Ideas in Ecology and Evolution 11: 19–28, 2018
doi:10.4033/iee.2018.11.3.n

Received 29 June 2016; Accepted 24 April 2018

New Idea

Meiosis decreases recombination load; Mitosis increases recombination load

Root Gorelick and Francis X. Villablanca

Root Gorelick (Root.Gorelick@carleton.ca), Department of Biology, School of Mathematics & Statistics, and Institute of Interdisciplinary Studies, Carleton University, 1125 Raven Road, Ottawa Ontario, Canada

Francis X. Villablanca (fvillabl@calpoly.edu), Biological Sciences Department, California Polytechnic State University, 1 Grand Avenue, San Luis Obispo, California, USA

Abstract

Chiasmata are necessary for proper chromosomal segregation, but can result in inadvertent recombination. Bernstein and Michod demonstrated that meiosis evolved as a means of error correction, not genetic mixing. Therefore meiotic recombination is not the *sine qua non* of sex, but is instead an epiphenomenon of imperfect meiotic error correction. By correcting against recombinant genotypes, meiosis reduces recombination load, thereby providing an unappreciated selective advantage for sex. Sex reducing recombination load should be integrated into population genetic models of multi-locus epistasis for maintenance of sex and may explain sequestration of germ lines in animals. We predict that eumetazoa have less recombination load than sexual organisms without a germ line. Mitosis largely lacks the error correction of meiosis, destroys linkage through ubiquitous mitotic recombination, and thereby increases recombination load, especially in co-adapted gene complexes. Meiosis and possibly karyogamy provide an unexpected benefit to sex, offsetting at least some of the famed costs of sex.

Recombination reduces fitness of co-adapted gene complexes

There is little doubt that the genome of almost any organism has co-adapted gene complexes (Wasserman 1968, Santos 2009). Unfortunately, it is effectively impossible to define what genes are, with a gene being somewhere between the size of a single nucleotide position and an entire linkage group. But, regardless, for genes in co-adapted gene complexes, there exists linkage disequilibrium between pairs or more of genes (Gorelick and Laubichler 2004). Though we cannot exactly define the units making up the complex, if those genes assort even somewhat independently, then fitness may be degraded, which is loss of the 'co-adapted' part of co-adapted gene complexes. The important thing is that recombination, which for simplicity here means crossing-over recombination, reduces linkage disequilibrium (Hartl and Clark 1989, Hedrick 2000, Gorelick and Laubichler 2004) and is predicted to reduce mean fitness of a population when it disrupts one or more co-adapted gene complexes. This reduction in fitness, when breaking up co-adapted gene complexes, is known as *recombination load* (Charlesworth and Charlesworth 1975, Lynch and Deng 1994, Allen and Lynch 2008).

Meiosis can provide a source of recombination that is generally corrected

Meiotic recombination may have evolved from mitotic recombination (Villeneuve and Hillers 2001, Marcon and Moens 2005), with meiosis evolving as an error-correcting mechanism, not as a source of recombination (Bernstein 1977, Bernstein et al. 1981, Bernstein et al. 1988). However, for the diametrically opposite view, that mitosis evolved from meiosis, see Garg and Martin (2016). We consider both below.

Meiotic recombination would not occur were it not for chiasmata of the synaptonemal complex. Roeder (1997) provides a summary of meiosis that places the chiasmata

into a mechanistic context: "During prometaphase, homologous chromosomes can become attached to microtubules from the same or opposite spindle poles. Only attachment to microtubules from opposite poles results in a stable configuration that is maintained until anaphase. If homologs attach to microtubules from the same pole they dissociate and try again. The recognition that chromosomes are properly oriented depends on the mechanical tension that results when homologs are pulled toward opposite spindle poles, *and this pulling is resisted by chiasmata*" (Roeder 1997: 2612; emphasis added). Importance of that physical tension was demonstrated using micromanipulating needles to apply tension to homologs that were attached to the same spindle pole. When an opposing force is applied, the otherwise unstable monopolar attachment is stabilized (Nicklas 1974) and dissociation does not occur. Twenty years after Roeder (1997), Ruchaud et al. (2007) answered the question of how tension signals that homologs are correctly oriented by providing a summary of the micromolecular structures throughout the cell that respond to the tension. Essentially, cell biologists view tension via chiasmata as necessary for proper segregation of chromosomes during meiosis (Villeneuve and Hillers 2001, Ruchaud et al. 2007). Consequently, if proper cell division is necessary and sufficient to explain the importance of chiasmata, then any contributions to recombination must, by definition, be secondary. Indeed, from this perspective, crossing over *recombination* is collateral damage from chiasmata.

The synaptonemal complex is in turn an essential part of DNA repair (Page and Hawley 2003, Barlow and Rothstein 2010), a point even made by the person who first elucidated Holliday junctions (Wilkins and Holliday 2009). "Recombination is required for proper segregation of homologous chromosomes during the first division of meiosis. Here chromosomes are subjected to programmed double strand breaks and the subsequent 5′ resection creates single strand overhangs that invade the homologous chromosome to form hetero-duplexes. In the majority of cases the following repair occurs by gene conversion but a poorly known proportion results in crossover of chromosomes." (Munch et al. 2014: 892). Therefore most *recombination intermediates* are resolved either via gene conversion, or via double-Holliday junction resolution, whereby the majority of crossing over is resolved, but a small proportion of crossing over recombinants persist. Herein, we are focused on crossing over recombination, or for simplicity, recombination and recombination load. In addition, though many biologists erroneously believe that recombination only occurs during meiosis, and not during mitosis, as we discuss below, mitosis and meiosis are related phenomena and recombination occurs in both. If recombination occurs in both, then we must consider how meiosis and mitosis each contribute to recombination load.

Meiosis decreases recombination load, while mitosis increases recombination load

If the synaptonemal complex results in recombinants, and if this were the selective advantage, then why is the same complex involved in recombination repair? Recombination may just be an epiphenomenon of both sex and the mechanisms resulting in meiotic divisions, whereby necessary gene conversion repair and double-Holliday junction resolution has gone awry and recombination intermediates then persist (Bishop and Zickler 2004). If meiosis evolved as a mechanism for cell division and ploidy reduction, resulting both in error and an error-correcting mechanism, but did not evolve as a source of recombination, then meiosis *reduces* additive genetic variance (Gorelick and Heng 2011). Likewise, if meiosis largely functions as a means of error-correction, and largely suppresses or corrects for recombination, then meiosis reduces or at least does not increase recombination load.

The primary reason most people erroneously believe that meiosis increases heritable variation is their uncritical acceptance of an error regarding independent segregation made by August Weismann (1891 [1892]). Weismann grossly overestimated the number of possibly independently segregated genomes from meiosis because he did not realize that each gamete needed to have one copy of each homologous chromosome (Gorelick and Heng 2011). For n pairs of chromosomes, Weismann (1891 [1892]) therefore thought that independent segregation resulted in $\binom{2n}{n} = \frac{2n!}{n!\cdot n!}$ different genotypes, whereas, with homologues, independent segregation only results in 2^n different genotypes (1891 [1892]). For six pairs of chromosomes ($2n$=12), this translates into Weismann thinking there was 15 times the variation due to segregation than we now know exists. For 23 pairs of chromosomes ($2n$=46), Weismann believed there was almost 100,000 times the variation due to segregation than we now know exists. Weismann was also misguided in desperately looking for some mechanism to increase heritable variation in order to resuscitate Darwin's theory of natural selection, which had been largely discredited or abandoned between 1859 and 1886 because there was no apparent variation upon which selection might act. As a final nail in the "uncritical acceptance" coffin, Weismann never considered that recombination was a source of heritable variation because recombination was not discovered by Morgan (1911) until just before Weismann's death.

The crux of how meiosis reduces recombination was encapsulated in Bernstein's work showing how synaptonemal complex formation allowed for detection and correction of double-stranded DNA errors (Bernstein 1977, Bernstein et al. 1981, Bernstein et al. 1988). In fact, evolutionary geneticists now realize that, "the initial

function of chromosome pairing was to *limit*, not enhance, recombination" (Wilkins and Holliday 2009: 3; italics in original). Even more telling with regards to recombination load, mitotic recombination lacks synaptonemal complexes hence, by contrast, could in fact contribute to the recombination rates. Relatively speaking, meiosis eliminates some of the recombination that it could otherwise contribute, while mitosis does not. Thus, meiosis decreases recombination load, while mitosis increases recombination load.

Mitotic versus meiotic recombination: relative rates and cumulative effects

Contemporary biologists often contend that meiosis is the source of heritable variation vis-à-vis crossing-over recombination, rather than via segregation as emphasized by Weismann (1891 [1892]) (but see Kirkpatrick and Jenkins 1989 for the importance of segregation). Plenty of recombination occurs during meiotic prophase I (Otto and Lenormand 2002), but crossing-over recombination also occurs during mitosis (Pontecorvo and Käfer 1958), albeit without synaptonemal complex formation, which may be required in meiotic recombination (Page and Hawley 2001). On average there are 1.56 recombination events per chromosome per meiotic division in eukaryotes (Otto and Lenormand 2002, Lambing et al. 2017), but only 0.8×10^{-4} recombination events per mitotic division (Mandegar and Otto 2007), meaning that meiotic recombination rates are typically much higher (probably about 20,000 times higher) than mitotic recombination rates per individual nuclear division (Pâques and Haber 1999). Compounding this disparity, recombination is much more likely to be between sister chromatids in mitosis than in meiosis (Pâques and Haber 1999, Villeneuve and Hillers 2001). Compensating for this disparity in most eukaryotes, there are far more mitotic divisions than meiotic divisions, such as in the yeast *Saccharomyces cerevisiae* for which much of the data on recombination rates was estimated. Therefore, because of the type of recombination (mitotic versus meiotic) and number of nuclear divisions, it is critical that we consider the possible cases in which more recombination is occurring via a mitotic path than a meiotic one. This situation is potentially most extreme in female eukaryotes if no germ line is present: they are in a body comprised of trillions of cells that were all formed via mitotic divisions (Bianconi et al. 2013). While there may be trillions of mitotic divisions, there may only be thousands or millions of meiotic divisions per generation. In addition, a long line of mitotic divisions can precede any single meiotic division. The cumulative number of recombination events due to many mitotic divisions preceding any meiotic recombination is much less pronounced in eumetazoa because of their sequestered germ lines, but seems particularly relevant for other eukaryotes. But does the higher number of mitotic cell divisions ever fully compensate for the lower rate of mitotic recombination, such that more recombination load is generated via mitosis than by meiosis? The answer to this may simply depend on the taxon in question.

By definition, recombination increases recombination load, but this can be no more ascribed to meiosis than mitosis. Because of the ubiquity of mitosis and mitotic recombination, even in cells destined for germ lines, sex by itself cannot be the primary determinant of the magnitude of recombination load, nor can recombination load be relegated only to sexual organisms. Though we acknowledge that meiotic and mitotic recombination probably occur at different hotspots (Pâques and Haber 1999), it is possible that this source of variation could be acted on by selection and the amount of recombination, and subsequent load could itself evolve (Ziolkowski and Henderson 2017, Ritz 2017).

Meiosis, mitosis, and co-adapted gene complexes

Lynch and Deng (1994: 257) showed that, "Sexual reproduction can lead to a reduction in the amount of expressed genetic variance when genes with like effects tend to be associated in the same parental individuals, that is, when there is coupling disequilibrium rather than the repulsion disequilibrium predicted under stabilizing selection." This speaks directly to co-adapted gene complexes and how sex should result in lower genetic variance, particularly under any degree of inbreeding, and because meiosis and karyogamy are the only times in a lifecycle when wholesale epigenetic resets occur. Indeed, most eukaryotes are more highly inbred than generally perceived (Shields 1982). Molecular phylogenies demonstrate that interbreeding organisms usually have very similar DNA, with well over 98% of their nucleotides lacking polymorphisms (Chen and Li 2001, Ebersberger et al. 2002, Unneberg et al. 2005). As a consequence, in sexually reproducing organisms, individuals *within* species should be *much* more closely related to individuals of their own species than to individuals in other species. So, for example, in a comparison of average synonymous divergence in 61 pairs of closely related animal populations, Roux et al. (2016) found a 10-30 times lower divergence between populations comprising single species (populations connected via genome-wide gene flow) than between species (genetically isolated). Most interbreeding occurs between individuals that look remarkably alike. From a more mechanistic perspective, most offspring do not travel far from their parents and breeding in philopatric systems results in inbreeding (Shields 1982). Because of typically extensive inbreeding, there is a higher probability that chromosomes are identical by descent than is

generally acknowledged. Therefore, even with recombination, co-adapted gene complexes would be more likely to remain intact.

However, what we assert here is far more general, i.e. that meiosis virtually always leads to a greater reduction in genetic variance than does mitosis. Meiosis preserves co-adapted gene complexes better than does mitosis, regardless of extent or forms of linkage disequilibrium and epistasis. The problem here is not so much an underappreciation of the error-correcting role of meiosis, so much as the woefully incorrect assumption that mitosis results in little or no genetic variation and no recombination. Somewhat akin to meiotic recombination, mitotic recombination (e.g. Lynch and Deng 1994, Avise 2008) is believed to be an error-correcting mechanism (aka somatic recombination; Stern 1936, Pontecorvo and Käfer 1958, Schoustra et al. 2007), albeit probably not nearly as good of one as is meiosis (Groden et al. 1990, Ellis et al. 1995, Serrano et al. 2011).

Meiotic versus mitotic heritability

In discussing how meiosis reduces additive genetic variance, especially when comparing meiotic with mitotic recombination, we need to be precise in defining additive genetic variance and its measurement. For instance, cancer researchers often speak of both meiotic and mitotic heritability. Modulo phenotypic variance, meiotic heritability is equivalent to additive genetic variance. Meiotic and mitotic heritability can both be measured using parent-offspring regression, albeit with very different notions of who are parents and offspring. We previously used meiosis and karyogamy to demarcate individuals (Gorelick 2012), which admittedly does not apply to mitotic heritability. With mitotic heritability, individuals are simply different cells or, alternatively, different nuclei possibly in a single coenocytic or syncytial cell. This distinction between cells and nuclei becomes important when cell division and nuclear division are uncoupled. Note that due to development of multicellular and multinuclear organisms and cell differentiation, mitotic heritability may be quite low because daughter cells often look far different from their mother cells, depending on what quantitative trait one is using to measure heritability. By contrast, with meiotic heritability, offspring almost always closely resemble their parents. The conflation of mitotic with meiotic heritability seems peculiar in light of the fact that recombination occurs in both meiosis and mitosis.

Multi-locus functional epistasis

Much research on evolutionary maintenance of sex focuses on epistasis and recombination, with the general conclusions that there is almost no part of parameter space in which sex will be maintained via epistasis, when assuming that only recombination associated with meiosis (not mitosis) tends to break up co-adapted gene complexes (Otto and Michalakis 1998, Otto and Nuismer 2004). In a sense, meiosis, associated with sex, would itself be breaking up epistatic interactions that could otherwise support sex. Therefore, population geneticists suspect that higher-order epistatic interactions, i.e. those simultaneously involving three or more loci, will be negligible in maintaining sex (e.g. Otto and Lenormand 2002, Otto and Nuismer 2004, Otto and Gerstein 2006). However, one would only come to this false conclusion by ignoring that mitotic recombination does a far better job of breaking up co-adapted gene complexes because of the large number of mitotic divisions and their cumulative effects. In addition, and conspicuously, current models are all really two-locus or additive sums of pairs of non-additive loci (Turelli and Barton 2006), in part because it is necessary but mathematically cumbersome dealing with multi-locus linkage disequilibrium (e.g. Kouyos et al. 2006). If sex vis-à-vis meiosis largely acts to suppress recombination and repair DNA, while mitosis causes substantial recombination without much error-correcting capability, then maybe we need to pay attention to multi-locus functional epistasis (Gorelick and Laubichler 2004, Hansen 2013). It is not obvious what population genetic predictions will be like once population genetic models have sex reducing recombination rates and include *bona fide* multi-locus functional epistasis. We suspect these models will more realistically address co-adapted gene complexes.

Eumetazoan germ lines

Lineages that sequester a germ line (Weismann 1892 [1893]), which we now believe to include most eumetazoa, benefit from a substantial selective advantage because meiosis reduces recombination load and mitosis increases recombination load. Eumetazoan germ lines are established soon after zygote formation, hence primordial germ cells and their predecessor pole cells have undergone few mitotic divisions prior to meiosis (Bendel-Stenzel et al. 1998, Mahowald 2001, De Loof et al. 2016). Eumetazoa therefore have a clear selective advantage by virtue of escaping the otherwise verdant recombination load generated by mitotic divisions because eumetazoan primordial germ cells undergo many fewer mitotic divisions than do cells that will lead to gamete production in non-eumetazoans. This not only begs the question of why germ lines have not evolved in large multicellular sponges, fungi (Ophisthokonta), plants (Archaeplastida), and stramenopiles (SAR supergroup), but also suggests that these other eukaryotes should have much greater recombination load compared with eumetazoans because they have many more mitotic divisions between their meiotic divisions. It may prove fruitful to empirically explore if this is indeed the case.

Variation in recombination rates and empirical tests

Models of selection and linkage predict lower genetic variation in regions of lower recombination, and data from multiple species support this prediction (Nachman 2002). Herein we are predicting reduced recombination and genetic diversity in areas with co-adapted gene complexes or a reduction in recombination load due to meiosis. More specifically we predict the recombination load (i.e. breakdown of linkage disequilibrium of co-adapted complexes) and genetic diversity will be greater due to mitosis than due to meiosis. Conversely, we also predict that linkage disequilibrium will be more frequent due to meiosis than to mitosis. An empirical test of our prediction would require a comparison of mitotic and meiotic divisions within the same individual (for example over time), or alternatively, a comparison across species that differ in germ line sequestration. Support for our prediction would be found if linkage disequilibrium were more common under meiosis than mitosis, and if genetic diversity were lower under meiosis than mitosis. The most powerful test would compare cell lines or individuals where all variation in the recombination rate (and thus linkage disequilibrium) was caused by mitotic versus meiotic cell divisions, with no contribution to rate differences due to any other factor. This best-case scenario is unlikely given the large number of factors that are known to affect recombination rate.

Genomic advances in fine scale mapping of F1 recombinant genotypes and analyses of SNPs and genetic diversity in naturally occurring populations have greatly informed our understanding of variation in recombination rates. Within population recombination rates are known to vary over four orders of magnitude (McVean 2000) and to show a similar range across a multitude of species (Ritz et al. 2017). This variation exists for a number of reasons. One suite of reasons is summarized as the population recombination rate or $N\mu rs$ (Nachman 2002): where N is the effective population size, with larger populations expected to have less linkage disequilibrium (Wall 2001); μ is the recurrent mutation rate and is expected to decrease diversity; r is the recombination rate and is expected to increase diversity; and s is the selection coefficient and is expected to act against novel recombinants and decrease diversity (Potapova and Gorbsky 2017). The parameter r is itself a function of: centromeric/telomeric position (Broman et al. 1998, Kong et al. 2002, Nachman 2002); presence or frequency of specific sequence motifs responsible for chiasmata formation (Kong et al. 2008); GC content (Birdsell 2002, Kong et al. 2002, Groenen et al. 2009); taxa, population, individual, and sex (Broman et al. 1998, Wilfert et al. 2007, Kong et al. 2008, Groenen et al. 2009, Kong et al. 2010); age and temperature (Rose and Baillie 1979, Kuliev and Verlinsky 2004); as well as feedback and homeostasis mechanisms (Ritz et al. 2017, Ziolkowski and Henderson 2017) and, yes, whether recombination is due to meiosis versus mitosis. Empirically, one would need to control for a large number of factors in order to test for differences in recombination rates or linkage disequilibrium due specifically to meiosis and mitosis. But, in theory, such a test is at least plausible. It may be more productive to explore individual recombination rates rather than population rates, and to compare the relative contribution of meiotic recombination to that of mitotic recombination. Importantly, comparisons within individuals would control for a large number of factors (except age).

No longer a need to explain the cost of sex

Meiosis provides advantages to populations that engage in sex, regardless of whether the sex is amphimixis, autogamy, automixis, premeiotic doubling, or gametic doubling (the latter two are when meiosis alternates with endomitosis, where the endomitotic division might occur either immediately before or after meiosis). Sex (meiosis) not only corrects genetic errors, epigenetic errors, and genomic errors (Gorelick and Heng 2011), but, by suppressing recombination, sex reduces recombination load. Suppression is through selection against mitotic recombinants or potentially through gene conversion or meiotic drive. Sex is much less of a conundrum in evolutionary biology if it reduces recombination load, but this is only clear if we consider that mitotic recombination can break up co-adapted gene complexes and thereby lead to increased recombination load. Reduction of recombination load is a sexual form of conservative bet hedging sensu Simons (2011). In addition, we strongly disagree with the usual assumption that genotypes remain intact with apomictic (aka mitotic) reproduction, but instead argue that mitotic replication, in and of itself, is a source of much genetic and genomic variation and recombination load. We agree with Heng (2007, 2009) who has emphasized that sex acts like an error-correcting filter, which is why mitotic divisions can so readily accumulate genomic abnormalities, as with cancer (Gorelick and Heng 2011, Abdallah et al. 2013). If this error-correcting filter of meiosis is lacking, then the genetic variation due to mitosis becomes evident.

If meiosis decreases recombination load, then this provides an obvious selective advantage for sex, largely obviating a rich literature begun by George Williams (2007, 2009), Michael Ghiselin (1974), and John Maynard Smith (1966, 1975) on the supposedly paradoxical costs of sex. Sex, vis-à-vis meiosis, as well as karyogamy (see below), may not increase additive genetic variance, but sex is still advantageous, even in highly inbred lineages because it decreases recombination load. In sexually reproducing organisms without germ line sequestration, recombination load contributed by mitosis should exceed the contribution by meiosis (1)

because of the much larger number of mitotic versus meiotic cell divisions and (2) because the higher number of mitotic cell divisions compensates for a lower mitotic recombination rate (per nuclear division). Therefore, in organisms with a germ line, the reduction in recombination load is due to elimination of a large number of mitotic recombination events in the germ line.

Did mitosis evolve from meiosis?

Cavalier-Smith (2010) proposed that meiosis and mitosis evolved simultaneously. However, his theory is based on a purely eubacterial origin of eukaryotes, without any archaebacterial contributions. Yet, eukaryotic ribosomes and histones are probably derived from archaea (Sandman et al. 1990, Woese et al. 1990), so we tentatively dismiss Cavalier-Smith's claim. Most other authors (e.g. Wilkins and Holliday 2009), assumed that meiosis evolved from mitosis. Here we want to briefly consider the opposite temporal order of evolution.

Garg and Martin (2016) proposed that eukaryotes evolved as a syncytial (more accurately, coenocytic) symbiosis of an archaebacterium with eubacterially-derived mitochondria, in which they proposed that mitosis arose as a modified form of meiosis. This is curious given the prevalence of syncytia and/or coenocytes amongst the immediate products of meiosis and karyogamy (e.g. Gorgoń et al. 2015, Yoshida 2016). However, Garg and Martin (2016) primarily base their novel order of meiosis evolving before mitosis on needing a way to reverse Muller's ratchet and their assumption that recombination only occurs in meiosis, not mitosis. In fact, they claim that mitosis evolved from meiosis via a loss of both recombination and reduction division. (Note, though, that Garg and Martin (2016: 1963) also make the ambiguous double negative claim that, "Our proposal lacks mitosing cells incapable of recombination."). We disagree with Garg and Martin's (2016) premise that recombination is absent from mitosis—we are only willing to concede that synaptonemal complex formation is lacking from mitosis. But Garg and Martin's (2016) theory is commensurate with mitosis increasing recombination load and meiosis decreasing it. A lineage would need some way of limiting recombination load, implying that meiosis could easily have evolved before mitosis, but not *vice versa*. The recombination load reduction ascribed here to meiosis would provide circumstantial evidence that mitosis evolved as a degenerate form of meiosis and that meiosis is eventually needed in all eukaryotic lifecycles to ameliorate recombination load, even if this meiosis is just automixis or autogamy.

Karyogamy also reduces recombination load

If sex is considered to be karyogamy, rather than meiosis, which was the traditional view prior to 1890 (Hertwig 1890, Cole 1930), then how does sex affect recombination load? Karyogamy is probably a modified form of meiosis (Gorelick and Carpinone 2009). Traditional meiosis contains two reduction divisions, while karyogamy only contains one reduction division, the cleavage division. Otherwise, meiosis and karyogamy are virtually identical. Karyogamy may be the elusive one-step meiosis. Therefore, if meiosis reduces recombination load, then so should karyogamy.

Here is a short synopsis of the parallels between meiosis and karyogamy. Both meiosis and karyogamy begin with a chromosomal duplication. This duplication has been noted in all species studied, including humans. That is, the first step in karyogamy, before egg nuclei 'fuse' with sperm nuclei (technically, before pronuclear association) is for both haploid nuclei to duplicate their chromosomes, meaning that zygotes have four copies of each chromosome. The last step in both meiosis and karyogamy is a reduction division. For meiosis, this means going from two copies of each chromosome to just one per nucleus. For karyogamy, this means going from four copies of each chromosome to two per chromosome during the cleavage division, which is not mitotic. Thus, if meiosis reduces recombination load, then so should its modified form, karyogamy.

Concluding Remarks

Like most objects of study in evolutionary biology, recombination load is complicated and shaped by many evolutionary mechanisms. Any recombination, whether it occurs during meiosis or mitosis, will affect recombination load if it disrupts a co-adapted gene complex. We have argued that the crux of study for recombination load is whether co-adapted gene complexes are broken-up or maintained. But the problem is that co-adapted gene complexes are themselves poorly understood, partly because of lack of study of multi-locus epistasis. If, as we have argued, meiosis and karyogamy reduce or correct recombination relative to what it could be, then both reduce recombination load. By contrast, mitosis should invariably increase recombination load, unless mitotic recombination is somehow suppressed. Essentially, we argue that meiosis reduces recombination load more than is currently accepted, and mitosis increases recombination load more than is currently accepted. Therefore, if we are correct, theories regarding the evolution of sex should incorporate a reduction of recombination load due to meiosis. Reduced recombination load should be

especially evident in lineages with germ lines, e.g. eumetazoans, because pre-meiotic germ cells (PGCs) eventually develop from the zygote after very few mitotic divisions. At least one important implication is that sex reducing recombination load ameliorates many of the costs of sex. In sexually reproducing organisms without germ line sequestration, recombination load contributed by mitosis should exceed the contribution by meiosis because of the much larger number of mitotic versus meiotic cell divisions and because of the relative rates of mitotic versus meiotic recombination. In organisms with a germ line, the reduction in recombination load is due to the elimination of a large number of mitotic recombination events in the germ line.

Acknowledgments

Thanks to the Natural Sciences and Engineering Research Council of Canada (NSERC) for a Discovery Grant to RG. Thanks to Mauro Santos and Mark Fitzpatrick for many helpful comments on an earlier version of this manuscript.

Referees

Mauro Santos - mauro.santos@uab.es
Universitat Autònoma de Barcelona

Mark Fitzpatrick – mark.fitzpatrick@utoronto.ca
University of Toronto

References

Abdallah, B. Y., Horne, S.D., Stevens, J.B., Liu, G., Ying, A.Y., Vanderhyden, B., et al. 2013. Single cell heterogeneity: Why unstable genomes are incompatible with average profiles. Cell Cycle 12:3640–3649. CrossRef

Allen, D. E., and M. Lynch. 2008. Both costs and benefits of sex correlate with relative frequency of asexual reproduction in cyclically parthenogenic *Daphnia pulicaria* populations. Genetics 179:1497–1502. CrossRef

Avise, J.C. 2008. Clonality: the genetics, ecology, and evolution of sexual abstinence in vertebrate animals. Oxford University Press, Oxford. CrossRef

Barlow, J.H., and R. Rothstein. 2010. Timing is everything: cell cycle control of Rad52. Cell Division 5. CrossRef

Bendel-Stenzel, M., Anderson, R., Heasman, J., and C. Wylie. 1998. The origin and migration of primordial germ cells in the mouse. Seminars in Cell & Developmental Biology 9:393–400. CrossRef

Bernstein, H. 1977. Germ line recombination may be primarily a manifestation of DNA repair processes. Journal of Theoretical Biology 69:371–380. CrossRef

Bernstein, H., Byers, G.S., and R.E. Michod. 1981. Evolution of sexual reproduction: importance of DNA repair, complementation, and variation. American Naturalist 117:537–549. CrossRef

Bernstein, H., Hopf, F.A., and R.E. Michod. 1988. Is meiotic recombination an adaptation for repairing DNA, producing genetic variation, or both? Pages 139–160 *in* R.E. Michod and B.R. Levin, editors. The evolution of sex: an examination of current ideas. Sinauer Associates, Sunderland.

Bianconi, E., Piovesan, A., Facchin, F., Beraudi, A., Casadei, R., Frabetti, F., et al. 2013. An estimation of the number of cells in the human body. Annals of Human Biology 40:463–471. CrossRef

Birdsell, J.A. 2002. Integrating genomics, bioinformatics, and classical genetics to study the effects of recombination on genome evolution. Molecular Biology and Evolution 19:1181–1197. CrossRef

Bishop, D.K., and D. Zickler. 2004. Early decision: meiotic crossover interference prior to stable strand exchange and synapsis. Cell 117:9–15. CrossRef

Broman, K.W., Murray, J.C., Sheffield, V.C., White, R.L., and J.L. Weber. 1998. Comprehensive human genetic maps: Individual and sex-specific variation in recombination. American Journal of Human Genetics 63:861–869. CrossRef

Cavalier-Smith, T. 2010. Origin of the cell nucleus, mitosis and sex: roles of intracellular coevolution. Biology Direct 5:7. DOI 10.1186/1745-6150-5-7. CrossRef

Charlesworth, B., and D. Charlesworth. 1975. An experiment on recombination load in *Drosophila melanogaster*. Genetical Research 25:267–274. CrossRef

Chen F.C., and W.H. Li. 2001. Genomic divergences between humans and other hominoids and the effective population size of the common ancestor of humans and chimpanzees. American Journal of Human Genetics 68:444–456. CrossRef

Cole, F.J. 1930. Early theories of sexual generation. Clarendon Press, Oxford.

De Loof, A., Schoofs, L., and R. Huybrechts. 2016. The endocrine system controlling sexual reproduction in animals: Part of the evolutionary ancient but well conserved immune system? General and Comparative Endocrinology 226:56–71. CrossRef

Ebersberger I., Metzler D., Schwarz, C., and S. Pääbo. 2002. Genome-wide comparison of DNA sequences between humans and chimpanzees. American Journal of Human Genetics 70:1490–1497. CrossRef

Ellis, N.A., Lennon, D.J., Proytcheva, M., Alhadeff, B., Henderson, E.E., and J. German. 1995. Somatic intragenic recombination within the mutated locus *BLM* can correct the high sister chromatid exchange phenotype of Bloom syndrome cells. American Journal of Human Genetics 57:1019–1027.

Garg, S.G., and W.F. Martin. 2016. Mitochondria, the cell cycle, and the origin of sex via a syncytial eukaryote common ancestor. Genome Biology and Evolution 8:1950–1970. CrossRef

Ghiselin, M.T. 1974. The economy of nature and the evolution of sex. University of California Press, Berkeley.

Gorelick, R. 2012. Mitosis circumscribes individuals; sex creates new individuals. Biology & Philosophy 27:871–890. CrossRef

Gorelick, R., and J. Carpinone. 2009. Origin and maintenance of sex: the evolutionary joys of self sex. Biological Journal of the Linnean Society 98:707–728. CrossRef

Gorelick, R., and H.H.Q. Heng. 2011. Sex reduces genetic variation: a multidisciplinary review. Evolution 65:1088–1098. CrossRef

Gorelick, R., and M.D. Laubichler. 2004. Decomposing multilocus linkage disequilibrium. Genetics 166: 1581–1583. CrossRef

Gorgoń, S., Krodkiewska, M., and P. Świątek. 2015. Ovary ultrastructure and oogenesis in *Propappus volki* Michaelsen, 1916 (Annelida: Clitellata). Zoologischer Anzeiger 257:110–118. CrossRef

Groden, J., Nakamura, Y., and J. German. 1990. Molecular evidence that homologous recombination occurs in proliferating human somatic cells. Proceedings of the National Academy of Sciences of the United States of America 87:4315–4319. CrossRef

Groenen, M.A.M., Wahlberg, R., Foglio, M., Cheng, H.H., Megens, H.J., Crooijmans, R., et al. 2009. A high-density SNP-based linkage map of the chicken genome reveals sequence features correlated with recombination rate. Genome Research 19:510–519. CrossRef

Hansen, T.F. 2013. Why epistasis is important for selection and adaptation. Evolution 67:3501–3511. CrossRef

Hartl, D.L., and A.G. Clark. 1989. Principles of population genetics (2nd edition). Sinauer Associates, Sunderland.

Hedrick, P.W. 2000. Genetics of populations (2nd edition). Jones and Bartlett, Sudbury.

Heng, H.H.Q. 2007. Elimination of altered karyotypes by sexual reproduction preserves species identity. Genome 50:517–524. CrossRef

Heng, H.H.Q. 2009. The genome-centric concept: resynthesis of evolutionary theory. BioEssays 31:512–525. CrossRef

Hertwig, O. 1890. Vergleich der ei- und samenbildung bei nematoden: eine grundlage für cellülare streitfragen. Archiv für mikroscopische Anatomie 36:1–138. CrossRef

Kirkpatrick, M., and C.D. Jenkins. 1989. Genetic segregation and the maintenance of sexual reproduction. Nature 339:300–301. CrossRef

Kong, A., Gudbjartsson, D.F., Sainz, J., Jonsdottir, G.M., Gudjonsson, S.A., Richardsson, B., et al. 2002. A high-resolution recombination map of the human genome. Nature Genetics 31:241–247. CrossRef

Kong, A., Thorleifsson, G., Gudbjartsson, D.F., Masson, G., Sigurdsson, A., Jonasdottir, A., et al. 2010. Fine-scale recombination rate differences between sexes, populations and individuals. Nature 467:1099–1103. CrossRef

Kong, A., Thorleifsson, G., Stefansson, H., Masson, G., Helgason, A., Gudbjartsson, D.F., et al. 2008. Sequence variants in the *RNF212* gene associate with genome-wide recombination rate. Science 319:1398–1401. CrossRef

Kouyos, R.D., Otto, S.P., and S. Bonhoeffer. 2006. Effect of varying epistasis on the evolution of recombination. Genetics 173:589–597. CrossRef

Kuliev, A., and Y. Verlinsky. 2004. Meiotic and mitotic nondisjunction: lessons from preimplantation genetic diagnosis. Human Reproduction Update 10:401–407. CrossRef

Lambing, C., Franklin, F.C.H. and C-J.R. Wang. 2017. Understanding and manipulating meiotic recombination in plants. Plant Physiology 173:1530–1542. CrossRef

Lynch, M., and H-W. Deng. 1994. Genetic slippage in response to sex. American Naturalist 144:242–261. CrossRef

Mahowald, A.P. 2001. Assembly of the *Drosophila* germ plasm. Pages 187–213 *in* L.D. Etkin and K.W. Jeon, editors. International Review of Cytology - a Survey of Cell Biology, Vol 203: Cell Lineage Specification and Patterning of the Embryo. Elsevier Academic Press, San Diego. CrossRef

Mandegar, M.A., and S.P. Otto. 2007. Mitotic recombination counteracts the benefits of genetic segregation. Proceedings of the Royal Society B-Biological Sciences 274:1301–1307. CrossRef

Marcon, E., and P.B. Moens. 2005. The evolution of meiosis: recruitment and modification of somatic DNA-repair proteins. BioEssays 27:795–808. CrossRef

McVean, G. 2000. What is driving male mutation? Current Biology 10:R834–R835. CrossRef

Morgan, T.H. 1911. Random segregation versus coupling in Mendelian inheritance. Science 34:384. CrossRef

Munch, K., Schierup, M.H., and T. Mailund. 2014. Unraveling recombination rate evolution using ancestral recombination maps. BioEssays 36:892–900. CrossRef

Nachman, M.W. 2002. Variation in recombination rate across the genome: evidence and implications. Current Opinion in Genetics & Development 12:657-663. CrossRef

Nicklas, R.B. 1974. Chromosome segregation mechanisms. Genetics 78:205–213.

Otto, S.P., and A.C. Gerstein. 2006. Why have sex? The population genetics of sex and recombination. Biochemical Society Transactions 34:519–522. CrossRef

Otto, S.P., and T. Lenormand. 2002. Resolving the paradox of sex and recombination. Nature Reviews Genetics 3:252–261. CrossRef

Otto, S.P., and Y. Michalakis. 1998. The evolution of recombination in changing environments. Trends in Ecology & Evolution 13:145–151. CrossRef

Otto, S.P., and S.L. Nuismer. 2004. Species interactions and the evolution of sex. Science 304:1018–1020. CrossRef

Page, S.L., and R.S. Hawley. 2001. *c(3)G* encodes a *Drosophila* synaptonemal complex protein. Genes & Development 15:3130–3143. CrossRef

Page, S.L., and R.S. Hawley. 2003. Chromosome choreography: the meiotic ballet. Science 301:785–789. CrossRef

Pâques, F., and J.E. Haber. 1999. Multiple pathways of recombination induced by double-strand breaks in *Saccharomyces cerevisiae*. Microbiology and Molecular Biology Reviews 63:349–404.

Pontecorvo, G., and E. Käfer. 1958. Genetic analysis based on mitotic recombination. Advances in Genetics 9:71–104. CrossRef

Potapova, T., and G.J. Gorbsky. 2017. The consequences of chromosome segregation errors in mitosis and meiosis. Biology 6:12. CrossRef

Ritz, K.R., Noor, M.A.F., and N.D. Singh. 2017. Variation in recombination rate: Adaptive or not? Trends in Genetics 33:364–374. CrossRef

Roeder, G.S. 1997. Meiotic chromosomes: it takes two to tango. Genes & Development 11:2600–2621. CrossRef

Rose, A.M., and D.L. Baillie. 1979. The effect of temperature and parental age on recombination and nondisjunction in *Caenorhabditis elegans*. Genetics 92:409–418.

Roux, C., Fraisse, C., Romiguier, J., Anciaux, Y., Galtier, N., and N. Bierne, N. 2016. Shedding light on the grey zone of speciation along a continuum of genomic divergence. PLoS Biology 14(12):e2000234. CrossRef

Ruchaud, S., Carmena, M., and W.C. Earnshaw. 2007. Chromosomal passengers: conducting cell division. Nature Reviews Molecular Cell Biology 8:798–812. CrossRef

Sandman, K., Krzycki, J.A., Dobrinski, B., Lurz, R., and J.N. Reeve. 1990. *HMf*, a DNA-binding protein isolated from the hyperthermophilic archaeon *Methanothermus fervidus*, is most closely related to histones. Proceedings of the National Academy of Sciences of the United States of America 87:5788–5791. CrossRef

Santos, M. 2009. Recombination load in a chromosomal inversion polymorphism of *Drosophila subobscura*. Genetics 181:803–809. CrossRef

Schoustra, S.E., Debets, A.J.M., Slakhorst, M., and R.F. Hoekstra. 2007. Mitotic recombination accelerates adaptation in the fungus *Aspergillus nidulans*. PLoS Genetics 3. DOI 10.1371/journal.pgen.0030068. CrossRef

Serrano, L., Liang, L., Chang, Y.M., Deng, L., Maulion, C., Nguyen, S., and J.A. Tischfield. 2011. Homologous recombination conserves DNA sequence integrity throughout the cell cycle in embryonic stem cells. Stem Cells and Development 20:363–374. CrossRef

Shields, W.M. 1982. Philopatry, inbreeding, and the evolution of sex. State University of New York Press, Albany.

Simons, A.M. 2011. Modes of response to environmental change and the elusive empirical evidence for bet hedging. Proceedings of the Royal Society B-Biological Sciences 278:1601–1609. CrossRef

Stern, C. 1936. Somatic crossing over and segregation in *Drosophila melanogaster*. Genetics 21:625–730.

Turelli, M., and N.H. Barton. 2006. Will population bottlenecks and multilocus epistasis increase additive genetic variance? Evolution 60:1763–1776. CrossRef

Unneberg P, Stromberg, M., Lundeberg, J., Jansson, S., and F. Sterky (2005) Analysis of 70,000 EST sequences to study divergence between two closely related *Populus* species. Tree Genetics & Genomes 1:109–115. CrossRef

Villeneuve, A.M., and K.J. Hillers. 2001. Whence meiosis? Cell 106:647–650. CrossRef

Wall, J.D. 2001. Insights from linked single nucleotide polymorphisms: what we can learn from linkage disequilibrium. Current Opinion in Genetics & Development 11:647–651. CrossRef

Wasserman, M. 1968. Recombination-induced chromosomal heterosis. Genetics 58:125–139.

Weismann, A. 1891 [1892]. Amphimixis or the essential meaning of conjugation and sexual reproduction [translators: E. B. Poulton, A. E. Shipley, L. J. Gould, E.R. Lankester, S. H. Vines, F. Gotch, and D. G. Ritchie]. Pages 100–222. Essays upon heredity and kindered biological problems - Volume 2. Clarendon Press, Oxford.

Weismann, A. 1892 [1893]. The germ-plasm: a theory of heredity [translator: Parker, W.N.]. Walter Scott, London.

Wilfert, L., Gadau, J., and P. Schmid-Hempel. 2007. Variation in genomic recombination rates among animal taxa and the case of social insects. Heredity 98:189–197. CrossRef

Wilkins, A.S., and R. Holliday. 2009. The evolution of meiosis from mitosis. Genetics 181:3–12.

Williams, G.C. 1966. Adaptation and natural selection: a critique of some current evolutionary thought. Princeton University Press, Princeton.

Williams, G.C. 1975. Sex and evolution. Princeton University Press, Princeton.

Woese, C.R., Kandler, O., and M.L. Wheelis. 1990. Towards a natural system of organisms: proposal for the domains Archaea, Bacteria, and Eucarya. Proceedings of the National Academy of Sciences of the United States of America 87:4576–4579. CrossRef

Yoshida, S. 2016. From cyst to tubule: innovations in vertebrate spermatogenesis. Wiley Interdisciplinary Reviews - Developmental Biology 5:119–131. CrossRef

Ziolkowski, P.A., and I.R. Henderson. 2017. Inter-connections between meiotic recombination and sequence polymorphism in plant genomes. New Phytologist 213:1022–1029. CrossRef