

# Preface

## Why Biocommunication of Soil Microorganisms?

Although research on signal-mediated interactions of microorganisms – especially prokaryotes – in the ocean is a broad field of investigation, research on communication between soil microorganisms is not as well developed in comparison. This contradicts the importance of the roles of soil bacteria on parasitic and symbiotic interactions with plants, animals, and fungi in dry, wetland, and wasteland ecologies and in flood waters and their consequences on terrestrial life. Additionally, it is equally important to investigate the main sources of genetic innovation, exchange, and storage of soil bacteria (such as decomposers, nitrogen fixers, disease suppressors, aerobes, anaerobes, actinobacteria, and sulfur oxidizers), i.e., the roles of phages, plasmids, and related genetic parasites. Focusing on these viral colonizers and viral-derived regulatory elements of all prokaryotic life is important because they determine the interactional competences of soil bacteria and their group identity, i.e., their competence in producing and emitting shared signal molecules, interpreting incoming messages via appropriate receptors, measuring them, and generating appropriate response behaviors. Although these factors have been investigated by physiological, chemical, and mechanistic perspectives, it has become increasingly clear that signal-mediated interactions, i.e., biocommunication processes, additionally rely on semiotic rules that have to be correctly followed or biocommunication will not occur. This means that the rules of signal use are not strict (natural) laws: although very conservative, rules of signal use may be changed or even generated *de novo* for adaptational purposes.

If we speak of biocommunication of soil microorganisms, we first must become clear with the up-to-date terms of communication (and with the signaling system, which is used to communicate what we call language). Therefore, we should rely on the results of the pragmatic turn in the philosophy of science discourse in the seventies and eighties of the last century, which was the result of a discourse between 1920 and 1980 to clarify the conditions for generating correct sentences in science.

Communication is defined as an interaction between at least two living agents, which share a repertoire of signs (which represents a kind of natural language) that are combined (according to syntactic rules) in varying contexts (according to pragmatic rules) to transport content (according to semantic rules).

These three levels of semiotic rules are complementary parts of any natural language or code. If one level is missing, according to Charles Morris (see Morris 1946), we cannot seriously speak of language or communication. So the most recent definition of communication is: sign-mediated and rule-governed interactions, i.e., interactions that depend on a commonly shared repertoire of signs and rules of sign-use. However, these features are lacking in abiotic interactions. Additionally, we know that mathematical and mechanistic theories of language are less helpful in investigations on natural languages and real-life communication processes because such theories cannot explain typical features of living agents that communicate, which are not formalizable, i.e., for which no algorithm is available, such as the *de novo*-generation (innovation) of sentences/sequences. This means that no natural language or code speaks or codes itself but needs living agents that are competent in using such languages or codes (Witzany 2010).

In the biology of the twentieth century, the physiology of all kinds of cells, tissues, organs, and organisms of all organismic kingdoms was the mainstream direction in biological research and experiments. In the 1970s, an increasing use of “communication” as a metaphor also occurred in biology. During the last decade of this period, interest in communication (no longer being used as a metaphor) within and between organisms overtook that of the pure physiological understanding of organisms. Cell-to-cell communication now dominates contemporary cell biology, including an enormous knowledge about a great variety of signaling pathways serving for both organization and coordination of production, release, uptake, and processing of “information” within and between cells.

In parallel, the use of “language” as a metaphor increased from the middle of the twentieth century with growing knowledge about the genetic code. Most of the processes that evolve, constitute, conserve, and rearrange the genetic storage medium DNA are terms that were originally used in linguistics, such as nucleic acid language, genetic code, “codes without commas” (F. Crick), coding, copying, translation, transcription, sequence homology, etc. Meanwhile, the linguistic approach also lost its metaphorical character and the similarity between natural languages/codes, and the genetic storage medium DNA are not only accepted but are adapted in epigenetics, bioinformatics, biolinguistics, protein linguistics, and biosemiotics. The advantage of methodical adaptation of communication and linguistic terminology is in having appropriate tools for differentiation at specific levels, which is otherwise difficult to describe nonreductively by pure physiology.

This means that language-like structures and communication processes occur at the bottom of living nature. Language and communication are not at all evolutionary inventions of humans, nor are they anthropomorphous adaptations to describe nonhuman living nature. It simply became, and still becomes, obvious that every coordination and organization within and between cells, tissues, organs, and organisms needs signs, i.e., chemical molecules that serve as signals or symbols

in messages or serve as vital indicators of environmental conditions. Because no code codes itself, as no language speaks itself, these signs need to be sensed and interpreted in a correct way by biological agents, i.e., there must be subjects/representatives of sign production and sign interpretation. This means that sensing, as well as interpretation, may fail with the result of nonappropriate behavior and even fatal consequences for cells, tissues, organs, and organisms.

The method of analyzing any part of a machine in detail to get a picture of its whole functional blueprint, which can then be used to reproduce or manipulate it, or to produce an even more perfect one (taking genetic engineering as an example), is still useful if we are dealing with machines. However, growing evidence of the aims of several biological processes makes it doubtful now whether investigating organisms with this mechanistic attitude will still be useful in the future:

### ***On the Interorganismic Level (Between Same and Related Organisms)***

Communication between cells, cellular parts, tissues, organs, and organisms is far from being a procedure, which can be reduced to mechanistic input/output or cause/reaction descriptions. It is evident today that communication processes between living organisms include a variety of circumstances and competences that must be fulfilled in parallel if communicative acts are to have successful consequences, such as common coordination.

First of all, no single organism is able to communicate as an emerging property. It must be a community, a society, or a swarm of organisms that each share an identity (group) and a competence to sense others as being part of this identity or not (self/nonself differentiation competence), even if this competence is shared genetically solely. To communicate, it is necessary that an organism has some skills that serve as signs (signals, symbols), such as chemical molecules either produced directly by itself or as secondary metabolites or even molecules in the surroundings that are not produced by the organism but can still be manipulated, according to the organismic needs.

Secondly, organisms must share a competence to use these signs in a coherent manner, which means using these signs in a strict temporal and spatial context. In most cases, it is not just one signaling molecule but several that are combined in a certain manner to transport messages (information). This represents a common feature of sign-use in communication processes, which is called their correct combination or syntax.

Thirdly, organisms are part of a habitat in which they live together with similar organisms of the same or related species, and in some cases, with an abundance of nonrelated organisms of other kingdoms. This context exactly represents the natural history of organismic swarms or communities in which they – and this is only a recently experienced feature – evolved and developed certain abilities to

appropriate response behaviors according to their survival. These include sensing, learning, and memory, which are the preconditions for faster adaptations.

Finally, the signaling molecules, which serve as signs, transport messages with meanings (semantics). The informational (semantic) content, which is transported, triggers certain response behaviors by the same or related, or even unrelated, organisms. Interestingly, the signal sequence or signal content does not necessarily depict a single meaning, i.e., function but can vary according to different situational contexts. This means that identical signs can transport a variety of different messages according to different contextual needs. This is important in very dense ecological habitats (as demonstrated below), for example, in the oral cavity of humans where communication of up to 500 different microbial species must function in order to prevent oral diseases. The different uses of identical signs (sequences) enable the generation of dialects within same species that can transport messages, which are microecosphere-specific. These include a very sensitive self/nonsself recognition between slightly differently adapted populations of the same species in the same ecological habitat.

Although sign-mediated interactions (i.e., communication processes) are very reliable in most cases, they do not function mechanistically in a strict sense. Syntax (combination), pragmatics (context), and semantics (content) must function in parallel to ensure and optimize coordination and thus survival of group members. These semiotic rules do not function mechanistically but may be varied, deleted, or, in certain circumstances, generated *de novo*. Additionally, semiotic rules do not function by themselves but need semiotic subjects, i.e., living organisms that use such rules. If no living organism is present, semiotic rules, signs, and communication are absent. Although highly conserved semiotic rules are modifiable, environmental circumstances, such as stress, trigger adaptational responses. In such cases, signals may transport new messages, which previously did not exist, broadening the communicative competences of organisms, i.e., broadening evolutionary capabilities. This is different in the case of abiotic processes, where semiotic (syntactic, pragmatic, semantic) rules of sign-use are unnecessary as natural laws are sufficient alone. No semiotic rules are used or necessary for water molecules to freeze into ice.

### ***On the Intraorganismic Level***

During the last 2 decades, more and more indicators replaced the mechanics of intracellular generation and use of signaling molecules by interactive information processing between parts of the cellular organism. Natural genetic engineering (Shapiro 2009) identified the whole processing of most steps and substeps of genetic content arrangement and rearrangement necessary for adaptational purposes in the fields of replication, transcription, translation, repair, marking (epigenetics), and immune functions. In contrast to former assumptions of DNA as a stable genetic information storage medium, which can be altered only by errors (mutations) or

damage, it became increasingly clear that the driving force of evolutionary novelty is a vast abundance of highly dynamic, mobile networking agents. These agents are active shortly after transcription out of the DNA storage medium and include RNAs such as the prominent tRNA, mRNA, and rRNA agents and a great variety of regulatory RNAs, most of them small, noncoding RNAs before translational processes into proteins (Witzany 2009). Also, transposons and/or retrotransposons, which represent mobile genetic elements, serve as competent genetic content operators.

Recent research indicates that all of these noncoding RNAs with its higher order regulatory functions, as well as the three prominent RNA agents mentioned above, and the whole range of transposable elements are remnants of former viral or viral-like agents (Villarreal 2005, 2009; Witzany 2010). It also became clear that the evolutionary role of viruses is not a derivative one as suggested by models that interpreted viruses (1) to be escaped as transcripts out of cellular organisms or (2) as descended from free-living bacteria and having lost their cellular functions, as with the regressive hypothesis. In contrast to this virus-first hypothesis is the identification of a high abundance of viral genetic sequences that are not found in any cellular DNA content (Forterre and Prangishvili 2009, Koonin 2009, Villarreal and Witzany 2010). This is in agreement with the early RNA world theory, where cellular life evolved after viruses. In this new perspective, cellular DNA is the preferred habitat for persistent viral settlers, which not only integrate but rearrange and transfer viral competences to the cellular host and therefore broaden cellular evolutive and developmental potentials.

The interrelation between nucleic acid language and linguistics is predominant in the field of bioinformatics, which is a successful tool in genetic comparison techniques such as phylogenetic analyses and comparative genomics. For several decades, it was assumed that the molecular syntax of genetic sequences determined the meaning (semantics) of these sequences according to Manfred Eigen. With the rise of epigenetics, it became clear that different marking (methylation) patterns of an identical genetic sequence can lead to different reading patterns and, consequently, to the production of different products from this genetic data set. Changing environmental circumstances such as stress or nutrient availability may alter these markings (histone modifications, methylation patterns), which may lead (not necessarily) to inheritable features (Jirtle and Skinner 2007). The evolution of epigenetic marking remained a mystery for a long time. According to the virus-first hypothesis, epigenetic marking is a viral competence. All viruses mark their genome in order to be able to differentiate self from nonself agents. If we assume that viruses are evolutionarily older than cellular life, epigenetic marking is a viral competence transferred to cellular life to broaden host informational content and evolutionary as well as developmental capabilities.

The integration of viral features to cellular hosts is not a rare event. Considering that viruses are ten times more abundant in the environment than cellular microorganisms, which all are infected by phages and plasmids, it seems rather doubtful that this rare habitat of cellular genomes contains free sequence space that is not subjected to competing viral settlers. Therefore, I predict that future investigations will show a much higher level of these persistent viral agents.

## ***In Vitro Analyses Lack Context-Dependent Behaviors of Real Life Habitats***

*In vitro* investigations focus on ecological setups, which do not represent the entire interactional context in which an organism is involved *in vivo*. The evolution and development of each organism depends on the *in vivo* habitat with its inter-, intra-, and transorganismic triggers on genetic reading patterns, which are absent from *in vitro* setups. Therefore, it is likely that isolated organisms in laboratory setups lack a variety of features, which would be triggered in *in vivo* habitats by natural circumstances such as symbiotic and parasitic microorganisms. This may lead to restricted conclusions on their intra- and interorganismic biocommunicative capabilities.

## ***Biocommunication of Soil Microorganisms***

As a consequence of these findings, I tried to integrate this biolinguistic and biocommunicative features into a uniform description of all key levels of communication within the organismic kingdoms of plants, fungi, animals, and bacteria, based on recent empirical data (Witzany 2010). Accordingly, biocommunication occurs on three levels: (1) intraorganismic, within an organism, (2) interorganismic, between the same or related species and (3) transorganismic, between organisms that are not related.

The biocommunicative approach demonstrates that cells, tissues, organs, and organisms coordinate and organize by communication processes and that genetic nucleotide sequence orders in cellular and noncellular genomes are structured like language, i.e., they follow combinatorial (syntactic), context-sensitive (pragmatic), and content-specific (semantic) rules. Without sign-mediated interactions, no vital functions within and between organisms can be coordinated. This feature is absent in nonliving matter. Additionally, the biocommunicative approach investigates natural genome editing competences of viruses and viral-like agents. Natural genome editing from a biocommunicative perspective is competent agent-driven generation and integration of meaningful nucleotide sequences into preexisting genomic content arrangements and the ability to (re)combine and (re)regulate them according to context-dependent (i.e., adaptational) purposes of the host organism.

It became increasingly clear that, particularly in these investigations, in contrast to the relatively rich database concerning the role of bacteria and their obligate viral settlers in the oceans, the basic knowledge of biocommunication in soil microorganisms is far from satisfactory. Although soil habitats are equally as important to terrestrial organisms as the sea is to aqueous organisms, main focus was not on soil organismic life. To give a recent overview on the biocommunication of soil microorganisms, Ajit Varma encouraged me to edit this book.

## ***Contributions to the biocommunication of soil microorganisms***

After the introduction in which a general overview on the key levels of communication of bacteria is given in the first section on intracellular biocommunication of soil bacteria, Stephen Abedon begins with the various levels of biocommunication of phages with soil microorganisms. Robert Armon gives a systematic overview on the interactional patterns of soil bacteria and their bacteriophages. Kurt Williamson reports on advances of our understanding of soil viral ecology. K.V. Srividhya and S. Krishnaswamy describe identification methods of persistent viral agents and their defectives (prophages and phage remnants) within soil microbials. Omar Bagasra and Gene Pace report on the important role of transposable elements in genome formatting of soil microbes. Makoto Kimura, Guanghua Wang, Natsuko Nakayama, and Susumu Asakawa investigate the role of bacteriophages on soil bacteria in rice paddies. Antonet Svircev, Susan Lehman, Peter Sholberg, Dwayne Roach, and Alan Castle investigate the phage mediated genetic exchange between soil microorganisms with their hosts. Brian Cheetham, Gabrielle Whittle, Michael Tang, and Margaret Katz identify a series of genetic elements within the *Dichelobacter nodosus* genome, which modulate expression of virulence determinants and are themselves controlled in a coordinated manner. Dalit Roth, Asaf Madi, Dror Y. Kenett, and Eshel Ben-Jacob introduce the Genome Holography method for the analysis of gene expression data. Margaret Riley reflects on the bacterial species concept in light of the large scope for horizontal gene transfer and on relevant methods for identification and measurement.

The second section on intercellular and transorganismic biocommunication of soil microorganisms starts with Katherine Pappas and Miguel Cevallos reporting on the plasmids of Rhizobiaceae, which receive, integrate, and release signals that profoundly determine bacterial–host cohabitation. Yves Dessaux, Emilie Chapelle, and Denis Faure differentiate two biocommunicative strategies in soil ecosystems such as quorum sensing and quorum quenching. Max Teplitski, Massimo Merighi, Mengsheng Gao, and Jayne Robinson report on the role of plasmids, transposons, and other viral defectives as effective tools for signal production for biocommunicative needs. Paul Paré, Huiming Zhang, Mina Aziz, Xitao Xie, Mi-Seong Kim, Xin Shen, and Jinlin Zhang investigate biocommunication of beneficial microbes that drive growth and development of plants. Max Teplitski and Sathish Rajamani investigate biocommunication between soil algae and bacteria. Ilona Pfeiffer reports on possible communication strategies between bacteria and fungi that cause antagonistic or symbiotic interactions between them. Ralf Oelmüller, Neeraj Shrivastava, Meghna Pohani, Kailash Upadhyaya, Irena Sherameti, Paul Murugan, Shashibala Singh, and Ajit Varma investigate symbiotic and transkingdom signaling of bacteria, plants, and fungi in the rhizosphere.

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