ENGINEERING AND INFORMATION PROBLEMS OF THE ICONIC APES INTO HUMANS TRANSITION

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Streszczenie

Artykuł stanowi przegląd różnych faktów związanych z domniemaną ewolucją człowieka z przodka wspólnego z małpami. Podejście bioinżynierskie wskazuje na znaczenie każdego szczegółu w konstrukcji organizmu dwunożnego. Ocena ewolucji małp i człowieka musi zatem uwzględniać nie tylko różnice genetyczne i ilość genów konieczną do przekształcenia, ale też ograniczenia takiej transformacji narzucone przez dobór naturalny, do jakich należy warunek funkcjonalności oraz rzeczywisty czas, jaki upływa pomiędzy dwiema korzystnymi mutacjami. Druga grupa problemów dotyczy konstrukcji mechanicznych składających się na dwunożny i czworonożny system lokomocji oraz systemów sterowania umożliwiających ruch na dwóch lub czterech nogach, a także możliwości wytworzenia form pośrednich między jednym a drugim. Konieczność zachowania bezpośredniej zależności szczegółów konstrukcyjnych od informacji zakodowanej w genach stanowi dodatkowy problem. W ten sposób staje się oczywistością konieczność zrewidowania idei ewolucji jednych organizmów w inne zachodzącej małymi krokami.

Słowa kluczowe: genom, dwunożność, funkcjonalność, dobór naturalny, bioinżynieria
Key words: genome, bipedalism, functionality, natural selection, bioengineering

1. Introduction

From a purely philosophical viewpoint, Darwin's theory may explain the "design" of organisms, and their wondrous diversity, as the result of natural

processes, the gradual accumulation of spontaneously arisen variations (mutations) sorted out by natural selection (Ayala, 2012). The objective of this study is to revisit the evolutionary proposition of the common ancestor of humans and apes from the perspective of genetics and mechanical engineering. Trying to answer the question "How can we recognize common ancestors?" Andrews (2015) suggests: "It would be a mistake to consider that our common ancestor with chimpanzees looked anything like either ourselves or like chimpanzees, but it is reasonable to look to see how much we share with chimpanzees, both genetically and morphologically."

Nowadays, bioengineering allows examination of "biological or medical application of engineering principles" (*Definition...,* 2018) in order to better understand mechanisms in life processes. Especially in research on the evolution of living beings, it is very advantageous to analyze engineering solutions like mechanics, optics (Parker, 2011), composite material properties (Zargar Kharazi et al., 2012) and even entire systems, such as echolocation in bats (Teeling, 2009). Informatics and computers are useful tools for gene analysis, which often involves large computational clusters consisting of hundreds of individual computers with the collective processing power of tens of thousands of individual laptop or desktop computers (*Human Genetics*..., 2018).

Perhaps one of the most difficult issues to address in evolutionary biology is the unimaginable transitional forms required between completely different technical devices applied to living organisms assumed to be related to each other. As an example one could mention the issues arising with the co-called "Light-switch theory" describing the commonly acknowledged fact that roughly 500 My ago nearly-blind organisms "suddenly and mysteriously evolved complex new visual systems" of diverse working principles (Lipson and Kurman, 2016).

Other problems arise with a further example, the Carabid ground beetles because of the high temperatures and chemical reactivity of their defense systems. Modification of such a system introducing any errors would result in the demise of the modified beetle, breaking the chain of evolutionary mutations. The fact is, molecular phylogenetic studies provide a different category of solutions than morphological classification. On the one hand some morphologically identical Carabid species are clearly divided into 8 isolated lineages based on phylogenetic criteria, but on the other hand, there are clearly distinguishable morphological species that "demonstrate only small evolutionary distances from one another" (Osawa and Su, 2004).

The paper below is an attempt to review principles concerning differences between human and ape construction from engineering perspectives of bipedal and quadrupedal locomotion, genetic differences between humans and apes, and possible transitional forms between genetic information and the technical construction of locomotion systems.

2. Genetic differences

Many popular publications promote the idea of genetic similarity between humans and apes. The American Museum of Natural History published the value 98.8% of "the same DNA" explaining that "human and chimp DNA is so similar because the two species are so closely related" (*DNA...,* 2018). Similarly, the Smithsonian Institution published percentage differences between humans and chimpanzee as 1.2%, humans and bonobo, and 1.6% humans and gorillas (*Genetic Evidence...,* 2018). These numbers correlate with the ones published in the most renowned journals, such as "Nature" (Waterson et al., 2005), "Science" (Fujiyama et al., 2002), or "American Journal of Human Genetics" (Chen & Li, 2001; Ebersberger et al., 2002).

Logically, one would expect that if similarity in DNA was poor, then it would be difficult to talk about a "common ancestor." Perhaps that is the reason why the obvious differences are ignored: chimps have 3 billion base pairs, man has 3.23 (7% more DNA); chimps have 18,759 protein coding genes, man has about 20,000 (ca. 6% more genes). Can we really expect 98.8% DNA sequence similarity if there are 6% more protein coding genes?

Bergman and Tomkins (2013) review a series of investigations that challenge these vogue genetic similarity percentages. They discuss the widely accepted assumption when obtaining such numbers that 95% of genome is ignored as junk. There is no ground, however, to omit 95% of the genome. If non-repetitive gene sequences are compared, only 76% of human genome is like the chimpanzee, but when the gaps, replacements, and "copy number variations" are considered, the total similarity of the genomes drops below 70%. Authors also discuss the genome structural differences, gene regulation differences, genome size and the Y-chromosome chasm. Similarly, Ebersberger et al. (2007) reported that "for about 23% of our genome, we share no immediate genetic ancestry with our closest living relative, the chimpanzee."

DNA sequences are available to download from genomic databases (*Genome Browser...,* 2018), and can be easily compared. An argument can be made that only exon coding sequences should be compared. If this is done the comparison rises to a not unreasonable value of 86-89%. In order to get the ~98.8% value reported in poor scientific literature, however, the numerous "indel" sequences (inserted or deleted base-pairs) in exons also have to be excluded (Tomkins, 2011). Obviously, if every difference is excluded we can get 100% identity but that would be a very trivial and misleading comparison.

3. Transition through mutations

With such clear differences between human and ape genes, one might ask a question about the transformability of one gene into another. Despite many hypotheses on genome evolution there is still no convincing model of gene

transformation. Brown (2002) dedicated an entire chapter discussing the hypotheses on genome evolution, admitting that none of them is proved with convincing evidence. Boussau and Daubin (2010) found unsatisfactory the existing models and propose their own model, which is also unconvincing.

The main problem with mutations is the fact that the vast majority of them are disadvantageous or neutral. Numerous diseases can be attributed to mutations. One of the more recently documented is autosomal recessive congenital cataracts (Irum et al., 2016). Advantageous mutations are rare. The succession of two advantageous mutations, being so much rarer, would not occur in any reasonable evolutionary time. Estimated for humans, the waiting time for two positive mutations is ca. 160 million years (Durrett and Schmidt, 2008). No model embedded in genetic reality can reduce the waiting time down to the 10 million years considered to have been required for human evolution, with all the necessary mutational steps to constitute the human genome. Some papers suggest even shorter time, e.g. that humans and chimpanzees shared a common ancestor 5-7 million years ago (Varki and Altheide, 2005; Scanes, 2018).

Clearly, under the demanding conditions of harsh natural selection, each mutational step must provide some advantage, or at least to not disable previously achieved advantages. Thus, the genetic information at each evolutionary mutational step must remain useful and lead to some desirable goal. However, this is by no means a trivial matter.

To illustrate the nature of the problem, that many biologists and non-engineers overlook, let us consider a highly pertinent example by a staunch proponent of such transitions, Carl Zimmer. He describes this in his blog for the National Geographic magazine called "The Loom" (Zimmer, 2005). It is the clever five step Doublet or Word Ladder from "Ape" to "Man"

1. Ape
2. Apt
3. Opt
4. Oat
5. Mat
6. Man

This seems to be a perfect example of just such a transition. Each step is clearly meaningful. If this step transition works for language games why shouldn't it work in nature and really turn an ape into a man? The issue that is completely overlooked is the nature of information. "Apt" does not refer to a modified "ape" that is intermediate in some theoretical meaning-sense to "Man". In reality only the combination of letters is intermediate, not the actual meaning of the information, and this is true for each step.

This example is meant to represent a gene transition, without considering multifactorial genetic causation at higher levels of physiological function (Noble, 2011). It is vital to understand the role of genes in causing traits (bits of the phenotype). A gene does not work alone. Instead its protein product interacts with protein products from other genes that together bring about a trait. As part of a progression of interactions, the gene products can be compared to words

in a sentence (Crompton, 1998), and all semantic sequences have "grammars" (syntax). If we look at Zimmer's word ladder, when "ape" changes to "apt" we have a shift from a noun to an adjective. This is a forbidden category change. The sentence, "The ape eats a banana", would become "The apt eats a banana", which is nonsense. The second step of the word ladder from "apt" to "opt" is another forbidden category change, from an adjective to a verb. The sentence, "His example is apt", becomes "His example is opt". Once again nonsense is produced. Even though the last two steps involve a shift from one noun to another: "Oat" to "Mat" to "Man", there are still subtle category changes. "Oat" describes a plant, "Mat" is a piece of coarse or resilient material. The sentence "Porridge is made from oats" is reasonable but "Porridge is made from mats" is unreasonable, or "The mat is made of rubber" is reasonable but "The man is made of rubber" is unreasonable.

This problem may seem obvious, almost trivial. Yet it is the same type of problem that has to be overcome when transitioning between genes that code for an ape's knee and genes that code for a human's knee. We can't just want the steps to work. Each step, each mutated gene, has to be functionally advantageous within its physiological context, otherwise not only will it not be selected for but, more likely, it will be immediately selected against.

Such "hopeful" transitions have also been explored by the famous neoatheist, Richard Dawkins. In his book "The Blind Watchmaker" (Dawkins, 2006) he describes a selection scenario of 41 generations that turn the extraordinary phrase:

"Y YVMQKZPFJXWVHGLAWFVCHQXYOPY"

into Shakespeare's immortal words, in his fabulous play "Hamlet",

"METHINKS IT IS LIKE A WEASEL".

The problem with Dawkins' scenario should now be readily apparent. A stage director would have a conniption if at the critical part and scene in Hamlet his/her actor could only recite that first meaningless phrase. The director would have them fired. Just so any natural selection would work against even the very first step eliminating it from the population. Selection would similarly work against all other meaningless phrases in the next 40 steps of the transition. Meaningful transitions, or as Darwin argued, selectively advantageous transitions have to be available at each and every step. Certainly, this is vital when considering a potential transition from an ape's knee to a human's knee.

Thus, mutations do not help to make the transition from an ape genome to a human genome because any intermediate combinations would not make sense and would result in non-functional knees. This is also true of epigenetic mechanisms, which were proposed decades ago (Ho and Saunders, 1979) and are still considered by some to be capable of opening up new evolutionary options (Jablonka, 2017). Even if epigenetic inheritance were involved in what authors call "adaptive evolution and macroevolution" transition from Ape to Apt and then to Opt remains non-meaningful and could not advance to man.

4. Transition between technical devices

To illustrate that, let us consider the text describing two simple devices. For example, we can write down two short texts describing two types of internal combustion engines: the four-stroke and the two-stroke ones. We can explore many transitional forms between the two texts; changing a few letters or a few words, or even a few sentences at each step, and still keeping some sense. However, most of our transitional forms are unable to function, because they describe neither a four-stroke engine, nor a two-stroke one. Thus, the functionality condition is not met, and almost none of the transitional forms between the two texts would be useful.

If we consider a "common ancestor" of the above two example texts, the problem appears to be completely unsolvable. We have to imagine a text describing something useful, which can be transformed into both a four-stroke engine and a two-stroke one. We are speaking about any descriptive text, while in nature genes are the technical text that enables fabrication of different devices from different work principles out of different materials in the living organism.

The same is observed in the case of the knee-joint, which is very different in humans and in apes. Let us imagine a "blind engineer" who is going to project and build a functional knee joint. The task is not just to produce randomly or selectively a series of specific words:
1. Femur (thigh bone),
2. Anterior cruciate ligament,
3. Fibular collateral ligament,
4. Transverse ligament,
5. Tibial collateral ligament,
6. Patellar ligament,
7. Meniscofemoral ligament,
8. Medial meniscus,
9. Lateral meniscus,
10. Posterior cruciate ligament,
11. Tibia (shin bone).

To obtain a functional knee, each of these "words" must contain technical data concerning sophisticated materials of certain chemical components, structure, elasticity and strength. Furthermore, one has to provide and to code somewhere the information on positioning of respective physical details (dimensions, shape, fixing points, etc.) and the way they are to be assembled. The task is far more complicated than putting together jigsaw puzzle pieces. Realizing, that "profound knowledge in functional and clinical anatomy is a prerequisite for efficient diagnosis in medical practice," (Meyer et al., 2017) we can only backtrack and speak about maintenance and service skills. The knowledge and skills of the "blind engineer" who projects and assembles the functional knee joint must be much more profound.

But the real problem in evolution of the human knee joint is that there is no way to assemble it out of the details prepared for the ape knee joint. No transitional

form between them is technically possible, and no technical solution like "common ancestor" is imaginable. How then can we imagine a step-by-step transformation of the genetic text describing an ape knee into the genetic text describing a human knee? How can we keep the sense, functionality and thus selectability of such a transitional series?

Despite superficial similarities, especially when seeing a gorilla stand up on his hind legs and "walk", there are many differences between apes and humans in constructional details (Rucki, Crompton, 2016). Apes have a prominent muzzle and a sloped cranial face. Apes have substantial labial salivary glands, man has almost none. Apes have four hands; man has two hands and, very obviously, two feet. Apes have a huge laryngeal sac in their chest to win their mates, man has a miniscule tube to lubricate his vocal chords. Male apes have an os baculum, male humans do not, etc. etc. etc. Consider just the average number of the coccygeal vertebrae, man differs more from apes than any two apes differ from one another:

- Man   4.2 (745 specimens)
- Chimpanzee   3.2 (47)
- Gorilla   3.0 (69)
- Orangutan   2.8 (56)
- Gibbon   2.7 (47)
- Siamang   2.6 (13)

Another noticeable difference is the presence of ischial callosities (bald buttock patches) found in gibbons, some chimpanzees, gorillas and orangutans. In man these callosities never have or will be found because the ischial tuberosities are completely padded by muscles arising from their entire surfaces, preventing skin from being pressed against the bone.

Features designed to keep balance during four-legged motion are the following:
- long arms (arm bones 120% larger than their leg bones),
- short legs with the knee cannot be straightened and must be continually loaded in flexion (bent leg),
- funnel-shaped ribs,
- opposable big toes (climbing activity instead of walking),
- projecting cervical vertebrae to support the forward projecting head, etc.

On the other hand, in humans, the center of gravity when in the upright position is right over the pelvic area. To achieve that and to ensure dynamic stability of the bipedal motion, there are many unique constructional characteristics of humans:
- shorter arms (approximately 70% of the size of leg bones),
- the curvature of the spine is "S" shaped in humans, unlike in apes,
- human knee joint is unique in that it can be locked in an upright position,
- human's scapula sits right on the back.

In humans, but not apes, the transverse metatarsal ligament binds the big toe. It is quite obvious that the opposable big toes in apes have more to do with climbing than with four-leg motion. In fact, for evolutionary theories, it turns thing from bad to worse, because its functionality leads to the completely different evolutionary direction of climbing instead of the development of bipedal walking. No wonder one was obliged to admit that the timing of the origins of bipedalism is uncertain (Best and Kamilar, 2018).

Moreover, the ratio of the power arm (the distance from the heel to the talocrural joint) to the load arm (that from the talocrural joint to the distal head of the metatarsals) differs markedly between the human and ape foot (Wang and Crompton, 2004). It minimizes muscle force at the talocrural joint by around 40%, reduces forces in the plantar musculature and aponeurosis and has a lower total of force in joints and muscles than do the ape feet. The observation that "chimpanzees and gorillas possess feet adapted for both arboreal and terrestrial substrates" (Gebo, 1992) emphasizes the fact that those constructional features are aimed at specific functions. In the case of apes, especially gorillas, it is possible to perform bipedal motion, but it is difficult and unnatural for monkeys and apes to maintain a vertical posture with their legs (Barnard et al., 2011).

The list above does not address the control software problem, which is substantially different between bipedal and quadrupedal robots. Evolutionary assumption that humans could "work out" the "walking control software" during the millions of years after their mechanic devices were already being used to walk, is against the known facts of natural selection and engineering knowledge. From the engineer's perspective, the development of bipedal robot design does not take into account any transitional form from a four-legged machine. A successful approach to bipedal robot design was reported by scholars at the University of Colombia (Roa et al., 2006). It is an iterative approach aimed at developing simple and effective control systems. The models, simulations and mechanics were based on knowledge of bipedal robot dynamics, and on system dynamics, but with no reference to four-legged prototypes. In fact, bipedal robots and four-legged ones differ so much, that building any transitional form between them both in mechanical and software terms would generate a series of additional insolvable problems (e.g. maintaining functionality after replacement of a detail or a unit). Considering engineering knowledge on bipedalism, it is very difficult to accept a hypothesis proposed e.g. by Druelle et al. (2017), that bipedality was the result of a developmental by-product.

In the demanding reality of natural selection, lack of usefulness means inability to survive. An organism unable to survive is unable to continue evolution. The condition to be met is that each and every of 500,000 generations is fully functional, which would be impossible had they, 30% of the genes constituting bipedal knee joints and 70% of genes for quadrupedal ones (or any other percentage different from 100%).

5. Conclusions

Bioengineering perspectives shed new light onto the issue of evolutionary development of human bipedality. The discussion about human evolution must address not just minor morphological differences and seemingly similar appearance, but constructional solutions of key importance. The engineering approach to the construction of bipedal and four-legged robots reveals the limitations posed by any kind of transitional forms.

It seems obvious with today's knowledge of the technical problems associated with transition from one mechanism into another, of the enormous amount of information needed for this transformation but always ensuring direct correlation of the information with the construction, of the hundreds of millions of years required for any two advantageous mutations to occur, and of the numerous technical differences between apes and humans, that no one would suggest a hypothesis like small-step evolution from one organism into another. Everything is against it:

- genetic programs in apes and humans are clearly not identical,
- the four-legged construction of apes is impossible to transform into the bipedal human construction, and no functional construction like a "common ancestor" is imaginable,
- the waiting time of 160 million years for even two advantageous mutations suggests that humans must have been humans for at least several hundreds of millions years, while commonly accepted evolutionary timescale leaves no more than 10 million years for human evolution.

The information presented seriously questions a trivial Darwinian generalization based on similarities in appearance. Proposed evolutionary models should be derived directly from the facts, omitting none of them; or, more generally, any theory must be based on facts instead of fitting facts to specious assumptions.

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Abstract

The paper summarizes various facts concerning presumptive human evolution from a common ancestor with apes. A bioengineering approach elegantly reveals the significance of each detail in construction of a bipedal organism. Evaluation of human and ape evolution must consider the genetic differences, the amount of genetic information to be transformed, the limitation of such

a transformation set by the condition of functionality and natural selection, and the waiting time between advantageous mutations. A second group of problems considers the mechanical construction of bipedal and quadrupedal solutions, the control systems required to enable movement using two or four legs, and any possible transitional forms between one and the other. The requirement to keep some direct correlation between transformation of genetic information and the respective constructional details poses another problem to be solved. The need to reconsider the proposition of small-step evolution of one organism into another becomes evidently clear.

Nota o autorach:

Mirosław Rucki, dr hab. inż., prof. nadzw. UTH Radom, Wydział Mechaniczny. Oprócz zainteresowań z zakresu Budowy i Eksploatacji Maszyn, zajmuje się biblistyką i historią chrześcijaństwa pierwszych wieków. Ukończył studia podyplomowe: pedagogiczne kształcenia zawodowego (Politechnika Poznańska), nauk o rodzinie (Papieski Wydział Teologiczny w Poznaniu) oraz biblijne (PWT we Wrocławiu). Należy do Stowarzyszenia Biblistów Polskich, Society of Biblical Literature oraz Chrześcijańskiego Forum Pracowników Nauki. Jest autorem lub współautorem dwóch książek recenzowanych i ponad 150 artykułów naukowych i referatów wygłoszonych na konferencjach z dziedziny budowy i eksploatacji maszyn, a także trzech książek i ponad dwudziestu artykułów w czasopismach punktowanych z dziedziny biblistyki.

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