## THE FIRST MEETING ON PLANT NEUROBIOLOGY

May 17 – 20, 2005 Accademia dei Georgofili Florence (Italy)

**Talk version** 

## Serial Endosymbiotic Theory (SET): The biosemiotic update 2005

Günther Witzany Vogelsangstraße 18c, A-5111-Buermoos/Salzburg – Austria witzany@sbg.at

**The Serial Endosymbiotic Theory** is so revolutionary because it reversed the evolution vector from ramification to merging. Eukaryotic cells, according to Margulis, are the result of merging several different ancestor genomes (Margulis 1996, 1999, 2004, Margulis et al. 2000, Margulis and Sagan 2002).

The important factor is the sequence of merging in symbiogenesis, i.e. the serial evolution. The first merger involved (1) thermoplasmic archaebacteria with motile spirochaeta-like eubacteria that (2) were able to swim, to the nucleocytoplasm. These forms were still anaerobic. This was followed by a merging with (3) aerobic organisms. This enabled them to survive the increasing oxygen concentrations. The final step was the merging with (4) photosynthetic bacteria. With this approach, the SET contradicts traditional theories of evolution, all of which firmly held that the direction lay in ramification and not in merging.

One integrated genome was sufficient in the merger of archae- and eubacterium, in the Proctista 2 integrated genomes were necessary, in the fungi 3, in animals at least 4, and in the plant kingdom (400 million years ago) at least 5, perhaps even 7 (Margulis 1996). Thus, the plant genome is the epitome of symbiogenetic evolution processes and represents the most complex integration process. Considering that the evolution of flowering plants took place only about 150 million years ago, and that their seeds and fruits provided the foundation for higher animals, then these revolutionary symbiogenetic processes are relatively young compared with evolutionary history as such (Margulis and Schwartz 1988).

The SET also supports her assumption by pointing out that most of the DNA found in the cytoplasm of animals, fungi, plants and protoctists comes from genes of bacteria that became organelles, and not from genetic drift or mutations. Eukaryotic genes that participate in information processing (translation, transcription etc.) show a close relationship to eubacteria. Genetic factors that control metabolic processes, however, more closely resemble those of archaebacteria.

Another advantage of the merging paradigm of the SET is a merging of entire gene-blocks. This demonstrates that complex genomic make-ups can be passed on directly and that the step-by-step development via chance mutations is outdated.

**Merging?** – **Communication!** Lynn Margulis uses in the SET the classic language of mechanistic biology to describe symbiogenesis: "merging" "fusion", "incorporation".

In fact, a multi-levelled, generative communication process rather than "fusion" is involved. Its success, however, depends on whether the necessary sign processes proceed according to rules or whether they fail. Moreover, the integration of genetic components into available genomes and therefore the creation of a new individual does not involve "incorporation", but rather a DNA/RNA - processing.

The pragmatic philosophy of biology (Witzany 1993, 2000) and the young science of biosemiotics (Kull 2005) demonstrate that life functions are *always* related to sign processes. ). "Life is distinguished from the nonliving world by its dependence on signs" (H.Pattee). More precisely: sign processes *regulate and constitute* life functions. If these sign processes are faulty, then life processes are compromised or terminated. These sign processes regulate life processes on different levels *simultaneously*: intracellularly, within the cell (DNA, RNA activities, messenger substances, etc.), and intercellularly as cell-cell communication. This is the intraorganismic level. In parallel, each organism also conducts species-specific (interorganismic) and transspecific (metaorganismic) communication processes.

Should the symbiosis lead to a symbiogenesis, to the development of a new species and thus to the disappearance of the formerly independent individuals, then the result is *generative* DNA-text processing in which genetically different gene pools are combined into *one* DNA text. This requires a recombination that assimilates the foreign data set, converting the external into the internal.

But, which genome editing competences are able to integrate an endosymbiontic genome in a host genome in respect to the former existing genome architecture. Manfred Eigen would ask how to think a correct rearrangement of the molecular genome grammar.

**Symbiogenesis by communicating organisms:** Over the last 25 years, tens of thousands of papers have been published in the field of molecular biology, genetics, biochemestry, epigenetics and similar disciplines. They outline in great detail the intracellular processes of recombinant DNA, splicing, RNA-editing, coding, copying, major and fine repairs, transcription, translation, RNA processing, insertion, the role of introns and exons in "reading" processes, the complementary roles of DNAs and RNAs, even the significance and indispensable structural function of non protein coding DNA (Cavalier-Smith and Beaton 1999, Sternberg 2002, Jaenisch and Bird 2003, Baluska et al. a/b 2004, Shapiro and Sternberg 2004, Schmitt and Paro 2004, True et al. 2004, Wang et al. 2004).

Successful DNA/RNA processing requires numerous, specifically tailored enzyme proteins. In all cases, text-processing enzyme proteins and also interacting RNAs are involved in very precisely conducting these varied DNA - processing steps. Any mistakes here typically have grave and often lethal consequences for the organism.

Today there are strong reasons, that this text processing on protein-coding DNA is overruled by the genome processing abilities of DNA coding not for proteins but for active micro-RNAs (Mattick 2001, Mattick and Gagen 2001, Spotswood and Turner 2002, Turner 2002, Mattick 2003, Mattick 2005, Shapiro and Sternberg 2005). Especially the recombination of two different genomes into one as happened in early symbiogenesis we can imagine through the text processing competences of active micro RNAs.

Active micro-RNAs control and integrate large-scale structures of the chromosome. The number of different micro-RNAs is estimated to exceed several 10 000. Some of the discovered tasks of these micro-RNAs are co-suppression, suppression of transposition,

position effect variegation, start-stop signals, RNA interference, imprinting, chromosomal methylation, transvection, transscriptional and posttransscriptional gene silencing along with numerous other RNA-DNA, RNA-RNA (trans-acting RNAs), RNA-protein interactions. These active RNAs are as competent as proteins in catalysing, signaling and switching.

Cellular differentiation and phenotypic variation results primarily from variations in this high order regulation, not in the proteins themselves or in their mutations. The phenotypic variation in complex organisms is the result of a *different use of a set of protein-coding core components*. The higher order regulation in non-protein-coding genome architecture is able to manage a larger genetic data set in its phenotypic range. As far as evolutionary processes are concerned, it is naturally much simpler to change or expand a number of very small control sequences than to duplicate an entire network of protein-coding DNA. Variations of this higher order regulation can create an enormous spectrum of different protein expression profiles and we can understand why <u>one and the same gene</u> can be used for "multiple protein meanings".

Language and communication: from *linguistic turn* to *pragmatic turn*: In referring to genetic codes, signaling pathways, transcription RNA editing, etc. in linguistic terminology in order to describe essential life processes, we can rely on an unspoken and uncritical preunderstanding of language and communication, i.e. on metaphysical and/or reductionistic prerequisites: We can say that (1.) we are working in standardized experimental setups and that theoretical preconditions are not very interesting. We can say that (2.) we refer to the world of objects in the language of exact natural science whose validity claim is founded on the laws of the physical world. We might assume that observed things have a direct empirical significance that need not be further questioned because the laws of physics correspond 1:1 with the material foundations of the linguistically constructive human brain (universal syntax). We might also assume (3.) an overlying meta-system in which human populations represent one of the subsystems that communicates within itself and with co-systems in an information-theoretical framework (Witzany 1995, 1998, 2002).

The theory of science discussion about "language" and "communication" lasted 60 years, aproximately from 1920 to 1980. It consisted of two phases, and its first result was (a) the *linguistic turn*, the second result being (b) the *pragmatic turn*.

The *linguistic turn* recognizes <u>in difference</u> to former metaphysical theories of knowledge that we do not understand phenomenas, causes, effects, relations, objects, things, but sentences. Without sentences we are not able to identify, to speak about, even to think about things of outer world. Only syntactically correct sentences which are in principle formalizable are able to depict physical reality. This universalizable language of objects guarantees precision of natural sciences. But the *linguistic turn* of logical empiricism had to abandon its effort to achieve the ultimate validity claim of a physicalistic universal language. And, <u>common</u> with former metaphysical theories of knowledge linguistic turn thinkers share a solus ipse subject of knowledge.

Following Wittgenstein's analysis of obying rules (Wittgenstein 1972: 80), the theory-ofscience discourse replaced the solipsistic subject of knowledge of subjectivism and objectivism with the "ultimate opinion" of an "indefinite community of investigators" of Ch.S. Peirce. The decisive change versus Descartes and Kant's solus-ipse subject of knowledge is the "community of interpretation" in the "community of investigators". *Scientific knowledge does not exist for a solus ipse subject, but only for members of a community of interpreters.* Intersubjective validity claims of scientific knowledge requires therefore linguistic communication of meaning and consensus formation via statements. The *pragmatic turn* founded the intersubjective-communicative character of thought, experience and research and was therefore able to avoid the omnipresent subject-object dichotomy and its unavoidable consequences, solipsism and objectivism or how Thomas McCarthy characterized the monological observer perspective:" "The monological approach preordained certain ways of posing the basic problems of thought and action: subject versus object, reason versus sense, reason versus desire, mind versus body, self versus other, and so on."

The semiotics of Ch.S. Peirce is helpful in respect to describe language and communication also in non-human nature, f.e. chemical molecules functioning <u>as signs</u> in signalling pathways. It can provide the irreducible conditions for the *appropriate* analyses of sign-usage and linguistic communication via a 3-levelled semiotics. According to Peirce, (1.) a sign designates (2.) (some)thing to (3.) an interpreter (which is not a solus ipse subject but member of a linguistic community). The correct relation between the signs obey (1) syntactic rules. (2) Semantic rules decide about correct designation of (some)thing, i.e correct meaning. (3) Pragmatic rules are decicive for correct relation of sign user/sign interpreter and signs, i.e. the concrete situational context in which the sign user uses signs. This 3 levels of semiotic rules are irreducible. *Each of the 3 elements of the sign function already presupposes in its function the other two*.

If someone reduces this principally irreducible 3-levelled relation to 2 or 1 level, he falls victim to an reductive fallacy,<sup>1</sup> as happened in metaphysics, ontologics, ontosemantics, empiricism in its different forms of objectivism, physicalism, materialism, mechanicism, naturalism, constructivism, systems theory.

Pragmatic philosophy of biology and a non-reductionistic 3-levelled biosemiotics enables a clear distinction between life and the non-living. The unbridgable gap between a mechanistic and the communicative concept is that rule-governed sign mediated interactions are restricted to living individuals (-in-populations) (Witzany 2005 a, b).

**Understanding communicative competences of plants:** If we deal with "language" and "communication" in multilevel communication processes of plants we could try to describe sign-use, to extract the semiotic (syntactic, semantic and pragmatic) rules that sign use

<sup>&</sup>lt;sup>1</sup> As described by Apel The most common of these are (Apel 1974):

<sup>•</sup> **Linguistic platonism of scientific models**. sign (1) without the signified (some)thing (2) and without sign interpreter (3): Abstraction from the (apriori of the) linguistic community. The *logic of science* in the linguistic turn: the linguistic expressions or the explanatory model are the reality.

<sup>•</sup> Idealism of consciousness. (3) without (1) and without (2): Abstraction from the linguistic community; Descartes, Kant, Fichte, Hegel, Husserl: subjective/objective reason is the reality. Language is only a secondary means.

<sup>•</sup> **Pansemiotics**, metaphysical semioticism. (3) and (1) without (2): Semiotic idealism: signs and sign interpreters are reality. Everything is sign.

<sup>•</sup> **Realism, materialism, pre-Kantian metaphysics**. (2) without (1) and without (3): Reality is solely the physical-chemical laws of the material world. Sign use and sign interpretation are pre-scientific constructions.

<sup>•</sup> **Positivism of the sensory data**. (2) and (3) without (1): Leibniz, Locke, Berkeley, Hume, Popper. The material function of the sensory organs adheres to a universal syntax that is identical to the laws of physics and chemistry.

<sup>•</sup> Solipsism, realism, ontosemantics, constructivism, systems theory. (2) and (1) without (3): Subjectless, syntactic-semantic phase of the *logic of science* in Wittgenstein 1, Carnap, Russel, Tarski: Abstraction from (apriori of) the linguistic community.

follows. Perhaps we can even find some rules by identifying the non-following of rules and its consequences. The semiotic rules we will find in describing sign-use within plants will differ from those found in describing sign-use between plants of the same species, or those between different plant species. These semiotic rules of sign-use will be different from sign-use between plants and (a) bacteria, (b) protoctists, (c) animals and (d) fungae.

But, step-by step, we will be able to discover the true nature of rule-governed signmediated interaction in plants, i.e. the *communicative competences* of plants. This is the correct way to understand the plant kingdom: not as an (quasi-extraterrestrial) 3<sup>rd</sup> person observer, but as *performative participants* in the global community of communicating nature, i.e. the *Mitwelt* that all living beings share.

## REFERENCES

Apel, K.O. (1974). Zur Idee einer transzendentalen Sprachpragmatik. Die Dreistelligkeit der Zeichenrelation und die "abstractive fallacy" in den Grundlagen der klassischen Transzendentalphilosophie und der sprachanalytischen Wissenschaftslogik. In Simon, J. (ed.) Aspekte und Probleme der Sprachphilosophie. Verlag Karl Alber, Freiburg/München, pp. 283-326.

Bais, H.P. et al. (2004). How plants communicate using the underground information superhighway. *Trends in Plant Science*, 9(1): 26-32.

Baluska F. et al. (2004 a). Eukaryotic Cells and their *Cell Bodies*: Cell Theory Revised. *Annals of Botany*, 94: 9-32.

Cavalier-Smith, T. and Beaton, M.J. (1999). The skeletal function of non-coding DNA: new evidence from ancient cell chimeras. *Genetics*, 106: 3-13.

Jaenisch, R. and Bird, A. (2003). Epigenetic regulation of gene expression: how the genome integrates intrinsic and environmental signals. *Nature genetics supplement*, 33: 245-254.

Kull, K. (2005). A brief history of Biosemiotics. *Journal of Biosemiotics*, 1: 1-34. Margulis, L. and Schwartz, K.V. (<sup>2</sup>1988). *Five Kingdoms*. W. H. Freeman and Company, New York.

Margulis, L. and Schwartz, K.V. (<sup>2</sup>1988). *Five Kingdoms*. W.H. Freeman, New York.

Margulis, L. (1996). Archaeal-eubacterial mergers in the origin of Eukarya: Phylogenetic classification of life. *Proceedings of the National Academy of Sciences of the USA*, 93: 1071-1076.

Margulis, L. (1999). Die andere Evolution. Spektrum Akademischer Verlag, Heidelberg.

Margulis, L., et al. (2000). The chimeric eukaryote: origin of the nucleus from the karyomastigont in an amitochondriate protists. *Proceedings of the National Academy of Sciences of the USA*, 97: 6954-6959.

Margulis, L. and Sagan, D. (2002). *Acquiring Genomes. A Theory of the Origin of Species*. Basic Books, New York.

Margulis, L. (2004). Serial endosymbiotic theory (SET) and composite individuality. Transition from bacterial to eukaryotic genomes. *Microbiology Today*, 31: 173-174.

Mattick, J.S. and Gagen, M.J. (2001). The Evolution of Controlled Multitasked Gene Networks: The Role of Introns and Other Noncoding RNAs in the Development of Complex Organisms. *Molecular Biology and Evolution*, 18(9): 1611-1630.

Mattick, J.S. (2001). Non-coding RNAs: the architects of eukaryotic complexity. *EMBO reports*, 2(11): 986-991.

Mattick, J.S. (2003). Challenging the dogma: the hidden layer of noncoding RNAs in complex organisms. *BioEssays*, 25(10): 930.

Mattick, J.S. (2005). Das verkannte Genom-Programm. Spektrum der Wissenschaft 3: 62-69.

McCarthy, T. (1984). Translator's Introduction. In: Habermas, J., *The Theory of Communicative Action* 1, Beacon Press, Boston. p. ix.

Schmitt, S. and Paro, R. (2004). A reason for reading nonsense. Nature, 429: 510-511.

Shapiro, J.A. and Sternberg, R.v. (2005). Why repetitive DNA is essential to genome function. *Biological Review*, 80: 1-24.

Spotswood, H.T. and Turner, B.M. (2002). An increasingly complex code. *The Journal of Clinical Investigation*, 110 (5): 577-582.

Sternberg, R.v. (2002). On the Roles of Repetitive DNA Elements in the Context of a Unified Genomic-Epigenetic System. *Annals of the New York Academy of Sciences*, 981: 154-188.

Trewavas, A. (2003). Aspects of Plant Intelligence. Annals of Botany, 92: 1-20.

Trewavas, A. (2004). Aspects of Plant Intelligence: an Answer to Firn. *Annals of Botany*, 93: 353-357.

True, H. et al. (2004). Epigenetic regulation of translation reveals hidden genetic variation to produce complex traits. *Nature*, 431: 184-187.

Turner, B. M. (2002). Cellular Memory and the Histone Code. Cell, 111: 285-291.

Walker, T.S. (2003). Root exudation and Rhizosphere Biology. Plant Physiology, 132: 44-51.

Wang, Y. et al. (2004). *Beyond the Double Helix: Writing and Reading the Histone Code*. Bock, G. and Goode, J. (eds.) Reversible Protein Acetylation. Novartis Foundation, 2004.

Wittgenstein, L. (1972). Philosophical Investigations. Basil & Blackwell, Oxford pp 80e.

Witzany, G. (1993). Natur der Sprache – Sprache der Natur. Sprachpragmatische Philosophie der Biologie. Königshausen & Neumann, Würzburg.

Witzany, G. (1995). From the "logic of the molecular syntax" to molecular pragmatism. *Evolution and Cognition*, 1(2): 148-168.

Witzany, G. (1998). Explaining and Understanding LIFE. Semiotica, 120(3/4): 421-438.

Witzany, G. (2000). *Life: The Communicative Structure. A New Philosophy of Biology*. Libri Books on Demand, Norderstedt.

Witzany, G. (2002). *Reduction of biological phenomena? Deficits of systems theory and the alternatives*. Sign Processes in Complex Systems, Schmitz, W. (ed), Mouton de Gruyter, Berlin/New York, pp 303-307.

Witzany, G. (2005 a). From biosphere to semiosphere to social lifeworlds. Biology as an understanding social science. *Journal of Biosemiotics*, 2 (forthcoming).

Witzany, G. (2005 b). Natural history of life: History of communication logics and dynamics. *SEED Journal*, (forthcoming).