Evolution of sexual reproduction

The **evolution of sexual reproduction** describes how sexually reproducing animals, plants, fungi and protists could have evolved from a common ancestor that was a single celled eukaryotic species.[1][2][3] There are a few species which have secondarily lost the ability to reproduce sexually, such as Bdelloidea, and some plants and animals that routinely reproduce asexually (by apomixis and parthenogenesis) without entirely losing sex. The evolution of sex contains two related, yet distinct, themes: its *origin* and its *maintenance*.

Ladybirds mating

The origin of sexual reproduction in prokaryotes is around 2 billion years ago (Gya) when bacteria started exchanging genes via the processes of conjugation, transformation, and transduction.[4] In eukaryotes, it is thought to have arisen in the Last Common Eukaryotic Ancestor (LECA), possibly via several processes of varying success, and then to have persisted.[5]

Pollen production is an essential step in sexual reproduction of seed plants.

Since hypotheses for the origins of sex are difficult to verify experimentally (outside of evolutionary computation), most current work has focused on the maintenance of sexual reproduction. The maintenance of sexual reproduction - specifically, of its dioecious form - in a highly competitive world had long been one of the major mysteries of biology, as both other known mechanisms of reproduction - asexual reproduction and hermaphroditism - possess apparent advantages over it. Asexual reproduction can proceed by budding, fission, or spore formation not involving union of gametes, which results in a much faster rate compared to sexual reproduction, where 50% of offspring are males, unable to produce offspring themselves. In hermaphoditic reproduction each of the two parent organisms required for the formation of a zygote can provide either the male or the female gamete, which leads to advantages in both size and genetic variance of a population.

Sexual reproduction must offer significant fitness advantages to a species because despite the two-fold cost of sex (see below), it dominates among multicellular forms of life, implying that the fitness of offspring produced outweighs the costs. Sexual reproduction derives from recombination, where parent genotypes are reorganized and shared with the offspring. This stands in contrast to single-parent asexual replication, where the offspring is identical to the parents. Recombination supplies two fault-tolerance mechanisms at the molecular level: *recombinational DNA repair* (promoted during meiosis because homologous chromosomes pair at that time) and *complementation* (also known as heterosis, hybrid vigor or masking of mutations).

Contents

Historical perspective

The issue features in the writings of Aristotle, and modern philosophical-scientific thinking on the problem dates from at least Erasmus Darwin (1731-1802) in the 18th century. August Weismann picked up the thread in 1889, arguing that sex served to generate genetic variation, as detailed in the majority of the explanations below. On the other hand, Charles Darwin (1809-1882) concluded that the effects of hybrid vigor (complementation) "is amply sufficient to account for the ... genesis of the two sexes". This is consistent with the repair and complementation hypothesis, described below. Biologists - including W. D. Hamilton, Alexey Kondrashov, George C. Williams, Harris Bernstein, Carol Bernstein, Michael M. Cox, Frederic A. Hopf and Richard E. Michod - have suggested several explanations for how a vast array of different living species maintain sexual reproduction.

Disadvantages of sex and sexual reproduction

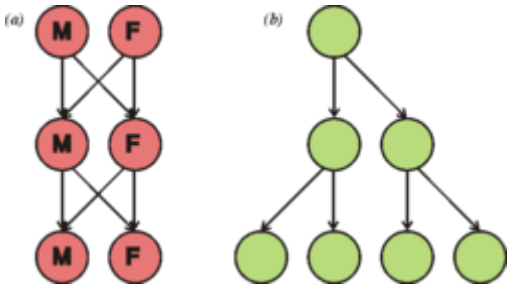
This section will briefly focus on the ostensible disadvantages of sexual reproduction as compared to relative advantages in asexual reproduction. Given that sexual reproduction abounds in multicellular organisms, this section is followed by a lengthy overview of theories aiming to elucidate the advantages of sex and sexual reproduction.

Population expansion cost of sex

An asexual population can grow much more rapidly with each generation. Assume the entire population of some theoretical species has 100 total organisms consisting of two sexes (i.e. males and females) with 50:50 male-to-female representation, and only the females of this species can bear offspring. If all capable members of this population procreated once, a total of 50

offspring would be produced (the *F1* generation). Contrast this outcome with an asexual species, where each member of the 100-organism population is capable of bearing young. If all capable members of this asexual population procreated once, a total of 100 offspring would be produced.

This idea is sometimes referred to as the **two-fold cost** of sexual reproduction. It was first described mathematically by John Maynard Smith.[6] In his manuscript Smith further speculated on the impact of an asexual mutant arising in a sexual population, which suppresses meiosis and allows eggs to develop by mitotic division into offspring genetically identical to the mother.[7] The mutant-asexual lineage would double its representation in the population each generation, all else being equal.



This diagram illustrates the *two-fold cost of sex*. If each individual were to contribute to the same number of offspring (two), *(a)* the sexual population remains the same size each generation, where the *(b)* asexual population doubles in size each generation.

Technically the problem above is not that of sexual reproduction but a problem of having a subset of organisms incapable of bearing offspring. Indeed some multicellular organisms (isogamous) engage in sexual reproduction but all members of the species are capable of bearing offspring.[8] The two-fold reproductive disadvantage assumes that males contribute only genes to their offspring and sexual females waste half their reproductive potential on sons.[7] Thus, in this formulation, the principal costs of sex is that males and females must successfully copulate (which almost always involves expending energy to come together through time and space).

Selfish cytoplasmic genes

Sexual reproduction implies that chromosomes and alleles segregate and recombine in every generation, but not all genes are transmitted together to the offspring.[7] There is a chance of spreading mutants that cause unfair transmission at the expense of their non-mutant colleagues. These mutations are referred to as selfish because they promote their own spread at the cost of alternative alleles or host organism, these include; nuclear meiotic drivers and selfish cytoplasmic genes.[7] Meiotic driver is defined as genes that distort meiosis to produce gametes containing themselves more than half the time and selfish cytoplasmic gene is a gene located in an organelle, plasmid, or intracellular parasite that modifies reproduction to cause its own increase at the expense of the cell or organism that carries it[7]

Genetic heritability cost of sex

A sexually reproducing organism only passes on ~50% of its own genetic material to each L2 offspring. This is a consequence of the fact that gametes from sexually reproducing species are haploid. Again however, this is not applicable to all sexual organisms. There are numerous species which are sexual but do not have a genetic-loss problem because they do not produce males or females. Yeast, for example, are isogamous sexual organisms which have two mating types which fuse and recombine their haploid genomes. Both sexes reproduce during the haploid and diploid stages of their life cycle and have a 100% chance of passing their genes into their offspring.[8]

Some species avoid the cost of 50% of sexual reproduction, although they have "sex" (in the sense of genetic recombination). In these species (e.g., bacteria, ciliates, dinoflagellates and diatoms), "sex" and reproduction occurs separately.[9][10]

Advantages of sex and sexual reproduction

The concept of sex includes two fundamental phenomena: the sexual process (fusion of genetic information of two individuals) and sexual differentiation (separation of this information into two parts). Depending on the presence or absence of these phenomena, the existing ways of reproduction can be divided into asexual, hermaphrodite and dioecious forms. The sexual

process and sexual differentiation are different phenomena, and, in essence, are diametrically opposed. The first creates (increases) diversity of genotypes, and the second decreases it by half.

Reproductive advantages of the asexual forms are in quantity of the progeny and the advantages of the hermaphrodite forms – in maximum diversity. Transition from the hermaphrodite to dioecious state leads to a loss of at least half of the diversity. So, the main question is to explain the advantages given by sexual differentiation, i.e. the benefits of two separate sexes compared to hermaphrodites rather than to explain benefits of sexual forms (hermaphrodite + dioecious) over asexual ones. It has already been understood that since sexual reproduction is not associated with any clear reproductive advantages, as compared with asexual, there should be some important advantages in evolution.[11]

Advantages due to genetic variation

For the advantage due to genetic variation, there are three possible reasons this might happen. First, sexual reproduction can combine the effects of two beneficial mutations in the same individual (i.e. sex aids in the spread of advantageous traits). Also, the necessary mutations do not have to have occurred one after another in a single line of descendants.[12] Second, sex acts to bring together currently deleterious mutations to create severely unfit individuals that are then eliminated from the population (i.e. sex aids in the removal of deleterious genes). However, in organisms containing only one set of chromosomes, deleterious mutations would be eliminated immediately, and therefore removal of harmful mutations is an unlikely benefit for sexual reproduction. Lastly, sex creates new gene combinations that may be more fit than previously existing ones, or may simply lead to reduced competition among relatives.

For the advantage due to DNA repair, there is an immediate large benefit of removing DNA damage by recombinational DNA repair during meiosis, since this removal allows greater survival of progeny with undamaged DNA. The advantage of complementation to each sexual partner is avoidance of the bad effects of their deleterious recessive genes in progeny by the masking effect of normal dominant genes contributed by the other partner.

The classes of hypotheses based on the creation of variation are further broken down below. Any number of these hypotheses may be true in any given species (they are not mutually exclusive), and different hypotheses may apply in different species. However, a research framework based on creation of variation has yet to be found that allows one to determine whether the reason for sex is universal for all sexual species, and, if not, which mechanisms are acting in each species.

On the other hand, the maintenance of sex based on DNA repair and complementation applies widely to all sexual species.

Protection from major genetic mutation

In contrast to the view that sex promotes genetic variation, Heng,[13] and Gorelick and Heng[14] reviewed evidence that sex actually acts as a constraint on genetic variation. They consider that sex acts as a coarse filter, weeding out major genetic changes, such as chromosomal rearrangements, but permitting minor variation, such as changes at the nucleotide or gene level (that are often neutral) to pass through the sexual sieve.

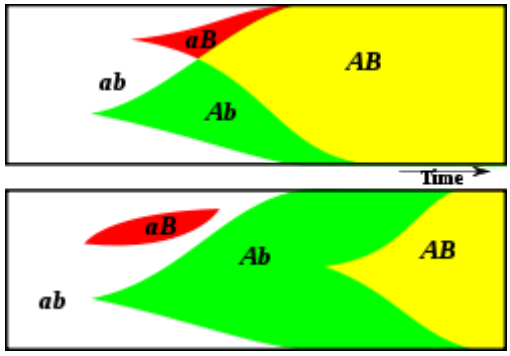
Novel genotypes

Sex could be a method by which novel genotypes are created. Because sex combines genes from two individuals, sexually reproducing populations can more easily combine advantageous genes than can asexual populations. If, in a sexual population, two different advantageous alleles arise at different loci on a chromosome in different members of the population, a chromosome containing the two advantageous alleles can be produced within a few generations by recombination. However, should the same two alleles arise in different members of an asexual population, the only way that one chromosome can develop the other allele is

to independently gain the same mutation, which would take much longer. Several studies have addressed counterarguments, and the question of whether this model is sufficiently robust to explain the predominance of sexual versus asexual reproduction.[15]:73–86

Ronald Fisher also suggested that sex might facilitate the spread of advantageous genes by allowing them to better escape their genetic surroundings, if they should arise on a chromosome with deleterious genes.

Supporters of these theories respond to the balance argument that the individuals produced by sexual and asexual reproduction may differ in other respects too – which may influence the persistence of sexuality. For example, in the heterogamous water fleas of the genus *Cladocera*, sexual offspring form eggs which are better able to survive the winter versus those the fleas produce asexually.



This diagram illustrates how sex might create novel genotypes more rapidly. Two advantageous alleles *A* and *B* occur at random. The two alleles are recombined rapidly in a sexual population (top), but in an asexual population (bottom) the two alleles must independently arise because of clonal interference.

Increased resistance to parasites

One of the most widely discussed theories to explain the persistence of sex is that it is maintained to assist sexual individuals in resisting parasites, also known as the Red Queen Hypothesis.[16][15]:113–117[17][18][19]

When an environment changes, previously neutral or deleterious alleles can become favourable. If the environment changed sufficiently rapidly (i.e. between generations), these changes in the environment can make sex advantageous for the individual. Such rapid changes in environment are caused by the co-evolution between hosts and parasites.

Imagine, for example that there is one gene in parasites with two alleles *p* and *P* conferring two types of parasitic ability, and one gene in hosts with two alleles *h* and *H*, conferring two types of parasite resistance, such that parasites with allele *p* can attach themselves to hosts with the allele *h*, and *P* to *H*. Such a situation will lead to cyclic changes in allele frequency - as *p* increases in frequency, *h* will be disfavoured.

In reality, there will be several genes involved in the relationship between hosts and parasites. In an asexual population of hosts, offspring will only have the different parasitic resistance if a mutation arises. In a sexual population of hosts, however, offspring will have a new combination of parasitic resistance alleles.

In other words, like Lewis Carroll's Red Queen, sexual hosts are continually "running" (adapting) to "stay in one place" (resist parasites).

Evidence for this explanation for the evolution of sex is provided by comparison of the rate of molecular evolution of genes for kinases and immunoglobulins in the immune system with genes coding other proteins. The genes coding for immune system proteins evolve considerably faster.[20][21]

Further evidence for the Red Queen hypothesis was provided by observing long-term dynamics and parasite coevolution in a "mixed" (sexual and asexual) population of snails (*Potamopyrgus antipodarum*). The number of sexuals, the number asexuals, and the rates of parasite infection for both were monitored. It was found that clones that were plentiful at the beginning of the study became more susceptible to parasites over time. As parasite infections increased, the once plentiful clones dwindled dramatically in number. Some clonal types disappeared entirely. Meanwhile, sexual snail populations remained much more stable over time.[22][23]

However, Hanley et al.[24] studied mite infestations of a parthenogenetic gecko species and its two related sexual ancestral species. Contrary to expectation based on the Red Queen hypothesis, they found that the prevalence, abundance and mean intensity of mites in sexual geckos was significantly higher than in asexuals sharing the same habitat.

In 2011, researchers used the microscopic roundworm *Caenorhabditis elegans* as a host and the pathogenic bacteria *Serratia marcescens* to generate a host-parasite coevolutionary system in a controlled environment, allowing them to conduct more than 70 evolution experiments testing the Red Queen Hypothesis. They genetically manipulated the mating system of *C. elegans*, causing populations to mate either sexually, by self-fertilization, or a mixture of both within the same population. Then they exposed those populations to the *S. marcescens* parasite. It was found that the self-fertilizing populations of *C. elegans* were rapidly driven extinct by the coevolving parasites while sex allowed populations to keep pace with their parasites, a result consistent with the Red Queen Hypothesis.[25][26] In natural populations of *C. elegans*, self-fertilization is the predominant mode of reproduction, but infrequent out-crossing events occur at a rate of about 1%.[27]

Critics of the Red Queen hypothesis question whether the constantly changing environment of hosts and parasites is sufficiently common to explain the evolution of sex. In particular, Otto and Nuismer [28] presented results showing that species interactions (e.g. host vs parasite interactions) typically select against sex. They concluded that, although the Red Queen hypothesis favors sex under certain circumstances, it alone does not account for the ubiquity of sex. Otto and Gerstein [29] further stated that “it seems doubtful to us that strong selection per gene is sufficiently commonplace for the Red Queen hypothesis to explain the ubiquity of sex.” Parker [30] reviewed numerous genetic studies on plant disease resistance and failed to uncover a single example consistent with the assumptions of the Red Queen hypothesis.

DNA repair and complementation

As discussed in the earlier part of this article, sexual reproduction is conventionally explained as an adaptation for producing genetic variation through allelic recombination. As acknowledged above, however, serious problems with this explanation have led many biologists to conclude that the benefit of sex is a major unsolved problem in evolutionary biology.

An alternative "informational" approach to this problem has led to the view that the two fundamental aspects of sex, genetic recombination and outcrossing, are adaptive responses to the two major sources of "noise" in transmitting genetic information. Genetic noise can occur as either physical damage to the genome (e.g. chemically altered bases of DNA or breaks in the chromosome) or replication errors (mutations)[31][32][33] This alternative view is referred to as the repair and complementation hypothesis, to distinguish it from the traditional variation hypothesis.

The repair and complementation hypothesis assumes that genetic recombination is fundamentally a DNA repair process, and that when it occurs during meiosis it is an adaptation for repairing the genomic DNA which is passed on to progeny. Recombinational repair is the only repair process known which can accurately remove double-strand damages in DNA, and such damages are both common in nature and ordinarily lethal if not repaired. For instance, double-strand breaks in DNA occur about 50 times per cell cycle in human cells [see DNA damage (naturally occurring)]. Recombinational repair is prevalent from the simplest viruses to the most complex multicellular eukaryotes. It is effective against many different types of genomic damage, and in particular is highly efficient at overcoming double-strand damages. Studies of the mechanism of meiotic recombination indicate that meiosis is an adaptation for repairing DNA.[34][35] These considerations form the basis for the first part of the repair and complementation hypothesis.

In some lines of descent from the earliest organisms, the diploid stage of the sexual cycle, which was at first transient, became the predominant stage, because it allowed complementation — the masking of deleterious recessive mutations (i.e. hybrid vigor or heterosis). Outcrossing, the second fundamental aspect of sex, is maintained by the advantage of masking mutations and the disadvantage of inbreeding (mating with a close relative) which allows expression of recessive mutations (commonly observed as inbreeding depression). This is in accord with Charles Darwin,[36] who concluded that the adaptive advantage of sex is hybrid

vigor; or as he put it, "the offspring of two individuals, especially if their progenitors have been subjected to very different conditions, have a great advantage in height, weight, constitutional vigor and fertility over the self fertilised offspring from either one of the same parents."

However, outcrossing may be abandoned in favor of parthenogenesis or selfing (which retain the advantage of meiotic recombinational repair) under conditions in which the costs of mating are very high. For instance, costs of mating are high when individuals are rare in a geographic area, such as when there has been a forest fire and the individuals entering the burned area are the initial ones to arrive. At such times mates are hard to find, and this favors parthenogenic species.

In the view of the repair and complementation hypothesis, the removal of DNA damage by recombinational repair produces a new, less deleterious form of informational noise, allelic recombination, as a by-product. This lesser informational noise generates genetic variation, viewed by some as the major effect of sex, as discussed in the earlier parts of this article.

Deleterious mutation clearance

Mutations can have many different effects upon an organism. It is generally believed that the majority of non-neutral mutations are deleterious, which means that they will cause a decrease in the organism's overall fitness.[37] If a mutation has a deleterious effect, it will then usually be removed from the population by the process of natural selection. Sexual reproduction is believed to be more efficient than asexual reproduction in removing those mutations from the genome.[38]

There are two main hypotheses which explain how sex may act to remove deleterious genes from the genome.

Evading harmful mutation build-up

While DNA is able to recombine to modify alleles, DNA is also susceptible to mutations within the sequence that can affect an organism in a negative manner. Asexual organisms do not have the ability to recombine their genetic information to form new and differing alleles. Once a mutation occurs in the DNA or other genetic carrying sequence, there is no way for the mutation to be removed from the population until another mutation occurs that ultimately deletes the primary mutation. This is rare among organisms. Hermann Joseph Muller introduced the idea that mutations build up in asexual reproducing organisms. Muller described this occurrence by comparing the mutations that accumulate as a ratchet. Each mutation that arises in asexually reproducing organisms turns the ratchet once. The ratchet is unable to be rotated backwards, only forwards. The next mutation that occurs turns the ratchet once more. Additional mutations in a population continually turn the ratchet and the mutations, mostly deleterious, continually accumulate without recombination.[39] These mutations are passed onto the next generation because the offspring are exact genetic clones of their parent. The genetic load of organisms and their populations will increase due to the addition of multiple deleterious mutations and decrease the overall reproductive success and fitness.

For sexually reproducing populations, studies have shown that single-celled bottlenecks are beneficial for resisting mutation build-up. Passaging a population through a single-celled bottleneck involves the fertilization event occurring with haploid sets of DNA, forming one fertilized cell. For example, humans undergo a single-celled bottleneck in that the haploid sperm fertilizes the haploid egg, forming the diploid zygote, which is unicellular. This passage through a single cell is beneficial in that it lowers the chance of mutations from being passed on through multiple individuals.[40] Further studies using *Dictyostelium discoideum* suggest that this unicellular initial stage is important for resisting mutations due to the importance of high relatedness. Highly related individuals are more closely related, and more clonal, whereas less related individuals are less so, increasing the likelihood that an individual in a population of low relatedness may have a detrimental mutation. Highly related populations also tend to thrive better than lowly related because the cost of sacrificing an individual is greatly offset by the benefit gained by its relatives and in turn, its genes, according to kin selection. The studies with *D. discoideum* showed that conditions of high relatedness resisted mutant individuals more effectively than those of low relatedness, suggesting the importance of high relatedness to resist mutations from proliferating.[41]

Removal of deleterious genes

This hypothesis was proposed by Alexey Kondrashov, and is sometimes known as the *deterministic mutation hypothesis*.[38] It assumes that the majority of deleterious mutations are only slightly deleterious, and affect the individual such that the introduction of each additional mutation has an increasingly large effect on the fitness of the organism. This relationship between number of mutations and fitness is known as *synergistic epistasis*.

By way of analogy, think of a car with several minor faults. Each is not sufficient alone to prevent the car from running, but in combination, the faults combine to prevent the car from functioning.

Similarly, an organism may be able to cope with a few defects, but the presence of many mutations could overwhelm its backup mechanisms.

Kondrashov argues that the slightly deleterious nature of mutations means that the population will tend to be composed of individuals with a small number of mutations. Sex will act to recombine these genotypes, creating some individuals with fewer deleterious mutations, and some with more. Because there is a major selective disadvantage to individuals with more mutations, these individuals die out. In essence, sex compartmentalises the deleterious mutations.

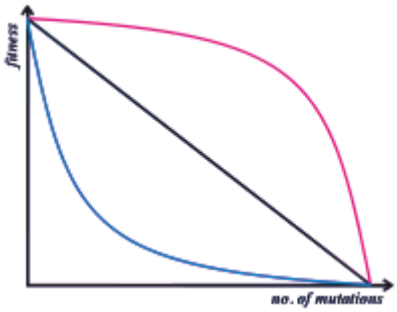


Diagram illustrating different relationships between numbers of mutations and fitness. Kondrashov's model requires *synergistic epistasis*, which is represented by the red line[42][43] - each subsequent mutation has a disproportionately large effect on the organism's fitness.

There has been much criticism of Kondrashov's theory, since it relies on two key restrictive conditions. The first requires that the rate of deleterious mutation should exceed one per genome per generation in order to provide a substantial advantage for sex. While there is some empirical evidence for it (for example in Drosophila[44] and E. coli[45]), there is also strong evidence against it. Thus, for instance, for the sexual species *Saccharomyces cerevisiae* (yeast) and *Neurospora crassa* (fungus), the mutation rate per genome per replication are 0.0027 and 0.0030 respectively. For the nematode worm *Caenorhabditis elegans*, the mutation rate per effective genome per sexual generation is 0.036.[46] Secondly, there should be strong interactions among loci (synergistic epistasis), a mutation-fitness relation for which there is only limited evidence.[47] Conversely, there is also the same amount of evidence that mutations show no epistasis (purely additive model) or antagonistic interactions (each additional mutation has a disproportionally *small* effect).

Other explanations

Geodakyan's evolutionary theory of sex

Geodakyan suggested that sexual dimorphism provides a partitioning of a species' phenotypes into at least two functional partitions: a female partition that secures beneficial features of the species and a male partition that emerged in species with more variable and unpredictable environments. The male partition is suggested to be an "experimental" part of the species that allows the species to expand their ecological niche, and to have alternative configurations. This theory underlines the higher variability and higher mortality in males, in comparison to females. This functional partitioning also explains the higher susceptibility to disease in males, in comparison to females and therefore includes the idea of "protection against parasites" as another functionality of male sex. Geodakyan's evolutionary theory of sex was developed in Russia in 1960-80 and was not known to the West till the era of the Internet. Trofimova, who analysed psychological sex differences, hypothesised that the male sex might also provide a "redundancy pruning" function.[48]

Speed of evolution

Ilan Eshel suggested that sex prevents rapid evolution. He suggests that recombination breaks up favourable gene combinations more often than it creates them, and sex is maintained because it ensures selection is longer-term than in asexual populations - so the population is less affected by short-term changes.[15]:85–86[49] This explanation is not widely accepted, as its assumptions are very restrictive.

It has recently been shown in experiments with *Chlamydomonas* algae that sex can remove the speed limit on evolution.[50]

An information theoretic analysis using a simplified but useful model shows that in asexual reproduction, the information gain per generation of a species is limited to 1 bit per generation, while in sexual reproduction, the information gain is bounded by $\sqrt{G}$, where G is the size of the genome in bits.[51]

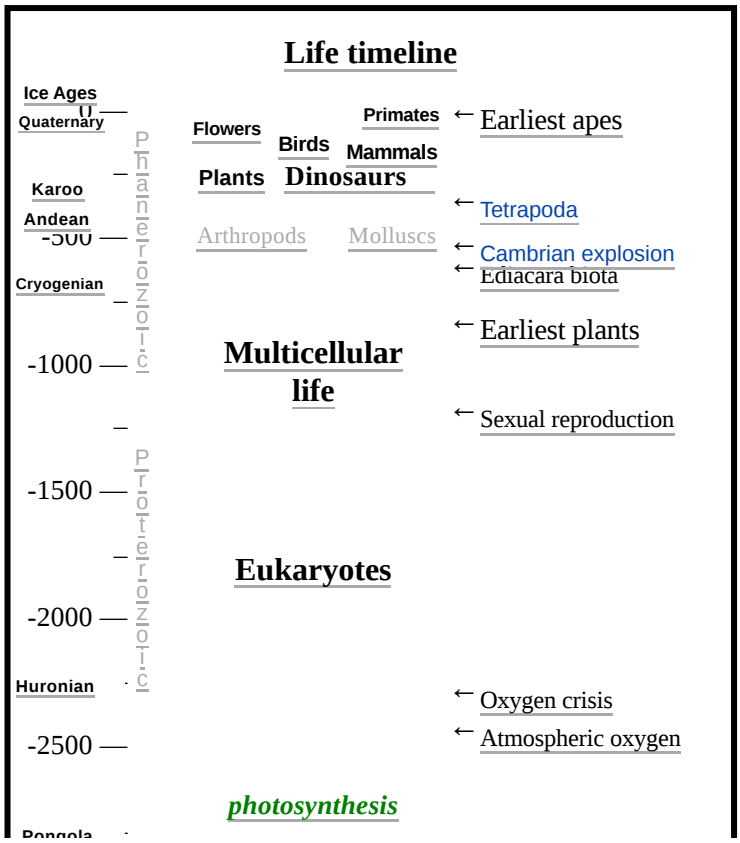
Libertine bubble theory

The evolution of sex can alternatively be described as a kind of gene exchange that is independent from reproduction.[52] According to the Thierry Lodé's "libertine bubble theory", sex originated from an archaic gene transfer process among prebiotic bubbles.[53][54] The contact among the pre-biotic bubbles could, through simple food or parasitic reactions, promote the transfer of genetic material from one bubble to another. That interactions between two organisms be in balance appear to be a sufficient condition to make these interactions evolutionarily efficient, i.e. to select bubbles that tolerate these interactions (“libertine” bubbles) through a blind evolutionary process of self-reinforcing gene correlations and compatibility.[55]

The "libertine bubble theory" proposes that meiotic sex evolved in proto-eukaryotes to solve a problem that bacteria did not have, namely a large amount of DNA material, occurring in an archaic step of proto-cell formation and genetic exchanges. So that, rather than providing selective advantages through reproduction, sex could be thought of as a series of separate events which combines step-by-step some very weak benefits of recombination, meiosis, gametogenesis and syngamy.[56] Therefore, current sexual species could be descendants of primitive organisms that practiced more stable exchanges in the long term, while asexual species have emerged, much more recently in evolutionary history, from the conflict of interest resulting from anisogamy.

Origin of sexual reproduction

Many protists reproduce sexually, as do the multicellular plants, animals, and fungi. In the eukaryotic fossil record, sexual reproduction first appeared by 1.2 billion years ago in the Proterozoic Eon.[57] All sexually reproducing eukaryotic organisms likely derive from a single-celled common ancestor.[1][35][58][53] It is probable that the evolution of sex was an integral part of the evolution of the first eukaryotic cell.[59][60] There are a few species which have secondarily lost this feature, such as Bdelloidea and some parthenocarpic plants.

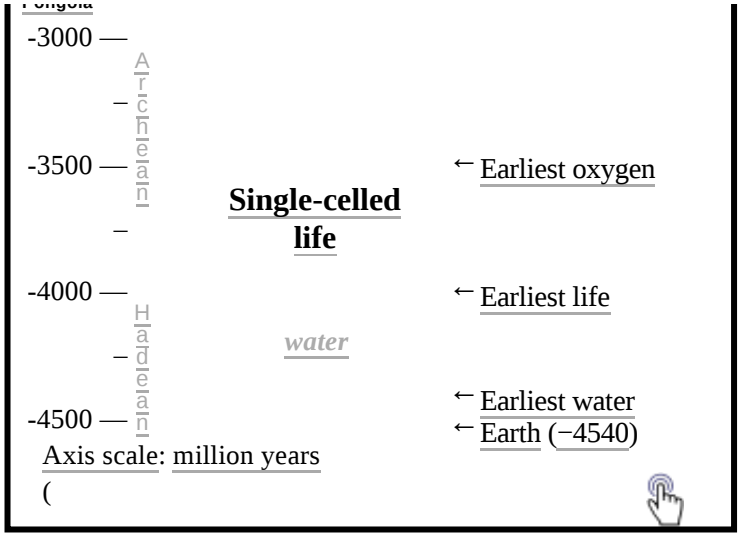


Diploidy

Organisms need to replicate their genetic material in an efficient and reliable manner. The necessity to repair genetic damage is one of the leading theories explaining the origin of sexual reproduction. Diploid individuals can repair a damaged section of their DNA via homologous recombination, since there are two

copies of the gene in the cell and if one copy is damaged, the other copy is unlikely to be damaged at the same site.

A harmful mutation in a haploid individual, on the other hand, is more likely to become fixed (i.e. permanent), since any DNA repair mechanism would have no source to recover the original undamaged sequence from.[31] The most primitive form of sex may have been one organism with damaged DNA replicating an undamaged strand from a similar organism in order to repair itself.[61]



Meiosis

If, as evidence indicates, sexual reproduction arose very early in eukaryotic evolution, the essential features of meiosis may have already been present in the prokaryotic ancestors of eukaryotes.[58][62] In extant organisms, proteins with central functions in meiosis are similar to key proteins in natural transformation in bacteria and DNA transfer in archaea.[62][63] For example, recA recombinase, that catalyses the key functions of DNA homology search and strand exchange in the bacterial sexual process of transformation, has orthologs in eukaryotes that perform similar functions in meiotic recombination[62] (see Wikipedia articles RecA, RAD51 and DMC1).

Natural transformation in bacteria, DNA transfer in archaea, and meiosis in eukaryotic microorganisms are induced by stressful circumstances such as overcrowding, resource depletion, and DNA damaging conditions.[55][62][63] This suggests that these sexual processes are adaptations for dealing with stress, particularly stress that causes DNA damage. In bacteria, these stresses induce an altered physiologic state, termed competence, that allows active take-up of DNA from a donor bacterium and the integration of this DNA into the recipient genome (see Natural competence) allowing recombinational repair of the recipients' damaged DNA.[64]

If environmental stresses leading to DNA damage were a persistent challenge to the survival of early microorganisms, then selection would likely have been continuous through the prokaryote to eukaryote transition,[56][62] and adaptative adjustments would have followed a course in which bacterial transformation or archaeal DNA transfer naturally gave rise to sexual reproduction in eukaryotes.

Virus-like RNA-based origin

Sex might also have been present even earlier, in the hypothesized RNA world that preceded DNA cellular life forms.[65] One proposed origin of sex in the RNA world was based on the type of sexual interaction that is known to occur in extant single-stranded segmented RNA viruses, such as influenza virus, and in extant double-stranded segmented RNA viruses such as reovirus.[66]

Exposure to conditions that cause RNA damage could have led to blockage of replication and death of these early RNA life forms. Sex would have allowed re-assortment of segments between two individuals with damaged RNA, permitting undamaged combinations of RNA segments to come together, thus allowing survival. Such a regeneration phenomenon, known as multiplicity reactivation, occurs in influenza virus[67] and reovirus.[68]

Parasitic DNA elements

Another theory is that sexual reproduction originated from selfish parasitic genetic elements that exchange genetic material (that is: copies of their own genome) for their transmission and propagation. In some organisms, sexual reproduction has been shown to enhance the spread of parasitic genetic elements (e.g.: yeast, filamentous fungi).[69]

Bacterial conjugation is a form of genetic exchange that some sources describe as “sex”, but technically is not a form of reproduction, even though it is a form of horizontal gene transfer. However, it does support the “selfish gene” part theory, since the gene itself is propagated through the F-plasmid.[61]

A similar origin of sexual reproduction is proposed to have evolved in ancient haloarchaea as a combination of two independent processes: jumping genes and plasmid swapping.[70]

Partial predation

A third theory is that sex evolved as a form of cannibalism: One primitive organism ate another one, but instead of completely digesting it, some of the “eaten” organism's DNA was incorporated into the DNA of the “eater”.[61][59]

Vaccination-like process

Sex may also be derived from another prokaryotic process. A comprehensive theory called “origin of sex as vaccination” proposes that eukaryan sex-as-syngamy (fusion sex) arose from prokaryan unilateral sex-as-infection, when infected hosts began swapping nuclearised genomes containing coevolved, vertically transmitted symbionts that provided protection against horizontal superinfection by other, more virulent symbionts.

Consequently, sex-as-meiosis (fission sex) would evolve as a host strategy for uncoupling from (and thereby render impotent) the acquired symbiotic/parasitic genes.[71]

Mechanistic origin of sexual reproduction

While theories positing fitness benefits that led to the origin of sex are often problematic, several theories addressing the emergence of the mechanisms of sexual reproduction have been proposed.

Viral eukaryogenesis

The viral eukaryogenesis (VE) theory proposes that eukaryotic cells arose from a combination of a lysogenic virus, an archaean, and a bacterium. This model suggests that the nucleus originated when the lysogenic virus incorporated genetic material from the archaean and the bacterium and took over the role of information storage for the amalgam. The archaeal host transferred much of its functional genome to the virus during the evolution of cytoplasm, but retained the function of gene translation and general metabolism. The bacterium transferred most of its functional genome to the virus as it transitioned into a mitochondrion.[72]

For these transformations to lead to the eukaryotic cell cycle, the VE hypothesis specifies a pox-like virus as the lysogenic virus. A pox-like virus is a likely ancestor because of its fundamental similarities with eukaryotic nuclei. These include a double stranded DNA genome, a linear chromosome with short telomeric repeats, a complex membrane bound capsid, the ability to produce capped mRNA, and the ability to export the capped mRNA across the viral membrane into the cytoplasm. The presence of a lysogenic pox-like virus ancestor explains the development of meiotic division, an essential component of sexual reproduction.[73]

Meiotic division in the VE hypothesis arose because of the evolutionary pressures placed on the lysogenic virus as a result of its inability to enter into the lytic cycle. This selective pressure resulted in the development of processes allowing the viruses to spread horizontally throughout the population. The outcome of this selection was cell-to-cell fusion. (This is distinct from the

conjugation methods used by bacterial plasmids under evolutionary pressure, with important consequences.)[72] The possibility of this kind of fusion is supported by the presence of fusion proteins in the envelopes of the pox viruses that allow them to fuse with host membranes. These proteins could have been transferred to the cell membrane during viral reproduction, enabling cell-to-cell fusion between the virus host and an uninfected cell. The theory proposes meiosis originated from the fusion between two cells infected with related but different viruses which recognised each other as uninfected. After the fusion of the two cells, incompatibilities between the two viruses result in a meiotic-like cell division.[73]

The two viruses established in the cell would initiate replication in response to signals from the host cell. A mitosis-like cell cycle would proceed until the viral membranes dissolved, at which point linear chromosomes would be bound together with centromeres. The homologous nature of the two viral centromeres would incite the grouping of both sets into tetrads. It is speculated that this grouping may be the origin of crossing over, characteristic of the first division in modern meiosis. The partitioning apparatus of the mitotic-like cell cycle the cells used to replicate independently would then pull each set of chromosomes to one side of the cell, still bound by centromeres. These centromeres would prevent their replication in subsequent division, resulting in four daughter cells with one copy of one of the two original pox-like viruses. The process resulting from combination of two similar pox viruses within the same host closely mimics meiosis.[73]

Neomuran revolution

An alternative theory, proposed by Thomas Cavalier-Smith, was labeled the Neomuran revolution. The designation "Neomuran revolution" refers to the appearances of the common ancestors of eukaryotes and archaea. Cavalier-Smith proposes that the first neomurans emerged 850 million years ago. Other molecular biologists assume that this group appeared much earlier, but Cavalier-Smith dismisses these claims because they are based on the "theoretically and empirically" unsound model of molecular clocks. Cavalier-Smith's theory of the Neomuran revolution has implications for the evolutionary history of the cellular machinery for recombination and sex. It suggests that this machinery evolved in two distinct bouts separated by a long period of stasis; first the appearance of recombination machinery in a bacterial ancestor which was maintained for 3 Gy, until the neomuran revolution when the mechanics were adapted to the presence of nucleosomes. The archaeal products of the revolution maintained recombination machinery that was essentially bacterial, whereas the eukaryotic products broke with this bacterial continuity. They introduced cell fusion and ploidy cycles into cell life histories. Cavalier-Smith argues that both bouts of mechanical evolution were motivated by similar selective forces: the need for accurate DNA replication without loss of viability.[74]

Questions

Some questions biologists have attempted to answer include:

- Why sexual reproduction exists, if in many organisms it has a 50% cost (fitness disadvantage) in relation to asexual reproduction?[9]
- Did mating types (types of gametes, according to their compatibility) arise as a result of anisogamy (gamete dimorphism), or did mating types evolve before anisogamy?[75][76]
- Why do most sexual organisms use a binary mating system?[77] Why do some organisms have gamete dimorphism?

References

1. Letunic, I; Bork, P (2006). "Interactive Tree of Life" (http://itol.embl.de/). Retrieved 23 July 2011.
2. m Letunic, I; Bork, P (2007). "Interactive Tree of Life (iTOL): An online tool for phylogenetic tree display and annotation" (http://itol.embl.de/help/17050570.pdf) (PDF). *Bioinformatics*. **23** (1): 127–8. doi:10.1093/bioinformatics/btl529 (https://doi.org/10.1093%2Fbioinformatics%2Fbtl529). PMID 17050570 (https://www.ncbi.nlm.nih.gov/pubmed/17050570).

3. Letunic, I; Bork, P (2011). "Interactive Tree of Life v2: Online annotation and display of phylogenetic trees made easy" (http://itol.embl.de/help/gkr201.pdf) (PDF). *Nucleic Acids Research*. **39** (Web Server issue): W475–8. doi:10.1093/nar/gkr201 (https://doi.org/10.1093%2Fnar%2Fgkr201). PMC 3125724 (https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3125724). PMID 21470960 (https://www.ncbi.nlm.nih.gov/pubmed/21470960).
4. Otto, Sarah (2014). "Sexual Reproduction and the Evolution of Sex" (https://www.nature.com/scitable/topicpage/sexual-reproduction-and-the-evolution-of-sex-824). *Scitable*. Retrieved 28 February 2019.
5. Goodenough, U.; Heitman, J. (1 March 2014). "Origins of Eukaryotic Sexual Reproduction" (http://cshperspectives.cshlp.org/lookup/doi/10.1101/cshperspect.a016154). *Cold Spring Harbor Perspectives in Biology*. **6** (3): a016154–a016154. doi:10.1101/cshperspect.a016154 (https://doi.org/10.1101%2Fcshperspect.a016154). ISSN 1943-0264 (https://www.worldcat.org/issn/1943-0264). PMC 3949356 (https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3949356). PMID 24591519 (https://www.ncbi.nlm.nih.gov/pubmed/24591519).
6. Smith, J. Maynard (1978). *The Evolution of Sex* (https://books.google.com/books?id=SbI5AAAAIAAJ&printsec=frontcover). Cambridge University Press. ISBN 9780521293020.
7. 1946-, Stearns, S. C. (Stephen C.) (2005). *Evolution : an introduction*. Hoekstra, Rolf F. (2nd ed.). Oxford [England]: Oxford University Press. ISBN 978-0199255634. OCLC 56964580 (https://www.worldcat.org/oclc/56964580).
8. Hoekstra, Rolf F. (1987). "The Evolution of Sexes". In Stearns, Stephen C. (ed.). *The Evolution of Sex and its Consequences* (https://books.google.com/books?id=1cQACAAAQBAJ&lpg=PP1&pg=PA59). Springer Basel AG. ISBN 9783034862738.
9. Ridley, Mark (2003). *Evolution* (3rd ed.). Wiley. p. 314. ISBN 9781405103459.
10. Beukeboom, L. & Perrin, N. (2014). *The Evolution of Sex Determination*. Oxford University Press, p. 5-6 [1] (https://books.google.com/books?id=d4cLBAAAQBAJ&lpg=PP1&hl=pt-BR&pg=PA5#v=onepage&q&f=false). Online resources, [2] (http://www.oup.co.uk/companion/beukeboom).
11. Crow J.F. (1994). Advantages of Sexual Reproduction, Dev. Gen., vol.15, pp. 205-213.
12. Goldstein, R N (2010). *36 Arguments for the Existence of God: A Work of Fiction*. Pantheon. ISBN 978-0-307-37818-7.
13. Heng HH; Heng, Henry H.Q. (2007). "Elimination of altered karyotypes by sexual reproduction preserves species identity". *Genome*. **50** (5): 517–524. doi:10.1139/g07-039 (https://doi.org/10.1139%2Fg07-039). PMID 17612621 (https://www.ncbi.nlm.nih.gov/pubmed/17612621).
14. Gorelick R, Heng HH; Heng (2011). "Sex reduces genetic variation: a multidisciplinary review". *Evolution*. **65** (4): 1088–1098. doi:10.1111/j.1558-5646.2010.01173.x (https://doi.org/10.1111%2Fj.1558-5646.2010.01173.x). PMID 21091466 (https://www.ncbi.nlm.nih.gov/pubmed/21091466).
15. Birdsell, JA; Wills, C (2003). *The evolutionary origin and maintenance of sexual recombination: A review of contemporary models*. *Evolutionary Biology*. **33**. pp. 27–137. doi:10.1007/978-1-4757-5190-1_2 (https://doi.org/10.1007%2F978-1-4757-5190-1_2). ISBN 978-1-4419-3385-0.
16. Matt Ridley 1995 *The Red Queen: Sex and the Evolution of Human Nature* 1995 Penguin.
17. MacIntyre, Ross J.; Clegg, Michael, T (Eds.), Springer. Hardcover ISBN 978-0306472619, ISBN 0306472619 Softcover ISBN 978-1-4419-3385-0.
18. Van Valen, L. (1973). "A New Evolutionary Law". *Evolutionary Theory*. **1**: 1–30.
19. Hamilton, W. D.; Axelrod, R.; Tanese, R. (1990). "Sexual reproduction as an adaptation to resist parasites" (https://www.ncbi.nlm.nih.gov/pmc/articles/PMC53943). *Proceedings of the National Academy of Sciences*. **87** (9): 3566–3573. doi:10.1073/pnas.87.9.3566 (https://doi.org/10.1073%2Fpnas.87.9.3566). PMC 53943 (https://www.ncbi.nlm.nih.gov/pmc/articles/PMC53943). PMID 2185476 (https://www.ncbi.nlm.nih.gov/pubmed/2185476).
20. Kuma, K.; Iwabe, N.; Miyata, T. (1995). "Functional constraints against variations on molecules from the tissue-level - slowly evolving brain-specific genes demonstrated by protein-kinase and immunoglobulin supergene families". *Molecular Biology and Evolution*. **12** (1): 123–130. doi:10.1093/oxfordjournals.molbev.a040181 (https://doi.org/10.1093%2Foxfordjournals.molbev.a040181). PMID 7877487 (https://www.ncbi.nlm.nih.gov/pubmed/7877487).
21. Wolfe KH, Sharp PM; Sharp (1993). "Mammalian gene evolution - nucleotide-sequence divergence between mouse and rat". *Journal of Molecular Evolution*. **37** (4): 441–456. doi:10.1007/BF00178874 (https://doi.org/10.1007%2FBF00178874). PMID 8308912 (https://www.ncbi.nlm.nih.gov/pubmed/8308912).

22. Jokela, Jukka; Dybdahl, Mark; Lively, Curtis (2009). "The Maintenance of Sex, Clonal Dynamics, and Host-Parasite Coevolution in a Mixed Population of Sexual and Asexual Snails". *The American Naturalist*. **174** (s1): S43–53. doi:10.1086/599080 (https://doi.org/10.1086%2F599080). JSTOR 10.1086/599080 (https://www.jstor.org/stable/10.1086/599080). PMID 19441961 (https://www.ncbi.nlm.nih.gov/pubmed/19441961).
23. "Parasites May Have Had Role In Evolution Of Sex" (https://www.sciencedaily.com/releases/2009/07/090706171542.htm). Science Daily. 31 July 2009. Retrieved 19 September 2011.
24. Hanley KA; Fisher RN; Case TJ (1995). "Lower mite infestations in an asexual gecko compared with its sexual ancestors". *Evolution*. **49** (3): 418–426. doi:10.2307/2410266 (https://doi.org/10.2307%2F2410266). JSTOR 2410266 (https://www.jstor.org/stable/2410266). PMID 28565091 (https://www.ncbi.nlm.nih.gov/pubmed/28565091).
25. Morran, Levi T.; Schmidt, Olivia G.; Gelarden, Ian A.; Parrish Rc, Raymond C.; Lively, Curtis M. (2011). "Running with the Red Queen: Host-Parasite Coevolution Selects for Biparental Sex" (https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3402160). *Science*. **333** (6039): 216–218. doi:10.1126/science.1206360 (https://doi.org/10.1126%2Fscience.1206360). PMC 3402160 (https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3402160). PMID 21737739 (https://www.ncbi.nlm.nih.gov/pubmed/21737739).
26. "Sex -- As We Know It -- Works Thanks to Ever-Evolving Host-Parasite Relationships, Biologists Find" (https://www.sciencedaily.com/releases/2011/07/110707141158.htm). Science Daily. 9 July 2011. Retrieved 19 September 2011.
27. Barrière A, Félix MA (July 2005). "High local genetic diversity and low outcrossing rate in Caenorhabditis elegans natural populations". *Curr. Biol*. **15** (13): 1176–84. arXiv:q-bio/0508003 (https://arxiv.org/abs/q-bio/0508003). doi:10.1016/j.cub.2005.06.022 (https://doi.org/10.1016%2Fj.cub.2005.06.022). PMID 16005289 (https://www.ncbi.nlm.nih.gov/pubmed/16005289).
28. Otto SP, Nuismer SL; Nuismer (2004). "Species interactions and the evolution of sex". *Science*. **304** (5673): 1018–1020. doi:10.1126/science.1094072 (https://doi.org/10.1126%2Fscience.1094072). PMID 15143283 (https://www.ncbi.nlm.nih.gov/pubmed/15143283).
29. Otto SP, Gerstein AC; Gerstein (August 2006). "Why have sex? The population genetics of sex and recombination". *Biochemical Society Transactions*. **34** (Pt 4): 519–22. doi:10.1042/BST0340519 (https://doi.org/10.1042%2FBST0340519). PMID 16856849 (https://www.ncbi.nlm.nih.gov/pubmed/16856849).
30. Parker MA (1994). "Pathogens and sex in plants". *Evolutionary Ecology*. **8** (5): 560–584. doi:10.1007/BF01238258 (https://doi.org/10.1007%2FBF01238258).
31. Bernstein H; Byerly HC; Hopf FA; Michod RE (1984). "Origin of sex". *J. Theor. Biol*. **110** (3): 323–51. doi:10.1016/S0022-5193(84)80178-2 (https://doi.org/10.1016%2FS0022-5193%2884%2980178-2). PMID 6209512 (https://www.ncbi.nlm.nih.gov/pubmed/6209512).
32. Bernstein H; Byerly HC; Hopf FA; Michod RE (1985). "Genetic damage, mutation, and the evolution of sex". *Science*. **229** (4719): 1277–81. doi:10.1126/science.3898363 (https://doi.org/10.1126%2Fscience.3898363). PMID 3898363 (https://www.ncbi.nlm.nih.gov/pubmed/3898363).
33. Bernstein H; Hopf FA; Michod RE (1987). *The Molecular Basis of the Evolution of Sex*. *Adv. Genet*. Advances in Genetics. **24**. pp. 323–70. doi:10.1016/S0065-2660(08)60012-7 (https://doi.org/10.1016%2FS0065-2660%2808%2960012-7). ISBN 9780120176243. PMID 3324702 (https://www.ncbi.nlm.nih.gov/pubmed/3324702).
34. Cox MM (2001). "Historical overview: searching for replication help in all of the rec places" (https://www.ncbi.nlm.nih.gov/pmc/articles/PMC37418). *Proc. Natl. Acad. Sci. U.S.A*. **98** (15): 8173–80. doi:10.1073/pnas.131004998 (https://doi.org/10.1073%2Fpnas.131004998). PMC 37418 (https://www.ncbi.nlm.nih.gov/pmc/articles/PMC37418). PMID 11459950 (https://www.ncbi.nlm.nih.gov/pubmed/11459950).
35. Bernstein H, Bernstein C, Michod RE (2011). “Meiosis as an evolutionary adaptation for DNA repair.” In “DNA Repair”, Intech Publ (Inna Kruman, editor), Chapter 19: 357-382 doi:10.5772/1751 (https://doi.org/10.5772%2F1751) ISBN 978-953-307-697-3 Available online from: http://www.intechopen.com/books/dna-repair/meiosis-as-an-evolutionary-adaptation-for-dna-repair
36. Darwin CR (1876). The effects of cross and self fertilisation in the vegetable kingdom. London: John Murray. [3] (http://darwin-online.org.uk/converted/published/1881_Worms_F1357/1876_CrossandSelfFertilisation_F1249/1876_CrossandSelfFertilisation_F1249.html) see page 462
37. Griffiths *et al.* 1999. Gene mutations, p197-234, *in* Modern Genetic Analysis, New York, W.H. Freeman and Company.

38. Kondrashov, A. S. (1988). "Deleterious mutations and the evolution of sexual reproduction". *Nature*. **336** (6198): 435–440. doi:10.1038/336435a0 (https://doi.org/10.1038%2F336435a0). PMID 3057385 (https://www.ncbi.nlm.nih.gov/pubmed/3057385).
39. Muller, H.J. (1964). "The Relation of Recombination to Mutational Advance". *Mutation Research*. **1**: 2–9. doi:10.1016/0027-5107(64)90047-8 (https://doi.org/10.1016%2F0027-5107%2864%2990047-8).
40. Niklas, Karl J. (1 January 2014). "The evolutionary-developmental origins of multicellularity" (http://www.amjbot.org/content/101/1/6). *American Journal of Botany*. **101** (1): 6–25. doi:10.3732/ajb.1300314 (https://doi.org/10.3732%2Fajb.1300314). ISSN 0002-9122 (https://www.worldcat.org/issn/0002-9122). PMID 24363320 (https://www.ncbi.nlm.nih.gov/pubmed/24363320).
41. Kuzdzal-Fick, Jennie J.; Fox, Sara A.; Strassmann, Joan E.; Queller, David C. (16 December 2011). "High Relatedness Is Necessary and Sufficient to Maintain Multicellularity in Dictyostelium". *Science*. **334** (6062): 1548–1551. doi:10.1126/science.1213272 (https://doi.org/10.1126%2Fscience.1213272). ISSN 0036-8075 (https://www.worldcat.org/issn/0036-8075). PMID 22174251 (https://www.ncbi.nlm.nih.gov/pubmed/22174251).
42. Ridley M (2004) *Evolution*, 3rd edition. Blackwell Publishing.
43. Charlesworth B, Charlesworth D (2010) *Elements of Evolutionary Genetics*. Roberts and Company Publishers.
44. Whitlock, M. C.; Bourguet, D. (2000). "Factors affecting the genetic load in Drosophila: synergistic epistasis and correlations among fitness components". *Evolution*. **54** (5): 1654–1660. doi:10.1554/0014-3820(2000)054[1654:fatgli]2.0.co;2 (https://doi.org/10.1554%2F0014-3820%282000%29054%5B1654%3Afatgli%5D2.0.co%3B2). PMID 11108592 (https://www.ncbi.nlm.nih.gov/pubmed/11108592).
45. Elena, S. F.; Lenski, R. E. (1997). "Test of synergistic interactions among deleterious mutations in bacteria". *Nature*. **390** (6658): 395–398. doi:10.1038/37108 (https://doi.org/10.1038%2F37108). PMID 9389477 (https://www.ncbi.nlm.nih.gov/pubmed/9389477).
46. Drake JW; Charlesworth B; Charlesworth D; Crow JF (April 1998). "Rates of spontaneous mutation" (https://www.ncbi.nlm.nih.gov/pmc/articles/PMC1460098). *Genetics*. **148** (4): 1667–86. PMC 1460098 (https://www.ncbi.nlm.nih.gov/pmc/articles/PMC1460098). PMID 9560386 (https://www.ncbi.nlm.nih.gov/pubmed/9560386).
47. Sohail, M; Vakhrusheva, OA; Sul, JH; Pulit, SL; Francioli, LC; van den Berg, LH; Veldink, JH; de Bakker, PIW; Bazykin, GA; Kondrashov, AS; Sunyaev, SR (2017). "Negative selection in humans and fruit flies involves synergistic epistasis" (https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6200135). *Science*. **356** (6337): 539–542. doi:10.1126/science.aah5238 (https://doi.org/10.1126%2Fscience.aah5238). PMC 6200135 (https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6200135). PMID 28473589 (https://www.ncbi.nlm.nih.gov/pubmed/28473589).
48. Trofimova, I. (2015). "Do psychological sex differences reflect evolutionary bi-sexual partitioning?". *American Journal of Psychology*. **128** (4): 485–514. doi:10.5406/amerjpsyc.128.4.0485 (https://doi.org/10.5406%2Famerjpsyc.128.4.0485). PMID 26721176 (https://www.ncbi.nlm.nih.gov/pubmed/26721176).
49. Eshel I, Feldman MW; Feldman (May 1970). "On the evolutionary effect of recombination". *Theoretical Population Biology*. **1** (1): 88–100. doi:10.1016/0040-5809(70)90043-2 (https://doi.org/10.1016%2F0040-5809%2870%2990043-2). PMID 5527627 (https://www.ncbi.nlm.nih.gov/pubmed/5527627).
50. Colegrave, N. (2002). "Sex releases the speed limit on evolution". *Nature*. **420** (6916): 664–666. doi:10.1038/nature01191 (https://doi.org/10.1038%2Fnature01191). PMID 12478292 (https://www.ncbi.nlm.nih.gov/pubmed/12478292).
51. David MacKay (2003). *Information Theory, Inference, and Learning Algorithms* (http://www.inference.phy.cam.ac.uk/itprnn/book.pdf) (PDF). Cambridge University Press, Cambridge. pp. 269–280.
52. Lesbarrères D (2011). "Sex or no sex, reproduction is not the question". *BioEssays*. **33** (11): 818. doi:10.1002/bies.201100105 (https://doi.org/10.1002%2Fbies.201100105). PMID 22009640 (https://www.ncbi.nlm.nih.gov/pubmed/22009640).
53. LODÉ T (2011). "Sex is not a solution for reproduction: the libertine bubble theory". *BioEssays*. **33** (6): 419–422. doi:10.1002/bies.201000125 (https://doi.org/10.1002%2Fbies.201000125). PMID 21472739 (https://www.ncbi.nlm.nih.gov/pubmed/21472739).
54. LODÉ T (2011). "The origin of sex was interaction, not reproduction (what's sex really all about), Big Idea" (http://www.pagepress.org/journals/index.php/eb/article/view/eb.2012.e1). *New Scientist*. **212** (2837): 30–31. doi:10.1016/S0262-4079(11)62719-X (https://doi.org/10.1016%2FS0262-4079%2811%2962719-X).

55. LODÉ T (2012). "Sex and the origin of genetic exchanges". *Trends Evol Biol*. **4**: e1. doi:10.4081/eb.2012.e1 (https://doi.org/10.4081%2Feb.2012.e1).
56. Lodé, T (2012). "Have sex or not ? Lessons from bacteria". *Sexual Dev*. **6** (6): 325–328. doi:10.1159/000342879 (https://doi.org/10.1159%2F000342879). PMID 22986519 (https://www.ncbi.nlm.nih.gov/pubmed/22986519).
57. Nicholas J. Butterfield, "Bangiomorpha pubescens n. gen., n. sp.: implications for the evolution of sex, multicellularity, and the Mesoproterozoic/Neoproterozoic radiation of eukaryotes" (http://paleobiol.geoscienceworld.org/cgi/content/abstract/26/3/386)
58. Bernstein H, Bernstein C (2010). "Evolutionary origin of recombination during meiosis". *BioScience*. **60** (7): 498–505. doi:10.1525/bio.2010.60.7.5 (https://doi.org/10.1525%2Fbio.2010.60.7.5).
59. Ploompuu, T. (1999). *Biosüsteemide mälu teooria* [*Why the eukaryotic cell memory was needed*]. *Schola Biotheoretica* (in Estonian). **XXV**. Tartu: Sulemees. pp. 51–56. ISBN 978-9985908150. Abstract in English available online: [4] (http://www.tlu.ee/~toenu/ingl/euk_rakk.htm)
60. Hörandl E, Speijer D (February 2018). "How oxygen gave rise to eukaryotic sex" (https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5829205). *Proc. Biol. Sci*. **285** (1872): 20172706. doi:10.1098/rspb.2017.2706 (https://doi.org/10.1098%2Frspb.2017.2706). PMC 5829205 (https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5829205). PMID 29436502 (https://www.ncbi.nlm.nih.gov/pubmed/29436502).
61. Olivia Judson (2002). *Dr. Tatiana's sex advice to all creation*. New York: Metropolitan Books. pp. 233–4. ISBN 978-0-8050-6331-8.
62. Bernstein, H., Bernstein, C. Evolutionary origin and adaptive function of meiosis. In "Meiosis", Intech Publ (Carol Bernstein and Harris Bernstein editors), Chapter 3: 41-75 (2013).
63. Bernstein H, Bernstein C. Sexual communication in archaea, the precursor to meiosis. pp. 103-117 in *Biocommunication of Archaea*. 2017. doi:10.1007/978-3-319-65536-9 (https://doi.org/10.1007%2F978-3-319-65536-9). ISBN 978-3-319-65535-2.
64. Michod RE, Wojciechowski MF, Hoelzer MA (1988). "DNA repair and the evolution of transformation in the bacterium Bacillus subtilis" (https://www.ncbi.nlm.nih.gov/pmc/articles/PMC1203263). *Genetics*. **118** (1): 31–39. PMC 1203263 (https://www.ncbi.nlm.nih.gov/pmc/articles/PMC1203263). PMID 8608929 (https://www.ncbi.nlm.nih.gov/pubmed/8608929).
65. Eigen M, Gardiner W, Schuster P, Winkler-Oswatitsch R (April 1981). "The origin of genetic information". *Scientific American*. **244** (4): 88–92, 96, et passim. doi:10.1038/scientificamerican0481-88 (https://doi.org/10.1038%2Fscientificamerican0481-88). PMID 6164094 (https://www.ncbi.nlm.nih.gov/pubmed/6164094).
66. Bernstein H, Byerly HC, Hopf FA, Michod RE (October 1984). "Origin of sex". *Journal of Theoretical Biology*. **110** (3): 323–351. doi:10.1016/S0022-5193(84)80178-2 (https://doi.org/10.1016%2FS0022-5193%2884%2980178-2). PMID 6209512 (https://www.ncbi.nlm.nih.gov/pubmed/6209512).
67. Barry RD (1961). "The multiplication of influenza virus. II. Multiplicity reactivation of ultraviolet irradiated virus". *Virology*. **14** (4): 398–405. doi:10.1016/0042-6822(61)90330-0 (https://doi.org/10.1016%2F0042-6822%2861%2990330-0). PMID 13687359 (https://www.ncbi.nlm.nih.gov/pubmed/13687359).
68. McClain ME, Spendlove RS (1966). "Multiplicity reactivation of reovirus particles after exposure to ultraviolet light" (https://www.ncbi.nlm.nih.gov/pmc/articles/PMC276440). *J Bacteriol*. **92** (5): 1422–1429. PMC 276440 (https://www.ncbi.nlm.nih.gov/pmc/articles/PMC276440). PMID 5924273 (https://www.ncbi.nlm.nih.gov/pubmed/5924273).
69. Hickey D (1982). "Selfish DNA: a sexually-transmitted nuclear parasite" (https://www.ncbi.nlm.nih.gov/pmc/articles/PMC1201875). *Genetics*. **101** (3–4): 519–531. PMC 1201875 (https://www.ncbi.nlm.nih.gov/pmc/articles/PMC1201875). PMID 6293914 (https://www.ncbi.nlm.nih.gov/pubmed/6293914).
70. DasSarma, Shiladitya (2007). "Extreme Microbes". *American Scientist*. **95** (3): 224–231. doi:10.1511/2007.65.224 (https://doi.org/10.1511%2F2007.65.224).
71. Sterrer W (2002). "On the origin of sex as vaccination". *Journal of Theoretical Biology*. **216** (4): 387–396. doi:10.1006/jtbi.2002.3008 (https://doi.org/10.1006%2Fjtbi.2002.3008). PMID 12151256 (https://www.ncbi.nlm.nih.gov/pubmed/12151256).
72. Bell, PJ (2001). "Viral eukaryogenesis: Was the ancestor of the nucleus a complex DNA virus?". *Journal of Molecular Biology*. **53** (3): 251–256. doi:10.1007/s002390010215 (https://doi.org/10.1007%2Fs002390010215). PMID 11523012 (https://www.ncbi.nlm.nih.gov/pubmed/11523012).

73. Bell, PJ (2006). "Sex and the eukaryotic cell cycle is consistent with a viral ancestry for the eukaryotic nucleus". *Journal of Theoretical Biology*. **243** (1): 54–63. doi:10.1016/j.jtbi.2006.05.015 (https://doi.org/10.1016%2Fj.jtbi.2006.05.015). PMID 16846615 (https://www.ncbi.nlm.nih.gov/pubmed/16846615).
74. Cavalier-Smith, Thomas (2006). "Cell evolution and Earth history: Stasis and revolution" (https://www.ncbi.nlm.nih.gov/pmc/articles/PMC1578732). *Philosophical Transactions of the Royal Society B: Biological Sciences*. **361** (1470): 969–1006. doi:10.1098/rstb.2006.1842 (https://doi.org/10.1098%2Frstb.2006.1842). PMC 1578732 (https://www.ncbi.nlm.nih.gov/pmc/articles/PMC1578732). PMID 16754610 (https://www.ncbi.nlm.nih.gov/pubmed/16754610).
75. T. Togashi, P. Cox (Eds.) *The Evolution of Anisogamy*. Cambridge University Press, Cambridge; 2011, p. 22-29.
76. Beukeboom, L. & Perrin, N. (2014). *The Evolution of Sex Determination*. Oxford University Press, p. 25 [5] (https://books.google.com/books?id=d4cLBAAAQBAJ&lpg=PP1&hl=pt-BR&pg=PA25#v=onepage&q&f=false). Online resources, [6] (http://www.oup.co.uk/companion/beukeboom).
77. Czárán, T.L.; Hoekstra, R.F. (2006). "Evolution of sexual asymmetry" (https://www.ncbi.nlm.nih.gov/pmc/articles/PMC524165). *BMC Evolutionary Biology*. **4**: 34–46. doi:10.1186/1471-2148-4-34 (https://doi.org/10.1186%2F1471-2148-4-34). PMC 524165 (https://www.ncbi.nlm.nih.gov/pmc/articles/PMC524165). PMID 15383154 (https://www.ncbi.nlm.nih.gov/pubmed/15383154).

Further reading

- Bell, Graham (1982). *The masterpiece of nature: the evolution and genetics of sexuality*. Berkeley: University of California Press. ISBN 978-0-520-04583-5.
- Bernstein, Carol; Harris Bernstein (1991). *Aging, sex, and DNA repair*. Boston: Academic Press. ISBN 978-0-12-092860-6.
- Hurst, L.D.; J.R. Peck (1996). "Recent advances in the understanding of the evolution and maintenance of sex". *Trends in Ecology and Evolution*. **11** (2): 46–52. doi:10.1016/0169-5347(96)81041-X (https://doi.org/10.1016%2F0169-5347%2896%2981041-X). PMID 21237760 (https://www.ncbi.nlm.nih.gov/pubmed/21237760).
- Levin, Bruce R.; Richard E. Michod (1988). *The Evolution of sex: an examination of current ideas*. Sunderland, Mass: Sinauer Associates. ISBN 978-0-87893-459-1.
- Maynard Smith, John (1978). *The evolution of sex*. Cambridge, UK: Cambridge University Press. ISBN 978-0-521-21887-0.
- Michod, Richard E. (1995). *Eros and evolution: a natural philosophy of sex*. Reading, Mass: Addison-Wesley Pub. Co. ISBN 978-0-201-40754-9.
- "Scientists put sex origin mystery to bed, Wild strawberry research provides evidence on when gender emerges" (http://www.msnbc.msn.com/id/27927661/). MSNBC. Retrieved 25 November 2008.
- Ridley, Mark (1993). *Evolution*. Oxford: Blackwell Scientific. ISBN 978-0-632-03481-9.
- Ridley, Mark (2000). *Mendel's demon: gene justice and the complexity of life*. London: Weidenfeld & Nicolson. ISBN 978-0-297-64634-1.
- Ridley, Matt (1995). *The Red Queen: sex and the evolution of human nature*. New York: Penguin Books. ISBN 978-0-14-024548-6.
- Szathmáry, Eörs; John Maynard Smith (1995). *The Major Transitions in Evolution*. Oxford: W.H. Freeman Spektrum. ISBN 978-0-7167-4525-9.
- Taylor, Timothy (1996). *The prehistory of sex: four million years of human sexual culture*. New York: Bantam Books. ISBN 978-0-553-09694-1.
- Williams, George (1975). *Sex and evolution*. Princeton, N.J: Princeton University Press. ISBN 978-0-691-08147-2.

External links

- Why Sex is Good (http://www.livescience.com/health/050330_sex_good.html)
- An essay summarising the different theories (http://www.philippwesche.org/old1/es.html), dating from around 2001
- http://www.evolocus.com/Textbooks/Geodakian2012.pdf