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From Umwelt to Mitwelt: Natural laws versus rule-governed sign-mediated interactions (rsi's)

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Abstract

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Within the last decade, thousands of studies have described communication processes in and between organisms. Pragmatic philosophy of biology views communication processes as rule-governed sign-mediated interactions (rsi's). As sign-using individuals exhibit a relationship to following or not-following these rules, the rsi's of living individuals differ fundamentally from cause-and-effect reactions with and between non-living matter, which exclusively underlie natural laws. Umwelt thus becomes a term in investigating physiological influences on organisms that are not components of rsi's. Mitwelt is a term for the investigation of all rsi's of organisms. Living organisms are never solus ipse subjects of semioses, but share common sets of rules and signs. Life depends decisively on symbiotic communities. Serial Endosymbiotic Theory proved that the evolution of higher eukaryotic superkingdom was a merger of ancestral bacteria. The integration of bacterial genomes into eukaryotic genomes was also a step from analog to symbolic genetic codes. Now we know, that so-called 'junk DNA' has higher order regulatory functions on genome architecture and protein coding DNA plays only the role of a structural vocabulary.

Keywords: Mitwelt; epigenetic apriori; symbiotic interdependence; geMetaCode.

1. The supplement of the *Umwelt*-concept with a *Mitwelt*-concept

Within the last decade, the tendency to describe interactions in and between organisms as communication processes has continued to grow. Intra- und interorganismic communication is supplemented by meta-organismic communication that is between members of different species, genera and organismic kingdoms. An explosion of research in the field

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1 of symbioses proved that, in fact, life on our planet is entirely dependent
2 upon functioning symbiotic interaction communities (Zook 1998; Kowal-
3 lik 1999; Wagner et al. 1999). A pragmatic philosophy of biology as basis
4 of a three-leveled biosemiotics found and justify communication processes
5 as rule-governed sign-mediated interactions (Witzany 1993a, 1993b, 1995,
6 2002a, 2002b, 2005b). Sign use by interaction partners simultaneously
7 obeys syntactic, semantic, and pragmatic rules in principle (Witzany
8 2005b, in press).

9 The conditions on the planet's surface *without* living organisms are de-
10 termined entirely by the sun's energy and the laws of physics and chemis-
11 try (Margulis 1999). A planet *with* living organisms, i.e., with biosemiotic
12 processes deviates considerably from this scheme. The gas composition
13 and temperature will vary in a manner that cannot be predicted exclu-
14 sively by the laws of physics and chemistry alone. Such a planet contains
15 incompatible gas mixtures and temperatures whose relatively stable bal-
16 ance is actively controlled by organisms.

17 The interaction between organisms and matter is one in which organ-
18 isms interpret and structure their abiotic environment according to bi-
19 ological principles. The relationship to other organisms is a communicative
20 one: their mutual behavior underlies changeable rules, within the frame of
21 natural laws, more precisely (semiotic) rules of sign use with which the bi-
22 ological individuals interact, i.e., coordinate and organize. The difference
23 is that organisms cannot develop such a 'to follow or not follow' relation-
24 ship with natural laws, but underlie them in the strict sense.

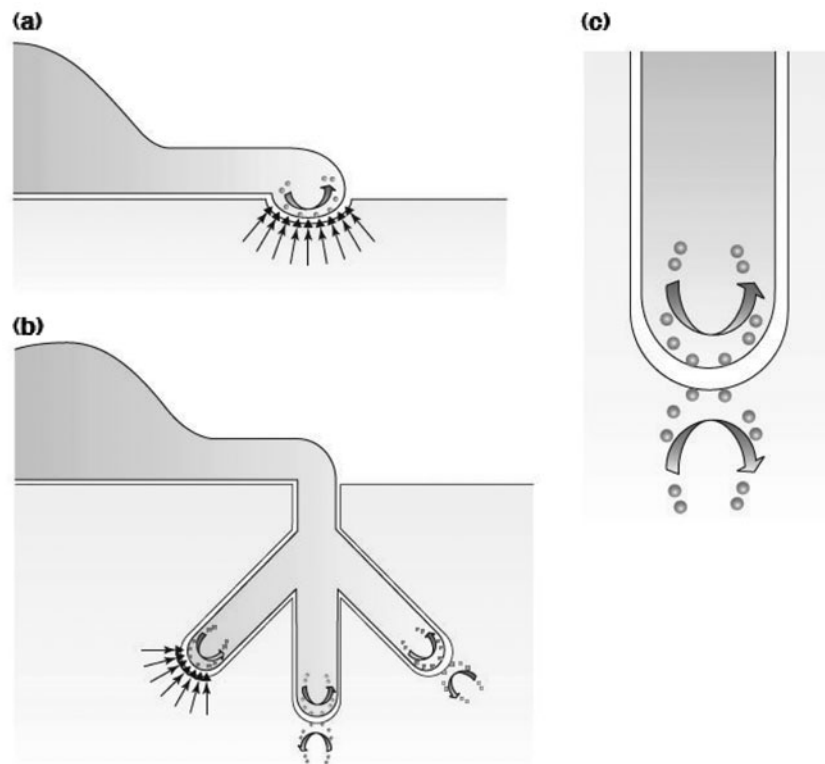
25 The *Umwelt* concept cannot do justice to the fundamental differences
26 between natural laws and rsi's because this concept reduces rsi's to the
27 information transmission effect and therefore to a level of coding and
28 decoding via an individual organism's physiological sensory organ. The
29 intersubjective-communicative character of the rsi's, and therefore the
30 relationship to following or not-following commonly shared rules of sign
31 use, does not manifest itself here.

32 In investigating communication processes in and between organisms, it
33 is therefore sensible to supplement the *Umwelt* concept with a *Mitwelt*
34 concept (Witzany in press). The *Mitwelt* concept underlines the difference
35 between the cause and effect reactions in natural laws and rsi's: *Umwelt*
36 thus becomes a helpful term in investigating those physiological influ-
37 ences on organisms that are not components of rsi's. *Mitwelt* is a term
38 for the integrative investigation of all rsi's of organisms, i.e., all intra-,
39 inter- and metaorganismic communication processes themselves and their
40 developmental history.

41 For example, plants maintain two types of membrane domains that re-
42 semble the neuronal and immunological synapses of animal cells (Baluska

1 et al. 2005). The *first* one transports Auxin and allows the highly plastic
 2 development of plants. The activity of this developmental plant synapse is
 3 modulated by two physical factors — light and gravity. The developmen-
 4 tal plant synapse assembles those molecules of non-living matter which
 5 are necessary to structure the plants non-biological environment accord-
 6 ing to biological principles, i.e., molecules become features of signs for
 7 an interpreting organism. There, the *Umwelt* term is useful in describing
 8 how organisms develop themselves by metabolizing within natural laws.

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35 Figure 1. 'Immunological plant synapses for cell-to-cell communication between plant host
 36 cells and their pathogens, parasites and symbionts. (a) Closely apposed plasma membranes
 37 of intruder and host cell during a penetration attempt. If the host cell succeeds in effectively
 38 forming a papilla then this synaptic cell-to-cell communication is terminated. (b) Alternat-
 39 ively, the intruder might penetrate deeply into the host plant cells and then immunological
 40 plant synapses support haustorial complexes and mycorrhizal arbuscles. (c) During the initia-
 41 tion of a Rhizobia-plant symbiosis, bacteria organize infection threads, the tips of which
 42 represent immunological plant synapses specialized for transporting bacteria deeply into root
 tissues' (figure 1 and text in Baluska et al. 2005: 108).

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1 The *second* type of plant synapse resembles the immunological synapse
2 of animal cells and allows plants to respond to pathogen and parasite at-
3 tacks (Baluska et al. 2005) as well as to establish stable symbiotic interac-
4 tions with rhizobia bacteria and fungal mycorrhiza (Baluska et al. 2005;
5 see also Estabrock and Yoder 1998; Yoder 1999; Keyes et al. 2000; Kah-
6 mann and Basse 2001; Engelberth et al. 2004; Imaizumi-Anraku et al.
7 2005).

8 A limited number of chemical messenger substances is available to
9 maintain and simultaneously conduct the communication between (a)
10 root cells of three different types, (b) root cells and microorganisms, (c)
11 root cells and fungi, and (d) root cells and insects (Bais et al. 2004; Call-
12 away 2002; Dessaux 2004; Dunn and Handelsman 2002; Teplitski et al.
13 2000; Walker 2003; Fleming 2005). The communication process in the
14 root zone is generally intra-, inter- and metaorganismic and requires a
15 high communicative competence in order to be successfully interactive
16 on all three levels and to distinguish messenger molecules from ‘noise’
17 (Federle and Bassler 2003; Hirsch et al. 2003; Sharma et al. 2003). Here,
18 the *Mitwelt* term is useful: its objects are primarily rule-governed sign-
19 mediated interactions, which depend on coherence of signs and three-
20 leveled rules, and not on natural laws alone.

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23 2. The epigenetic a priori of semioses

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25 As in the case of semiotics, biosemiotics also depends on the a priori of
26 bodies, i.e., living organisms: without living organisms there are *no* intra-
27 inter and metaorganismic semioses, transcription, translation, copying,
28 coding, splicing, self-splicing (group I and group II introns), i.e., the
29 whole complexity of semiotic processes. Rule-governed sign-mediated
30 interactions depend on living bodies in principle. Living bodies are the
31 *epigenetic a priori of semioses*. Only in rare exceptions living bodies are
32 monads, but they are in any case involved in a commonly shared rule-
33 constituted genetic set up with their descendants.

34 If signs are used by humans, there is, according to Peirce, a non-
35 reducible three leveled relationship between (1) the sign-user/sign-
36 interpreter and (2) the signs which designate (3) (some)thing. According
37 to Morris the relationship: (a) between sign-user/sign-interpreter and
38 signs is subject to pragmatic rules, (b) between signs and the designated
39 (some)thing is subject to semantic rules (c) between signs and signs is
40 subject to syntactic rules. According to Wittgenstein (1968) rule obeying
41 sign-users/interpreters are never *solus ipse* subjects (as with Descartes,
42 Kant, Hegel, Husserl, Carnap, Frege, Russel, Tarski, and Popper) but

1 always *performative participants* of communicating communities. Using/
2 interpreting signs is social interacting.

3 Integrating this pragmatic turn thinkers we are able to avoid the main
4 problem of all variations of philosophy of consciousness: how to make
5 the move from a state of *solus ipse* consciousness to a state of mutual
6 agreement, coordination and cooperation.

7 Therefore, semiotics as well as biosemiotics are really social sciences
8 (Witzany 2005b). Their research is directed towards signs, their use, their
9 meaning, their syntactic combinations (Noeth 2000; Kull 2005). Because
10 one sign alone is not a sign and without a sign-using community there is
11 neither meaning, nor interpretation or linguistic action, i.e., active sign
12 use, the social component is the decisive one. In Wittgenstein's language
13 game it is the analysis of obeying rules, in Peirce it is the 'ultimate opin-
14 ion' of an 'indefinite community of investigators' which refutes the *solus*
15 *ipse* subject of knowledge of Descartes and Kant in principle.¹ It is never
16 the role of an interpreter, because 'the interpreter' as *solus ipse* subject
17 doesn't exist (Witzany 2005b). Interpreting is a social action, and the 'in-
18 terpretant' is an internalized commonly shared background knowledge of
19 a historically evolved linguistic community.

20 From this point of reflection we can describe sign use in non-human
21 nature also. But not from an monological *solus ipse* perspective as a cog-
22 nitive simulation of an (quasi-) extraterrestrial observer, but with the
23 knowledge that living bodies are involved in social lifeworlds which de-
24 pend on social lifeworlds of (a) the same and parallel (b) other species,
25 genera, organismic kingdoms. All living organisms of the eukaryotic
26 superkingdom *depend decisively* on functioning symbioses with microbial
27 social lifeworlds. In examining the cells of the human body, 10 percent
28 stem from the human individual and up to 90 percent are symbiotic mi-
29 croorganisms (Blech 2000).

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32 **3. Evolution of the eukaryotic superkingdom by genomic integration**

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34 Another example applying the *Mitwelt* concept is the Serial Endosymbi-
35 otic Theory. The SET is so revolutionary because it reversed the evolu-
36 tion vector from ramification to unification. Eukaryotic cells, according
37 to Margulis, are the result of merging several different ancestor genomes,
38 that of (1) thermoplasmic archaeobacteria with (2) motile spirochaeta-like
39 eubacteria. This was followed by a merging with (3) aerobic organisms.
40 The final step was the merging with (4) photosynthetic bacteria. One inte-
41 grated genome was sufficient in the merger of archae- and eubacterium.
42 In the protocista two integrated genomes were necessary, in the fungi

1 three, in animals at least four, and in the plant kingdom (350 million years
2 ago) at least five. (Margulis 1996, 1999, 2004; Margulis and Schwartz
3 1988; Margulis et al. 2000; Margulis and Sagan 2002; Cavalier-Smith
4 2002; Stechmann and Cavalier-Smith 2003).

5 From the biosemiotic point of view this symbiogenetic process was
6 a change *from metaorganismic* communication, i.e., rsi's between two in-
7 dividuals who lived in symbiosis, to an *intraorganismic* communication
8 process. In the latter, two different genomes integrated into one at the
9 correct sequences, at the correct genome ratio, (i.e., the genome architec-
10 ture). It had to involve a correct integration of entire gene-blocks. The
11 SET demonstrates that complex genomic makeups can be passed on di-
12 rectly and not through step-by-step development via chance mutations
13 (Witzany 2005b). One scenario of how this integration process of two dif-
14 ferent genomes could take place can be imagined by the phenomenon of
15 horizontal gene transfer (Wagner et al. 1999; Wolf 1999, 2000; Jain et al.
16 1999; Jain et al. 2003; Xie et al. 2004; Timmis et al. 2004). As suggested
17 (Witzany 2005a, 2005b, in press) these (symbiogenetic and HGT) pro-
18 cesses are not changes in aggregate status solely but undoubtable bio-
19 semiotic ones: They are highly competent DNA textprocessing proce-
20 dures (Frost et al. 2005; Bordenstein and Reznikoff 2005; Gogarten and
21 Townsend 2005). Thomas and Nielsen identified 17 steps of integration
22 performance (see Fig. 2).

23 The DNA transfer between prokaryote cells include transformation,
24 transduction and conjugation which depend on certain mobile genetic
25 elements such as plasmids, bacteriophages and transposons. In this
26 processes that 'agents' are the 'natural genetic engineers' (Frost et al.
27 2005).

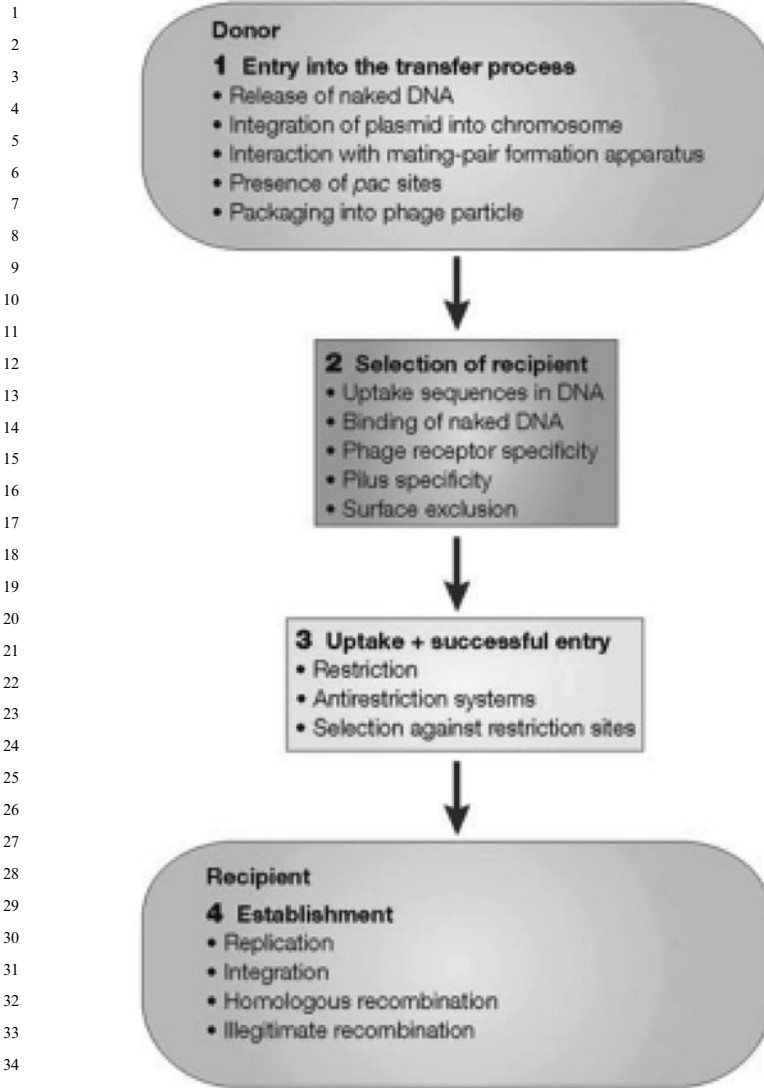
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30 **4. Analog — symbolic (prokaryotic genome — eukaryotic genome)**

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32 The step from prokaryotic to eukaryotic cells and the recombination of
33 up to 5 (or maybe even 7) different genomes into one, as occurred in the
34 evolution of plant cells was also the step from a nearly complete analog
35 proteinencoding DNA to a genome architecture of analog and increas-
36 ingly symbolic sequences (Witzany 2005b). As higher-developed eukary-
37 otic multicellular organisms show, this analog/symbolic ratio changed
38 into a proportion in humans, for example, of 3 percent proteinencoding
39 DNA (which is nearly identical to that of mice, namely 99 percent) and
40 97 percent non-proteinencoding DNA.

41 Ten years ago this non-proteinencoding DNA was not the center of
42 research interests and therefore named 'junk' DNA. While there is no



36 Figure 2. 'The process of horizontal gene transfer. A schematic outlining the stages through
37 which DNA must go on its journey from donor to recipient bacteria. The process begins with
38 DNA in a potential donor cell becoming available and ends when this DNA becomes a func-
39 tional part of a recipient cell's genome' (figure and text in Thomas and Nielsen 2005: 719).

1 relation between the complexity of organisms and the quantity of protein-
 2 coding DNA, but an obvious relation between complexity of organisms
 3 and non-protein coding DNA, this ‘junk’ DNA became interesting. It
 4 does not code for proteins but for RNAs, especially for a type of micro-
 5 RNAs (Cavalier-Smith and Beaton 1999; Mattick 2001, 2003, 2005; Mat-
 6 tick and Gagen 2001; Shapiro and Sternberg 2005). These micro-RNAs
 7 are as competent as proteins in DNA/RNA editing. Some may term this
 8 discrete structure of eukaryotic DNA (that doesn’t indicate analogous for
 9 what it codes) digital (Emmeche and Hoffmeyer 2005). But this informa-
 10 tion theoretical description is a more or less technical term, whereas ‘sym-
 11 bolic’ is a better description for the phenomena as such (Cvrcková and
 12 Markos 2005; Witzany 2005b).

13 Some of the discovered tasks of these micro-RNAs are co-suppression,
 14 suppression of transposition, position effect variegation, start-stop sig-
 15 nals, RNA interference, imprinting, chromosomal methylation, transvec-
 16 tion, transcriptional and posttranscriptional gene silencing along with
 17 numerous other RNA-DNA, RNA-RNA (trans-acting RNAs), RNA-
 18 protein interactions (Mattick and Gagen 2001). Today we may say that
 19 cellular differentiation and phenotypic variation results primarily from
 20 variations in this high-order regulation, not in the proteins themselves,
 21 thus non-protein coding DNA bears the architecture of eukaryotic com-
 22 plexity (Mattick 2001).

23

24

25 **5. Structural (protein-code-) vocabulary and its higher-order regulation**

26

27 The phenotypic variation in complex organisms is then the result of a *dif-*
 28 *ferent use* of a set of protein coding core components. We can say that in
 29 higher eukaryotic organisms we find 3 percent protein coding DNA as the
 30 structural vocabulary and 97 percent non-protein coding DNA which has
 31 higher-order regulatory and constitutional functions that are decisive for
 32 expression, differentiation, development, (i.e., coordinated expression in
 33 time). I postulated these higher order regulatory and constituting func-
 34 tions as a consequence of the pragmatic philosophy of biology approach
 35 already in 1993 and in a further developed version in 2000 in terms like
 36 ‘innovation-code, text-generating-code, evolution-code’ (Witzany 1993b,
 37 1997, 2000).

38 In an article in S.E.E.D. Journal (Witzany 2005b), I put it in concrete
 39 as the genome-editing *MetaCode*. This non-protein coding *geMetaCode*
 40 has regulatory and constituting functions in chromosomal methylation.
 41 These functions decide about different signaling pathways of the same
 42 genetic setups through different rules of gene silencing and special start

1 and stops via alternative splicing. With this chromosomal methylation,
 2 organisms are able to handle ‘multiple protein meanings’ (Ast 2005) of
 3 one and the same genetic data set. As shown by some epigeneticists, these
 4 (*geMetaCode*-) functions are influenced and altered by environmental
 5 and other influences which are heritable but *do not involve or depend on*
 6 *mutations* of the DNA itself (Jenuwein and Allis 2001; Spotswood and
 7 Turner 2002; Sternberg 2002; Turner 2000, 2002; Jaenisch and Bird 2003;
 8 True et al. 2004; Wang et al. 2004; Waterland and Jirtle 2004).

9 The proposed *geMetaCode* integrates the features of (1) non-
 10 protein-coding DNA, (2) DNA which codes alternatively for (micro)RNAs
 11 and proteins, which depends on situational contexts and (3) the protein-
 12 coding DNA. This enables the (epigenetic) body and genome to interact
 13 *in time* over the whole lifetime, in the expression pathways of early devel-
 14 opment, the body axis, extremities, up until the adult individual. Or, as in
 15 plants, the endless growth and development (Trewavas 2001, 2003, 2005)
 16 based on *one and the same* protein coding vocabulary. The latter is used
 17 depending on the developmental context as epigenetic orientation of the
 18 plants, and therefore by the non-protein-coding regulatory, constitutional
 19 and generating functions of *geMetaCode*.

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22 6. Genetic backup insurance against mutational faults

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24 Plants can overwrite their genetic code they inherited from their parents
 25 and revert to that of their grand or great-grandparents (Lolle et al. 2005;
 26 Weigel and Juergens 2005; Pearson 2005). This contradicts traditional
 27 DNA textbook conviction that children simply receive combinations of
 28 the genes carried by their parents. Now a backup code was found that
 29 can bypass unhealthy sequences inherited from the parents and revert
 30 to the healthier sequences possessed by their grandparents or great-
 31 grandparents. As shown by a research team, plants are able to replace ab-
 32 normal code sequences of their parents with the regular code possessed by
 33 earlier generations.

34 Is it therefore necessary that not only the genetic setup of the parents is
 35 inherited but also that of the grand-parents and former ancestors? What
 36 is proposed is that higher order regulating micro RNAs — which func-
 37 tion as expressions of *geMetaCode* — ensure ancestor genome structures,
 38 which overrule protein-coding DNA under certain circumstances like
 39 stress. Such stress situations that could be dangerous for survival, could
 40 trigger plants to revert to the genetic setup of their ancestors which per-
 41 haps is more competent to deal with this circumstances than that of their
 42 parents.

1 It means that the (pragmatic) situational context of a living plant body
 2 (neuronal, hormonal, inflammatory, immune, stress) may induce epige-
 3 netic intervention on *geMetaCode*, i.e., active micro-RNA's activate a
 4 certain signaling pathway network which is able to restructure semantics
 5 of a genetic setup. By initiating methylation- and histone-modifications,
 6 certain silencings, start and stops, alternative splicing processes constitute
 7 alternative sequences, so that in existing genome architecture not the in-
 8 herited parental sequences are translated and transcribed but the backup
 9 copy of grand or great-grandparents.

10 Under normal conditions, genetic setup is in use, which stems from the
 11 parents. These research results are indications that not only a combina-
 12 tion of parental genes is inherited, but also ancestral genome-regulating
 13 features in 'non-coding' DNA, which enables alternative splicing path-
 14 ways, i.e., a *different use and multiple protein meanings of one and the*
 15 *same genetic data set* (Lolle et al. 2005; Weigel and Juergens 2005; Pear-
 16 son 2005).

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18

19 7. Conclusions

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21 This contribution could be an approach to resolve the contradiction of
 22 neo-Darwinism and neo-Lamarckism: The protein-coding DNA is not
 23 subject to evolutionary remodifications that lead to new abilities or new
 24 organisms, but is subject to chance mutations which can alter *existing*
 25 genotypes. The non-protein coding DNA, with its higher-order regulatory
 26 functions is subject to evolutionary remodifications *that are heritable but*
 27 *also reversible* and that regulate the structural vocabulary of protein-
 28 coding DNA. The *geMetaCode* is subject of encoding acquired abilities,
 29 i.e., to higher-order regulatory and constitutional functions, which may
 30 reorganize *and generate* new and altered genotypes with phenotypic con-
 31 sequences by alternative use of *one and the same* protein-coding DNA.

32

33

34 Note

35

- 36 1. The 'ultimate opinion' of the 'indefinite community of investigators' of Peirce doesn't
 37 resolve the discrepancy between (artificial) scientific languages and the ultimate meta-
 38 language of everyday language. Only the pragmatic action theory was able to found and
 39 justify rule-governed sign-mediated interactions as the a priori of the intersubjective-
 40 communicative character of thought, research, progress of knowledge, *and* everyday
 41 language. In contrast with Peirce, the pragmatic action theory doesn't focus on the inter-
 42 preter of signs in a process of interpretation, but on the *preconditions* for his ability to
 interpret, i.e., his a priori reliance on a social lifeworld that was the basis for his learning

1 to speak and to act communicatively. In my opinion, Josiah Royce with his 'community
2 of interpretation' followed by George Herbert Mead and his 'community of universal
3 discourse' were more radical in reaching a post-Kantian communicative community as
4 subject of knowledge.
5

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