6. Superfast Evolution via Trans- and Interspecies Biocommunication

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This chapter introduces to provide a thought model for the real speed of evolution as a combination of selective, permutative, and constructive elements. It introduces hypotheses on genetic biocommunication within and across species and mainly deals with the three types of adaptations in herbivores, carnivores, and omnivores where biocommunication is of paramount importance: adaptations in the food chain, adaptations to the environment (historical, via selection), and interspecies competition. Two major ideas are put forward in the chapter: firstly, a basic design principle in organisms which ensures that parts of the genetic code are interchangeable in single processing units that are

readable across species, even across biological kingdoms. Secondly, active (subconscious) selection of probability for the sex of the offspring by parents (by females at the time of conception, by males shortly before ejaculation) combined with continuous adaptations of the genetic material in the sperm of the fathers. In this way, evolution might be speeded up to the pace we experience it in organisms with natural selection being only one important aspect. One still can only speculate about constructive elements of evolution, however, the hypotheses described in the chapter definitely provide various reasons for starting intense academic discussion. This book chapter attempts to do science in a completely new way the authors like to call neo-Aristotelian. It takes results from scientific investigations, and aims, via logical thinking and extrapolation (and sheer judging in some cases) to come up with a concise hypothesis on important elements of evolution. Various experiments, which might prove or undermine the ideas, are suggested in the course of the train of thought. The authors look forward to future developments in this field, and responses, results and reactions from fellow scientists.

1. Introduction

Biocommunication denotes communication within or amongst species from all the empires and kingdoms in biology (intraspecies communication, interspecies communication). Communication denotes a process by which information is exchanged between individuals through a common system of symbols, signs or, behavior. In this chapter the authors concentrate on hypotheses on genetic biocommunication within and across animal species (carnivores, herbivores, omnivores). Three different types of biocommunication are dealt with: communication with the past (concerning the proposed permutative element of evolution), communication with other organisms (concerning parts of the genetic code that are interchangeable in single processing units across species, even across biological kingdoms, in the proposed selective element of evolution), and communication with the environment and the

partner (concerning the proposed constructive element of evolution). Based on sound scientific evidence and developed further by contemplation these hypotheses shall aim at stimulating further discussion, ideas, research projects and insights.

Regarding further aspects of biocommunication including vocalizations or signs via semiochemicals such as pheromones that are not treated here at all the reader is referred to a vast amount of literature that is available elsewhere in form of articles and books (see, e.g., Witzany, 2010; Witzany and Baluska, 2012; Witzany, 2012; Witzany, 2014 and references therein).

2. Motivation

It's all about survival and the resources that are available to the individual. As a start of the train of ideas and hypotheses presented in this chapter, the authors relate the trigger for biocommunication to these two factors. Reason: As long as the animal is well fed, there is no reason to learn. However, there is definitely a reason to learn when it is hungry. And especially when it is regularly hungry. Similar arguments hold for further paramount resources besides food, and survival itself. In the following, the chapter will deal only with the extremes of herbivores (animals that feed on plants) and carnivores (animals that feed on meat), assuming that omnivores are in relation to the ideas presented below a simple mixture of the two extremes. The chapter will also make occasional references to plants, however, a theory of biocommunication in plants of the authors is on-going work and will be reported elsewhere. Springer devoted its extensive book series Signaling and Communication in Plants to this theme, with one of them concentrating on biocommunication (Witzany and Baluska, 2012).

Paramount properties of carnivorous animals such as lions and eagles are their mobility and competitiveness. For herbivores such as cattle or sheep the need to detect habitats of plants that serve as food and the need to open up new habitats is of utmost importance. In both cases biocommunication is of great significance.

2.1 Adaptations in biocommunication

The tree types of adaptations in herbivores and carnivores where biocommunication is of paramount importance are adaptations in the food chain, adaptations to the environment (historical, selection) and interspecies competition. Below, each of them will be treated in more detail. Generally it can be said that the faster such adaptations are represented in the genome of the respective animal, the higher is its chance of survival. Reticulate evolution makes perfect sense: the relationships between species or higher taxa cannot be represented in simple forking diagrams as previously assumed (phylogenetic network as opposed to the older concept of a phylogenetic tree). Sometimes even parts of the fork fuse again (hybridization and combination of two species).

2.2 Adaptations in the food chain

Adaptations in the carnivore food chain are equivalent to adaptations between prey and predator. The authors propose that carnivores adapt their genetic code to keep pace with improvements of their prey and vice versa. Such adaptation might take place via interspecies exchange of information. The classical paper on horizontal gene transfer (which would be one way to transport hereditary information across) starts with the sentence "*Gene flow from parent to child is the basic of heredity. Gene flow between unrelated organisms, even across biological kingdoms, may be a cornerstone of evolution.*" (Amábile-Cuevas and Chicurel, 1993).

Horizontal gene transfer (HGT, also known as lateral gene transfer) denotes the movement of genetic information between species, via selectable and easily transferred genomic islands (Peter and Townsend, 2005). Heritable HGT has been shown between Eubacteria and Archaea (Nelson *et al.*, 1999), between prokaryotes and unicellular eukaryotes (Andersson, 2005; Doolittle, 1998), from bacteria to multicellular eukaryotes (Hottopp *et al.*, 2007), from eukaryotes to prokaryotes (HGT to *Escherichia coli* from a eukaryotic host, Doolittle *et al.*, 1990) and between eukaryotes (Daniels *et al.*, 1990), the latter one being even by far not as rare as previously assumed (Andersson *et al.*, 2003). HGT facilitates the

acquisition of novel gene functions (such as antibiotic resistance) and can speed up evolution, either for the recipient or in case of parasitic genetic elements for themselves (Peter *et al*., 2002).

HGT can also be detrimental if the gene has no function, if it is incompatible with existing genes, or if it is a selfishly replicating mobile element (Vogan and Higgs, 2011). Possible pathways for interspecies gene transfer are phagocytosis, introgression via interspecies hybrids (Goodman *et al*., 1999), symbiosis (intimate contact of the host with symbionts, such as gene transfer between eukaryotic cells with plastids or mitochondria) and transfection (Peter, 2003). Such interspecies exchange of information increases the organism's knowledge about the environment. As Keeling and Palmer put it in their 2008 Nature Reviews Genetics article on HGT in eukaryotic evolution, *you are what you eat, what you live on, what lives on you and what lives in you* (Keeling and Palmer, 2008). Members of the same species were found to differ dramatically in gene content: in a study by Welch *et al*. (Welch *et al*., 2002) three *E. coli* genomes were sequenced. Less than 40% of the genome was common to all three bacteria!

Herbivores on the other hand do not adapt their genetic code to keep pace with improvements of their predators, but adapt to new food sources: They use the existing genetic potential in their genes to change themselves — their historic gene pool (permutation by recession). See below for ideas on non-coding DNA (junk DNA) and how it might be storage for the gene pool of the ancestors of a certain individual.

Plants might do it completely different altogether. HGT was found to be especially frequent in the early evolution of land plants, when a completely new environment had to be conquered by the organisms, and fast genetic learning was of great significance (Yue *et al*., 2012). Keeling and Palmer (Keeling and Palmer, 2008) stress the important role of HGT in adaptation to certain specialized niches and the highly variable impact of HGT in different lineages.

An interesting example for HGT is the 70-kDa heat-shock protein (HSP70) gene that is found in various organisms in three domains of life (archaebacteria, eubacteria, and eukaryotes), but not in their common ancestor (Gupta and Golding, 1993). HSP70 is one
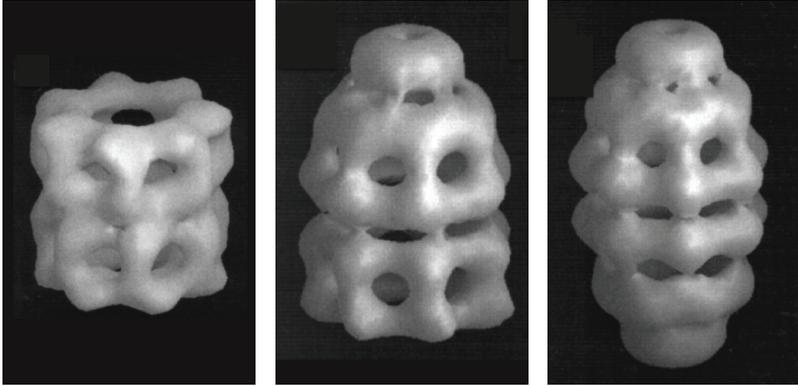
Figure 1.   Chaperonins such as GroEL/GroES (HSP60) and HSP70 are proteins that help misfolded proteins to fold correctly. The gene that codes for HSP70 appears in all three domains of life, but not in the common ancestor, and is a classic example for horizontal gene transfer (Gupta and Golding, 1993). The structure in the images consists of a double ring chaperonin GroEL (left image) that can be capped with one or two chaperonins GroES (middle and right images) and that provides safe space for protein repair (Roseman *et al.*, 1996). © Cell Press. Image reproduced with permission.

of the greatest inventions in nature: it is a chaperonin protein (Fig. 1) that helps misfolded proteins to fold correctly (Hartl, 1996). Chaperonins were also the first molecules for which protein–protein interactions were imaged in real time on the single molecule level (Viani *et al.*, 2000). HSP70 is the most conserved protein present in all organisms that is known to date. What if the most substantial inventions are generally not kept within one species, but distributed to all species? Would this be a hint that all life on Earth works together and helps each other to sustain? Not on the individual level, but on the species level and beyond? After all, we are altogether here on Spaceship Earth (as Buckminster Fuller, one of the great thinkers of the 20th century, used to call it in his classic 1968 book Operating Manual for Spaceship Earth) and need each other for survival.

2.3 Adaptations to the environment

Adaptations to the environment can happen via two different ways: first, historically, by going back in the genome to genes that

proved to be successful in the given environment (permutation by recession), and secondly, via innovation and selection. Intraspecies lateral gene transfer (see, e.g., Schubert *et al.*, 2009) and hereditary learning from each other (for reproduction, for the exchange of food sources) are important related aspects.

2.4 Intraspecies competition

In intraspecies competition genetic communication with the own species becomes important. The basic question is how to become attractive for potential mates.

3. Basic Design Principles in Organisms: Main Ideas

Two main ideas that are proposed in this chapter: firstly, a basic design principle in organisms, which ensures that parts of the genetic code are interchangeable in single processing units that are readable across species, even across biological kingdoms. Secondly, active (subconscious) selection of the probability for the sex of the offspring by fathers and mothers (at different times though), combined with continuous adaptations to the environment of the genetic material in sperm of the fathers.

The genetic code is uniform in most organisms: the same codons stand for the same proteins (Griffiths *et al.*, 2000). Due to this common language across species, it is possible to exchange readable blocks of genetic information, not just within species, but across all branches of the phylogenetic tree (or rather phylogenetic network, given all the cross-cuttings, short-cuts, and connections that have been found so far).

This readability and uniformity of the genetic code across known life forms (from viruses to bacteria to humans, with a few exceptions, such as in plastids and mitochondria, and in in the nuclear genome of some protozoans) can be called a universal basic design principle of organisms. The nature and message of DNA represent a universal language of life on Earth.

The interdependence and interconnectedness of all life forms on Earth shall be illustrated in one example: even pests such as socially

parasitic ants turn out to be protectors when the host needs protection in face of attacks by a predator (Adams *et al.*, 2013). Such switching from parasite to protector, from being harmful to being beneficial, might happen often in the interaction of organisms, and might therefore bring sense to bilateral horizontal gene transfer between predator and prey. In the end, all living species form an ecosystem, and depend on each other. We need to sustain each other. It cannot be that herbivores eat all the plants; because otherwise no breathable oxygen would be produced any more and all the herbivores would asphyxiate and/or starve to death. There might be very elaborate higher order control systems written in our genomes, control systems that ensure the survival of life itself. Mutualism, an association between two organisms, often from different species, that benefits both partners, might be the rule, and not the exception.

3.1 The selective element of evolution and its lateral transfer: single processing units that are readable across species

The authors propose that the information exchange takes place in single processing units that are readable across species. Why this has evolved we cannot say. But it is striking that the genetic code is the same across species, with just a few notable exceptions. Only mitochondria (who have their own genetic material, which is handed down from the mother to the offspring) use a slightly varied form, as do plastids, and also some microorganisms (Kay, 2000).

3.2 The permutative element of evolution: permutation by recession or innovation

The authors propose that in the process of courtship the DNA of man and woman is compared for similar blocks, not just in the current coding genome of the future parents, but back in time for many generations (this information is partially stored in the non-coding DNA, see below). The more generations one has to go

back to detect similarities, the more valuable this individual is concerning its genetic material. In a large gene pool, such permutation is not necessary, because the information is readily available from various individuals (i.e., many parallel evolution strains). However, in cases of a small gene pool, i.e., close relationships in past generations, many similar data blocks exist and permutation by recession or innovation becomes a necessity. Small genetic gene pools speed up evolution, either via differentiation into various species, who would occupy different ecological niches (cf. Darwin finches) or by a better adaptation to the environment. In a large gene pool, the common traits are confirmed. The constructive element of evolution is more dominant in large gene pools, whereas the permutative element is dominant in small gene pools.

In the proposed approach concerning the permutative element in evolution, permutation by innovation and selection is accompanied by permutation by recession. Permutation by recession indicates that if the genome provided by the parents is not good enough, the organism can access earlier genes, e.g., the ones from grandparents or other ancestors, perhaps going back in time very very long, and incorporate them in its genome (Weigel and Jurgens, 2005; Pearson, 2005; Lolle *et al.*, 2005; Ledford, 2013).

The genome can repair itself and can even reverse mutations. Examples for this are transposable elements and rare cases of children who inherit disease-causing mutations but show only mild symptoms, perhaps because some of their cells have reverted to a normal and healthier genetic code (Pearson, 2005). A transposable element (transposon, jumping gene, Nobel prize 1983 for Barbara McClintock) is non-coding DNA that has been unambiguously shown to be important in higher plant genome function and evolution (Buchers *et al.*, 2012). Such elements can change their position within the genome, sometimes creating or reversing mutations and altering the cell's genome size. Transposable elements might be involved in the permutation by recession. They can also be transferred horizontally. Schaack and co-workers (Schaack *et al.*, 2010) argue that the introduction of transposable elements by horizontal

transfer in eukaryotic genomes has been a major force propelling genomic variation and biological innovation.

One example for permutation by recession is a scientific study that shows that in certain plants (Arabidopsis, cress), where genes from the parent generation were modified so that they are bad for the daughter generation, the daughter generation goes back to the respective gene of the grandparents or even great-grandparents (Pearson, 2005; Lolle *et al.*, 2005). Cress overturns textbook genetics! Mendel's laws describe the inheritage of traits linked to single genes on chromosomes in the cell nucleus. Sometimes traints do not segregate in accordance with Mendel's laws. Examples for such non-Mendelian inheritage are extranuclear inheritance via genetic material present in mitochondria and plastids, gene conversion, infectious heredity (new genetic material introduced via infectious particles such as viruses), genome imprinting, where genes are epigenetically marked before transmission, altering their levels of expression, mosaicism, where the individual has different genetic material in its cells, due to mutations — if this occurs in egg or sperm cells, the new information is hereditatry, and trinucleotide repeat disorders.

The research result by Lolle *et al.* (2005) on non-Mendelian genetics in Arabidopsis implicates that apart from the genes inherited from the parents, there is some kind of storage for the genes from previous generations. The authors propose to investigate non-coding DNA (also known as junk DNA) as a candidate for the storage space for the genomes of the ancestors. In some organisms, non-coding DNA takes up a major fraction of the genome: In the case of humans, for example, up to 98% of the DNA is non-coding.

Parts of the non-coding DNA are transcribed and result in RNA pieces that do not code for proteins. What if they are not at all junk, but in fact very important and contain important information concerning, e.g., our past, the genome of our ancestors (and thereby a backup genome for our offspring), information about environments, etc.? Important information might be stored in the DNA at various hierarchical levels, some of which not yet described by
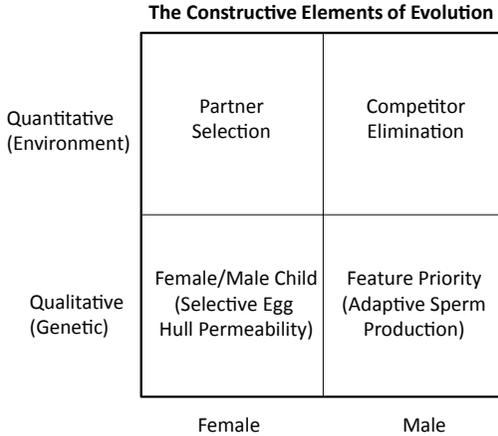
researchers. 76% of the human genome's non-coding DNA sequences are transcribed and nearly half of the genome is accessible to genetic regulatory proteins such as transcription factors. The research project ENCODE for example has revealed that some 80% of the human genome is biochemically active (see http://www.genome.gov/10005107 and references there).

Another storage option proposed in the scientific literature is a template directed process that makes use of an ancestral RNA-sequence cache (Lolle, 2005). The results presented in the Lolle *et al.*, 2005 paper elicited various rebuttal papers, and major discussions (Peng *et al.*, 2006; Mercier *et al.*, 2008; Ledford, 2013; Hopkins *et al.*, 2013). What is true we do not know yet.
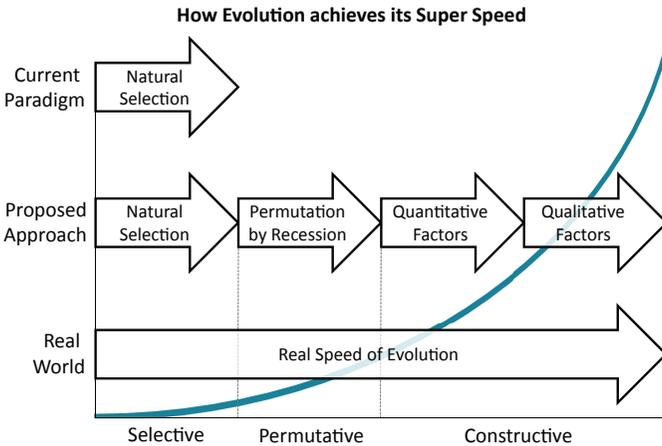
3.3 The constructive element of evolution: tuneable probability of the sex of the offspring and continuous adaptations to the environment

Natural selection and permutation by recession are just two of the proposed factors, and can alone not explain the superfast speed at which evolution takes place. The authors therefore propose a constructive element in evolution, consisting of quantitative and qualitative factors (Figs. 2 and 3).

The assumption from which the authors start their train of thinking is that when a woman gives birth to a girl it is a proof of genetic advantages of the respective partners, whereas when she gives birth to a boy, the boy first has to prove in the next generation that his genetic material is good enough to produce a girl with his partner. The authors propose a four-quadrant selection matrix for the constructive element of evolution (Fig. 2), containing quantitative and qualitative elements. Quantitatively, the woman selects the partner, and the man eliminates competitors. The quantitative constructive elements of evolution depend on the environment. Qualitatively, the woman can control via changing the permeability of her egg hull if she will get a male or female child (by either letting a spermatozoon bearing the Y or the X chromosome pass and fertilize the egg, Fig. 4). On the side of the male, such

The Constructive Elements of Evolution

	Female	Male
Quantitative (Environment)	Partner Selection	Competitor Elimination
Qualitative (Genetic)	Female/Male Child (Selective Egg Hull Permeability)	Feature Priority (Adaptive Sperm Production)

Figure 2.   The constructive elements of evolution. Male and female contribute to the speed of evolution of their offspring, via actions that either depend on genetics or the environment.

How Evolution achieves its Super Speed

Figure 3.   The main hypotheses put forward in this chapter. Evolution depends on selective, permutative, and constructive elements. Together they determine the speed of evolution, as we know it. See text.

qualitative contributions stem from feature priority coming from adaptive sperm production. Female humans are born with about 200,000 eggs in their ovaries, whereas men always produce sperm afresh.

Figure 4. Sperm and egg fusing. Here, the authors put forward the hypothesis that properties of the parents, the environment and compatibility of their genes actively determine the probability whether the joint child will be male or female. Public domain image.

In most countries, for as long as records have been kept, more boys than girls have been born. The secondary sex ratio (the ratio between male and female offspring) in people for the entire world population is 101 males to 100 females (CIA, 2015).

In times of a large choice of potential male partners (which is often equivalent to times of peace) a woman has the possibility to select the most compatible man as father of her child. In case of an excellent compatibility, the probability to give birth to a female is higher (80% as opposed to 50%), whereas if they are not compatible, it would be lower (20% as opposed to 50%). Reason for that is that every healthy female has the ability to reproduce and pass on her genetic material. Males on the other hand are in competition. Martinez *et al.* (2012) showed that in the US the number of children per woman (for women aged 22–44 years) crucially depends on education: A woman with no high school diploma statistically gives birth to 2.5 children, a woman with high school diploma gives birth to 1.8 children, and a woman with some college gives birth to 1.5 kids. With a Bachelor degree or higher, every woman mothers 1.1 kids. If one looks at the respective numbers of the males fathering these children, one notices a discrepancy. Men admit the fathering

of much fewer children. The respective percentage of illegitimate children becomes higher when looking at lower social classes. The probability of a male to produce legitimate offspring therefore increases with social class. With decreasing educational background the share of illegitimate children increases, which means that the genetic competition between males are higher. In times of crises such as wars, when fewer men are available, the compatibility between couples is not as likely. In cases of low genetic (and social) compatibility, there is a higher likelihood for a baby boy to be born (see treatment of the wartime sex ratio below). A lot of this selection process takes place via smell, where the women prefer the smell of men with genes different to their own, enlarging the gene portfolio of their offspring (Wedekind, 1994).

Wedekind showed in the so-called smelly T-shirt experiment that women preferred the smell of T-shirts worn by men with different genes from themselves, and thereby unconsciously select sex partners who help to put the offspring at some genetic advantage, due to the new and different genes from the partner. In times of war, when the sample of eligible men is smaller, women need to take what they get to produce offspring.

Wartime increases the sex ratio (Bernstein, 1958; Gellatly, 2009) between boys and girls: there is a statistically significant increase in the fraction of male births toward the end and immediately after both world wars. The year after World War I ended, an extra two boys were born for every 100 girls in the UK, compared to the year before the war started (Gellatly, 2009). In a subgroup of especially fertile couples after World War I, for example, from 1,178 children 55.3% were sons (Bernstein, 1958). The sex ratio remained high for about 18 months after WWI (Bernstein, 1958).

The fact that more male offspring are born after a war might corroborate the hypothesis of a tuneable probability of the sex of the offspring: at times during which not too many men with suitable genetic material for the respective women might be available, more boys are born, whose genetic material needs to go through one more iteration (generation) before a girl is born.

Various attempts have been made to determine differences in Y and X chromosome bearing spermatozoa, and using them in influencing the sex of the offspring, e.g., in *in vitro* fertilization. Where on the other hand the partner might know best if a baby boy or a baby girl would be best with the respective partner under the given circumstances. The classical phase-contrast microscopy work by Shettles on the nuclear morphology of human spermatozoa (Shettles, 1960) gave rise to the widely held idea that spermatozoa bearing the X chromosome (resulting in girls) swim faster than spermatozoa carrying the smaller Y chromosome (resulting in boys). Until recently, modern methods showed no morphological difference between human X and Y spermatozoa (Hossain *et al.*, 2001; Grant, 2006) and also no difference in swimming velocity of X and Y bearing bovine sperm (Penfold *et al.*, 1998). However, measurements of sperm surfaces with the atomic force microscope, a powerful instrument that allows for measurements on living cells down to the nanoscale, revealed that the associations of several structural measurements of the sperm cell head are promising candidates for development of a new method of sperm sexing (Carvalho *et al.*, 2013).

The authors also propose that men, under the influence of smell and other environmental factors, can influence the race of their X or Y bearing sperm by active control of the viscosity of their prostate liquid and thereby also actively contribute to the probability of the sex of the offspring. Sperm is continuously produced based on the most recent information, but for control of the sex of the offspring this system is too slow — therefore the authors propose the variable medium provided by the prostate liquid as selective medium. The prostate system seems much too complex to simply provide a low friction environment for the spermatozoa. It might be that it is a highly elaborately system controlled by lymphatic information, with environmental feedback, contributing to male reproduction and the tuneable probability of the sex of the offspring. It remains to be investigated if changes in the viscosity of prostate fluid and any resulting motility of sperm yielding male or female offspring exist. If so, another constructive element of evolution has been

identified. The potential involvement of a lymphatic information system for the prostate shall be investigated by further research.

Further aspects of interest: correlations of the secondary sex ratio with the frequency of incest over many generations need to be established in further research. Via the alignment via the junk DNA, the system is well informed about the size of the gene pool and accordingly adopts the implementation velocity of new genetic material. In this respect, specific properties of offspring resulting from incest and biological bastards are also of high interest. It would also be interesting to take a closer look at the sex ratio in children who result from a rape. However, there were no data to be found on the sex ratio of children after a rape. This might be an area of no-go research, which is societally taboo. Also of interest is research on how populations with a limited gene pool such as the Inuit acquire new genetic material. Isolated Inuit groups formerly had their young girls spend the night with strangers; the resulting children enlarged the gene pool. Also here information on the sex ratio would be very informative.

4. Summary, Discussion and Outlook

Various ideas regarding biocommunication within and amongst species, even across time, have surfaced in this chapter. The proposed part of the permutative element of evolution, where single organisms can access the genomes of their ancestors and accordingly even reverse back mutations, is an example for biocommunication with the past. The authors also treated a certain selective aspect of evolution, where parts of the genetic code are transferred to other organisms, even across biological kingdoms, in single processing units — this is an example for genetic communication with other organisms, and might even be a sign of the importance of sustaining life as a whole as opposed to single individuals — the highly conserved gene for the heat shock protein HSP70, which is now — thanks to lateral gene transfer — present in all three domains of life, but not in the common ancestor, is an intriguing example for collaboration of life forms. The third type of

biocommunication treated here refers to information exchange with the environment and between the partners, and is dealt with in the authors' proposal concerning a constructive element of evolution.

The major new ideas put forward by the authors are that the real speed of evolution results from three major elements: the selective element of evolution (which comprises mutation and selection, and parts of the genetic code that are interchangeable in single processing units across species, even across biological kingdoms), the permutation by recession element of evolution (where the organism can actively change bad genes back to the ones of ancestors, here the authors propose that non-coding DNA might provide the required storage space for such large amounts of data) and a constructive element of evolution, that is comprised of quantitative and qualitative elements, and is mainly concerned with which traits are passed on via male or female offspring.

What is life is still a question we cannot answer, let alone what is the meaning and goal of life (if any)? Is there a motivation of evolution? Why is the genetic code (i.e., the rules by which genetic material is translated into proteins in organisms) uniform across species? Did this uniformity stay the same with time, with evolution, to keep on ensuring that genetic material can be exchanged across biological kingdoms?

Many questions remain, and a lot of research needs to be done. Thinking about biocommunication and evolution will certainly provide interesting pieces for the puzzle we need to assemble to understand the complex network of life and its elaborate ways of communication.

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