

The Kilimanjaro hypothesis: sex as a conserver of replicative fidelity and an adaptation to unstable environments

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Abstract

A problem at the heart of evolutionary biology is to explain how natural selection maintains high-fidelity genetic replication when the genes that specify the enzymes that replicate DNA are themselves subject to mutation. Other problems include explaining why virtually all multicellular and many unicellular organisms reproduce sexually, and why some animals, such as peacocks and birds of paradise, have evolved extravagant ornaments and complex mating rituals that appear to be detrimental. I present a simple “Kilimanjaro hypothesis” that tackles all three problems. Since the genes that specify the proteins that replicate DNA can mutate, replicative fidelity must vary between individuals. I note that many organisms choose their mates by responding to various complex behaviors, physical displays, and biochemical mechanisms, often generated by the interaction of many gene products acting together. I propose that natural selection consistently adds unnecessary complexity to the mechanisms that transfer genetic material between individuals. Since most mutations are harmful, mutator mutations are likely to disrupt these mechanisms - which must reduce the chance of individuals with error-prone replisomes mating successfully. Many puzzling biological phenomena among sexual organisms can be explained along these lines. The migration and spawning of Atlantic salmon and the complex displays of birds of paradise may, for example, be best understood as “tests” to establish that potential sexual partners possess genes for high-fidelity genetic replication. Animals that have developed physical handicaps that appear harmful, such as peacocks, and animals that undertake remarkable migrations, such as arctic terns and monarch butterflies, may be extreme examples of such tests. I also provide suggestions for experiments to test the hypothesis.

Introduction

Imagine a woman who announces publicly she will have sex with any man, but only on the summit of Mount Everest. Moreover, the potential partners must solve a challenging Sudoku puzzle that they pick up on the way, and (so that she can choose quickly) they must write – *display* – their solutions in large numerals on a banner that they bring along. If practical, this would be a reasonable mating strategy for both sexes: both mother and father would likely have better-than-average genes. In this paper, I suggest that many plants and animals adopt similar strategies, setting up practical “obstacle courses” for potential mates. They may also demand complicated physical displays, all of which can only be generated by the interaction of many genes. For example, Atlantic salmon follow a similar strategy to climbing Mount Everest when they migrate from saltwater to freshwater and then swim up rivers to reach their spawning grounds. Peahens prefer to mate with peacocks with large and symmetrical *displays* comprising the cocks’ considerably elongated upper tail feathers. The hypothesis presented here, however, also tackles two more fundamental problems in evolutionary biology: why sex is so ubiquitous and how replicative fidelity is maintained. (This essay will not detail how high-fidelity replication might have originally evolved. Briefly, it seems likely that special

conditions might be required for fidelity to increase. Very stable conditions might be necessary, possibly combined with serial colonization of successive sites. In most cases, I would expect fidelity to decrease, usually slowly but sometimes rapidly. I am unaware of any literature discussing how increased fidelity can evolve.) Mutations must occasionally arise in all genes, including those that specify the proteins that replicate the genetic material – the nucleic acid polymerases and their associated proteins. Some of these mutations must reduce fidelity without actually being fatal. Lineages that replicate with reduced fidelity must therefore exist in all biological kingdoms, although we do not know how common they are. Moreover, we have to consider small changes in fidelity. The mutation rate in humans has been estimated to be around 2.5×10^{-8} mutations per nucleotide site per generation [Nachman, 2000]. Could a human (or another animal) identify an individual with a mutation rate of, say, 2.5×10^{-7} ? This is important. If ten times as many mutations were to arise, we can assume that more are likely to land in the genes encoding replisomes, making the problem worse. (Replisomes are the complex molecular machines that replicate DNA. They comprise many proteins, including DNA polymerases, exonucleases, ligases, helicases, etc.)

There is another critical issue: as Duffy pointed out, if a biological entity is “suddenly thrust into an environment that it’s not well adapted to . . . there is a larger fraction of potentially beneficial mutations available and having a nonzero mutation rate would be preferable to all descendants always staying exactly the same” [Duffy, 2018]. In other words, strong new selective pressures may increase the proportion of beneficial mutations, and weaker or more consistent selection may reduce it. During periods of strong selection, slightly lower-fidelity replisomes may therefore be preferable and may be selected. At later times, however, low fidelity becomes a problem: firstly, because once the population is well-adapted to its new environment, most subsequent mutation is undesirable, and, secondly, because mutations may arise in the replisome genes themselves. Fortunately, some individuals in a large population are likely to retain high fidelity, so appropriate mate selection can in principle restore fidelity, but some means of identifying high-fidelity individuals is required. Fidelity is valuable, and it may increase or decrease, but a safe long-term strategy for all life forms is to conserve it. The hypothesis presented here is based on the premise that the more genes are involved in both mate selection and the physical or biochemical mechanism of mating – including genes that usually do something else – the lower the chance that low-quality replisome genes with many mutator mutations will be selected or transferred by males during mating. The hypothesis suggests that many puzzling features of animals and plants are there to conserve fidelity.

Multifactorial mate selection

The peacock’s tail has clearly evolved in response to female mate choice, and it has the potential to indicate increased mutation because many genes are required to make it, and defects in any of these genes are likely to disrupt its appearance. Takahashi *et al.* studied feral peafowl in Japan and found that peahens did not prefer peacocks with more symmetrical tails or of greater length, or had more ocelli. However, the authors noted that tails showed a small variance among males across populations. One interpretation is therefore that most peacocks already had low mutation rates (possibly because tail-selection provides a very effective filter), leaving females to focus on other attributes. Therefore, a reasonably well-formed tail may act as a peacock “entrance exam”, with peahens not seeking perfection in tails. (Much of the remaining variation in tails may come, in any case, from environmental factors.) A better human analogy may therefore be a woman who looks for a partner on the summit of a mountain such as Kilimanjaro, which many men can climb. Getting to the summit might be her entrance exam – after that, she uses other criteria to make her final

choice. Recognizing that many species do use a multifactorial approach to mate selection, I have named my conjecture the “Kilimanjaro hypothesis”.

Natural phenomena that can be explained by the Kilimanjaro Hypothesis

The Kilimanjaro hypothesis can explain many puzzling features and behaviors of complex organisms. For example, many species complete long migrations each year. You might expect natural selection to favor lineages that avoid the risk and energy expenditure of such long journeys. Migratory populations persist, however, in many species. Arctic terns complete the longest migrations known in the animal kingdom, with birds nesting in Iceland and Greenland completing annual round-trip migrations that are over 70,000 km. The species is successful, with an estimated two million individuals, possibly because migration acts as an effective filter of fidelity. In many migratory species, “breakaway” populations that either do not migrate or migrate less far exist, but they do not generally outcompete the populations completing longer migrations. Atlantic salmon can migrate from freshwater to the ocean and then return. Both sexes undertake dangerous journeys, including adapting to changing salinity, leaping up waterfalls, avoiding predators, and swimming in shallow water, usually returning to mate in the streams where they hatched. “Landlocked” lineages that spend their entire lives in freshwater exist, but populations that migrate from the ocean to freshwater to breed are more numerous. Some invertebrates are migratory. Some populations of monarch butterflies do not migrate, but many North American populations east of the Rocky Mountains complete a dangerous multi-generational migration between overwintering sites (the largest being in Michoacán in Mexico, where around 150 million monarchs overwinter) and their northern breeding grounds, mainly near the Great Lakes. It seems that selective or genetic advantages compensate for the dangers of migration. Note that this cycle requires four generations to complete, so many of the genetically-encoded behaviors and physiological changes required for migration cannot be conserved by selection en route. Other animal features and behaviors that require the interaction of many gene products could provide similar benefits. Birdsong is an example of a behavior that can only be produced by individuals with many functional genes that must specify the proteins that make the physical structures of the syrinx, appropriate instinctive behavior, and the ability to learn by imitation. Any deviation from the norm in a particular individual is broadcast to their neighbors. Humans are attracted to partners with athleticism and pretty faces (which are close to, but not identical to, average faces [Perrett, 1994]), as well as intelligence and a sense of humor, both of which are the product of an extraordinarily complex organ – the human brain. Invertebrates may adopt similar strategies. For example, fireflies receive and transmit encoded flashed messages to attract mates, while medflies and some spiders perform complex dances. Male fiddler crabs wave their enlarged claws in a species-specific pattern to attract females. Females decide whether to approach males based on male traits, including the wave rate and claw size, but characteristics of the male’s burrow including depth and temperature then determine whether mating occurs in a multifactorial selection process [Backwell and Passmore 1996]. Corrals may provide another example since they synchronize their spawning by monitoring water temperatures, light, and the moon’s cycles (or tides). In other species, including plants and fungi, complex biochemical mechanisms are in operation that could prevent the transfer or recombination of low-fidelity replisome genes. For example, the fertilization of flowering plants involves multilayered signaling pathways, with many gene products that are expressed in both pollen and the female tissues (figure 1). The Kilimanjaro hypothesis suggests that some of this complexity is unnecessary but that such biochemical “lock-and-key” mechanisms can reduce the chance that low-fidelity lineages will successfully reproduce.

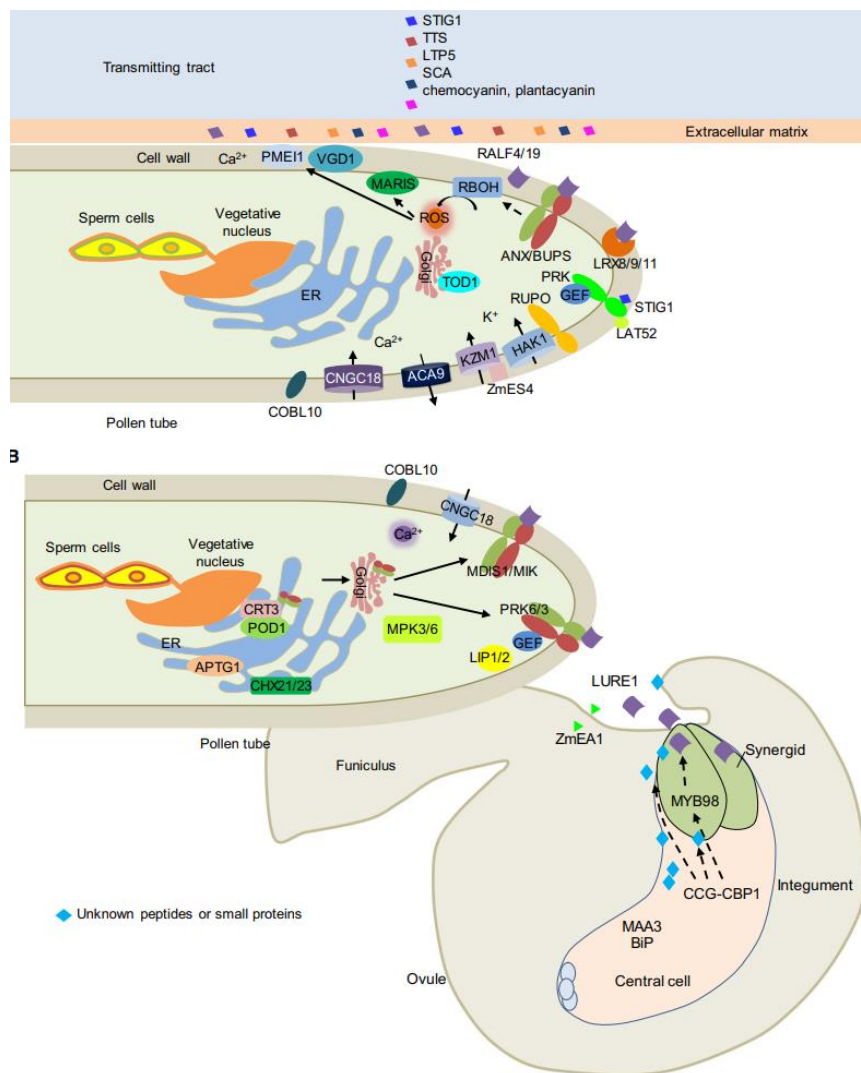


Figure 1. Fertilization in flowering plants. Pollen tube elongation in the maternal tissue and navigation to the ovule require intimate successive cell–cell interactions between the tube and female tissues [Li et al., 2018]. This procedure can create complex tests for pollen grains (which should be thought of as haploid organisms that are capable of producing sperm) using multilayered signaling pathways that involve many gene products, which can weed out the more error-prone lineages.

Note that trends in sexual selection may vary when selective pressures vary. For example, Takahashi et al. studied feral peafowl in Japan, where they are presumably not well-adapted. They may therefore have been subject to strong selection for several generations, meaning that a higher proportion of mutations than usual would be beneficial (see below). This means that peahens putting less emphasis on well-formed tails might have been selected in Japan.

The evolution of sexual reproduction

It is interesting to contemplate how life must have existed before sexual reproduction evolved. Ancient asexual biological lineages must have existed as quasispecies, meaning that they were similar to modern asexual biological entities such as viruses, occurring as diverging phylogenetic trees that form “clouds” of rapidly-mutating related genotypes. (Presumably, simple mechanisms

that allowed recombination between lineages soon evolved, like those of viruses, because they allow beneficial mutations on different branches of the tree to be brought together as single lineages.) As noted above, when a biological entity's environment is stable, it will eventually become well-adapted to that environment, such that very few changes in nucleic acid bases and amino acids in sequences can provide an advantage. After long selection in a stable environment, therefore, almost all mutations are harmful and high-fidelity replication becomes particularly advantageous. Presumably, natural selection can then remove most of the mutator mutations that arise since they will be linked to the mutations they generated. Since life exists today (and since asexual self-replicating entities such as viruses also exist) we know that such systems can be stable and were so in the remote past. Early life might therefore have persisted in a limited number of stable environments, but lineages that spread to more changeable environments would be predicted to lose fidelity (because selection for high fidelity would be reduced), become unstable, and have limited longevity. By introducing complex structural or biochemical lock-and-key mechanisms and allowing mate selection, sexual reproduction may have allowed ancient life forms to move from stable to less-stable environments. Moreover, error-prone lineages that acquired beneficial mutations could easily recombine sexually with high-fidelity lineages to create new, well-adapted, stable lineages. Sexual reproduction can, therefore, plausibly be seen as an adaptation to unstable environments. A similar argument can explain why sex is so popular among complex organisms since many are subject to strong selection and may need to recover replicative fidelity when it is lost in otherwise well-adapted individuals.

Fisher's runaway selection and Zahavi's handicap principle

Other hypotheses have been put forward to explain the development of the exaggerated features that are sometimes produced by sexual selection in animals. In the early 20th century, Ronald Fisher suggested that any slight preference in females for a male character, such as slightly longer tails in birds, might set up a positive feedback cycle. The preferred trait and the female preference for it would increase together. In this model, females would continue to prefer males with long tails even if they were so long that the individuals possessing them were not the best survivors. In 1975, Amotz Zahavi made an alternative proposal. He suggested that animal traits that confer handicaps may evolve by sexual selection because they "test the quality" of the individuals that possess them [Zahavi, 1975]. These two hypotheses, and the Kilimanjaro hypothesis, are all distinct. Both the Kilimanjaro hypothesis and Zahavi's handicap principle suggest that sought-after characters can advertise the quality of genes whose effects would otherwise be hidden. Fisher's "runaway" sexual selection, however, says the selected characters are attractive in themselves simply because they have become "fashionable" in that particular population. The Kilimanjaro hypothesis emphasizes complexity and proposes that these sought-after characters are typically the product of many genes (to show up mutations effectively), but they can be either beneficial (such as strong muscles and intelligent brains) or harmful (such as the massive tail of a peacock); by contrast, Zahavi suggests that the sought-after characters must "lower the fitness of the selected sex in relation to the main ecological problems of the species" and must squander scarce resources [Zahavi, 1975]. According to both runaway selection and the handicap principle, species and populations with greater handicaps (such as peafowl and migratory species such as arctic terns and Atlantic salmon) are expected to be at a selective disadvantage compared to comparable groups with more modest handicaps. The Kilimanjaro hypothesis says that such species and populations may be at a long-term selective advantage compared to comparable groups, and may thrive, if the handicaps successfully reduce the transmission and selection of error-prone replicome genes.



Figure 2. The extraordinary symmetry of a peacock's tail, with the positions and lengths of feathers being carefully controlled to produce regular spacing of the "eyes". In 1975, Amotz Zahavi proposed the "handicap principle" to explain the evolution of features such as these [Zahavi. 1975]. The principle suggests that by squandering scarce resources by growing and maintaining such features, peacocks and other animals show potential mates that they are of "good quality" and are selected. However, the handicap would be almost identical without the elaborate markings and exact symmetry, suggesting that these features have some other benefit. Moreover, the barbs outside the eye areas of the feathers are sparse, suggesting that selection favors reduced, rather than enhanced, weight - although enhanced weight would increase the handicap. The Kilimanjaro hypothesis notes that a well-formed tail shows that the peacock has an intact set of genes for making tails, suggesting a low mutation rate. Similarly, a female that recognizes a well-formed tail has an intact set of genes for tail-recognition.

Other mutations

Note that the mate-selection strategies discussed above can also show up other genetic defects that would otherwise be hidden. Complex behaviors, displays, and biochemical mechanisms can expose mutations in "house-keeping" genes that are active in all cell types, such as ribosomal and cell-cycle proteins, histones, mitochondrial proteins, and factors for transcription, RNA splicing, translation, and protein processing.

Suggestions for experimental and observational testing of the Kilimanjaro hypothesis

Several scientific approaches could test the Kilimanjaro Hypothesis. Similar studies could be performed with any convenient sexual organisms, including yeasts, protists, insects (such as *Drosophila* or flour beetles), flowering plants, fish, birds, or mammals (possibly in captivity, for example, in zoos.) Gene sequencing is probably necessary to allow the unambiguous interpretation of results. I suggest focusing on polymerases, but other replisome genes could be included. (I imagine performing these experiments with *Drosophila*, but other species could be used.) I suggest an experimental approach along the following lines:

- (1) sequence polymerase genes in wild organisms from large, stable populations, which can be assumed to replicate with high fidelity.

(2) Take samples from individuals and sequence their polymerase genes, and/or profile their DNA. (One or more rounds of reproduction may be necessary to obtain material to sequence small organisms.) Identify lineages with mutations in polymerase genes, which are expected to show increased mutation rates in most cases, and lineages with few mutations or none.

(3) Set up colonies, starting each with a single pair. Found several colonies with low-fidelity individuals and several with high-fidelity individuals. Polymerase and other genes can be sequenced (or DNA can be profiled) to confirm the identities of high and low-fidelity colonies.

(4) Now introduce high-fidelity individuals into low-fidelity colonies, and low-fidelity individuals into high-fidelity colonies; use sequencing to compare the rates at which the two classes of polymerase genes invade their respective colonies.

The Kilimanjaro hypothesis predicts that high-fidelity genes will replicate and spread faster than low-fidelity ones. It would be very interesting to perform the experiment to, but it can also be thought of as a thought-experiment: (1) replisome genes *must* sometimes be subject to mutation; (2) some of these mutations *must* affect fidelity negatively; (3) the resulting extra mutations *must* eventually affect, negatively, whatever criteria are used for mate selection by the species; (4) lineages with high fidelity *must* outcompete low-fidelity lineages over time.

A second experimental approach would compare the health, well-being, genetic fidelity, number of individuals, etc., over several generations of two populations. In one population, individuals would be free to choose their mates, while in the comparison population mating would be limited to preselected pairs selected at random by the experimenter. I expect the first population to outperform the second over time. Again, sequencing, DNA profiling, etc., could confirm the involvement of mutations affecting fidelity.

A third approach would test whether applying intense selective pressures encourages the emergence of low-fidelity lineages. [Studies along these lines may have been carried out already – I will investigate when I have time.] For example, colonies could be sustained on unsuitable foods or exposed to toxic compounds. Novel behaviors could also be selected, for example, by eliminating *Drosophila* or other insects that are attracted to electrical insect killers by UV lamps. Evolutionary theory suggests that low-fidelity lineages will be more prevalent after strong selection and rapid adaptation. It would be important to prevent or limit recombination because, as discussed, mate selection might conserve fidelity. For example, mating could be limited to preselected pairs.

A fourth suggestion is observational. Since the Kilimanjaro Hypothesis suggests that long migrations reduce the prevalence of mutator mutations, it predicts that migratory lineages will tend to infiltrate non-migratory populations rather than the reverse. This prediction could be investigated in migratory and related non-migratory populations by constructing phylogenetic trees based on DNA sequences.

Conclusions

Zahavi pointed out that more than one hypothesis can explain the evolution of sought-after characters [Zahavi, 1975]. Likewise, I am not claiming that the handicap principle (or any other theory of evolution) is wrong. In the example given above in the introduction, if a man carried a bunch of flowers to the summit of a mountain to impress a woman, he would be applying the handicap principle. It might work. Similarly, a trait that initially evolved as a test of fidelity might

become “fashionable” in particular species and so become exaggerated to a maladaptive degree; such selection could be considered “runaway”. I suggest, however, that the Kilimanjaro hypothesis provides a more straightforward and more universal explanation of most of the surprising features and behaviors that other hypotheses of sexual selection seek to explain while also shedding light on the ubiquity of sexual reproduction and the preservation of replicative fidelity.

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