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Meiotic drive and genome evolution in vascular land plants

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Abstract

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Meiotic drive is a deviation from Mendelian inheritance where genetic elements are preferentially inherited by the surviving egg cell. This can profoundly impact chromosome (and genome) size and structure. Across vascular plants, heterosporous lineages typically have fewer chromosomes than homosporous lineages. The underlying mechanism causing this disparity has been debated for over half a century. Although reproductive mode has been identified as critical to these patterns, the symmetry of meiosis during sporogenesis has been overlooked as a cause of the difference in chromosome numbers. In most heterosporous plants, meiosis during megasporogenesis is asymmetric, meaning one of the four meiotic products survives to become the egg, and the three polar bodies die. Comparatively, meiosis is symmetric in homosporous megasporogenesis and all meiotic products survive. The symmetry of meiosis is important because asymmetric meiosis enables meiotic drive and associated genomic changes. Here we review how meiotic drive impacts genome evolution, what we would expect to see in lineages without meiotic drive, and finally what the first homosporous plant genomes tell us about patterns of evolution concerning meiotic drive.

25

Introduction

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Meiotic drive is a deviation from Mendelian inheritance where genetic elements are preferentially inherited by the germ line (Sandler and Novitski, 1957; Pardo-Manuel de Villena and Sapienza, 2001b). This occurs via the asymmetry of female meiosis in terms of cell fate: of the four meiotic products, only one survives to become the egg cell and the three polar bodies do not enter the germ line (Fig 1A, Burt and Trivers, 2009; Schmerler and Wessel, 2011; Haig, 2020). In heterozygotes, a driving allele can rapidly rise to fixation by taking advantage of a functionally asymmetric meiotic spindle pole, which will be preferentially transmitted into the surviving egg cell (Pardo-Manuel de Villena and Sapienza, 2001b; Fishman and Willis, 2005; Finseth, 2023). Regardless of fitness consequences, a drive locus can become fixed in a population rapidly, sometimes within a handful of generations (e.g., Fishman and Willis, 2005). Consequently, meiotic drive can have profound impacts on the genome. Drive can favor the inheritance of certain chromosomal rearrangements and morphologies, altering a species' karyotype and chromosome number (Pardo-Manuel de Villena and Sapienza, 2001a; Burt and Trivers, 2009; Fishman *et al.*, 2014; Baack *et al.*, 2015; Lindholm *et al.*, 2016; Blackmon *et al.*,

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42 2019; Boman *et al.*, 2024). In addition, meiotic drive is thought to affect critical parts of the cell
43 that would not be under selection otherwise. For example, drive can lead to increased centromere
44 size and sequence diversity (Henikoff, Ahmad and Malik, 2001; Malik and Bayes, 2006; Zedek
45 and Bureš, 2016; Finseth, Nelson and Fishman, 2021). Meiotic drive has been described across
46 eukaryotes (e.g., Foster and Whitten, 1991; Lindholm *et al.*, 2016; Zedek and Bureš, 2016;
47 Lampson and Black, 2017), but has not previously been explored as a potential mechanism for
48 the remarkable difference in genome structure and chromosome number among vascular land
49 plants. Meiotic drive can only occur during asymmetric meiosis—a trait of most heterosporous
50 plants, but not homosporous plants. Therefore, meiotic drive cannot happen in homosporous
51 lineages, and the absence of drive may be part of the reason we see such distinct genomic
52 differences between homosporous and heterosporous plants.

53

54 Across vascular land plant lineages, there is great diversity and disparity of genome size and
55 structure. Specifically, flowering plants have smaller average nuclear genomes and lower
56 chromosome numbers than most pteridophytes (ferns and lycophytes), a pattern that is correlated
57 with a difference in reproductive mode (Klekowski and Baker, 1966; Wagner and Wagner, 1979;
58 Nakazato *et al.*, 2008; Leitch and Leitch, 2013). Flowering plants and some pteridophytes are
59 heterosporous, and reproduce via separate megaspores and microspores that develop into female
60 and male gametophytes. Female meiosis is typically asymmetric in heterosporous plants and
61 male meiosis is symmetric (Fig. 1A, B). In contrast, most species of pteridophytes are
62 homosporous, and they reproduce by one type of spore which germinates into a gametophyte
63 capable of producing eggs, sperm, or both; all homosporous meiosis is symmetric (Fig. 1C).
64 Homospory is the ancestral character state in land plants whereas heterospory is thought to have
65 evolved as many as 11 times (Bateman and DiMichele, 1994). Importantly, the transition to
66 heterospory is often accompanied by distinct changes in genome structure, including a decrease
67 in chromosome number and genome size (Clark *et al.*, 2016; Carta, Bedini and Peruzzi, 2020).
68 An important caveat is that gymnosperms—the heterosporous seed plant lineage sister to
69 flowering plants—have large genomes. However, they have relatively low chromosome numbers
70 that have been fairly static over time (Li *et al.* in prep). Their large genome sizes are due to the
71 accumulation of repetitive elements (e.g., Nystedt *et al.*, 2013). In addition, while gymnosperms
72 have experienced a few potential ancient WGD events (Li *et al.*, 2015; One Thousand Plant
73 Transcriptomes Initiative, 2019; Stull *et al.*, 2021) they may not undergo significant genome
74 downsizing (Ickert-Bond *et al.*, 2020) and have lower rates of genome evolution relative to
75 flowering plants (De La Torre *et al.*, 2017).

76

77 Several mechanisms have been proposed to explain the differences in genome organization
78 between homosporous and heterosporous plants (Klekowski and Baker, 1966; Wagner and
79 Wagner, 1979; Hafler and Soltis, 1986; Hafler, 1987; Barker and Wolf, 2010; Leitch and
80 Leitch, 2013; Kinosian, Rowe and Wolf, 2022). The most well-supported have been differences
81 in the number of rounds of ancient whole genome duplications (WGDs) and subsequent re-
82 diploidization (Klekowski and Baker, 1966; Wagner and Wagner, 1979; Hafler, 1987; Barker,

83 2013; Kinosian, Rowe and Wolf, 2022). Interestingly, homosporous and heterosporous lineages
84 have experienced roughly the same number of rounds of WGDs, but likely different mechanisms
85 or at least rates of diploidization (One Thousand Plant Transcriptomes Initiative, 2019; Li *et al.*,
86 2021; McKibben, Finch and Barker, 2024), Li *et al.* in prep). Following a WGD, diploidization
87 can proceed rapidly in flowering plants via a reduction in chromosome number (dysploidy) and
88 extensive gene deletions (Wendel, 2015; Li *et al.*, 2021). It has been proposed that pteridophytes
89 undergo some genomic restructuring following WGDs, but their diploidization process appears
90 to involve limited chromosome loss accompanied by gene silencing rather than deletion
91 (Haufler, 1987; Barker, 2013), Li *et al.* in prep). Over the multiple rounds of WGD in their
92 history, homosporous pteridophyte chromosome numbers have increased despite their repeated
93 return to diploid inheritance.

94

95 In addition to the dynamics of WGDs and diploidization, we propose that meiotic drive may be
96 an important force behind differences in genome evolution across vascular land plants,
97 specifically due to fundamental differences in meiosis related to spore production between
98 heterosporous and homosporous plants. Traditionally defined meiotic drive can only happen with
99 asymmetric meiosis (Sandler and Novitski, 1957; Fishman and Willis, 2005), which is well-
100 documented in heterosporous plants (e.g., Lindholm *et al.*, 2016; Haig, 2020; Finseth, 2023).
101 Homosporous plants have strictly symmetric meiosis, eliminating the possibility of traditionally
102 defined meiotic drive and any genome restructuring it can cause. Other types of drive can occur
103 in symmetric meiosis, although these processes typically occur after meiosis and are expected to
104 have different effects on the genome (Lindholm *et al.*, 2016). Here we review how meiotic drive
105 impacts genome evolution across vascular land plants, what genome characteristics we would
106 expect to see in a lineage without meiotic drive, how post-meiotic drive may be influencing
107 pteridophyte genomes, and conclude with future directions for incorporating meiotic drive into
108 the growing body of work on plant genome evolution.

109

110 **The influence of meiotic drive on heterosporous genome structure**

111

112 Meiotic drive can happen by several mechanisms, including centromere and chromosome drive.
113 These types of drive are likely important forces shaping heterosporous plant genome structure, as
114 they can lead to drastic changes in chromosome number and karyotype morphology. For
115 example, centromere drive causes accelerated centromere evolution despite these structures
116 being essential to cell division (Henikoff, Ahmad and Malik, 2001; Malik and Bayes, 2006;
117 Zedek and Bureš, 2016). Centromere drive results from competition among chromosomes to be
118 transmitted to a gamete during asymmetric meiosis and results in selection for particular
119 centromere morphologies (Henikoff, Ahmad and Malik, 2001; Finseth, 2023). In angiosperms,
120 the four meiotic products are arranged in a line with the surviving cell that becomes the gamete
121 typically at one end (Huang and Russell, 1992; Bell, 1996). Larger centromeres have a stronger
122 kinetochore-spindle connection, resulting in the larger centromere (and attached homolog) being
123 preferentially moved to the end of the set of meiotic products where it becomes the egg cell

124 (Dudka and Lampson, 2022). Competition among chromosomes to be transmitted to the egg can
125 lead to an increase in the centromere size to increase the strength of the kinetochore-spindle
126 connection. While this has been demonstrated in mice, the mechanism of centromere drive may
127 be more complex in plants (Finseth, 2023). For example, centromere size is correlated with
128 genome size and chromosome number in plants (Bennett *et al.*, 1981; Zhang and Dawe, 2012),
129 suggesting that centromere size does not simply increase in plants due to drive. Different
130 proteins may mediate the strength of kinetochore attachment in plants (Talbert and Henikoff,
131 2022; Finseth, 2023; Majka *et al.*, 2023), but additional work is needed to understand the
132 mechanisms at play. Although the biology of centromere drive and its impacts are complex in
133 plants, two of the best examples of centromere-associated meiotic drive—the D locus in *Mimulus*
134 (Fishman and Saunders, 2008) and Ab10 in maize (Dawe *et al.*, 2018)—are from flowering plants.
135

136 Driving centromeres can be part of large, non-recombining regions that harbor deleterious alleles
137 (Finseth *et al.*, 2022). This can have major negative fitness consequences in both males and
138 females (Fishman and Kelly, 2015) and can lead to hybrid inviability between populations
139 (Henikoff, Ahmad and Malik, 2001; Talbert and Henikoff, 2022), but also select for
140 chromosome fusions which reduce overall chromosome number (Pardo-Manuel de Villena and
141 Sapienza, 2001a; Lindholm *et al.*, 2016). This is most prevalent in lineages with monocentric
142 chromosomes, where fused centromeres directly increase the strength of the centromere-spindle
143 fiber bond (Chmátal *et al.*, 2014; Ruckman *et al.*, 2020). For example, Robertsonian
144 translocations are preferentially transmitted in humans despite deleterious effects (Daniel, 2002;
145 Poot and Hochstenbach, 2021; Talbert and Henikoff, 2022). Chromosomes with a derived fusion
146 are also preferentially transmitted in *Drosophila* (Stewart *et al.*, 2019). In *Mimulus* it is thought
147 that chromosome fissions supported by meiotic drive are responsible for chromosome number
148 doubling, not polyploidy (Fishman *et al.*, 2014). There is evidence that centromere drive can
149 favor chromosome fusions in one species of butterfly, but conserve chromosome structure by
150 selecting against chromosome fusions in another (Boman *et al.*, 2024). In addition, there is
151 increased rate variation in chromosome number evolution in monocentric (compared to
152 holocentric) insects, which could be explained by meiotic drive being present or absent
153 depending on the lineage (Ruckman *et al.*, 2020). Chromosome fusions favored by meiotic drive
154 could be part of how heterosporous plants cytologically downsize following WGD; the absence
155 of meiotic drive in homosporous plants would eliminate this process as a mechanism for genome
156 downsizing.

157

158 To counteract the negative effects of centromere drive, centromere histone H3 (CenH3) is
159 frequently under positive selection in lineages with asymmetric meiosis (Zedek and Bureš, 2016;
160 Finseth, Nelson and Fishman, 2021). CenH3 mediates the attachment to the kinetochore and is
161 thought to respond epigenetically in strong centromere drive systems and alter the strength of
162 centromeres (Malik and Henikoff, 2002; Allshire and Karpen, 2008). Notably, CenH3 is under
163 purifying selection in lineages with symmetric meiosis because no centromere drive is taking

164 place (Zedek and Bureš, 2016). Centromere drive causes the rapid evolution of what is otherwise
165 a conserved genetic element, and subsequently alters the genome in unique ways.

166

167 Like centromere drive, chromosome drive can also have strong effects on an organism's
168 karyotype that results in changes to the morphology and number of chromosomes. In
169 chromosome drive, different morphologies (meta-, acro-, or telocentric chromosomes) are
170 favorably inherited depending on the system (Burt and Trivers, 2009; Dudka and Lampson,
171 2022). This is known to occur in mammals, where a change in the polarity of meiotic drive (i.e.,
172 which meiotic product survives) favors a specific chromosome morphology, causing rapid
173 rearrangement of chromosome structure and number (Blackmon *et al.*, 2019). For example, in
174 mammals, it is typical to have some species with a high frequency of metacentric chromosomes
175 and others with a high frequency of acrocentric chromosomes (Pardo-Manuel de Villena and
176 Sapienza, 2001b; Burt and Trivers, 2009). Such bimodal karyotypes within groups are less
177 common in angiosperms, perhaps because the polarity of meiosis is relatively weak (Huang and
178 Russell, 1992). Most angiosperms have symmetric karyotypes comprising mostly metacentric
179 chromosomes (Stebbins and Others, 1971; Weiss-Schneeweiss and Schneeweiss, 2013). Some
180 angiosperms, mainly monocots with large genomes, have asymmetric karyotypes with variable
181 chromosome size and centromere positions (Stedje, 1989; Choi *et al.*, 2008; Hamouche *et al.*,
182 2010; McKain *et al.*, 2012). Research in the Brassicaceae suggests that an asymmetric karyotype
183 is perhaps a transition state between two favored chromosome morphologies (Mandáková and
184 Lysak, 2008; Lysak *et al.*, 2009). This could be created by drive if the polarity of meiosis
185 recently changed due to a hybridization or speciation event. As part of chromosome drive,
186 rearrangements can be preferentially transmitted by meiotic drive, as shorter chromosomes are
187 more likely to end up in the oocyte; therefore, deletions are favored over inversions or
188 translocations (Burt and Trivers, 2009). If one chromosome is shorter than its homolog due to
189 gene deletion it may be preferentially inherited via chromosomal drive. This could potentially be
190 part of why angiosperms delete genes quickly following diploidization.

191

192 In summary, centromere and chromosomal drive influence genome structure by the preferential,
193 non-Mendelian inheritance of chromosomes with particular features. The specific traits favored
194 by drive depend on the biological system, but some favored features include larger centromeres,
195 diverse centromeres, particular centromere positions, a diversity of chromosome rearrangements
196 and structure, plus smaller genomes and chromosomes. It is important to note that there are many
197 ways in which angiosperm megasporogenesis happens (Huang and Russell, 1992; Kaur,
198 Kathpalia and Koul, 2024), all having different types of cells develop into the megaspore
199 resulting in variation in the potential mechanisms of meiotic drive. These include monosporic
200 megasporogenesis, where one of four one-nucleate cells result survives; disporic
201 megasporogenesis, where one of two two-nucleate cells survives; and tetrasporic
202 megasporogenesis where one four-nucleate cell develops to form the embryo sac (e.g., Haig,
203 1990, 2020; Drews and Koltunow, 2011) Meiotic drive would be the strongest in a monosporic
204 system, and present but less strong in a disporic system. In tetrasporic megasporogenesis, the egg

205 cell develops much later, and within an embryo derived from one genetic background (Yadegari
206 and Drews, 2004); drive would act much differently and potentially be less strong than in the
207 other two types of megasporogenesis. Interestingly, megasporogenesis in heterosporous ferns
208 could potentially have stronger meiotic drive than in seed plants. Megasporogenesis in the fern
209 *Marsilea* produces eight tetrads of megaspores, and in each tetrad just one megaspore survives.
210 However, of the eight total megaspores, only one survives to maturity (Bell, 1981). Instead of
211 1/4 of potential megaspores surviving in angiosperm monosporic sporogenesis, in *Marsilea* only
212 1/32 megaspores are ultimately viable. Interestingly, spores are produced in a tetrad with no
213 polarity as to which megaspore survives (Bell 1985). In any case, the potential for meiotic drive
214 may be part of the reason heterosporous plants, in particular angiosperms, have a large diversity
215 of genome organization that evolves relatively rapidly. Competition among centromeres and
216 chromosomes in plant lineages with meiotic drive may lead to lower chromosome numbers
217 especially if fusions are favored in their drive systems. In contrast, the absence of meiotic drive
218 in homosporous plants could be why we see a comparative lack of diversity and slower evolution
219 in their genome structure and organization such as largely stable and high chromosome numbers
220 over time.

221

222 **Meiotic drive and symmetric meiosis**

223

224 In contrast to the genomes of the heterosporous angiosperms, the genomes of plants with
225 symmetric meiosis—namely homosporous pteridophytes—cannot be influenced by traditionally
226 defined meiotic drive. Female meiotic drive requires asymmetric meiosis for the preferential
227 inheritance of certain genetic elements to the egg or megaspore. Homosporous pteridophytes
228 have a unique kind of symmetric meiosis, different from that of male meiosis in heterosporous
229 plants. In leptosporangiate ferns, spores are produced via four rounds of mitosis and one round of
230 meiosis (Fig. 1C). In eusporangiate ferns, hundreds of spores are produced in tetrads via one
231 round of meiosis, akin to male meiosis in heterosporous plants (Brown and Lemmon, 2001). In
232 these plants without meiotic drive, we expect to see relatively slow rates of centromere
233 evolution, limited selection pressure on chromosome size and morphology, and larger genomes.

234

235 Previous work has shown that centromere drive is not present in lineages with symmetric meiosis
236 (Zedek and Bureš, 2016). Evidence for this comes from molecular evolutionary analyses of
237 histones, in particular CenH3. In lineages with asymmetric meiosis, CenH3 is often rapidly
238 evolving with signals of positive selection, but evolutionary constrained and under purifying
239 selection in organisms with symmetric meiosis (Zedek and Bureš, 2016; Finseth, Nelson and
240 Fishman, 2021). This is thought to be a result of centromere histones rapidly evolving to
241 counteract the changes caused by centromere drive. Rapid histone evolution is not expected or
242 observed in lineages with symmetric meiosis because centromeres are conserved in the absence
243 of meiotic drive. It is not yet possible to analyze the centromeres of homosporous fern and
244 lycophyte genomes because they have proven difficult to detect in these large and repetitive
245 genomes (F.-W. Li, Pers. Com). If centromere drive occurs in any of these species, we would

246 expect to see large, diverse, and potentially growing centromeric regions with rapid evolution of
247 centromere histones (Malik and Bayes, 2006; Zedek and Bureš, 2016).

248

249 The absence of centromere or chromosome drive in homosporous plants means no preferential
250 inheritance of certain karyotypes, chromosome morphologies, or rearrangements (Burt and
251 Trivers, 2009). This could be part of the reason why homosporous pteridophytes have relatively
252 stable chromosome structures (Wagner and Wagner, 1979; Bomfleur, McLoughlin and Vajda,
253 2014; Clark *et al.*, 2016), uniform chromosome sizes (Manton, 1950; Wagner and Wagner, 1979;
254 Nakazato *et al.*, 2008; Clark *et al.*, 2016), and relatively slow rates of chromosome number
255 evolution (Li *et al.* in prep). The size range variation in homosporous fern chromosomes is only
256 31-fold, compared to 1300-fold in heterosporous angiosperms (Clark *et al.*, 2016). It has been
257 hypothesized that this stability and uniformity is due to a limit on the amount of genetic material
258 in each chromosome (Liu *et al.*, 2019), but also may come from the lack of meiotic drive
259 resulting in little selection pressure on various features of their chromosomes. Despite the
260 extensive research on pteridophyte cytology (e.g., Manton 1950), limited information has been
261 published on their chromosome morphology. From this small dataset (Table 1), we see several
262 taxa with mostly acrocentric chromosomes. Although it is hard to draw meaningful conclusions
263 without more data, it is worth noting that in some lineages with meiotic drive, Robertsonian
264 translocations lead to the fusion of acrocentric chromosomes to form metacentric chromosomes
265 with increased centromere size and strength (Daniel, 2002; Dudka and Lampson, 2022). The
266 frequency of acrocentric chromosomes reported here may be evidence that meiotic drive is
267 indeed not happening in homosporous ferns and lycophytes. Further studies on homosporous and
268 heterosporous pteridophyte chromosome morphology and karyotype structure, ideally in a
269 phylogenetic context, are needed to understand what processes are influencing these traits.

270

271 Although meiotic drive may not occur in homosporous plants, other types of drive can operate in
272 organisms with symmetric meiosis. These types of transmission ratio distortion occur post-
273 meiotically, and so are different from the classical definition of meiotic drive (Sandler and
274 Novitski, 1957; Pardo-Manuel de Villena and Sapienza, 2001b; Fishman and Willis, 2005). One
275 example of post-meiotic drive is spore drive. This has been characterized in fungi, and occurs
276 when a particular haplotype kills spores with an alternative haplotype (Raju, 1994; Grognet *et al.*
277 *et al.*, 2014; Harvey *et al.*, 2014; Lindholm *et al.*, 2016). Spore drive is best characterized in
278 ascomycete fungi, where the spores are packaged together in an ascus. The proximity of spores
279 in an ascus allows for a killer haplotype to kill or disable neighboring spores with an alternate
280 haplotype. Similar spore production occurs in pteridophytes with spores packaged in a
281 sporangium. Spore drive has not been tested in ferns, but reductions in spore numbers within a
282 sporangium has been observed across populations of homosporous ferns (Barker and Hickey,
283 2006; A. L. Grusz, Pers. Ob.) which suggests it could occur. In addition, dispersal can also
284 influence spore drive, with drive being more prevalent if spores do not travel far from one
285 another (Lindholm *et al.*, 2016). Studies have shown that the majority of fern spores disperse
286 only a few meters from the parent plant (Conant, 1978; Rose and Dassler, 2017), but because

287 ferns produce vast numbers of spores some do travel great distances (e.g., Tryon, 1970). The
288 greater spores disperse from one another, the less selective pressure for spore drive (Lindholm *et*
289 *al.*, 2016), although no studies to date have looked at this type of spore competition in ferns and
290 lycophytes.

291

292 Another example of post-meiotic drive is male drive, which occurs when a drive locus kills
293 sperm with a target locus (e.g. Taylor, 1994; Presgraves, Severance and Wilkinson, 1997).
294 Similar to spore drive, one genotype will kill another genotype regardless of the fitness
295 consequences (Rice, 2013; Lindholm *et al.*, 2016). There is limited research on fern sperm
296 competition, but observational studies note competition in the archegonium before sperm meet
297 the egg (Lopez-Smith and Renzaglia, 2008). Further work is needed to understand competition
298 and potential male drive among sperm of homosporous plants, as well as other plant lineages
299 with flagellate sperm.

300

301 Because of fundamental differences in meiosis, meiotic drive cannot happen in homosporous
302 pteridophytes in the same way as in heterosporous plants. Post-meiotic drive can still influence
303 the genomes of homosporous plants by removing certain genotypes but likely does not shape the
304 genome in the same ways as meiotic drive. Several homosporous pteridophyte genome
305 assemblies are now published (Fang *et al.*, 2021; Huang *et al.*, 2022; Marchant *et al.*, 2022; Yu
306 *et al.*, 2023; Li *et al.*, 2024), giving us insight into what plant genome structure looks like
307 without female meiotic drive. Perhaps most striking is that these species have highly conserved
308 intra- and intergenomic synteny over millions of years (Huang *et al.*, 2022; Li *et al.*, 2024). An
309 exception is *Ceratopteris richardii*, which has a rate of fractionation rivaling many angiosperm
310 species (Nakazato *et al.*, 2006; Marchant *et al.*, 2022). Broad patterns in homosporous
311 pteridophytes suggest that, while genic diploidization occurs, there are limited mechanisms for
312 cytologically restructuring the genome following WGD. Thus, meiotic drive may be important
313 for reducing chromosome number and the extensive rearrangements observed following
314 polyploidy in flowering plant genomes compared to those of ferns and lycophytes.

315

316 **Conclusions and future work**

317

318 Here we have covered how meiotic drive may be a potential mechanism behind the disparity in
319 genome architecture among land plants, specifically influencing chromosome number and
320 structure of heterosporous plants. Other types of drive can occur in homosporous lineages, but
321 not meiotic drive, as traditionally defined, because sporogenesis is symmetric. Although the
322 symmetry of meiosis has not been explicitly discussed before in the context of homosporous
323 plants, other authors have noted that genome evolution is likely dependent on the mechanics of
324 meiosis (e.g., Burt and Trivers, 2009; Lindholm *et al.*, 2016; Kinosian, Rowe and Wolf, 2022;
325 Finseth, 2023). Here we discuss a few ways to investigate how drive or other types of
326 transmission ratio distortion might affect homosporous vascular land plant genomes.

327

328 Consistent with the absence of meiotic drive, past studies have shown that homosporous ferns
329 have strong Mendelian inheritance (Andersson-Kottö, 1927; Dederá and Werth, 1987). Ferns
330 have relatively low gene densities compared to flowering plants (Rabinowicz *et al.*, 2005; Wolf
331 *et al.*, 2015), perhaps because of a lack of meiotic drive selecting for genome downsizing. The
332 rate of evolution of meiosis related genes is greater in heterosporous angiosperms than in
333 homosporous pteridophytes, suggesting that different selection pressures, perhaps one of those
334 being meiotic drive, are acting on meiosis in these lineages (Li *et al.* in prep). As expected with
335 the absence of meiotic drive, CenH3 does not appear to be rapidly evolving in ferns and
336 lycophytes (Zedek and Bures 2016), but the analysis combined homosporous and heterosporous
337 genera with a mixture of symmetric and asymmetric meiosis. More focused molecular
338 evolutionary analyses of CenH3 and other proteins in heterosporous versus homosporous plants
339 would provide further insight into the pattern. In addition, there is a positive correlation between
340 long terminal repeat retrotransposon (LTR-RT) insertion time with haploid nuclear genome size
341 in pteridophytes, as well as a notable difference in insertion time between homosporous and
342 heterosporous plants (Baniaga and Barker, 2019). LTR-RTs have a high birth but low death rate
343 in homosporous ferns, with the inverse occurring in heterosporous lycophytes (Wang *et al.*,
344 2021; Yu *et al.*, 2023). Transposons are known to be associated with meiotic drive, although the
345 exact transmission mechanisms depend on the system (Eickbush, Young and Zanders, 2019;
346 Vogan *et al.*, 2021). Building on these observations, future work could look more explicitly for
347 evidence of drive or transmission ratio distortion in homosporous plants and investigate the
348 mechanics of homosporous meiosis.

349

350 Finding natural examples of meiotic drive can be challenging, as a driving or target locus is often
351 rapidly fixed in a population, and therefore undetectable. However, these can reemerge following
352 a hybridization event, or even be part of hybrid sterility (Lindholm *et al.*, 2016). An example of
353 this is in yellow monkeyflowers, where hybrids between *Mimulus guttatus* and *M. nasutus*
354 exhibit strong female meiotic drive and the driving locus is nearly fixed in only a handful of
355 generations (Fishman *et al.*, 2001; Fishman and Willis, 2005; Finseth, Nelson and Fishman,
356 2021). Testing for such cryptic drive systems could be a potential avenue of research in
357 pteridophytes, specifically in those with known hybrid sterility. Pteridology has a rich history of
358 work on hybrid species, including studies on the model system *Ceratopteris* (e.g., Hickok, 1973;
359 Hickok and Klekowski, 1974). Genomic resources available for *Ceratopteris* (Nakazato *et al.*,
360 2006; Marchant *et al.*, 2022) would make testing for drive in a hybrid mapping population
361 feasible (e.g., Fishman and Willis 2005). While the drive mechanism would likely not be the
362 same in pteridophytes as in flowering plants, detecting transmission ratio distortion in
363 pteridophytes would be insightful and help create a path for future work.

364

365 A drive mechanism that could be happening in homosporous plants is spore drive. In fungi,
366 spores are affected by drive when a certain genotype kills an alternative genotype. Considering
367 the large number of spores produced by both eusporangiate and leptosporangiate lineages, the
368 ingredients for spore drive are present. DNA expression studies have identified spore drive

369 systems, revealing that the driving element can lethally target specific genes (Urquhart and
370 Gardiner, 2023). A consistent reduction in spore number per sporangium in leptosporangiate
371 ferns has been observed (Barker and Hickey, 2006; A. L. Grusz, Pers. Ob.), suggesting
372 something may be happening during sporogenesis to reduce spore number. Additional work
373 counting spores could better characterize this pattern. If more concrete patterns of spore
374 reduction are observed and connected to a spore drive system, the model fern *Ceratopteris* could
375 help understand the genetic mechanisms for homosporous spore drive.

376
377 Other processes outside of meiotic and related drive systems could affect chromosome number
378 and genome size in vascular plants. Population size can be a greater force on chromosome
379 number than meiotic drive. For example, in *Carnivora* smaller populations had greater variation
380 in chromosome number than large populations (Jonika *et al.*, 2024). Another hypothesis for the
381 evolution of chromosome number is the minimum interaction theory, which postulates smaller
382 chromosomes are selected to reduce reciprocal translocation (Imai *et al.*, 1986). Under minimum
383 interaction theory, chromosome numbers are predicted to increase as more chromosomes are
384 needed to contain the genome. Exploring ecology and natural history in homosporous plants is
385 also another avenue to understand their distinct genome organization outside of meiotic drive. It
386 is well-established that the rate of molecular evolution is higher and genome size is smaller in
387 plants with shorter life cycles, compared to those with longer life cycles (Cavalier-Smith, 2005;
388 Smith and Donoghue, 2008). A correlation between the type of sporogenesis and nuclear genome
389 size has been made in angiosperms, where species that undergo disporic or tetrasporic
390 megasporogenesis have larger genomes than those with monosporic sporogenesis (Bharathan,
391 1996). There is also a correlation between vascular structure (i.e., the presence or absence of
392 tracheids) and genome size (Cavalier-Smith, 2005). Heterosporous ferns (Salviniales) and
393 *Selaginella* have tracheids and small genome sizes, but gymnosperms and the heterosporous
394 lycophyte *Isoetes* lack tracheids and have large genomes (Cavalier-Smith, 1978; Leitch *et al.*,
395 2005). Comparing life history and genome traits in a phylogenetic context could help tease apart
396 complex interactions between these variables.

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398 The proliferation of a selfish element is key in meiotic drive systems, yet the mechanisms by
399 which this occurs are incredibly varied (Burt and Trivers, 2009; Lindholm *et al.*, 2016; Saupe
400 and Johannesson, 2022). Therefore, if meiotic drive occurs in pteridophytes it is probably distinct
401 from drive in angiosperms, fungi, or animals. The absence of meiotic drive would help explain
402 large and stable genomes, uniform chromosome sizes, relatively static chromosome numbers
403 following WGDs, as well as the current challenges with assembling centromeres in fern and
404 lycophyte genomes. Although almost certainly only one piece of the puzzle, researching meiotic
405 drive in homosporous plants is important to broaden our understanding of the unique genomes of
406 this lineage.

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410 **Acknowledgments**

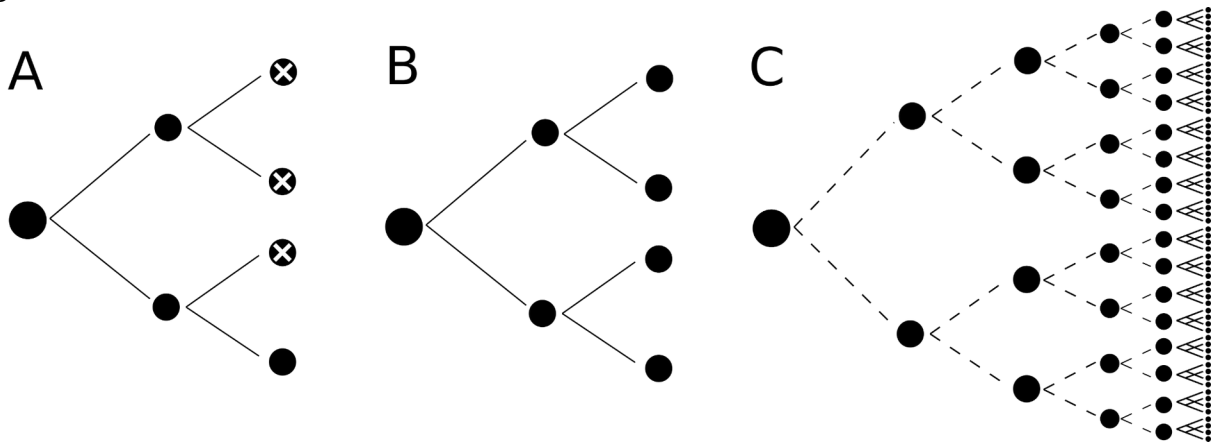
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416 **Table 1.** Chromosome morphology for homosporous and heterosporous pteridophytes.

Taxon	Reproductive mode	Chromosome morphology	Citation
<i>Claytosmunda claytoniana</i>	homosporous	acrocentric, very few metacentric	(Tatuno and Yoshida, 1967)
<i>Osmundastrum cinnamomeum</i>	homosporous	acrocentric, very few metacentric	(Tatuno and Yoshida, 1967)
<i>Plenasium banksiaefolium</i>	homosporous	acrocentric, very few metacentric	(Tatuno and Yoshida, 1967)
<i>Hymenophyllum barbatum</i>	homosporous	acrocentric, some metacentric	(Tatuno and Takei, 1969)
<i>Asplenium incisum</i>	homosporous	acrocentric, very few metacentric	(Tatuno and Kawakami, 1969)
<i>Pteris</i>	homosporous	acrocentric	(Kawakami, 1971)
<i>Regnellidium diphyllum</i>	heterosporous	Submetacentric and subtelo-centric	(Kuriachan, 1994)
<i>Selaginella</i>	heterosporous	Metacentric, telocentric	(Takamiya, 1993; Marcon, Barros and Guerra, 2005)
<i>Danaea</i>	homosporous	submetacentric	(Benko-Iseppon, Rodrigues and da Fonsêca, 2000)
<i>Acrostichum</i>	homosporous	subtelocentric	(Marcon, Barros and Guerra, 2003)
<i>Doryopteris triphylla</i>	homosporous	telocentric	(Neira <i>et al.</i> , 2017)

417 **Figures**

418 **Figure 1.** Examples of different types of meiosis. In each panel, the far left circle depicts the
 419 sporocyte, and succeeding divisions proceeding to the right. Solid lines indicate meiosis and
 420 dotted lines indicate mitosis. A) Heterosporous female meiosis, where only one meiotic product
 421 survives (can be on either top or bottom) and the remaining three polar bodies die; B)
 422 Heterosporous male meiosis, where all meiotic products survive; C) Leptosporangiate
 423 sporogenesis where 64 spores are generated through four rounds of mitosis and one round of
 424 meiosis.
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448 **Glossary**

449 **Transmission ratio distortion** - unequal inheritance of parental alleles in the offspring
450 population

451 **Meiotic drive** - disproportional inheritance of alleles, chromosomes, or other genome structures
452 during asymmetrical meiosis.

453 **Spore drive** - typically occurring in fungi, one haplotype will kill the alternative haplotype.

454 **Male drive** - biased transmission which occurs during or after male meiosis. This typically
455 involves an allele that kills certain sperm cells.

456 **Sporogenesis** - the generation of a spore cell by meiosis (in heterosporous plants) or mitosis (in
457 homosporous plants)

458 **Megasporogenesis** - creation of spores that will develop into a female gametophyte
459 (megagametophyte)

460 **Microsporogenesis** - creation of spores that will develop into a male gametophyte
461 (megagametophyte)

462 **Homosporous** - an organism that produces one type of spore. This spore develops into a
463 gametophyte which can produce male and/or female gametes.

464 **Heterosporous** - an organism that produces two types of spores. These are the mega- and
465 microspores, which develop into gametophytes capable of producing eggs or sperm, respectively.

466 **Pteridophyte** - a plant classified as a fern or lycophyte. This group is paraphyletic but is
467 important functionally because all taxa are seedless vascular plants.

468 **Leptosporangiate fern** - ferns that produce sporangia with a long stalk that arise from a single
469 epidermal cell. Their spore production proceeds from a single spore mother cell through four
470 rounds of mitosis and one round of meiosis to form 64 spores.

471 **Eusporangiate fern** - ferns that produce sporangia with a short or no stalk that arise from
472 several epidermal cells. Hundreds to thousands of spores are produced in each sporangium via
473 meiosis.

474 **Metacentric** - a chromosome with the centromere positioned in the middle, with both arms
475 being the same length.

476 **Acrocentric** - a chromosome with the centromere close to one end, with one arm being much
477 longer than the other.

478 **Telocentric** - a chromosome where the centromere is at one end, causing there to be effectively
479 only one arm rather than two.

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