Evolutionary Origin of Recombination during Meiosis

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Recent evidence indicates that meiosis arose very early in eukaryotic evolution, which suggests that essential features of meiosis were already present in the prokaryotic ancestors of eukaryotes. Furthermore, in extant organisms, proteins with central functions in meiosis are similar in sequence and function to key proteins in bacterial transformation. In particular, RecA recombinase—which performs the central functions of DNA homology search and strand exchange in bacterial transformation—has orthologs in eukaryotes that carry out similar functions in meiotic recombination. Both transformation and meiosis (including meiotic recombination) in eukaryotic microorganisms are induced by stressful conditions, such as overcrowding, resource depletion, and DNA-damaging conditions, suggesting that these processes are adaptations for dealing with stress. If such environmental stresses were a persistent challenge to the survival of early microorganisms, then continuity of selection through the prokaryote to eukaryote transition probably would have followed a course in which bacterial transformation naturally gave rise to the recombination process that is central to eukaryote meiosis.

The origin of meiosis, and in particular meiotic recombination, is an unresolved mystery in biology. We hypothesize in this article that meiotic recombination, a key part of the sexual process in eukaryotes, arose from the sexual process of transformation in bacteria. We also consider evidence bearing on the alternative view that meiosis evolved from mitosis, insofar as it is relevant to the origin of meiotic recombination.

Transformation, the sexual process in bacteria, and meiosis, an intrinsic part of sex in eukaryotes, are prevalent and fundamentally important processes in nature. These processes promote increased efficiency of recombinational repair of DNA damage (Bernstein et al. 1985, Michod et al. 2008)—an adaptive advantage that may explain their prevalence. We therefore hypothesize that meiotic recombination arose from bacterial transformation, assuming that, because of its adaptive importance, the evolution of sex was a continuous process from bacteria to eukaryotes.

Cavalier-Smith (2002) and Wilkins and Holliday (2009), on the other hand, have presented the view that meiosis originated from mitosis. It is clear that meiosis and mitosis share many features related to chromosome segregation and cell division. However, we think it probable that these features emerged largely as subsequent adaptations in both processes after the evolution of the eukaryotic cell from its prokaryotic progenitors. Since our focus is the origin of meiotic recombination and also the initial event that gave rise to meiosis (not subsequent adaptations), we do not include a detailed consideration of the similarities of meiosis and mitosis here.

The five principal lines of evidence supporting the hypothesis that meiotic recombination arose from bacterial transformation are (1) the core genes for meiotic recombination were present very early in eukaryotic evolution, possibly in the common ancestor of all eukaryotes; (2) the direct prokaryotic ancestors of eukaryotes were capable of transformation; (3) orthologs of the RecA recombinase, an enzyme that plays a central role in transfomation, also play a central role in meiotic recombination; (4) other gene functions (aside from RecA orthologs) that are important to meiosis have similar functions in transformation; and (5) transformation in bacteria and mating of eukaryotic microorganisms (protists) are induced by similar types of stress that may be associated with DNA damage.

Meiosis and transformation have fundamental similarities

Meiosis and transformation are key stages of the sexual cycles of eukaryotes and bacteria, respectively. Both processes are complex adaptations coded for by many genes. Meiosis occurs in the nucleus of diploid eukaryotic cells of the germ line, whereby nonsister homologous chromosomes (originating from the fusion of gametes from different parents) align and undergo genetic recombination. The recombined genome is then passed on to a haploid gamete, which forms a diploid progeny cell upon union with another gamete.

Bacterial transformation, similar to meiosis, occurs within a bacterial cell, whereby nonsister homologous chromosomes (or parts of chromosomes) originating from different parent cells align and undergo genetic recombination. The recombined DNA is passed on to a progeny bacterium.

The core genes for meiosis were very likely present in the common ancestor of all eukaryotes

Sexual reproduction involving meiosis is widespread among eukaryotes; however, until recently it was unclear whether the capacity for meiosis was fundamental to eukaryotes. One important reason for this uncertainty was that certain well-studied human pathogenic protists, thought to have diverged early in the eukaryotic lineage, were presumed to be asexual. However, several of these organisms have been shown to be capable of, or to recently have had the capability for, meiosis and sex. For instance, *Giardia intestinalis*, a common intestinal protozoan parasite, was once regarded as an early diverging lineage of eukaryotes that might represent a stage of eukaryotic evolution predating the emergence of meiosis. However, the presence of a core set of meiotic genes, including five meiosis-specific genes, along with other recent evidence, indicates that *G. intestinalis* is capable of meiosis and, therefore, sexual reproduction (Ramesh et al. 2005, Poxleitner et al. 2008). Protozoan parasites of the genus *Leishmania*, which cause widespread and devastating human diseases, were recently shown to have a sexual cycle (Akopyants et al. 2009). *Trichomonas vaginalis*, a parasitic protist, causes a range of infections in humans and is thought to have diverged from the eukaryotic lineage at an early point. Neither meiosis nor sex has been observed in *T. vaginalis*; however, this organism proved to have orthologs of 27 of 29 genes known to function in meiosis, including eight of nine genes tested that are specific to meiosis (Malik et al. 2008). This finding suggests that *T. vaginalis* is currently or was recently sexual. This observation and other related findings led to the conclusion that the core genes necessary for meiosis were probably present in the common ancestor of all eukaryotes (Malik et al. 2008).

Likelihood that an ancestor of eukaryotes was capable of transformation

The idea that transformation evolved into meiosis depends on the assumption that the prokaryotic progenitor of the eukaryotic cell lineage was capable of transformation. Current evidence suggests that eukaryotes arose more than 1.5 billion years ago (Javaux et al. 2001). The crucial event was probably the development of a stable relationship between an anaerobic host bacterium and a smaller, internalized aerobic bacterium.

We next consider the likelihood that this early ancestor of the eukaryotic lineage was capable of transformation. The internalized aerobe provided a capacity for respiration and eventually evolved into the mitochondrion. Sixty-seven prokaryote species (in seven different phyla) have been shown to be naturally competent for transformation (Johnsborg et al. 2007). As we improve our understanding of the

behavior of other bacterial species under crowded conditions, such as in biofilms, we will most likely discover many further examples of transformation. Therefore, the capacity for natural transformation among bacterial species is probably widespread.

Genome sequence analysis indicates that extant mitochondria are most closely related to extant α-proteobacteria, suggesting that an α-proteobacterium was the ancestor of mitochondria (Gray et al. 1999, Muller and Martin 1999). On the basis of computational analysis, research has shown that the common ancestor of α-proteobacteria contained between 3000 and 5000 genes and was an aerobic, free-living, motile bacterium with pili and surface proteins for host cell interaction (Boussau et al. 2004). Analysis of gene sequence data not only strongly supports a monophyletic origin of mitochondria from an α-proteobacterial ancestor but also implies that mitochondria emerged only once in evolution (Gray et al. 1999). Several extant species of α-proteobacteria undergo natural transformation, including *Agrobacterium tumefaciens* (Demaneche et al. 2001), *Methylobacterium organophilum* (O'Connor et al. 1977), and *Bradyrhizobium japonicum* (Raina and Modi 1972). A phylogenetic analysis led researchers to conclude that the ancient anaerobic bacterial host of the internalized protomitochondrion is an archaebacterium (Cox CJ et al. 2008). Among extant archaebacteria, transformation has been described in *Methanococcus voltae* (Bertani and Baresi 1987, Patel et al. 1994) and *Methanobacterium thermaautotrophicum* (Worrell et al. 1988). Thus, it is likely that when the eukaryotic lineage arose, presumably by the establishment of an endosymbiotic relationship of an archaebacterium with an α-proteobacterium, at least one and possibly both of the participants were capable of transformation.

Possible α-proteobacterial origin of genes central to meiosis

During the evolution of mitochondria from an ancestral α-proteobacterium, much of the genetic material of the α-proteobacterium was transferred to, and became integrated into, the host genome. Phylogenetic studies suggest that 630 or more genes were transferred from the α-proteobacterial genome to the eukaryotic nuclear genome (Gabaldon and Huynen 2003); therefore, if the ancestral α-proteobacterium were capable of transformation, as are some of its extant relatives, its genes encoding proteins necessary for transformation may have become integrated into the early eukaryotic nuclear genome. In extant organisms, the *RecA/Rad51/Dmc1* gene family plays a central role in both transformation and meiotic recombination. The *RecA* genes detected in eukaryotes show a high level of sequence similarity to *RecA* genes from proteobacteria, and it has been suggested that endosymbiotic transfer of the *RecA* gene from early mitochondria to the nuclear genome of ancestral eukaryotes may be the cause (Lin et al. 2006). Thus it appears that a gene central to meiotic recombination originated as a bacterial gene central to transformation.

Role of RecA recombinase in bacterial transformation

In this section, we discuss the central role of the RecA protein in bacterial transformation, and later we show that orthologs of the RecA protein play a similar central role in meiotic recombination, as illustrated in figure 1. Our current understanding of the transformation process in α-proteobacteria is not well developed. However, the molecular mechanisms of transformation in *Bacillus subtilis* and *Streptococcus pneumoniae* have been well studied. The RecA protein is essential for transformation both in *B. subtilis* and in *S. pneumoniae* (Claverys et al. 2009). Expression of the *RecA* gene is induced during the development of competence for transformation in *B. subtilis* (Cheo et al. 1992) and *S. pneumoniae* (Mortier-Barriere et al. 1998). In *B. subtilis* transformation, the entering single-stranded DNA (ssDNA) and RecA protein interact to form striking filamentous structures that emanate from the pole containing the competence machinery and extend into the cytosol (Kidane and Graumann 2005). These structures are considered to represent dynamic RecA/ssDNA nucleofilaments that scan the resident chromosome for regions of homology and bring the entering ssDNA to the corresponding region, where strand exchange occurs (Kidane and Graumann 2005). Similarly, the ε-proteobacterium *Helicobacter pylori* is naturally competent for transformation by a process that employs RecA (Fischer and Haas 2004).

Cox MM (1991) analyzed the experimental evidence of the molecular interactions of bacterial RecA protein with DNA. He concluded on mechanistic grounds that the RecA protein evolved as the central component of a recombinational repair system for dealing with DNA damage. This conclusion further suggests that the role of RecA in bacterial transformation is to repair damaged DNA. Although RecA functions in bacterial processes other than transformation that involve integration of exogenous DNA (i.e., conjugation and transduction), transformation—involving the uptake of exogenous DNA from the surrounding medium followed by integration—was probably the ancestral function. In the next section, we present evidence that RecA orthologs have a central role in meiotic recombination.

Recombinational repair is not limited to transformation in bacteria or meiosis in eukaryotes. It can also occur at lower frequency between sister chromosomes during vegetative growth of bacteria and in somatic cells of eukaryotes. However, in these latter cases, double-strand damages that occur before the replication leading to the formation of the sister chromosomes cannot be accurately repaired, since neither sister can provide an intact template for the other in the region of damage. This problem is overcome in transformation and in meiosis, because a unique feature of these sexual processes is that they involve recombination between non-sister chromosomes. Thus, the sexual processes provide the opportunity for efficient and accurate repair of double-strand damages, a feat that could not otherwise be accomplished.

It could be argued that the function of RecA in transformation and the function of RecA orthologs in meiotic recombination evolved independently of one another from repair functions of RecA in vegetative cells of bacteria and eukaryotes, respectively. However, we consider it a simpler explanation that RecA was already actively involved in recombinational repair during the sexual process of transformation, and that its function in the sexual process of meiosis was a continuation of its previous role.
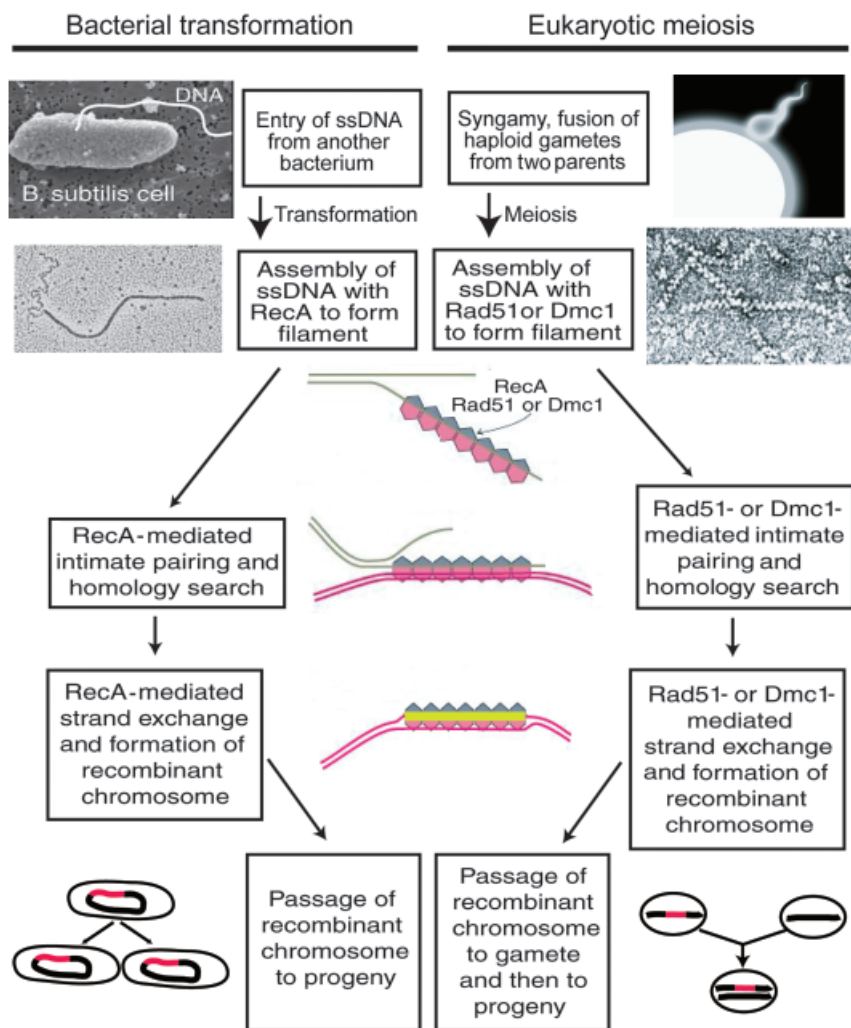

Figure 1. Similarities of bacterial transformation and eukaryotic meiotic recombination. ssDNA, single-stranded DNA.

Role of RecA orthologs in eukaryotes

The homologous recombination machinery and its mechanism of action and regulation appear to be highly conserved among eukaryotes. The *Rad51* and *Dmc1* genes in the eukaryotic yeasts *Saccharomyces cerevisiae* and *Schizosaccharomyces pombe* are orthologs of the bacterial *RecA* gene. The *Dmc1* gene has also been identified in the protists *Giardia, Trypanosoma, Leishmania, Entamoeba,* and *Plasmodium* (Ramesh et al. 2005). The Rad51 and Dmc1 recombinases interact with ssDNA to form a filamentous intermediate, called a presynaptic filament, which initiates recombination (Sauvageau et al. 2005, San Filippo et al. 2008). Whereas Dmc1 recombinase acts only during meiosis, Rad51 recombinase acts both in meiosis and somatic DNA repair. During meiosis, Rad51 uses mainly the sister chromatid as the repair template, whereas Dmc1 predominantly uses the homologous chromosome. The yeast Rad51 recombinase, like the bacterial RecA recombinase, catalyzes ATP (adenosine triphosphate)-dependent homologous DNA pairing and strand exchange (Sung 1994). The Dmc1 recombinase has an overall similarity to the bacterial RecA recombinase in tertiary structure (Story et al. 1993). These observations suggest that the yeast Rad51 and Dmc1 recombinases that act in meiosis, and the bacterial RecA recombinase that acts in transformation, are similar in function, which is in accord with the idea that meiotic recombination evolved from transformation.

We now discuss evidence that RecA orthologs play a central role in meiosis, not only in protists but in multicellular eukaryotes, as well. RecA orthologs function in meiosis in mice, humans, chickens, nematodes, *Arabidopsis*, rice, and lilies. A mouse *RecA* gene ortholog is expressed at a high level in the testis and ovary, suggesting that the protein product of this gene is involved in meiotic recombination (Shinohara et al. 1993). Mutations in the mouse *Dmc1* gene cause sterility, an inability to complete meiosis, and failure of intimate pairing of homologous chromosomes (Pittman et al. 1998, Yoshida et al. 1998). In the meiotic pachytene nuclei of the nematode *Caenorhabditis elegans*, resistance to DNA damage caused by X-irradiation depends on the *Rad51* gene (Takenami et al. 2000). Expression of a *RecA* gene ortholog also occurs in chicken testis and ovary and in human testis. The human meiosis–specific recombinase Dmc1 forms nucleoprotein complexes on ssDNA that promote a search for homology and perform DNA strand exchange, the two essential steps of genetic recombination (Sehorn et al. 2004, Bugreev et al. 2005).

In the lily, the *Lim15* and *Rad51* genes are orthologs of the yeast *Dmc1* and *Rad51* genes, respectively. Lily Rad51 and Lim15 proteins colocalize on chromosomes in various stages of meiotic prophase I, forming discrete foci (Terasawa et al. 1995). The proteins in these foci are thought to participate in the search for and pairing of homologous DNA sequences. In the plant *Arabidopsis thaliana*, meiosis requires Rad51 (Li et al. 2004) and Dmc1 (Couteau et al. 1999). In rice, an ortholog of *Dmc1* is essential for meiosis and plays an

important role in the pairing of homologous chromosomes (Deng and Wang 2007). Thus, it appears that in both animals and plants, RecA-like proteins have a significant role in meiotic recombination.

In general, RecA and its orthologs play very similar roles in the recombination events during transformation and meiosis. In both cases, the RecA protein or its equivalent assembles on ssDNA to form a presynaptic filament that then captures a duplex DNA molecule and searches for homology in the latter. Upon locating homology in the duplex molecule, the presynaptic molecule is able to form DNA joints (figure 1). These joints then undergo further processing, leading to the completion of the recombination event.

Other gene functions common to transformation and eukaryotic recombination

Preceding the assembly of the RecA recombinase or its equivalent on ssDNA to form a presynaptic filament, the proteins RPA (replication protein A) in eukaryotes and single-strand-binding protein (SSB) in bacteria are involved in processing the ssDNA. Unless these proteins are removed, they will prevent loading of the recombinase by steric hindrance. Certain recombinase accessory factors, termed recombination mediator proteins, have orthologs in eukaryotes and bacteria. Recombination mediator proteins can overcome the inhibitory effects of RPA and SSB proteins on the assembly of the RecA-type proteins with DNA to form the presynaptic filaments (Claverys et al. 2009). The recombination mediator proteins are critical for the efficiency of homologous recombination *in vivo*; thus, accessory proteins, beyond the recombinase itself, function both in transformation and in eukaryotic homologous recombination.

Aspects of meiosis needed to deal with larger genomes

To explain the more complex nature of meiosis compared with the simpler process of transformation, we need to consider the size of eukaryotes' genomes versus those of prokaryotes. For instance, yeast cells, which have some of the smallest genomes among eukaryotes, contain about three times more DNA than the average size of the largest prokaryotes (eight to nine megabase pairs; Vellai et al. 1998). The cells of higher animals and plants generally have 40 to 1000 times more DNA than *Escherichia coli* (Lodish et al. 1995).

If, as we propose, the earliest eukaryotes had a relatively simple sexual process analogous to bacterial transformation, then adaptive innovations may have emerged as the genome expanded to allow this sexual process to function in the more organized and efficient manner that characterizes meiosis. In particular, as analyzed by Forterre and Gadelle (2009), "topoisomerases probably originated when more complex DNA genomes (long linear or circular DNA molecules) were selected in the course of evolution." One particular topoisomerase that has received much attention is Spo11. Forterre and Gadelle (2009) found Spo11 to be a eukaryotic homolog of the A subunit of Topo IIB, similar to

the archaeal Topo IIB. Topoisomerases have evolved different functions among different eukaryotic lineages. Although the biochemical function of Spo11 is well conserved (i.e., double-strand break formation), in some species of eukaryotes (mice and yeast), double-strand breaks play a role in chromosome pairing and synapsis; in other species, such as *Drosophila melanogaster*, chromosomes pair through a different recombination-independent mechanism (McKim and Hayashi-Hagihara 1998).

Because our hypothesis deals specifically with the evolutionary roots of meiosis, we have not attempted to detail the important changes that must have taken place as meiosis evolved further from its roots. For instance, it is beyond the scope of our proposal to attempt an explanation of the evolution of the suppression of sister chromatid separation during the first meiotic division or the absence of chromosome replication during the second meiotic division.

Differences between transformation and meiosis

In this section, we address whether the differences between transformation and meiosis in extant organisms are large enough to rule out the possibility of fundamental evolutionary relatedness.

One difference between transformation and meiosis is that transformation depends on the uptake of macromolecular DNA derived from another cell, whereas meiosis is preceded by the fusion of haploid gametes (syngamy). In most transforming bacterial species, the donor DNA for subsequent transformation becomes available because of autolysis of some cells in the population. However, *Neisseria gonorrhoeae,* a β-proteobacterium, can donate DNA for transformation using a secretion system (termed type IV secretion) that avoids donor-cell autolysis and death (Hamilton and Dillard 2006). Thus, cell death of one partner is a usual, but not necessary, precondition for transformation. Transfer of genomic DNA between two viable bacterial cells may have been the precondition that gave rise to the fusion of two cells (syngamy) in the transition to the eukaryote state.

Another difference between transformation and meiosis is that transformation is thought ordinarily to involve the transfer of only a small fraction of the donor genome to the recipient, whereas meiosis typically involves two whole genomes. Although transformation is usually studied in the context of the partial transfer of DNA, evidence suggests that DNA transfer can be substantial. In *B. subtilis* transformation, when the donor DNA is derived from protoplast lysates, the length of continuous DNA incorporated into the recipient cell can be greater than 1271 kilobases, which corresponds to about one-third of the whole genome length (Saito et al. 2006). There is also evidence that the whole chromosome from protoplast lysates can be incorporated into competent recipient cells (Akamatsu and Taguchi 2001). Thus, the transfer of the entire genome or a substantial fraction of it between two bacteria may have been another precondition that gave rise to the fusion of two gametes in eukaryotes.

A further difference between meiosis and transformation is that meiosis can be broken down into four steps, three of which have no counterparts in transformation. In brief, the four steps of meiosis are (1) premeiotic chromosome reduplication, (2) pairing and recombination between nonsister homologous chromosomes (i.e., homologous chromosomes of different parental origin), and (3–4) two successive divisions ending in the formation of haploid gametes. Transformation involves only the second step. Nevertheless, recombination between nonsister homologous chromosomes is generally regarded as the hallmark and key adaptive feature of meiosis, although changes in other processes, such as cell-cycle regulation and sister chromatid cohesion, are also important. This key adaptation may have therefore emerged in bacteria as the process of transformation, and then, during the early evolution of eukaryotes, evolved into the more organized process of meiotic recombination. Other features of meiosis, such as the meiotic spindle and cell-cycle control, employ gene products that at least partially overlap with those used in mitosis. Such gene products very likely evolved for simultaneous usage in similar roles in both processes, with some divergence of function.

Transformation in bacteria and mating of protists are induced by stress

For bacteria and protists, sexual reproduction is ordinarily facultative, and their sexual cycles are induced by stressful conditions. In bacteria, competence for transformation is typically induced by high cell density, nutritional limitation, or DNA-damaging conditions. For instance, in the α-proteobacteria species *Rhizobium japonicum* and *Methylobacterium organophilum*, development of competence for transformation occurs near the end of exponential growth, when the bacteria become crowded (Raina and Modi 1972, O'Connor et al. 1977). In the γ-proteobacterium *Haemophilus influenzae*, transformation occurs most efficiently at the end of exponential growth, as cells approach stationary phase (Goodgal and Herriott 1961). In *B. subtilis*, competence for transformation is induced toward the end of logarithmic growth, especially under conditions of amino acid limitation (Anagnostopoulos and Spizizen 1961), and is also induced by ultraviolet light, a DNA-damaging agent (Michod et al. 1988). In many streptococci, including *Streptococcus mutans*, development of competence for transformation is associated with high cell density and biofilm formation (Aspiras et al. 2004). In *S. pneumoniae*, transformation is induced by the DNA-damaging agents mitomycin C and fluoroquinolone (a topoisomerase inhibitor), as well as by aminoglycoside antibiotics (Claverys et al. 2006).

Induction of the meiotic sexual cycle in yeast similarly involves stress. For instance, in the yeast *S. pombe*, sexual development is induced when the supply of nutrients becomes limiting (Davey et al. 1998), or when the cells are exposed to hydrogen peroxide (which causes oxidative stress and DNA damage; Bernstein and Johns 1989). Exposure to hydrogen peroxide or mechanical damage to hyphae induces

sexual reproduction in *Phytophthora cinnamomi*, an oomycete (Reeves and Jackson 1974). In the unicellular green alga *Chlamydomonas reinhardi*, depletion of the nitrogen source in the growth medium leads to differentiation of vegetative cells into gametes (Sager and Granick 1954). In the multicellular green algae *Volvox carteri*, sex is induced in response to oxidative stress (Nedelcu and Michod 2003), as well as by heat shock (Kirk and Kirk 1986). In the paramecium tetrahymena, mating can be regularly initiated by washing, which induces rapid starvation (Elliott and Hayes 1953). The budding yeast *S. cerevisiae* proliferates mitotically as diploid cells when nutrients are plentiful; when starved, the organism undergoes meiosis to form haploid spores (Herskowitz 1988).

Observations such as those described in this section suggest that facultative sex in bacteria and protists is often an adaptive response to stressful environmental conditions, as would be expected if transformation and meiosis were related adaptations.

An alternative view that meiosis is derived from mitosis

As mentioned above, Wilkins and Holliday (2009) proposed that meiosis evolved from mitosis. In their alternate proposal, they cite four novel steps in meiosis not present in mitosis: (1) the pairing of homologous chromosomes, (2) the occurrence of extensive recombination between nonsister chromatids during pairing, (3) the suppression of sister-chromatid separation during the first meiotic division, and (4) the absence of chromosome replication during the second meiotic division. The authors further note that although the simultaneous appearance of these novel steps seems impossible, their step-by-step appearance as a result of natural selection of separate mutations also seems highly problematic, because the entire sequence is required for the reliable production of haploid chromosome sets. The authors then propose how meiosis may have originated from mitosis, even given these difficulties.

We note here, however, that if the essential processes of meiotic recombination are derived from bacterial transformation, some of the difficulties presented in Wilkins and Holliday's (2009) alternate view may be explained. For instance, steps 1 and 2 may have been derived from the pairing of DNA molecules of different parental origin and the recombination that occurs between them during transformation.

Although we consider that the core recombinational machinery used in meiosis is descended directly from the recombinational machinery used in transformation, this idea is compatible with the joint use of some gene products in both mitosis and meiosis, as these processes evolved from simpler bacterial processes. Indeed, it is possible that some gene products that evolved initially for use in mitosis were later used in meiosis, as well; thus, the idea that meiosis arose from transformation and the idea that meiosis arose from mitosis are not necessarily mutually exclusive. However, if it is assumed that meiosis arose only after mitosis was established, there would

have been an extended period (while mitosis was evolving) when there was no meiosis, and therefore no sex, in eukaryotes. This assumption appears to be contradicted by evidence that the basic machinery for meiosis was present very early in eukaryote evolution (Malik et al. 2008).

Persistent stress as the selective force governing the evolution of transformation and meiosis

Sexual processes are widespread in nature, and in all kingdoms sex is universally based on RecA-like proteins (Volodin et al. 2009). However, there is currently no consensus among biologists about the specific selective forces maintaining the sexual processes of transformation and meiosis. One view is that transformation and meiosis are primarily adaptations for repairing DNA damage (Bernstein et al. 1985, Michod et al. 2008); another view is that these processes are primarily adaptations for promoting allelic variation (Otto and Gerstein 2006, Vos 2009). Since both transformation and meiosis (in protists) are induced by stressful conditions, these processes may have been selected as adaptive responses to these stresses. Desiccation, starvation for particular nutrients, or high temperatures can cause the production of reactive oxygen species and genome damage. It is very likely that these stresses, as well as overcrowding accompanied by depletion of resources, mechanical damage, and direct exposure to DNA-damaging agents, were persistent problems for early microorganisms. Adaptive responses to these stresses probably include many different signaling pathways; some of these may be specifically linked to meiosis in different eukaryotes. Nevertheless, a common problem during meiosis is the need to deal with damage in germline DNA through recombinational repair—the only known repair process that can accurately repair double-strand damages. Even in obligate sexual organisms (e.g., humans) there are consistent endogenous sources of stress, such as reactive oxygen species, produced as byproducts of cellular respiration. The average number of double-strand breaks per cell in human DNA occurring at each cell generation is about 50 (Vilenchik and Knudson 2003). Thus, meiotic recombination is likely to have been maintained as a DNA repair process to protect germline DNA from the lethal consequences of such damages. If potentially lethal DNA damages have been a persistent long-term challenge to cellular survival, then the protection provided by recombinational repair should have been preserved during the transition from prokaryote transformation to eukaryote meiosis.

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