. Whereas the potential to divide seems to remain unlimited throughout the whole stem cell lineage, the progressive propagation of each bud cell is accompanied by a sequential restriction of the division capacity down to the division arrest, terminal differentiation, and death so that each bud cell gives rise to a limited cell (subsub)progression with a limited number of progeny cells. An asymmetric cell (sub)progression is a steady state system. At the base of this system, the asymmetric division of the first (primordial) stem cell yields the second stem cell and the first bud cell. The newly formed second stem cell remains inactive for a long period of time during which the first bud cell progressively propagates producing the first limited cell (subsub)progression. Within a limited cell (subsub)progression, the cells first propagate at the fastest rate producing a growing number of transit amplifying cells. After a critical number of division rounds is reached,

the cells become committed to undergo differentiation into one or more directions of specialization. Differentiating cells propagate at the lower rate and, when a critical number of division rounds is reached, they become mature specialized cells which do not divide and become exhausted by performing their special functions. At certain critical point of the history of the first limited cell (subsub)progression, the second stem cell divides producing the third stem cell and the second bud cell so that the exhausted first limited cell (subsub)progression becomes replaced by the newly formed second limited cell (subsub)progression. Since the potential to divide remains unlimited throughout the stem cell lineage, the asymmetric cell (sub)progression produces unlimited number of limited cell (subsub)progressions which replace each other in consecutive order. So, an asymmetric cell (sub)progression can maintain near a constant number of cells. The establishment of asymmetric cell (sub)progressions during life history of an individual cell progression may result in their diversification as well (as, for example, in Vertebrata including Mammalia).

In Mammalia, the zygote is considered as a truly totipotent cell in the sense that it is the progenitor of all of the four hundred or more ontogenetic cell types and subtypes (Vickaryous MK and Hall BK 2006) which are generated within the cell association during the life history of mammalian individual cell progression. The totipotency is usually retained by early progeny of the mammalian zygote up to the eight-cell stage so that two or more genetically equivalent cell associations may be occasionally formed within the same individual cell progression. Subsequently, the progressive cell propagation gives rise to a growing number of cells with more restricted potential. Traditionally, these cells have been subdivided into two groups: pluripotent embryonic stem cells and multipotent adult stem cells (Anderson DJ *et al* 2001, Gage FH and Verma IM 2003, Petersen BE and Terada N 2001). In mammalian embryo, first the inner cell mass (ICM) cells, then the epiblast cells, and finally the primordial germ cells are pluripotent embryonic stem cells that can be isolated and propagated *in vitro* displaying in culture an almost unlimited proliferation capacity and retaining a relatively normal and stable karyotype and the ability to differentiate into the most broad spectrum of ontogenetic cell types and subtypes (Czyz J and Wobus AM 2001, Eiges R and Benvenisty N 2002, Hadjantonakis AK and Papaioannou VE 2001, Hoffman LM and Carpenter MK 2005, Odorico JS *et al* 2001, Pera MF and Trounson AO 2004, Rossant J 2001, Stojkovic M *et al* 2004, Wobus AM and Boheler KR 2005). In the intact embryo, however, pluripotent embryonic stem cells persist for only a limited number of cell division rounds. This period of expansion of pluripotent embryonic stem cells is accompanied by the generation of primordial multipotent adult stem cells each of which gives rise to an asymmetric cell (sub)progression with cell differentiation in one or more directions of specialization. In this respect, the embryonic stem cells are precursors of adult stem cells. In contrast to traditional view, more recent findings (Anderson DJ *et al* 2001, Hawley RG and Sobieski DA 2002, Kuehnle I and Goodell MA 2002, Lemoli RM *et al* 2005) suggest that adult stem cells retain pluripotency. The only difference between embryonic and adult stem cells is that the propagation of embryonic stem cells is characterized by symmetric kinetics whereas the propagation of adult stem cells is characterized by asymmetric kinetics. Just the transition from symmetric to asymmetric kinetics of cell propagation is essential for establishment of asymmetric cell (sub)progressions within the cell association.

Once established, each asymmetric cell (sub)progression occupies its own domain within the cell association. In such domain, stem cell is usually located in especially carefully protected area, a stem cell niche (Fuchs E *et al* 2004, Li L and Xie T 2005, Ohlstein B *et al* 2004, Spradling A *et al* 2001, Watt FM and Hogan BLM 2000). If the stem cell divides, one daughter cell is retained as a stem cell but the other becomes bud cell and must leave the stem cell niche to enter an area occupied by limited cell (subsub)progressions. Since limited cell (subsub)progressions replace each other in consecutive order, near constant number of cells can be maintained within their area. The newly formed bud cell first enters a section occupied by a pool of transit amplifying cells and proceeds through a number of division rounds at the fastest rate providing a renewal of this pool. The transit amplifying cells are regularly committed to enter the next section occupied by a pool of differentiating cells which propagate at the lower rate. Finally, the differentiating cells are regularly committed to enter a section occupied by a pool of mature specialized cells which become inevitably exhausted by performing their functions. So, each domain occupied by an asymmetric cell (sub)progression consists of two areas: a stem cell niche with one stem cell and an area occupied by limited cell (subsub)progressions. In turn, the area occupied by limited cell (subsub)progressions consists of three sections: a section occupied by a pool of transit amplifying cells, a section occupied by a pool of differentiating cells, and a section occupied by a pool of mature specialized cells. Within each domain occupied by an asymmetric cell (sub)progression, its cells put together a well-proportioned unit. This unit is a very stable dynamic system being able to exist eternally owing to the very fine coordination of the whole cascade of the cell propagation, cell elimination, and cell differentiation events. Using inflow of negative entropy from environment, this unit can maintain sufficiently high degree of organization, so ensuring endless self-renewal. Stem cell lineage plays a key role in this unit. It is namely the source of preservation of genetic fidelity and the source of self-renewal of the whole asymmetric cell (sub)progression. Stem cells remain undifferentiated while simultaneously producing highly specialized cells. The splitting of the stem cell progeny into two separate cell groups that drastically differ in division frequency and division number is assumed as a consequence of a selective pressure in evolution of cell association types to avoid the negative results of mutations. On the one hand, this splitting allows to reduce the division frequency of just those cells that reside permanently in the cell association and so ensures the protection against accumulation of mutations. The division of these cells is very rare and is protected so sufficiently that they may divide unlimited number of times. On the other hand, the splitting allows to reduce the number of cell division rounds in the group of intensively proliferating cells and therefore to minimize the rate of malformation arising out of deleterious mutations. Also non-deleterious mutations in intensively proliferating cells do not accumulate since this progeny of the stem cell soon or later leaves the cell association. So, the splitting provides asymmetric cell (sub)progression with the property to exist beyond the number of cell divisions that leads to a significant risk in deleterious mutation.

After establishment of asymmetric cell (sub)progressions, the cell association consists of four categories of cells: adult stem cells, transit amplifying cells, differentiating cells, and mature specialized cells. Despite considerable efforts, adult stem cells remain the least studied cell category because they are extremely difficult to isolate from the cell association and propagate *in vitro*. Attempts to isolate adult stem cells are hindered by

their extreme rarity in the cell association and by the absence of appropriate markers which can be used to distinguish stem cells from bud cells and transit amplifying cells. Attempts to propagate adult stem cells *in vitro* are hindered by the intrinsic asymmetric kinetics of their propagation (Sherley JL 2002). Therefore, it is not surprisingly that reports on isolation and propagation of adult stem cells are highly questionable and data on studying the behaviour of derived cells *in vitro* or *in vivo* are usually controversial and difficult to interpret. Nevertheless, more recent findings (Henson NL *et al* 2005, Young HE 2004, Young HE *et al* 2005) provide data that allow to assume that adult stem cells are embryonic stem cell-like with respect to their unlimited potency to proliferate and differentiate *in vitro*. Transit amplifying cells show unlimited potency to proliferate but are restricted in their potency to differentiate. Differentiating cells are restricted in their potency to proliferate and are characterized by further restriction in their potency to differentiate. Mature specialized cells divide very rarely, if any, and are usually terminally differentiated. Different asymmetric cell (sub)progressions look alike when compared by their stem cells or transit amplifying cells. Differences between asymmetric cell (sub)progression types become first apparent by the examination of differentiating cells.

Asymmetric cell (sub)progressions superpose each other within the cell association and convert it into a steady-state system which balances cell propagation, cell elimination, and cell differentiation events to maintain the numbers of stem cells, transit amplifying cells, differentiating cells, and mature specialized cells, allowing the cell association to rapidly grow at the same time it is developing structurally and functionally.

Finally, the establishment of specific pattern of interactions between different types of asymmetric cell (sub)progressions within mammalian wall and regional diversification of this pattern contribute to the complexity of mammalian cell association. To describe this pattern, Mammalian Wall Formula is proposed (Tirjatkin N 2007).

Conclusions

Above, I have shown that the investigation of life from information processing perspective allows recognition in living world of complete hierarchy of universal life patterns and many important specific life patterns making the understanding of life complexity amazingly easy.

Living world – an extremely complex network composed of huge numbers of different chemical reactions continuously creating an enormously complex matrix composed of bewildering numbers of different chemicals involved in these reactions – becomes at once comprehensible as soon as one becomes familiar with how such basic chemical reactions as DNA transcription, RNA translation, and catalysis arrange in strong hierarchy of such life patterns as GENs, cells (GENomes), individual cell progressions, and the general cell progression.

Formation of cell associations during life history of animal individual cell progressions becomes more comprehensible if a notion of a closed and orientable surface is used. In contrast to abstract mathematical surface, the real biological surface is made up not by dimensionless points but by three-dimensional matrix with embedded cells. So, it is

actually a closed and orientable wall, since there is a distance between its two sides. The thickness of the wall may have regional differences in magnitude. Additionally, the two sides of the wall can be differently designated according to their orientation to interior or exterior of the cell association. To avoid confusion, one must be aware that the wall is not a boundary of the cell association but just its body.

Ontogenetic cell diversification during life history of mammalian individual cell progressions becomes at once comprehensible as soon as one becomes familiar with how the most regular spatiotemporal patterns of differential genome expression – asymmetric cell (sub)progressions – emerge and diversify. Additionally, it becomes more comprehensible if Mammalian Wall Formula is used which describes how specific pattern of interactions between different types of asymmetric cell (sub)progressions within mammalian wall emerges and diversifies regionally.

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Understanding life, constructing life

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Understanding life and constructing life are two fundamental problems at the very base of bio(techno)logical research and development respectively. These problems are intricately interwoven reflecting that science evolves by continuous exchange of facts and ideas between research and development. Understanding life is the only way to become able to construct it. Constructing life is the best way to improve life understanding. However, despite of much effort, life continues to be notoriously difficult to understand and construct. Here, I show that the investigation of life from information processing perspective makes life understanding sufficient enough for successful life constructing.

Without sufficient life understanding, successful life constructing is impossible. Unfortunately, most of the empirical and theoretical investigation in bio(techno)logical research and development is largely analytical. Although recent few decades were marked by very active implementation of synthetic approach (Andrianantoandro E *et al* 2006, Barrett CL *et al* 2006, Drubin DA *et al* 2007, Heinemann M and Panke S 2006, Ideker T *et al* 2001, Kitano H 2002, Mesarovic MD *et al* 2004, Westerhoff HV and Palsson BO 2004, Wolkenhauer O 2001), understanding life (Anbar M 2001, Bedau MA 1998, Dix DE 2002, Emmeche C 1997, Harold FM 2001, Kornberg A 1991, Penzlin H 2009) and constructing life (Andrianantoandro E *et al* 2006, Bedau MA *et al* 2000, Chopra P and Kamma A 2006, Drubin DA *et al* 2007, Endy D 2005, Heinemann M and Panke S 2006, Kim KJ and Cho SB 2006, Szostak JW *et al* 2001) remain unsolved fundamental problems.

The investigation of life from information processing perspective allows recognition in living world of complete hierarchy of universal life patterns and many important specific life patterns (Tirjatkin N 2005a, 2005b, 2005c, 2007, 2008a, 2008b). Here, I claim that the familiarity with these patterns is a prerequisite for both sufficient life understanding and successful life constructing.

Patterns of information processing in living world

Subcellularly, the information processing involves two tightly coupled reactions: genome expression and genome replication. During genome expression, information is converted first from DNA into RNA (transcriptome) form by DNA transcription, then from RNA into polypeptide (proteome) form by RNA translation, and finally from polypeptide into metabolite (metabolome) form by catalysis.

It is important to note that the genome is a limited set of genes and each gene is usually expressed separately to be fully converted into the corresponding element of the cell structure or function. For each gene, its own sequence DNA transcription -> RNA translation -> catalysis can be determined. This directed sequence of chemical reactions builds the most fundamental unit of information processing in the living world. This life pattern can be called the gene expression network (abbreviated GEN). Additionally, in some GENs, the obligatory sequence of chemical reactions can be restricted or

extended. So, in many GENs, end products are polypeptides functioning always as substrate molecules and never as catalysts. In many other GENs, end products are RNAs that never become translated into polypeptides, but function always at the level of RNA as substrate molecules. On the other hand, in many GENs, products of DNA transcription or RNA translation undergo post-transcriptional or post-translational processing respectively.

Since the genes are usually associated in a genome, the corresponding GENs are organised in more complicated unit of information processing in the living world. This life pattern can be called the genome expression network (abbreviated GENome). This life pattern is roughly equal to the cell. Whereas gene and genome are notions that refer to how information is stored in the living world, GEN and GENome refer to how the gene and genome work. The GENome can be considered as a highly regular composition of interacting GENs. During information processing in particular GEN, it is just the job of other GENs to provide necessary elements for gene expression machinery. Collectively, GENs in GENome work to replicate the complete genome so that the life history of the single cell begins with one cell but ends with two. Generally, the cell life history begins at the point where two newly produced sister cells halve the matrix inherited from the mother cell and each starts a self-dependent life. What the newborn cell has to do is just what its mother done: it starts its own genome expression which results in genome replication and in division in two daughter cells. In particular cell, the GENome is suited to specific subset of sources of mass, impulse (momentum), and energy to produce their usable forms essential for the cell life.

Thus, subcellularly, all chemical reactions are organized highly regular: first into gene expression networks and then into genome expression networks.

Supercellularly (supracellularly), the information processing involves other two important reactions: genome multiplication and genome diversification. Mechanism of genome multiplication is always the same: the genome replication by genome expression. On the contrary, mechanisms of genome diversification differ greatly ranging from the spontaneous sequence mutation to the highly regulated sequence transfer.

Progressive genome replication by genome expression leads to much more complicated unit of information processing in the living world. This life pattern can be called the genome multiplication network. Progressive genome replication is usually associated with progressive cell propagation producing a cell progression: one cell -> two cells -> four cells -> eight cells -> and so on… The entire living world is the only one cell progression which arose from one single primordial cell. However, the genome diversification produces cell progressions each of which is specified by a particular individual genome and can be called individual cell progression. Respectively, the entire living world can be considered as a growing composition of an increasing number of individual cell progressions. Spatiotemporal organization of a particular individual cell progression mostly depends upon whether the cells divide symmetrically or asymmetrically, whether the asymmetric cell divisions occur occasionally or regularly, whether the asymmetric cell division is associated with symmetric or asymmetric kinetics of the cell propagation, whether the cells will be rather randomly dispersed in

space to become autonomous in behaviour or remain in an association to form cell colony (primary, secondary, etc.), whether the cell association grows continuously or is a steady state system, and so on.

The entire living world is the only one cell progression which arose from one single primordial cell and has 3 or 4 billions years of uninterrupted history. It represents the most complicated unit of information processing in the living world. This life pattern can be called the genome diversification network or the general cell progression. The present-day biosphere is merely a tiny slice from it, a visible top of iceberg in ocean of time. The ancient part of this gigantic life pattern leaves very scarce traces.

Thus, supercellularly, chemical reactions are organized highly regular too: first into genome multiplication networks and then into the genome diversification network.

Understanding terrestrial life

Explicit recognition in the living world of complete hierarchy of universal life patterns and many important specific life patterns (Tirjatkin N 2005a, 2005b, 2005c, 2007, 2008a, 2008b) makes the understanding of life complexity and life diversity on the Earth amazingly easy.

The living world – an extremely complex network composed of huge numbers of different chemical reactions continuously creating an enormously complex matrix composed of bewildering numbers of different chemicals involved in these reactions – becomes at once comprehensible as soon as one becomes familiar with how such basic chemical reactions as DNA transcription, RNA translation, and catalysis arrange in strong hierarchy of life patterns shown in the table:

Table. Complete hierarchy of universal life patterns

Level	Life pattern…	… is roughly equal to:
4	Genome diversification network	General cell progression (living world or biosphere)
3	Genome multiplication network	Individual cell progression
2	Genome expression network (GENome)	Cell
1	Gene expression network (GEN)	

The general cell progression occupies the apex of the hierarchy. Most likely, it is unique and merits its own name (for example, Zoe). Other three life patterns in this hierarchy are doubtlessly universal. Their innumerable variations underlie the life diversity at corresponding levels.

Therefore, it is reasonable to have at least three taxonomic hierarchies (or genealogies): first for GENs, second for cells (GENomes), and third for individual cell progressions. It is important to note that, in addition to abstract taxonomic genealogies, such individual living things as GENs, cells (GENomes), and individual cell progressions also arrange in concrete genealogy and that this concrete genealogy is just the general

cell progression. According to the nature of universal life patterns in hierarchy, this concrete genealogy is one single genealogy of individual cell progressions at lower resolution, one single genealogy of cells (GENomes) at middle resolution, but a multiple N_1-fold genealogy of GENs at higher resolution where N_1 is a number of genes in genome (or GENs in GENome) of the primordial cell from which the general cell progression arose. Both abstract and concrete genealogies may be presented in form of a tree-like drawing (dendrogram). Some individual cell progressions may produce cell associations in form of true trees.

If combined with taxonomic hierarchies embracing diversity of corresponding life patterns, the complete hierarchy of universal life patterns provides basic reference frame for secure orientation within the living world. Additionally, this basic reference frame is suited very well for ordering of innumerable specific life patterns: they either disclose specific reciprocal relations between some GENs within any cells (GENomes), between some cells within any individual cell progressions, or between some individual cell progressions within the general cell progression or disclose specific reciprocal relations between some universal life patterns and environment. In addition to conventional specific life patterns, many important specific patterns of information processing in living world have been recognized (Tirjatkin N 2005a, 2005b, 2005c, 2007, 2008a, 2008b).

Constructing life *in silico*

Explicit recognition in the living world of complete hierarchy of universal life patterns and many important specific life patterns (Tirjatkin N 2005a, 2005b, 2005c, 2007, 2008a, 2008b) makes life understanding sufficient enough for successful life constructing.

There are large numbers of life definitions (for review see, for example, Popa R 2004). However, no one can be used for life constructing. It is important to note that the non-living and living are undistinguishable from the perspective of mass, impulse, and energy processing. The difference becomes apparent only from the perspective of information processing: life originates by coupling of genome replication to genome expression and develops by continuous genome multiplication and genome diversification. This statement defines exactly what life is from information processing perspective. However, it is a minimal definition of life. By contrast, maximal definition of life must contain an extension pointing out that, after origin of the Life on the Earth, history of the Earth is inseparable from the history of the living world: it is obvious that the geosystems and biosystems coevolve and the geoecosystems and bioecosystems emerge at the interface of this coevolution (Tirjatkin N 2008a).

The proposed minimal definition reveals life as a special case of information processing and suggests that the simplest way to construct life is the programming.

Using knowledge on patterns of information processing in the living world, I have already obtained first positive results by means of the simplest C++ programs (*www.nikita-tirjatkin.de*). Each program must be compiled to produce an executable code which then conducts the corresponding experiment for *in silico* life construction

every time it runs. By contrast to known applications, these programs explicitly construct in the memory of computer genome-containing objects with genome-based information processing: gene expression networks, genome expression networks, etc. For simplicity, *in silico* life (InSiLi) is constructed by instantiation of uncomplicated object types. However, all these object types can be easily replaced by more realistic or – why not! – by more unrealistic object types depending on research and/or development aims.

Perspectives

InSiLi strongly supports the claim that the familiarity with patterns of information processing in the living world is a prerequisite for both sufficient life understanding and successful life constructing. Now, we understand life good enough to construct it at least *in silico*.

Although extremely simple, InSiLi can be anticipated as starting point for broad family of sophisticated research and development tools. Bridging the gap between life understanding and life constructing, these tools would put bio(techno)logical research and development in a new perspective. On the one hand, they might contribute to the improvement of life understanding until we become able to construct life *ex silico* too. On the other hand, they might contribute to the improvement of life quality itself. Indeed, knowledge on patterns of information processing provides real opportunity for development of a variety of *in silico*, *in vitro*, and/or *in vivo* models being suited for simulation of differential genome expression during normal or pathologic ontogenesis and histogenesis to discover relevant pathways of disease pathogenesis and reveal appropriate targets and agents for disease diagnosis and therapeutic interventions.

Being extremely simple, InSiLi is comprehensible for the broadest scientific and non-scientific audience suggesting that the life understanding and life constructing are much easier than expected. Using knowledge on patterns of information processing in the living word, everyone can construct her or his own version of *in silico* life and so contribute to the solution of the most exciting fundamental problems of bio(techno)logical research and development.

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