

Mating system and the evolution of recombination rates in seed plants

| | |
|------------------|--|
| Journal: | <i>Journal of Evolutionary Biology</i> |
| Manuscript ID | Draft |
| Manuscript Type: | Research Article |
| Keywords: | Plants, Recombination, Life history traits, Selfing, Longevity, Genetic map length |
| | |

SCHOLARONE™
Manuscripts

MATING SYSTEM AND THE EVOLUTION OF RECOMBINATION RATES IN SEED PLANTS

July 17, 2024

Abstract

Meiotic recombination is a central mechanism underlying sexual reproduction among eukaryotes. In many species, the recombination rate is strongly constrained by chromosome size, as the number of crossovers per chromosome generally ranges between one and no more than a few (around three to five). Yet, recombination rates are variable and can evolve between species, in particular when they differ in their reproductive system. According to theory, indirect selection towards higher recombination rates is expected to be stronger in populations with a non-random mating system, such as selfing species compared to randomly mating species. To test for the impact of the mating system on the evolution of recombination rates, we leveraged a dataset with genetic maps, genome sizes, chromosome numbers and life history traits in 200 seed plant species. After controlling for the chromosome size effect, the phylogeny and map quality, we found a joint positive effect of the mating system and longevity on recombination rates, with higher recombination rates in mixed-mating and selfing species. We also found that mixed-mating and selfing species had a significantly higher number of crossovers in larger chromosomes than outcrossing species, suggesting selection for relaxed crossover interference in these former species. Our results point to the mating system as an important factor potentially shaping the evolution of recombination despite the strong constraints imposed on the number of crossovers per chromosome.

Keywords: Plants, Recombination, Life history traits, Selfing, Longevity, Genetic map length

MATING SYSTEM AND THE EVOLUTION OF RECOMBINATION RATES IN SEED PLANTS

20 Introduction

21 Meiotic crossovers occur in all sexually reproducing eukaryotes, and lead to the reciprocal exchange of genetic
22 material between homologous chromosomes. The average number of crossovers per chromosome is typically
23 comprised between one and three in most species (Stapley et al. 2017; Fernandes et al. 2018; Brazier and
24 Glémén 2022), which is usually thought to reflect mechanical constraints acting on chromosomal segregation
25 during the first meiotic division: at least one crossover per bivalent seems required to ensure the proper
26 disjunction of homologs, while too many crossovers may possibly impair correct segregation (Koehler et al.
27 1996 – but see Fernandes et al. 2018). However, genetic variation for the number and position of crossovers
28 along chromosomes can be observed at different scales: between broad taxa, between closely related species,
29 between populations of the same species and between individuals from the same population (e.g. Stapley
30 et al. 2017; Dumont, Broman, and Bret A Payseur 2009; Johnston et al. 2016; Brazier and Glémén 2022;
31 Peñalba et al. 2020; Samuk et al. 2020). Besides their effect on chromosomal segregation, crossovers also
32 lead to genetic recombination, eroding linkage disequilibria (LD) among loci. While an important amount
33 of theoretical work has explored the conditions under which breaking LD may provide a selective advantage
34 (Lenormand and Sarah P Otto n.d.; Agrawal 2006; Sarah P. Otto 2009), assessing whether such indirect
35 benefits may explain patterns of recombination variation between populations and species remains difficult
36 (Dapper and Bret A. Payseur 2017; Ritz, Noor, and Singh 2017).

37 Theoretical models have identified different mechanisms generating indirect selection on recombination
38 rates, corresponding to different possible sources of LD among selected loci. Selection may generate LD in the
39 presence of epistatic interactions among loci, since fitter combinations of alleles tend to increase in frequency.
40 When selection remains constant in space and time, breaking these fitter allelic combinations decreases the
41 mean fitness of offspring ("recombination load"). Nevertheless, increased recombination may be favored
42 when LD impedes adaptation, which is the case when LD is negative (meaning that beneficial alleles tend
43 to be associated with deleterious alleles at other loci). Epistatic interactions generate negative LD when the
44 combined effect of beneficial alleles at different loci is decreased compared to the multiplicative expectation,
45 a situation described as negative epistasis. However, negative epistasis can favor high recombination rates
46 only when it is sufficiently weak, so that the recombination load is not too strong (N. H. Barton 1995).
47 In finite populations, an additional source of negative LD is selective interference (also known as the Hill-
48 Robertson effect; Hill and Robertson 1966; Felsenstein 1974): indeed, while the stochasticity of mutation
49 and reproduction in finite populations may generate either positive or negative LD, situations where LD
50 is negative tend to persist longer, favoring increased recombination rates (Felsenstein and Yokoyama 1976;
51 Nicholas H Barton and Sarah P Otto 2005; Keightley and Sarah P Otto 2006; Hartfield, Sarah P Otto, and
52 Keightley 2010; Roze 2021; Bergman, Sarah P Otto, and Feldman 1995).

MATING SYSTEM AND THE EVOLUTION OF RECOMBINATION RATES IN SEED PLANTS

53 A possible approach to assess whether recombination rate variation may be explained by such indirect
54 selective forces could consist in testing to what extent populations or species that differ in some biological or
55 ecological characteristics present systematic differences in recombination rates, in a way that would corre-
56 spond to theoretical predictions. For example, the models cited above predict that recombination rates may
57 be higher in populations that have undergone recent episodes of directional selection, either due to nega-
58 tive epistasis or to selective interference between linked beneficial mutations (favoring genetic modifiers that
59 increase recombination). While this prediction is corroborated by the fact that increased recombination is
60 observed more often than decreased recombination after artificial selection experiments (Table 1 in Sarah P.
61 Otto and Nick H. Barton 2001), assessing whether a natural population has recently undergone directional
62 selection is generally difficult.

63 Interestingly, the mating system of organisms can vary greatly among species (sometimes among popula-
64 tions from the same species), and may have strong effects on indirect selection on recombination. In partic-
65 ular, self-fertilization is a common reproductive mode in hermaphroditic species, about 20% of Angiosperm
66 species being predominantly selfing (Barrett 2002). The effect of selfing on the evolution of recombination
67 stems both from the increase in homozygosity of individuals caused by inbreeding, and from correlations
68 in homozygosity among loci that are generated as long as some level of outcrossing is maintained in the
69 population. As shown by the recent analysis of Stetsenko and Roze (2022) focusing on the effect of deleteri-
70 ous mutations, the decreased efficiency of recombination caused by homozygosity has two contrasted effects
71 on the evolution of a recombination modifier: (1) it decreases indirect selection by reducing the effect of
72 the modifier on effective recombination rates (indirect selection on recombination vanishing under complete
73 selfing); (2) it increases the magnitude of LD, enhancing indirect selection on recombination. As a result,
74 selection for recombination (either due to selective interference or to negative epistasis) is often predicted
75 to be maximal for selfing rates slightly below one. Additionally, and as shown previously by Roze and
76 Lenormand (2005), correlations in homozygosity among loci generated by partial selfing may strongly favor
77 recombination in the presence of a particular form of negative epistasis (negative dominance-by-dominance
78 epistasis). In that case, selection for recombination may be maximized for moderate selfing rates (see Figure
79 5c in Stetsenko and Roze 2022).

80 These theoretical results thus show that self-fertilization should generally enhance indirect selection for
81 recombination, except under complete selfing. Do partially selfing species exhibit higher recombination
82 rates than outcrossing ones? Cytological studies from different genera of Angiosperms suggest that it may
83 indeed be the case, as self-pollinating species tend to show higher numbers of chiasmata per bivalent than
84 outcrossing species from the same genus (Roze and Lenormand 2005; Ross-Ibarra 2007). This positive
85 correlation was found to be significant across all species, as well as within each genus (Roze and Lenormand
86 2005). Furthermore, comparisons of the genetic maps of the highly selfing *Arabidopsis thaliana* and of its
87 outcrossing relative *Arabidopsis lyrata* also show higher recombination rates in *A. thaliana* (Kuittinen et al.

MATING SYSTEM AND THE EVOLUTION OF RECOMBINATION RATES IN SEED PLANTS

88 2004; Hansson et al. 2006; Kawabe et al. 2006). Since then, the number of species for which genetic maps
89 are available keeps increasing rapidly, opening new possibilities to test whether recombination rates tend to
90 correlate with certain biological traits of organisms.

91 In this article, we present an analysis of a dataset consisting of about 200 plant species for which genome
92 size, number of chromosomes and genetic map length are available. Species were categorized based on their
93 mating system and other life-history traits. The results show that species classified as mixed mating or selfing
94 tend to have higher chromosome map lengths than outcrossing species, thus confirming the positive effect
95 of selfing on recombination found in previous studies. Furthermore, mixed-mating and selfing species with
96 larger chromosomes tend to have higher numbers of crossovers per chromosome than species with smaller
97 chromosomes, while this trend is not observed in outcrossing species. Among the other traits tested, only
98 longevity showed a significant association with recombination, with medium-lived species presenting lower
99 recombination rates than short-lived or long-lived species.

100 Materials and Methods

101 Recombination dataset

102 The original dataset with total genetic map length (cM), number of chromosomes and genome physical
103 size (Mb) was retrieved from Stapley et al. (2017). We added genetic map length and genome sizes for
104 24 new species to the 184 species already in Stapley et al. (2017). This final dataset contained a list of
105 208 species. We returned to original publications to retrieve the exact ploidy level, the number of markers
106 on the final map and the number of progeny. In order to properly control for the chromosome size effect
107 already assessed in this data (Stapley et al. 2017), we also defined new genomic variables, such as the average
108 chromosome genetic map length (cM/chromosome) and the residuals of the linear regression of recombination
109 rates (cM/Mb) as a function of average chromosome size (Mb).

110 Life History Traits

111 Based on a literature search, we gathered Life History Traits data for every species (Table S1). We first
112 retrieved mating system information, using the coarse classification outcrossing / mixed / selfing, when
113 directly given in the literature. To complete the characterization of the mating system, we collected other
114 reproductive traits: sexual system (andromonoecy, dioecy, gynodioecy, hermaphroditism, monoecy), self
115 incompatibility (SI) status (self-incompatible and self-incompatible) and outcrossing rate, which we used to
116 characterize the mating system: dioecious and SI species were classified as outcrossing; based on outcrossing
117 rate (t) we classified species as outcrossing for $t > 0.80$, mixed for $0.2 < t < 0.8$ and selfing for $t < 0.2$. We
118 added the life form (herb, liana, shrub, tree, vine) and the life span (annual, biannual, perennial), which are
119 associated with the mating system. In addition it has been proposed that long life-span should select more

MATING SYSTEM AND THE EVOLUTION OF RECOMBINATION RATES IN SEED PLANTS

recombination (Burt and Bell 1987), although the underlying mechanism is unclear. As some categories were represented by only a few species and some traits were correlated, we defined three categories reflecting longevity: annual species, perennial non-woody species (herbs and vines), and woody perennials (trees, shrubs and lianas). We also included the cultivation status (cultivated, wild), as domestication has been also proposed to select higher recombination rate because of recent and prolonged episodes of directional selection (Ross-Ibarra 2007; Burt and Bell 1987). Finally, we categorized species as diploid (ploidy level = 2) or polyploid (ploidy level > 2). We added more phylogenetic levels (class, family) and we grouped species in large phylogenetic families (Superasterids, Lilioids + Alismatids Superrosids, Commelinids, Magnoliids, Basal eudicots, Conifers). The full dataset is available as Table S1.

129 Phylogenetic signal

We used the 'phytools' R package to manipulate phylogenetic tree data and to statistically test for a phylogenetic signal (Revell 2024). The phylogenetic time-calibrated supertree used for the comparative phylogenetic dataset was retrieved from Smith and Brown (Smith and Brown 2018). Tip labels were curated to remove subspecies and cultivar annotations and one tip per species was retained. Species missing in the tree were assigned randomly to a sister species of the same genus. The tree was forced to be ultrametric. We computed two phylogenetic signal metrics, Blomberg's K and Pagel's lambda. We also fitted three evolution models (Brownian Motion, Ornstein-Ulhenbeck and Early Burst) to the distribution of recombination rates, chromosome genetic map length and the residuals of the regression presented above.

138 Statistical analyses

All statistical analyses were performed on R version 4.3.3 (R Core Team 2022). Linear regressions were performed with the R base function 'lm'. We used the 'caper' R package to fit Phylogenetic Generalized Linear models with the function 'pgls' (Orme et al. 2018). We performed a forward stepwise model selection based on Anova and AIC/BIC criterion. We tested the significance of predictors with the 'anova' R function. The validity of the models was evaluated by visually checking the normality of the residuals (Q-Q plot and histogram), the homoscedasticity of the residuals, and the observed vs. fitted values and the residuals vs. fitted values to detect correlated errors.

146 Results

147 Dataset

After removing species with no information on the mating system, we kept 200 plant species, including 190 angiosperms and 10 gymnosperms. The map quality was globally good with 20 species with more than 200 markers (18 maps without information on the number of markers). The minimal number was 82 markers and

MATING SYSTEM AND THE EVOLUTION OF RECOMBINATION RATES IN SEED PLANTS

151 the highest number was 64,263 markers, with a median number of 998 markers. The number of progenies
152 ranged from 43 to 3,480, with a median number of 149 progenies. We had a sampling covering the whole
153 angiosperm phylogeny plus a few gymnosperms (Figure S1). A few families had a lot of species (e.g. Poaceae,
154 Fabaceae, Rosaceae and Brassicaceae had more than 10 species), but a majority of species was the single
155 representative of their family.

156 Among the 200 species, the number of chromosomes ranged from 5 to 90, with 170 diploid and 30
157 polyploids. We had 45 selfing species, 37 mixed mating species and 118 outcrossing species (including 21
158 dioecious species). Seventy-four species were long-lived (woody perennial), 47 were medium-lived (non-
159 woody perennial) and 79 short-lived species (annual). We had 49 self-compatible species (SC) and 56 self-
160 incompatible (SI). We had 109 cultivated and 91 wild species, though some species can be both cultivated
161 and wild.

162 Control for the strong chromosome size effect

163 Based on previous studies (Brazier and Glémén 2022; Haenel et al. 2018) we postulated that chromosome size
164 was the main determinant of recombination rates. Indeed we confirmed the strong negative correlation (log-
165 log relationship) between chromosome size and recombination rate in our dataset (Figure 1A). Commelinids
166 and conifers had amongst the largest chromosome size, while other plant species were on a lower range
167 of chromosome size. The average genetic map length was significantly yet only weakly correlated with
168 chromosome size (Spearman's $\rho = 0.21$, $p = 0.002$, Figure 1B) and not with the number of chromosomes
169 (Spearman's $\rho = -0.05$, $p = 0.49$, Figure S2). The distribution of chromosome genetic map length was
170 fat-tailed with a few chromosomes larger than 200 cM (range 44-347 cM/chromosome, Figure 1C). Finally,
171 average chromosome map lengths varied homogeneously among phylogenetic families, except for Lilioids +
172 Alismatids and basal Eudicots counting only a few species (Figure 1D, compare with recombination rates
173 (cM/Mb) in Figure 2 in Stapley et al. 2017). Overall our results suggest that the absolute number of COs
174 per chromosome (i.e. average chromosome genetic map length) are susceptible to evolve in a reasonable
175 range independently of chromosome size.

176 Weak phylogenetic signal

177 After controlling for the chromosome size effect, we also investigated how recombination rates evolved
178 amongst the plant phylogeny. In order to test the significance and strength of the phylogenetic signal,
179 we estimated two phylogenetic signal metrics (Blomberg's K and Pagel's lambda) and fitted three competing
180 phylogenetic models (Brownian Motion, Ornstein-Uhlenbeck and Early-burst) to the continuous distribu-
181 tion of chromosome average genetic length and the residuals of the regression of recombination rates as
182 a function of average chromosome size (Table 1). Blomberg's K were not significantly different from zero
183 while Pagel's Lambda was around 0.5, both indicating a weak phylogenetic signal. Based on the maximum

MATING SYSTEM AND THE EVOLUTION OF RECOMBINATION RATES IN SEED PLANTS

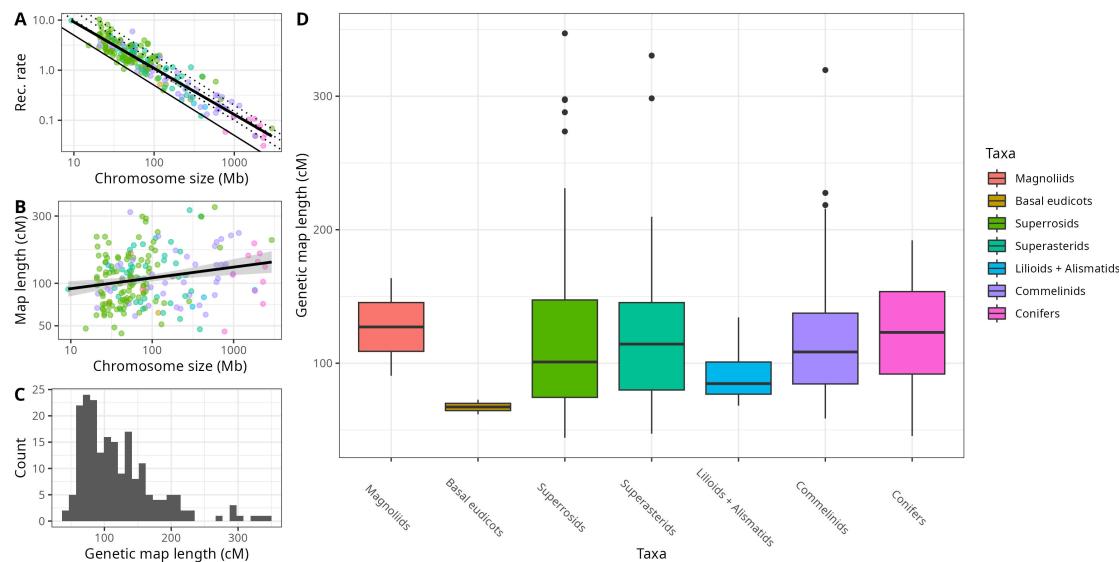


Figure 1: Distribution of recombination rates and genetic map length ($n = 200$ species). (A) Average chromosome size (Mb, log scale) is negatively correlated with recombination rates (cM/Mb, log scale). (B) Average genetic map length (cM) is weakly correlated to average chromosome size (Mb). (C) Density of chromosome genetic map length. (D) Boxplots of chromosome genetic map length per phylogenetic family. Compare with recombination rates (cM/Mb) in Figure 2 in Stapley et al. (2017).

184 Log-Likelihood criterion, the Ornstein-Uhlenbeck phylogenetic model was always preferred, suggesting that
 185 the recombination rate evolved under a constrained range.

Table 1: Phylogenetic signal for the two proxies of recombination rates. Blomberg's K and Pagel's Lambda (and their respective p-value) and the Log-Likelihood of the three phylogenetic models (Brownian Motion, Ornstein-Uhlenbeck and Early-burst, respectively). The best model according to the Log-Likelihood criterion is in bold.

| Trait | K | K p-value | λ | λ p-value | Log-lik BM | Log-lik OU | Log-lik EB |
|--------------------|------|-----------|-----------|-------------------|------------|-----------------|------------|
| Genetic map length | 0.09 | 0.117 | 0.46 | 0.01 | -1155.09 | -1091.53 | -1155.09 |
| Residuals | 0.1 | 0.032 | 0.47 | 0.01 | -173.16 | -110.77 | -173.16 |

186 Joint effect of the mating system and longevity

187 Based on ANOVAs and AIC/BIC criterion, we run a step forward model selection for Linear Regression
 188 and Phylogenetic Generalized Least Squares (Table S2). For both average chromosome map length and the
 189 residuals, the two significant predictors were always the mating system first, then longevity based on ANOVA
 190 ($p < 0.05$) and AIC (lower AIC value). However these effects were weak (Figure S3, S4), as the null model
 191 was always preferred by the BIC criterion. The effect of other life history traits was weak or null. The more
 192 complex models including both mating system and longevity were significantly better than the two models
 193 with a single predictor, except for the Linear Model with the average chromosome map length as response
 194 variable ($df = 2$, $F = 1.9095$, $p = 0.151$). The effect was stronger when the phylogeny was accounted for
 195 ($p = 0.035$ for 'lm' vs. $p = 0.008$ for 'pgls'). Overall, we observed a joint effect of the mating system and
 196 longevity on proxies of recombination rates (Figure 2, S5).

MATING SYSTEM AND THE EVOLUTION OF RECOMBINATION RATES IN SEED PLANTS

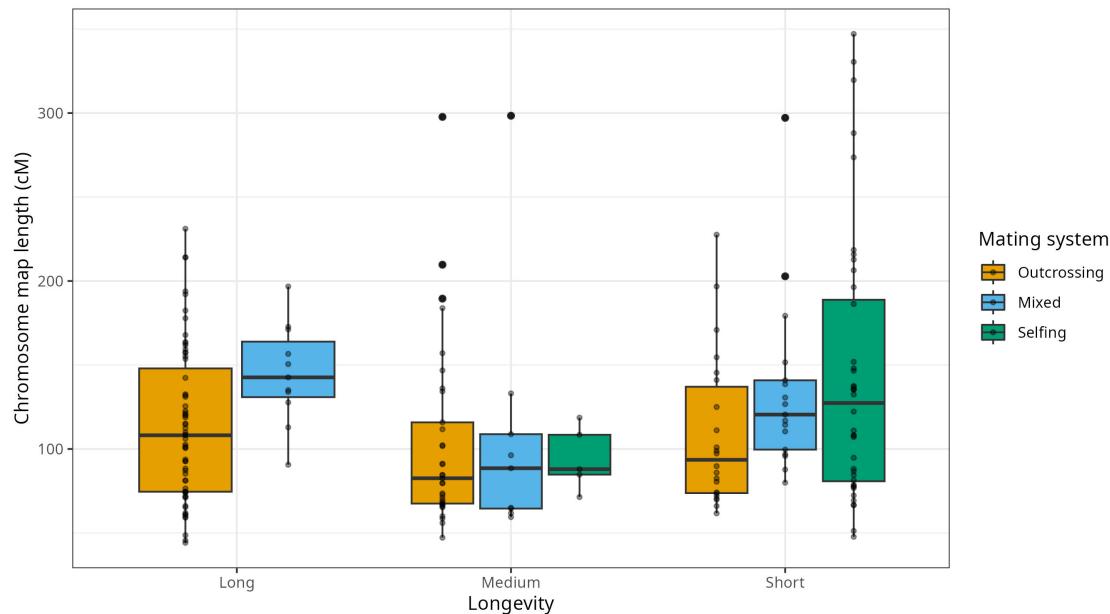


Figure 2: Recombination rates depend on the mating system and longevity. (A) The combined effect of the mating system and longevity on the average chromosome genetic map length. Each point is a species ($n = 200$ species).

Table 2: Model fit and parameter estimates of the best model (PGLS residuals = mating system + longevity, $\lambda = 0.480$, F-statistic = 4.069, df = 195, p = 0.0034, Adjusted R-squared = 0.0581). Significance codes: 0 *** 0.001 ** 0.01 * 0.05 . 0.1 ' 1.

| Response | Df | p | Parameter | Estimate | Std. Error | t | p |
|---------------|----|-----------|------------------|----------|------------|---------|----------|
| Mating system | 2 | 0.0078 ** | (Intercept) | -0.0789 | 0.2145 | -0.368 | 0.7133 |
| | | | Mixed-mating | 0.1805 | 0.0824 | 2.1898 | 0.0297 * |
| | | | Selfing | 0.1857 | 0.0891 | 2.0839 | 0.0385 * |
| Longevity | 2 | 0.0443 * | Medium longevity | -0.2201 | 0.0941 | -2.3395 | 0.0203 * |
| | | | Short longevity | -0.0741 | 0.0994 | -0.7461 | 0.4565 |

197 As a final model we selected the Phylogenetic Generalized Least Squares with the residuals as a response
 198 variable ($\lambda = 0.480$, F-statistic = 4.069, df = 195, p = 0.003433, Adjusted R-squared = 0.0581, Table
 199 2) where selfing and mixed mating species had significantly higher recombination than outcrossing species
 200 whereas medium-lived species had significantly lower recombination (Table 2). Both the mating system and
 201 longevity were significant in the ANOVA (df = 2, Sum of Squares = 0.0076, Mean Squares = 0.0038, F =
 202 4.9710, p = 0.0078, and df = 2, Sum of Squares = 0.0048, Mean Squares = 0.0024, F = 3.1666, p = 0.0443,
 203 respectively). The validity of the model was successfully assessed with diagnostic plots. The model with the
 204 average genetic map length yielded similar results.

205 We observed the same results when we plotted the joint effect of the mating system and longevity on
 206 recombination rates (Figure 2, S5). Outcrossing species had on average lower recombination rates for the
 207 three longevity categories though the difference was less clear in medium-lived species. On average, selfing
 208 and mixed mating system species had higher recombination rates. There was no selfing species in long-lived

209 species. Medium-lived species had lower recombination rates on average, with globally a maximum of two
 210 COs per chromosome (i.e. 100 cM) while long and short-lived generally exceeded two COs.

211 **Selection for higher recombination varies among phylogenetic families**

212 We investigated if there could be a family-specific effect of the mating system or longevity. Our phylogenetic
 213 sampling was sparse across the plant phylogeny but we managed to subset three independent families with
 214 at least ten species each and two species for each mating system. The family-specific selfing effect was not
 215 clear among the three families (Figure 3A). The increased recombination rate in selfing species was clear in
 216 Poaceae but weak or even reversed in Brassicaceae and Fabaceae. We observed only a few mixed-mating
 217 species. For Fabaceae and Poaceae we observed a clear short-lived effect with increased recombination rates
 218 (Figure 3B). We did not have enough medium-lived species to conclude for Brassicaceae. We did not have
 219 enough samples to investigate the joint effect or to perform a proper statistical analysis.

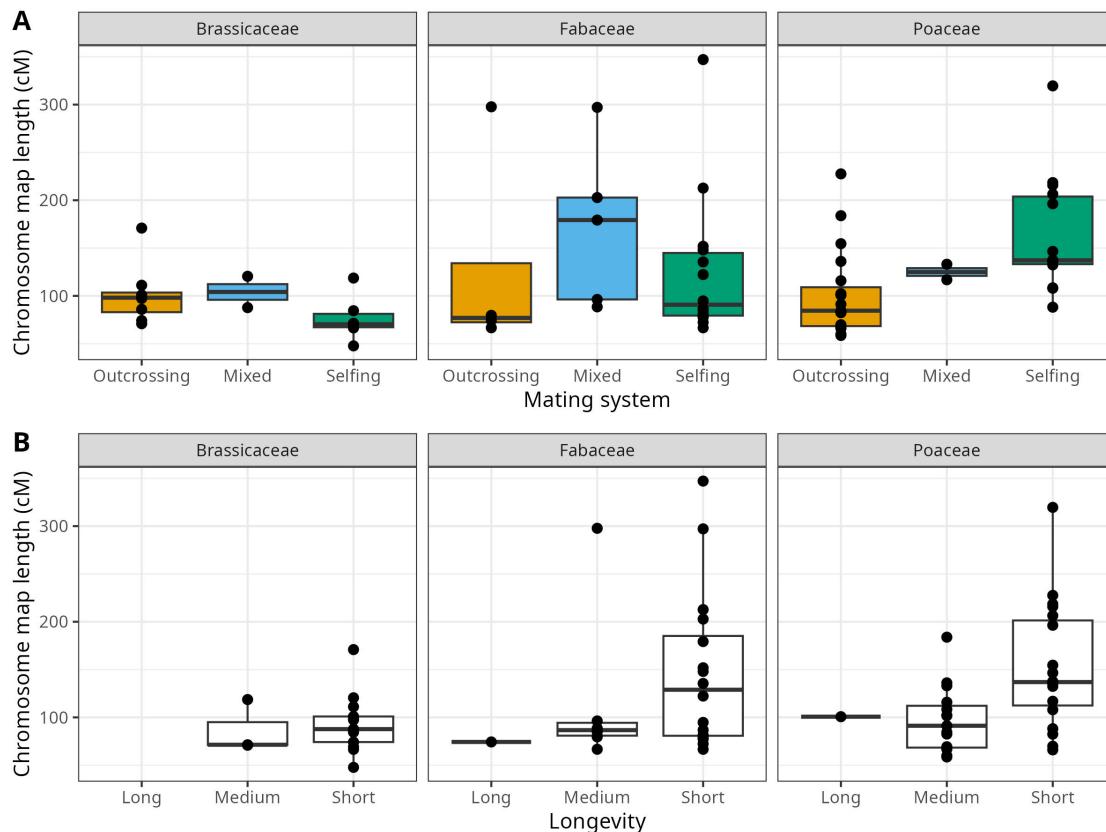


Figure 3: Chromosome genetic map length as a function of the mating system (same colors as in Figure 2)
 or longevity in three different phylogenetic families ($n = 91$ species). Each point is a species.

MATING SYSTEM AND THE EVOLUTION OF RECOMBINATION RATES IN SEED PLANTS

220 Selection towards extra crossovers in selfing and mixed mating species

221 We analyzed the dataset slightly differently by considering that there is one mandatory CO per chromosome
 222 and then the additional number of CO can increase or not with chromosome size, depending on the strength
 223 of CO interference. If CO interference is limited, larger chromosomes should have on average a higher
 224 number of COs. On the contrary, if interference is the limiting factor, evolution towards more COs on larger
 225 chromosomes should be prevented. We tested this idea by analyzing separately for each mating system the
 226 slope of the average chromosome genetic map length as a function of chromosome physical size (Figure 4).
 227 Species with larger chromosomes seemed to have more COs per chromosome in selfing and mixed-mating
 228 species but not in outcrossing species. The intercept was similar among the three mating systems (Figure 4).
 229 We tested the significance of this effect with a PGLS model with an interaction term between the chromosome
 230 size and the mating system. We also used the number of chromosomes as a covariate, since the Genome
 231 Wide Recombination Rate can be increased by increasing the total number of chromosomes (chromosome
 232 genetic map length = chromosome size*mating system + number of chromosomes, $\lambda = 0.468$, F-statistic =
 233 3.732, df = 193, p = 0.0016, Adjusted R-squared = 0.0761). There was a trend for the interaction between
 234 chromosome size and the mating system (p = 0.056), as well as a trend for the number of chromosomes (p
 235 = 0.071; see Table S3 for model fit and parameters). While there was a slight trend for the chromosomal
 236 genetic map length to increase with chromosome size in selfing species (interaction chromosome size:selfing,
 237 coefficient = 0.069, std. error = 0.0359, t = 1.9229, p = 0.056), the number of chromosomes had a negative
 238 effect on the chromosomal genetic map length (coefficient = -0.946, std. error = 0.5213, t = -1.8147, p =
 239 0.0711).

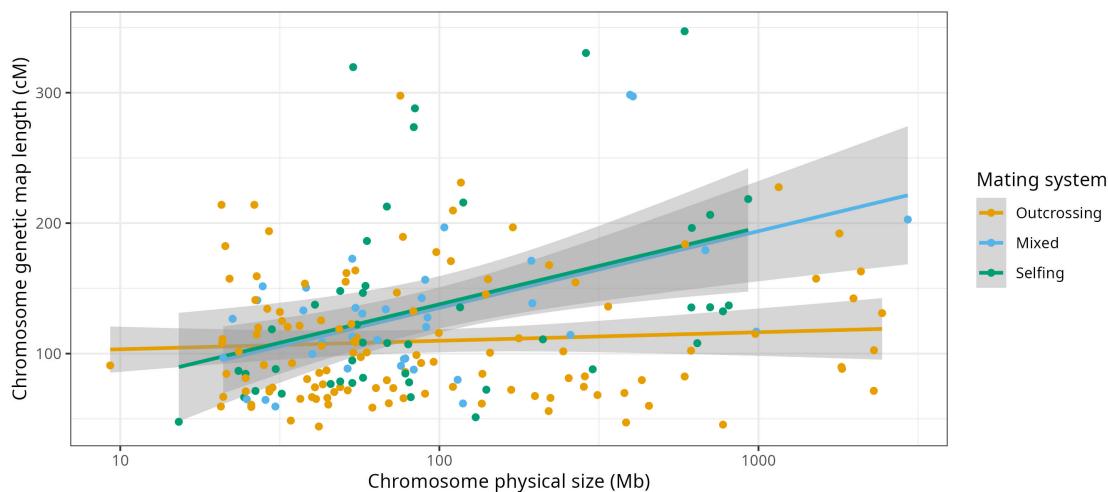


Figure 4: Selection towards higher CO rates in larger chromosomes for selfing and mixed-mating species (n = 118, 37 and 45 for outcrossing, mixed-mating and selfing species, respectively). The linear regression line and its 95% confidence interval for each mating system were estimated with the ggplot2 'geom_smooth' function (Wickham 2016).

240 **The effect is robust to map quality**

241 In order to control if the mating system and longevity effect were robust to differences in map quality among
242 species, we tested the influence of marker density and number of progenies on the significance of the results.
243 We added either marker density or number of progenies to the Phylogenetic Generalized Least Squares model
244 with the residuals as a response variable. Marker density had a significant positive effect on recombination
245 rates ($p = 0.028035$, see parameter estimates in Table S4) but it did not change the significance of selfing
246 and medium-lived species ($p = 0.0469$ and 0.0318 , respectively) while mixed-mating species remained as a
247 trend ($p = 0.0681$). Progeny number was not significant at all ($p = 0.5988$).

248 **Discussion**

249 In order to test for an effect of the mating system on the evolution of recombination rates, we compared
250 genetic maps in 200 plant species differing by their mating system and other life-history traits. We found
251 a joint positive effect of the mating system and longevity on recombination rates with variation across
252 phylogenetic families. We also found that mixed-mating and selfing species had a significantly higher number
253 of crossovers in larger chromosomes compared to outcrossing species. These results have implications for the
254 evolution of recombination given the constraints imposed on the number of crossovers per chromosome.

255 **Higher CO rates in selfing and mixed-mating species**

256 Among life history traits, the mating system has the main significant effect on recombination rates after
257 controlling for the strong chromosome size effect. Indeed, chromosome size is a major determinant of re-
258 combination rates in Eukaryotes (Brazier and Glémin 2022; Stapley et al. 2017; Haenel et al. 2018) but
259 our results show that the average chromosome genetic map length (i.e. the average number of COs) is only
260 weakly proportional to chromosome size. The average number of COs per chromosome varies between one
261 and four for most species, with some species exceeding six COs per chromosome (300 cM). Despite con-
262 straints on the number of COs per chromosome, as supported by the choice of the OU model (Table 1),
263 there is still possible variation upon which selection can act.

264 Selfing and mixed-mating species have higher recombination rates on average than outcrossing species,
265 thus supporting the theoretical predictions of a positive effect of selfing on recombination(Roze and Lenor-
266 mand 2005; Stetsenko and Roze 2022). Under realistic parameter values, Stetsenko and Roze (2022) found
267 that selfing increases selection for recombination to compensate for the decreased efficacy of recombination.
268 However, they predict that selection for recombination vanishes for selfing rates approaching one as, in this
269 case, homozygosity is too high for recombination to have an effect. This results in a non-monotonic increase
270 in recombination with selfing, with the selfing rate maximizing selection for recombination depending on pa-
271 rameter values, but typically being quite high. Our data are not precise enough to directly assess the nature

MATING SYSTEM AND THE EVOLUTION OF RECOMBINATION RATES IN SEED PLANTS

272 of the relationship between selfing rate and recombination rate. However, we observed the main difference
273 between outcrossing and mixed-mating + selfing, with no significant difference between mixed mating and
274 selfing, which is in agreement with the non-linear relationship predicted by theory assuming particular forms
275 of epistasis between deleterious mutations.

276 Our study also matches well with previous empirical results. Cytological measures of the number of chiasmata per bivalent per meiosis in several plant genera tend to confirm this overall increase of recombination
277 with selfing (reviewed in Roze and Lenormand 2005 and Ross-Ibarra 2007). This positive correlation was
278 found to be significant across all species as well as within genera (Roze and Lenormand 2005). However,
279 chiasma frequency only represents an indirect measure of the genome-wide recombination rate and is only
280 available in a dozen genera. Similar results were found from genetic maps, pointing at higher recombina-
281 tion rates in the highly selfing *Arabidopsis thaliana* compared to its outcrossing relative *Arabidopsis lyrata*
282 (Hansson et al. 2006; Kawabe et al. 2006; Kuittinen et al. 2004), but it was only in a single pair of species.
283

284 We observed a significant joint effect of the mating system and longevity. Recombination rates are similar
285 at the extreme life-spans, in short and long-lived species (annual and woody perennial, respectively), while
286 medium-lived species (perennial non-woody species such as herbs and vines) experience lower recombination
287 rates on average. Taking longevity into account reveals a stronger effect of the mating system in short-
288 and long-lived species than in medium-lived species (note that long-lived selfing species are exceedingly rare
289 and absent from our dataset). In mammals, Burt and Bell (Burt and Bell 1987) proposed that a long
290 life-span should select more recombination but the mechanism remains unclear. In plants, a meta-analysis
291 on chiasma frequencies found lower recombination in perennials than in annual species, but they did not
292 distinguish medium- and long-lived perennials and did not control for the mating system as we did (Koella
293 1993).

294 **Indirect evidence of reduced CO interference to increase the CO number**

295 The CO number per chromosome per meiosis is strongly constrained by CO assurance and interference
296 (Wang et al. 2015). While CO assurance guarantees at least one CO, the maximum number of COs is
297 strongly limited by CO interference, up to a maximum of four COs in most species (Brazier and Glémén 2022;
298 Stapley et al. 2017). This limited evolvability probably explains why the mating system and longevity have
299 a marginal effect that is significant only after controlling for the strong chromosome size effect. The proxies
300 of recombination rates have a weak phylogenetic signal and the Ornstein-Uhlenbeck model of evolution is
301 always preferred, suggesting stabilizing selection on the number of COs.

302 However indirect selection on the strength of CO interference might be a possible mechanism to allow
303 evolution towards a higher CO number, especially in non-random mating populations. The strength of CO
304 interference itself varies dramatically among species (Sarah P. Otto and Bret A. Payseur 2019) and CO
305 interference is thought to evolve in finite populations as a way to reduce selective interference among loci

MATING SYSTEM AND THE EVOLUTION OF RECOMBINATION RATES IN SEED PLANTS

306 (Nicholas H Barton and Sarah P Otto 2005; Keightley and Sarah P Otto 2006; Roze and Nick H Barton 2006).
307 Indeed we observe a higher number of COs per chromosome in mixed-mating and selfing species, particularly
308 in larger chromosomes, while this trend is not observed in outcrossing species. This suggests that the higher
309 number of COs in mixed-mating and selfing species may evolve through relaxed CO interference allowing
310 more COs to occur on the same chromosome. On the contrary, CO interference may have remained strong
311 in outcrossing species, limiting the CO number to its minimum independently of chromosome size.

312 One interesting question is whether one or two extra COs are sufficient to efficiently compensate for
313 the reduced efficiency of selection due to selfing. Considering that most of the genetic shuffling is done via
314 the independent assortment of chromosomes (inter-chromosomal shuffling), a more efficient way to increase
315 the recombination rate would be increasing the chromosome number to produce more COs on the whole
316 (Veller, Kleckner, and Nowak 2019). Selection for increased number of COs per chromosome, increased by
317 the effect of selfing, should thus be stronger in species with a small number of chromosomes. The number
318 of COs per chromosome can evolve more rapidly than the number of chromosomes, possibly on the same
319 timescale as selfing rates (Henderson and Bomblies 2021; Whitehead et al. 2018). It is thus more likely that
320 the number of chromosomes constrains the evolution of CO number rather than being the direct target of
321 selection for increased genetic shuffling. We found that at a chromosome level, the number of chromosomes
322 was negatively associated with the chromosome genetic map length, though not significantly. At a genome
323 wide level, Stapley et al. (2017) found a weak positive effect of chromosome number on the genome wide
324 recombination rate (cM/Mb) in plants, but not in animals and fungi.

325 **Strength and limitations of our dataset**

326 The effect of the mating system and longevity is moderate, most likely because it is biologically much
327 weaker than the dominant chromosome size effect. We were able to detect it by leveraging a large curated
328 dataset from Stapley et al. (2017) plus 24 new species with a sampling across seed plants (angiosperms and
329 gymnosperms). We also found that the results were robust to differences in map quality (approximated by
330 marker density and number of progeny).

331 However, our dataset remains limited to detect complex effects. The interaction between chromosome
332 size and the mating system is only a trend. We did not detect significant effects for other life-history traits,
333 despite strong expectations for some of them (e.g. cultivation status). There is multiple evidence of an effect
334 of domestication on recombination rates in plants (Ross-Ibarra 2007; Dreissig, Mascher, and Heckmann
335 2019; Fuentes et al. 2021; Schreiber et al. 2022). However, we were not able to distinguish cultivated and
336 domesticated species in our dataset and many species can be either strongly domesticated or wild relative
337 populations. For such traits, a pairwise sampling of closely related species/populations with contrasted life
338 history traits (wild vs. domesticated) should be more powerful than our large unstructured sampling. In
339 particular, comparing species with the same number of chromosomes and similar genome size would avoid

MATING SYSTEM AND THE EVOLUTION OF RECOMBINATION RATES IN SEED PLANTS

340 the strong confounding effect of chromosome size. It is likely that such an approach would also strengthen
341 the detection of the effect of the mating system.

342 It is difficult to empirically test theories on the evolution of recombination and comparative analyses are
343 a valuable approach as a first step to identify relevant factors. Despite the limitations discussed above, our
344 results point to the mating system as an important factor potentially shaping the evolution of recombination.
345 Further detailed studies of recombination patterns in species with contrasting selfing rates is a promising
346 approach to better understand the forces acting on the evolution of recombination and, in turn, the evolution
347 of selfing rates.

348 **Competing interests**

349 The authors declare no conflicts of interest.

350 **Data availability**

351 All scripts and data necessary to reproduce this study are available at the OSF repository
352 <https://osf.io/XXX>.

353 **References**

- 354 Agrawal, Aneil F. (2006). "Evolution of Sex: Why Do Organisms Shuffle Their Genotypes?" In: *Current*
355 *Biology* 16.17, R696–R704. doi: [10.1016/j.cub.2006.07.063](https://doi.org/10.1016/j.cub.2006.07.063).
- 356 Barrett, Spencer C. H. (2002). "The Evolution of Plant Sexual Diversity". In: *Nature Reviews Genetics* 3.4,
357 pp. 274–284. doi: [10.1038/nrg776](https://doi.org/10.1038/nrg776).
- 358 Barton, N. H. (1995). "A General Model for the Evolution of Recombination". In: *Genetical Research* 65.2,
359 pp. 123–144. doi: [10.1017/S0016672300033140](https://doi.org/10.1017/S0016672300033140).
- 360 Barton, Nicholas H and Sarah P Otto (2005). "Evolution of Recombination Due to Random Drift". In:
361 *Genetics* 169.4, pp. 2353–2370.
- 362 Bergman, Aviv, Sarah P Otto, and Marcus W Feldman (1995). "On the Evolution of Recombination in
363 Haploids and Diploids: I. Deterministic Models". In: *Complexity* 1.1, pp. 57–67.
- 364 Brazier, Thomas and Sylvain Glémén (2022). "Diversity and Determinants of Recombination Landscapes in
365 Flowering Plants". In: *PLOS Genetics* 18.8. Ed. by Ian R. Henderson, e1010141. doi: [10.1371/journal.pgen.1010141](https://doi.org/10.1371/journal.pgen.1010141).
- 367 Burt, Austin and Graham Bell (1987). "Mammalian Chiasma Frequencies as a Test of Two Theories of
368 Recombination". In: *Nature* 326.6115, pp. 803–805. doi: [10.1038/326803a0](https://doi.org/10.1038/326803a0).

MATING SYSTEM AND THE EVOLUTION OF RECOMBINATION RATES IN SEED PLANTS

- 369 Dapper, Amy L. and Bret A. Payseur (2017). "Connecting Theory and Data to Understand Recombination
370 Rate Evolution". In: *Philosophical Transactions of the Royal Society B: Biological Sciences* 372.1736,
371 p. 20160469. DOI: [10.1098/rstb.2016.0469](https://doi.org/10.1098/rstb.2016.0469).
- 372 Dreissig, Steven, Martin Mascher, and Stefan Heckmann (2019). "Variation in Recombination Rate Is Shaped
373 by Domestication and Environmental Conditions in Barley". In: *Molecular Biology and Evolution* 36.9.
374 Ed. by Michael Purugganan, pp. 2029–2039. DOI: [10.1093/molbev/msz141](https://doi.org/10.1093/molbev/msz141).
- 375 Dumont, Beth L, Karl W Broman, and Bret A Payseur (2009). "Variation in Genomic Recombination Rates
376 Among Heterogeneous Stock Mice". In: *Genetics* 182.4, pp. 1345–1349. DOI: [10.1534/genetics.109.105114](https://doi.org/10.1534/genetics.109.105114).
- 377 378 Felsenstein, Joseph (1974). "The Evolutionary Advantage of Recombination". In: *Genetics* 78.2, pp. 737–756.
379 DOI: [10.1093/genetics/78.2.737](https://doi.org/10.1093/genetics/78.2.737).
- 380 381 Felsenstein, Joseph and Shozo Yokoyama (1976). "The Evolutionary Advantage of Recombination. II. Indi-
382 vidual Selection for Recombination". In: *Genetics* 83.4, pp. 845–859.
- 383 Fernandes, Joiselle Blanche et al. (2018). "Unleashing Meiotic Crossovers in Hybrid Plants". In: *Proceedings
384 of the National Academy of Sciences* 115.10, pp. 2431–2436. DOI: [10.1073/pnas.1713078114](https://doi.org/10.1073/pnas.1713078114).
- 385 Fuentes, Roven Rommel et al. (2021). "Domestication Shapes Recombination Patterns in Tomato". In:
386 *Molecular Biology and Evolution*. Ed. by Michael Purugganan, msab287. DOI: [10.1093/molbev/msab287](https://doi.org/10.1093/molbev/msab287).
- 387 Haenel, Quiterie et al. (2018). "Meta-Analysis of Chromosome-Scale Crossover Rate Variation in Eukaryotes
388 and Its Significance to Evolutionary Genomics". In: *Molecular Ecology* 27.11, pp. 2477–2497. DOI: [10.1111/mec.14699](https://doi.org/10.1111/mec.14699).
- 389 Hansson, Bengt et al. (2006). "Comparative Gene Mapping in *Arabidopsis Lyrata* Chromosomes 1 and 2 and
390 the Corresponding *A. Thaliana* Chromosome 1: Recombination Rates, Rearrangements and Centromere
391 Location". In: *Genetical Research* 87.2, pp. 75–85. DOI: [10.1017/S0016672306008020](https://doi.org/10.1017/S0016672306008020).
- 392 Hartfield, Matthew, Sarah P Otto, and Peter D Keightley (2010). "The Role of Advantageous Mutations
393 in Enhancing the Evolution of a Recombination Modifier". In: *Genetics* 184.4, pp. 1153–1164. DOI: [10.1534/genetics.109.112920](https://doi.org/10.1534/genetics.109.112920).
- 394 395 Henderson, Ian R. and Kirsten Bomblies (2021). "Evolution and Plasticity of Genome-Wide Meiotic Re-
396 combination Rates". In: *Annual Review of Genetics* 55.1, annurev-genet-021721-033821. DOI: [10.1146/annurev-genet-021721-033821](https://doi.org/10.1146/annurev-genet-021721-033821).
- 397 398 Hill, W. G. and Alan Robertson (1966). "The Effect of Linkage on Limits to Artificial Selection". In: *Genetical
399 Research* 8.3, pp. 269–294. DOI: [10.1017/S0016672300010156](https://doi.org/10.1017/S0016672300010156).
- 400 Johnston, Susan E et al. (2016). "Conserved Genetic Architecture Underlying Individual Recombination
401 Rate Variation in a Wild Population of Soay Sheep (*Ovis Aries*)". In: *Genetics* 203.1, pp. 583–598. DOI:
402 [10.1534/genetics.115.185553](https://doi.org/10.1534/genetics.115.185553).

MATING SYSTEM AND THE EVOLUTION OF RECOMBINATION RATES IN SEED PLANTS

- 403 Kawabe, Akira et al. (2006). "Comparative Gene Mapping in *Arabidopsis Lyrata* Chromosomes 6 and 7 and
404 *A. Thaliana* Chromosome IV: Evolutionary History, Rearrangements and Local Recombination Rates".
405 In: *Genetical Research* 88.1, pp. 45–56. DOI: [10.1017/S0016672306008287](https://doi.org/10.1017/S0016672306008287).
- 406 Keightley, Peter D and Sarah P Otto (2006). "Interference among Deleterious Mutations Favours Sex and
407 Recombination in Finite Populations". In: *Nature* 443.7107, pp. 89–92.
- 408 Koehler, Kara E. et al. (1996). "Recombination and Nondisjunction in Humans and Flies". In: *Human
409 Molecular Genetics* 5.Supplement_1, pp. 1495–1504. DOI: [10.1093/hmg/5.Supplement_1.1495](https://doi.org/10.1093/hmg/5.Supplement_1.1495).
- 410 Koella, Jacob C. (1993). "Ecological Correlates of Chiasma Frequency and Recombination Index of Plants".
411 In: *Biological Journal of the Linnean Society* 48.3, pp. 227–238. DOI: [10.1111/j.1095-8312.1993.tb00889.x](https://doi.org/10.1111/j.1095-8312.1993.tb00889.x).
- 412 Kuittinen, Helmi et al. (2004). "Comparing the Linkage Maps of the Close Relatives *Arabidopsis Lyrata* and
413 *A. Thaliana*". In: *Genetics* 168.3, pp. 1575–1584. DOI: [10.1534/genetics.103.022343](https://doi.org/10.1534/genetics.103.022343).
- 414 Lenormand, Thomas and Sarah P Otto (n.d.). "The Evolution of Recombination in a Heterogeneous Envi-
415 ronment". In: (), p. 16.
- 416 Orme, David et al. (2018). *Caper: Comparative Analyses of Phylogenetics and Evolution in r*. Manual.
- 417 Otto, Sarah P. (2009). "The Evolutionary Enigma of Sex". In: *The American Naturalist* 174.S1, S1–S14. DOI:
418 [10.1086/599084](https://doi.org/10.1086/599084).
- 419 Otto, Sarah P. and Nick H. Barton (2001). "Selection for Recombination in Small Populations". In: *Evolution*
420 55.10, pp. 1921–1931. DOI: [10.1111/j.0014-3820.2001.tb01310.x](https://doi.org/10.1111/j.0014-3820.2001.tb01310.x).
- 421 Otto, Sarah P. and Bret A. Payseur (2019). "Crossover Interference: Shedding Light on the Evolution of
422 Recombination". In: *Annual Review of Genetics* 53.1, pp. 19–44. DOI: [10.1146/annurev-genet-040119-093957](https://doi.org/10.1146/annurev-genet-040119-093957).
- 423 Peñalba, Joshua V. et al. (2020). "Genome of an Iconic Australian Bird: High-quality Assembly and Linkage
424 Map of the Superb Fairy-wren (*Malurus Cyaneus*)". In: *Molecular Ecology Resources* 20.2, pp. 560–578.
425 DOI: [10.1111/1755-0998.13124](https://doi.org/10.1111/1755-0998.13124).
- 426 R Core Team (2022). *R: A Language and Environment for Statistical Computing*. Manual. R Foundation for
427 Statistical Computing. Vienna, Austria.
- 428 Revell, Liam J. (2024). "phytools 2.0: An Updated R Ecosystem for Phylogenetic Comparative Methods
429 (and Other Things)." In: *PeerJ* 12, e16505. DOI: [10.7717/peerj.16505](https://doi.org/10.7717/peerj.16505).
- 430 Ritz, Kathryn R., Mohamed A.F. Noor, and Nadia D. Singh (2017). "Variation in Recombination Rate:
431 Adaptive or Not?" In: *Trends in Genetics* 33.5, pp. 364–374. DOI: [10.1016/j.tig.2017.03.003](https://doi.org/10.1016/j.tig.2017.03.003).
- 432 Ross-Ibarra, J. (2007). "Genome Size and Recombination in Angiosperms: A Second Look". In: *Journal of
433 Evolutionary Biology* 20.2, pp. 800–806. DOI: [10.1111/j.1420-9101.2006.01275.x](https://doi.org/10.1111/j.1420-9101.2006.01275.x).
- 434 Roze, Denis (2021). "A Simple Expression for the Strength of Selection on Recombination Generated by
435 Interference among Mutations". In: *Proceedings of the National Academy of Sciences* 118.19, e2022805118.
436 DOI: [10.1073/pnas.2022805118](https://doi.org/10.1073/pnas.2022805118).

MATING SYSTEM AND THE EVOLUTION OF RECOMBINATION RATES IN SEED PLANTS

- 439 Roze, Denis and Nick H Barton (2006). "The Hill–Robertson Effect and the Evolution of Recombination".
440 In: *Genetics* 173.3, pp. 1793–1811.
- 441 Roze, Denis and Thomas Lenormand (2005). "Self-Fertilization and the Evolution of Recombination". In:
442 *Genetics* 170.2, pp. 841–857. DOI: [10.1534/genetics.104.036384](https://doi.org/10.1534/genetics.104.036384).
- 443 Samuk, Kieran et al. (2020). "Natural Selection Shapes Variation in Genome-wide Recombination Rate in
444 *Drosophila Pseudoobscura*". In: *Current Biology* 30.8, 1517–1528.e6. DOI: [10.1016/j.cub.2020.03.053](https://doi.org/10.1016/j.cub.2020.03.053).
- 445 Schreiber, Mona et al. (2022). "Recombination Landscape Divergence between Populations Is Marked by
446 Larger Low-Recombining Regions in Domesticated Rye". In: *Molecular Biology and Evolution*. Ed. by
447 Michael Purugganan, msac131. DOI: [10.1093/molbev/msac131](https://doi.org/10.1093/molbev/msac131).
- 448 Smith, Stephen A. and Joseph W. Brown (2018). "Constructing a Broadly Inclusive Seed Plant Phylogeny".
449 In: *American Journal of Botany* 105.3, pp. 302–314. DOI: [10.1002/ajb2.1019](https://doi.org/10.1002/ajb2.1019).
- 450 Stapley, Jessica et al. (2017). "Variation in Recombination Frequency and Distribution across Eukary-
451 otes: Patterns and Processes". In: *Philosophical Transactions of the Royal Society B: Biological Sciences*
452 372.1736, p. 20160455. DOI: [10.1098/rstb.2016.0455](https://doi.org/10.1098/rstb.2016.0455).
- 453 Stetsenko, Roman and Denis Roze (2022). "The Evolution of Recombination in Self-Fertilizing Organisms".
454 In: *Genetics* 222.1. Ed. by A Agrawal, iyac114. DOI: [10.1093/genetics/iyac114](https://doi.org/10.1093/genetics/iyac114).
- 455 Veller, Carl, Nancy Kleckner, and Martin A. Nowak (2019). "A Rigorous Measure of Genome-Wide Genetic
456 Shuffling That Takes into Account Crossover Positions and Mendel's Second Law". In: *Proceedings of the*
457 *National Academy of Sciences* 116.5, pp. 1659–1668. DOI: [10.1073/pnas.1817482116](https://doi.org/10.1073/pnas.1817482116).
- 458 Wang, Shunxin et al. (2015). "Meiotic Crossover Patterns: Obligatory Crossover, Interference and Home-
459 ostasis in a Single Process". In: *Cell Cycle* 14.3, pp. 305–314. DOI: [10.4161/15384101.2014.991185](https://doi.org/10.4161/15384101.2014.991185).
- 460 Whitehead, Michael R. et al. (2018). "Plant Mating Systems Often Vary Widely Among Populations". In:
461 *Frontiers in Ecology and Evolution* 6, p. 38. DOI: [10.3389/fevo.2018.00038](https://doi.org/10.3389/fevo.2018.00038).
- 462 Wickham, Hadley (2016). *Ggplot2: Elegant Graphics for Data Analysis*. Springer-Verlag New York.

463 **Supplementary figures**

MATING SYSTEM AND THE EVOLUTION OF RECOMBINATION RATES IN SEED PLANTS

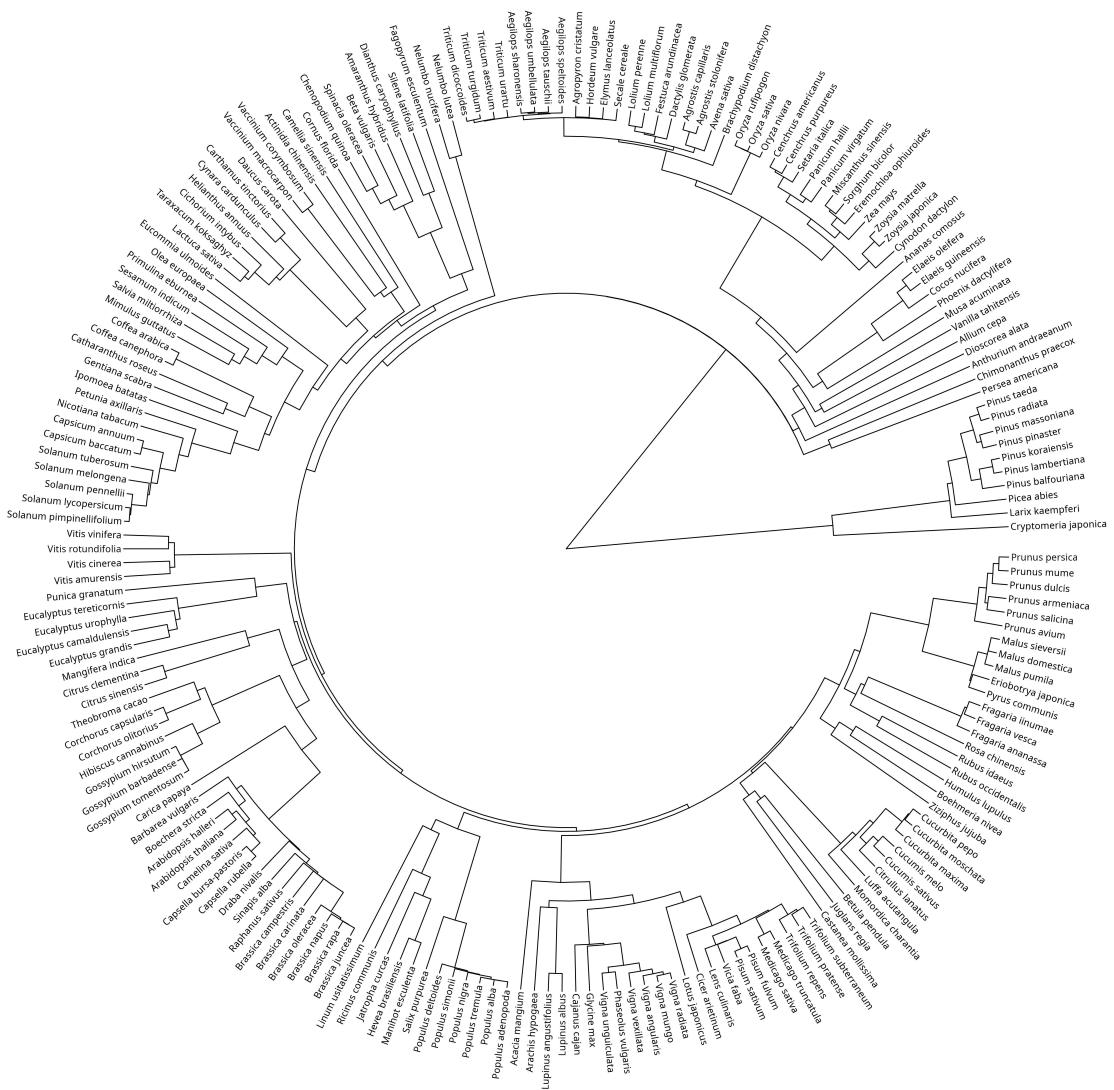


Figure S1: Phylogeny of the complete dataset based on the ultra-metric tree from Smith and Brown (2018).

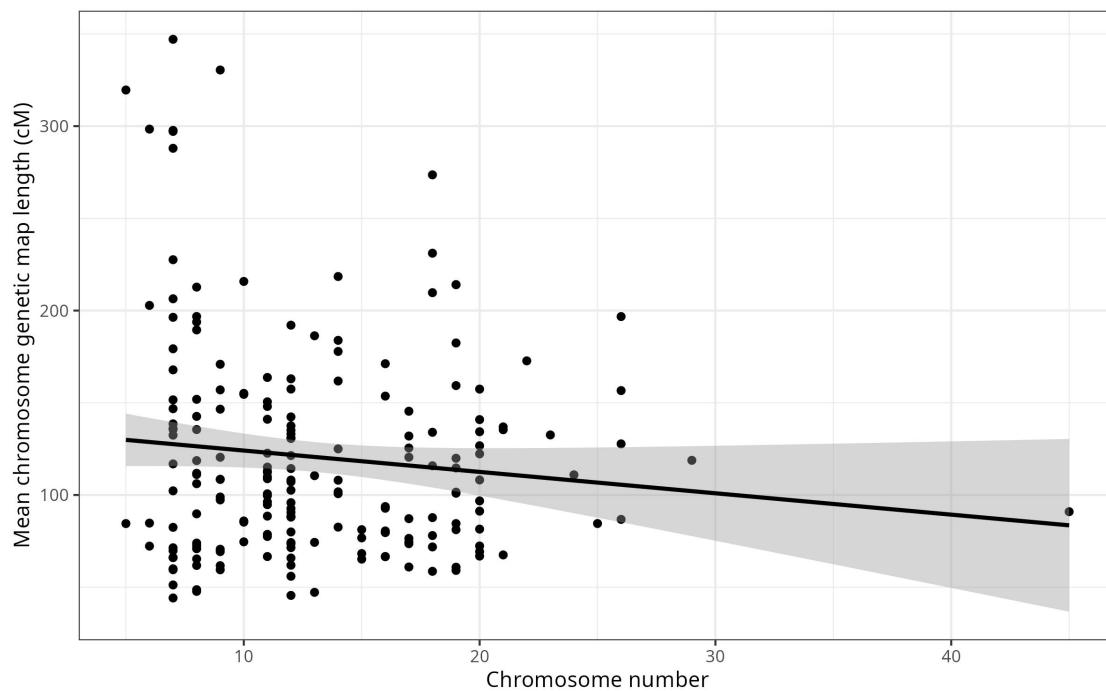


Figure S2: Average chromosome map length is not correlated with the haploid chromosome number (Spearman's $\rho = -0.08$, $p = 0.27$).

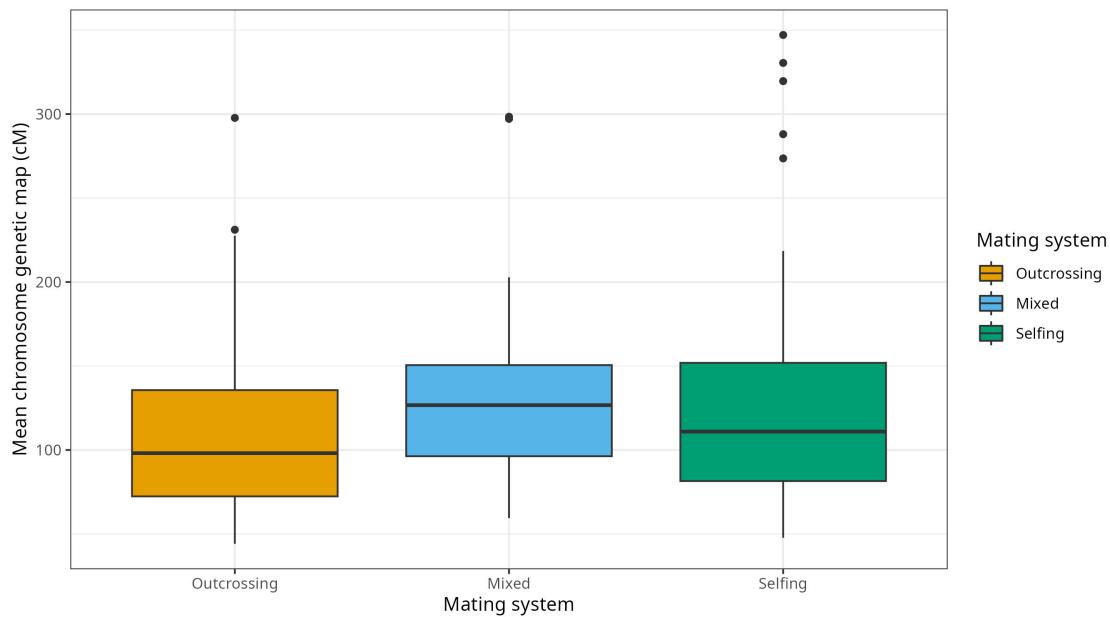


Figure S3: Chromosome map length as a function of the mating system.

MATING SYSTEM AND THE EVOLUTION OF RECOMBINATION RATES IN SEED PLANTS

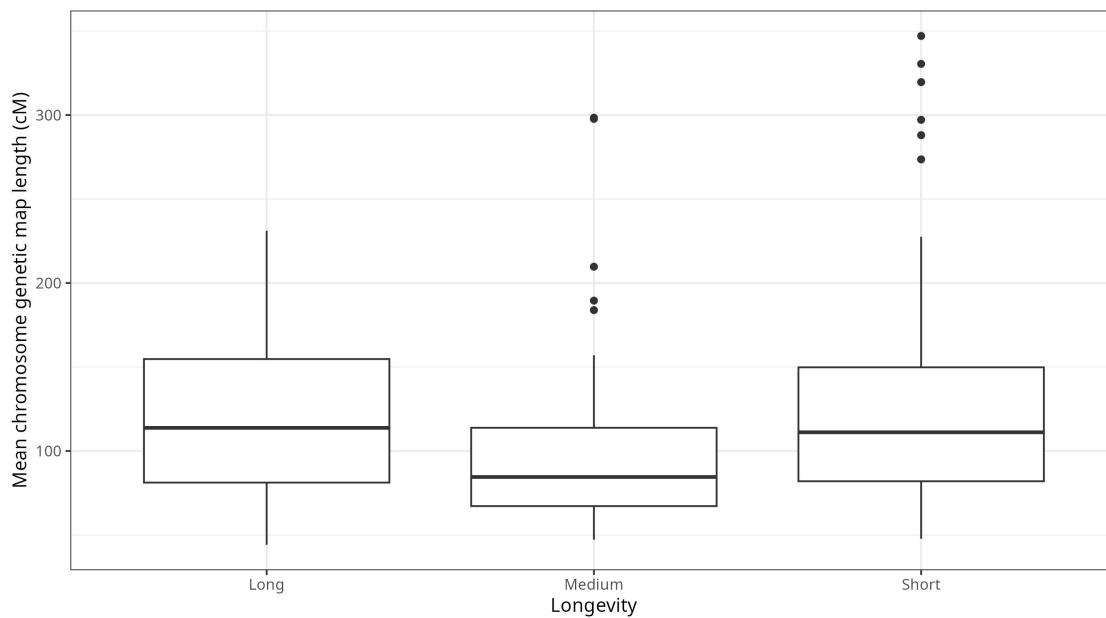


Figure S4: Chromosome map length as a function of longevity.

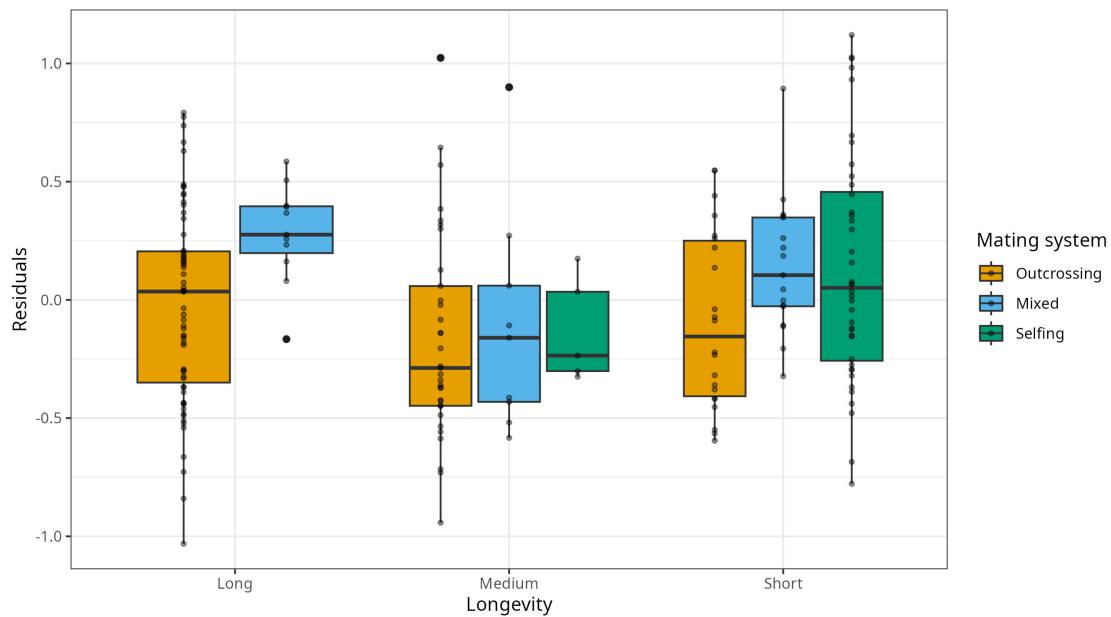


Figure S5: The recombination rates depend on the mating system and longevity. The combined effect of the mating system and longevity on the residuals of the regression recombination rate (cM/Mb) as a function of chromosome size(Mb).

⁴⁶⁴ Supplementary tables

Table S1: Complete dataset with genetic map length, genome size, genomic characteristics (e.g. ploidy, number of chromosomes) and life history traits, associated with references.

Table S2: Forward model selection steps for the chromosome genetic map length and the residuals of the regression recombination rate as a function of chromosome size. The Anova p-value and AIC/BIC values are provided for each 'lm' and 'pgls' model.

Table S3: Model fit and parameters estimates for the 'pgls' model testing the effect of the mating system, chromosome size, the interaction of the mating system and chromosome size, and the number of chromosomes. Chromosome genetic map length = mating system*chromosome size + chromosome number.

Table S4: Model fit and parameters estimates for the 'pgls' model testing the effect of marker density and number of progeny. Chromosome genetic map length = mating system + longevity + marker density + number of progeny.

groupfamilygenusspeciescultivationlife_formwoodinesslife_spanlongevitysexual_systemmating_system
AngiospermActinidiaceaeActinidiaActinidia chinensis cultivated Liana woody Perennial Long Dioecy Outcrossing
AngiospermAmaranthaceaeAmaranthusAmaranthus hybridus wild Herb non_ woody Annual Short Monoecy
AngiospermChenopodiaceaeBetaBeta vulgaris cultivated Herb non_ woody Biannual Short Hermaphrodism
AngiospermChenopodiaceaeChenopodiumChenopodium quinoa cultivated Herb non_ woody Annual Short
AngiospermChenopodiaceaeSpinaciaSpinacia oleracea cultivated Herb non_ woody Biannual Short Dioecy
AngiospermAmaryllidaceaeAlliumAllium cepa cultivated Herb non_ woody Biannual Short Hermaphrodism C
AngiospermAnacardiaceaeMangiferaMangifera indica cultivated Tree woody Perennial Long Hermaphrodism
AngiospermApiaceaeDaucusDaucus carota cultivated Herb non_ woody Biannual Short Hermaphrodism O
AngiospermApocynaceaeCatharanthusCatharanthus roseus wild Herb non_ woody Perennial Long Hermap
AngiospermAraceaeAnthuriumAnthurium andraeanum wild Herb non_ woody Perennial Long Monoecy Outc
AngiospermArecaceaeCocosCocos nucifera cultivated Tree woody Perennial Long Monoecy Mixed NA 0.72
AngiospermArecaceaeElaeisElaeis guineensis cultivated Tree woody Perennial Long Monoecy Outcrossing
AngiospermArecaceaeElaeisElaeis oleifera cultivated Tree woody Perennial Long Monoecy Outcrossing NA
AngiospermArecaceaePhoenixPhoenix dactylifera cultivated Tree woody Perennial Long Dioecy Outcrossin
AngiospermAsteraceaeCarthamusCarthamus tinctorius cultivated Herb non_ woody Annual Short Hermaph
AngiospermAsteraceaeCichoriumCichorium intybus cultivated Herb non_ woody Perennial Long Hermaphro
AngiospermAsteraceaeCynaraCynara cardunculus cultivated Herb non_ woody Biannual Short Hermaphrod
AngiospermAsteraceaeHelianthusHelianthus annuus cultivated Herb non_ woody Annual Short Hermaphrod
AngiospermAsteraceaeLactucaLactuca sativa cultivated Herb non_ woody Annual Short Hermaphrodism Se
AngiospermNANANAWild Herb non_ woody Perennial Long Hermaphrodism Outcrossing SINA 28894.11420
AngiospermBetulaceaeBetulaBetula pendula wild Tree woody Perennial Long Monoecy Outcrossing SINA 21
AngiospermBrassicaceaeArabidopsisArabidopsis halleri wild Herb non_ woody Perennial Long Hermaphrod
AngiospermBrassicaceaeArabidopsisArabidopsis thaliana wild Herb non_ woody Annual Short Hermaphrod
AngiospermBrassicaceaeBarbareaBarbarea vulgaris wild Herb non_ woody Annual _ Perennial Short Herma
AngiospermBrassicaceaeBoecheraBoechera stricta wild Herb non_ woody Perennial Long Hermaphrodism
AngiospermBrassicaceaeBrassicaBrassica rapa cultivated Herb non_ woody Annual Short Hermaphrodism
AngiospermBrassicaceaeBrassicaBrassica carinata cultivated Herb non_ woody Annual Short Hermaphrod
AngiospermBrassicaceaeBrassicaBrassica juncea cultivated Herb non_ woody Biannual Short Hermaphrod
AngiospermBrassicaceaeBrassicaBrassica napus cultivated Herb non_ woody Biannual Short Hermaphrod
AngiospermBrassicaceaeBrassicaBrassica oleracea cultivated Herb non_ woody Biannual Short Hermaphro
AngiospermBrassicaceaeBrassicaBrassica rapa cultivated Herb non_ woody Biannual Short Hermaphrodism
AngiospermBrassicaceaeCamelinaCamelina sativa cultivated Herb non_ woody Annual Short Hermaphrod
AngiospermBrassicaceaeCapsellaCapsella bursa-pastoris wild Herb non_ woody Annual Short Hermaphrod
AngiospermBrassicaceaeCapsellaCapsella rubella wild Herb non_ woody Annual Short Hermaphrodism Sel
AngiospermBrassicaceaeDrabaDraba nivalis wild Herb non_ woody Perennial Long Hermaphrodism Selfing
AngiospermBrassicaceaeRaphanusRaphanus sativus cultivated Herb non_ woody Annual Short Hermaphrod
AngiospermBrassicaceaeSinapisSinapis alba cultivated Herb non_ woody Annual Short Hermaphrodism O
AngiospermBromeliaceaeAnanasAnanas comosus cultivated Herb non_ woody Perennial Long Hermaphrod
AngiospermCalycanthaceaeChimonanthusChimonanthus praecox wild Shrub woody Perennial Long Herma
AngiospermCannabaceaeHumulusHumulus lupulus cultivated Liana woody Perennial Long Dioecy Outcrossing
AngiospermCaricaceaeCaricaCarica papaya cultivated Tree woody Perennial Long Dioecy Outcrossing NAN
AngiospermCaryophyllaceaeDianthusDianthus caryophyllus wild Herb non_ woody Perennial Long Hermap
AngiospermCaryophyllaceaeSileneSilene latifolia wild Herb non_ woody Perennial Long Dioecy Outcrossing
AngiospermConvolvulaceaeIpomoeaIpomoea batatas cultivated Herb non_ woody Perennial Long Hermap
AngiospermCornaceaeCornusCornus florida wild Tree woody Perennial Long Hermaphrodism Outcrossing S
AngiospermCucurbitaceaeCitrullusCitrullus lanatus cultivated Vinenon_ woody Annual Short Monoecy Mix
AngiospermCucurbitaceaeCucumisCucumis melo cultivated Vinenon_ woody Annual Short Hermaphrodism
AngiospermCucurbitaceaeCucumisCucumis sativus cultivated Vinenon_ woody Annual Short Monoecy Mix
AngiospermCucurbitaceaeCucurbitaCucurbita maxima cultivated Vinenon_ woody Annual Short Monoecy M
AngiospermCucurbitaceaeCucurbitaCucurbita moschata cultivated Vinenon_ woody Annual Short Monoecy
AngiospermCucurbitaceaeCucurbitaCucurbita pepo cultivated Vinenon_ woody Annual Short Monoecy Mix
AngiospermCucurbitaceaeLuffaLuffa acutangula cultivated Vinenon_ woody Annual Short Monoecy Mixed N
AngiospermCucurbitaceaeMomordicaMomordica charantia cultivated Herb non_ woody Annual Short Dioec
AngiospermDioscoreaceaeDioscoreaDioscorea alata cultivated Herb non_ woody Perennial Long Dioecy O
AngiospermEricaceaeVacciniumVaccinium corymbosum cultivated Shrub woody Perennial Long Hermaphrod

AngiospermEricaceae*Vaccinium* *Vaccinium macrocarpon* cultivated Shrub woody Perennial Long Hermaphrodite
AngiospermEucommiaceae*Eucommia* *Eucommia ulmoides* wild Tree woody Perennial Long Dioecy Outcrossing
AngiospermEuphorbiaceae*Hevea* *Hevea brasiliensis* cultivated Tree woody Perennial Long Hermaphrodism
AngiospermEuphorbiaceae*Jatropha* *Jatropha curcas* cultivated Shrub woody Perennial Long Hermaphrodism
AngiospermEuphorbiaceae*Manihot* *Manihot esculenta* cultivated Shrub woody Perennial Long Hermaphrodite
AngiospermEuphorbiaceae*Ricinus* *Ricinus communis* wild Shrub woody Perennial Long Monoecy Outcrossing
AngiospermFabaceae*Acacia* *Acacia mangium* wild Tree woody Perennial Long Hermaphrodism Outcrossing
AngiospermFabaceae*Arachis* *Arachis hypogaea* cultivated Herb non-woody Annual Short Hermaphrodism Self-incompatibility
AngiospermFabaceae*Cajanus* *Cajanus cajan* cultivated Herb non-woody Perennial Long Hermaphrodism Mixed
AngiospermFabaceae*Cicer* *Cicer arietinum* cultivated Herb non-woody Annual Short Hermaphrodism Self-incompatibility
AngiospermFabaceae*Glycine* *Glycine max* cultivated Herb non-woody Annual Short Hermaphrodism Self-incompatibility
AngiospermFabaceae*Lens* *Lens culinaris* cultivated Herb non-woody Annual Short Hermaphrodism Self-incompatibility
AngiospermFabaceae*Lotus* *Lotus japonicus* wild Herb non-woody Perennial Long Hermaphrodism Self-incompatibility
AngiospermFabaceae*Lupinus* *Lupinus albus* cultivated Herb non-woody Annual Short Hermaphrodism Self-incompatibility
AngiospermFabaceae*Lupinus* *Lupinus angustifolius* wild Herb non-woody Annual Short Hermaphrodism Self-incompatibility
AngiospermFabaceae*Medicago* *Medicago sativa* cultivated Herb non-woody Perennial Long Hermaphrodism
AngiospermFabaceae*Medicago* *Medicago truncatula* wild Herb non-woody Annual Short Hermaphrodism Self-incompatibility
AngiospermFabaceae*Phaseolus* *Phaseolus vulgaris* cultivated Herb non-woody Annual Short Hermaphrodism
AngiospermFabaceae*Pisum* *Pisum fulvum* wild Herb non-woody Annual Short Hermaphrodism Mixed NANA
AngiospermFabaceae*Pisum* *Pisum sativum* cultivated Vine non-woody Annual Short Hermaphrodism Mixed
AngiospermFabaceae*Trifolium* *Trifolium pratense* wild Herb non-woody Perennial Long Hermaphrodism Outcrossing
AngiospermFabaceae*Trifolium* *Trifolium repens* wild Herb non-woody Perennial Long Hermaphrodism Outcrossing
AngiospermFabaceae*Trifolium* *Trifolium subterraneum* wild Herb non-woody Annual Short Hermaphrodism
AngiospermFabaceae*Vicia* *Vicia faba* cultivated Herb non-woody Annual Short Hermaphrodism Mixed SCN/
AngiospermFabaceae*Vigna* *Vigna angularis* cultivated Vine non-woody Annual Short Hermaphrodism Self-incompatibility
AngiospermFabaceae*Vigna* *Vigna mungo* cultivated Vine non-woody Annual Short Hermaphrodism Self-incompatibility
AngiospermFabaceae*Vigna* *Vigna radiata* cultivated Vine non-woody Annual Short Hermaphrodism Self-incompatibility
AngiospermFabaceae*Vigna* *Vigna unguiculata* cultivated Vine non-woody Annual Perennial Short Hermaphrodism
AngiospermFabaceae*Vigna* *Vigna vexillata* wild Vine non-woody Perennial Long Hermaphrodism Mixed SCN/
AngiospermFagaceae*Castanea* *Castanea mollissima* cultivated Tree woody Perennial Long Monoecy Outcrossing
AngiospermGentianaceae*Gentiana* *Gentiana scabra* wild Herb non-woody Perennial Long Hermaphrodism
AngiospermGesneriaceae*Primulina* *Primulina eburnea* wild Herb non-woody Perennial Long Hermaphrodism
AngiospermJuglandaceae*Juglans* *Juglans regia* cultivated Tree woody Perennial Long Monoecy Outcrossing
AngiospermLamiaceae*Salvia* *Salvia miltiorrhiza* cultivated Herb non-woody Perennial Long Hermaphrodism
AngiospermLauraceae*Persea* *Persea americana* cultivated Tree woody Perennial Long Hermaphrodism Mixed
AngiospermLinaceae*Linum* *Linum usitatissimum* cultivated Herb non-woody Annual Short Hermaphrodism Self-incompatibility
AngiospermLythraceae*Punica* *Punica granatum* cultivated Tree woody Perennial Long Hermaphrodism Mixed
AngiospermMalvaceae*Corchorus* *Corchorus capsularis* cultivated Herb non-woody Annual Perennial Short Hermaphrodite
AngiospermMalvaceae*Corchorus* *Corchorus olitorius* cultivated Herb non-woody Annual Perennial Short Hermaphrodite
AngiospermMalvaceae*Gossypium* *Gossypium barbadense* cultivated Shrub woody Perennial Long Hermaphrodism
AngiospermMalvaceae*Gossypium* *Gossypium hirsutum* cultivated Shrub woody Perennial Long Hermaphrodism
AngiospermMalvaceae*Gossypium* *Gossypium tomentosum* wild Shrub woody Perennial Long Hermaphrodism
AngiospermMalvaceae*Hibiscus* *Hibiscus cannabinus* cultivated Herb non-woody Annual Perennial Short Hermaphrodite
AngiospermMalvaceae*Theobroma* *Theobroma cacao* cultivated Tree woody Perennial Long Hermaphrodism
AngiospermMusaceae*Musa* *Musa acuminata* cultivated Herb non-woody Perennial Long Hermaphrodism Mixed
AngiospermMyrtaceae*Eucalyptus* *Eucalyptus camaldulensis* wild Tree woody Perennial Long Hermaphrodism
AngiospermMyrtaceae*Eucalyptus* *Eucalyptus grandis* wild Tree woody Perennial Long Hermaphrodism Outcrossing
AngiospermMyrtaceae*Eucalyptus* *Eucalyptus tereticornis* wild Tree woody Perennial Long Hermaphrodism Mixed
AngiospermMyrtaceae*Eucalyptus* *Eucalyptus urophylla* wild Tree woody Perennial Long Hermaphrodism Outcrossing
AngiospermNelumbonaceae*Nelumbo* *Nelumbo lutea* wild Herb non-woody Perennial Long Hermaphrodism
AngiospermNelumbonaceae*Nelumbo* *Nelumbo nucifera* wild Herb non-woody Perennial Long Hermaphrodism
AngiospermOleaceae*Olea* *Olea europaea* cultivated Tree woody Perennial Long Hermaphrodism Outcrossing
AngiospermOrchidaceae*Vanilla* *Vanilla x tahitensis* cultivated Vine non-woody Perennial Long Hermaphrodite
AngiospermPedaliaceae*Sesamum* *Sesamum indicum* cultivated Herb non-woody Annual Short Hermaphrodite
AngiospermPhrymaceae*Erythranthe* *Erythranthe guttata* wild Herb non-woody Annual Short Hermaphrodite
AngiospermPoaceae*Aegilops* *Aegilops sharonensis* wild Herb non-woody Annual Short Hermaphrodism Mixed

AngiospermPoaceaeAegilopsAegilops speloideswildHerbnon_woodyAnnualShortHermaphrodismOutc
AngiospermPoaceaeAegilopsAegilops tauschiiwildHerbnon_woodyAnnualShortHermaphrodismSelfingI
AngiospermPoaceaeAegilopsAegilops umbellulatawildHerbnon_woodyAnnualShortHermaphrodismSelI
Angiosperm https://doi.org/10.1007/s00122-018-3148-91426968453.71428571428659.9785714285714I
AngiospermPoaceaeAgrostisAgrostis capillariswildHerbnon_woodyPerennialLongHermaphrodismOutc
AngiospermPoaceaeAgrostisAgrostis stoloniferawildHerbnon_woodyPerennialLongHermaphrodismOut
AngiospermPoaceaeAvenaAvena sativacultivatedHerbnon_woodyAnnualShortHermaphrodismSelfingN
AngiospermPoaceaeBrachypodiumBrachypodium distachyonwildHerbnon_woodyAnnualShortHermaph
AngiospermPoaceaeCenchrusCenchrus americanuscultivatedHerbnon_woodyAnnualShortHermaphrod
AngiospermPoaceaeCenchrusCenchrus purpureuswildHerbwoodyPerennialLongHermaphrodismOutc
AngiospermPoaceaeCynodonCynodon dactylonwildHerbnon_woodyPerennialLongHermaphrodismOut
AngiospermPoaceaeDactylisDactylis glomeratawildHerbnon_woodyPerennialLongHermaphrodismOutc
AngiospermPoaceaeElymusElymus lanceolatuswildHerbnon_woodyPerennialLongHermaphrodismOut
AngiospermPoaceaeEremochloaEremochloa ophiuroideswildHerbnon_woodyPerennialLongHermaphro
AngiospermPoaceaeLoliumLolium arundinaceumwildHerbnon_woodyPerennialLongHermaphrodismOut
AngiospermPoaceaeHordeumHordeum vulgarecultivatedHerbnon_woodyAnnualShortHermaphrodismS
AngiospermPoaceaeLoliumLolium multiflorumwildHerbnon_woodyAnnual_PerennialShortHermaphrod
AngiospermPoaceaeLoliumLolium perennewildHerbnon_woodyPerennialLongHermaphrodismOutcross
AngiospermPoaceaeMiscanthusMiscanthus sinensiswildHerbnon_woodyPerennialLongHermaphrodism
AngiospermPoaceaeOryzaOryza nivarawildHerbnon_woodyAnnualShortHermaphrodismSelfingNANA2
AngiospermPoaceaeOryzaOryza rufipogonwildHerbnon_woodyPerennialLongHermaphrodismMixedNA
AngiospermPoaceaeOryzaOryza sativacultivatedHerbnon_woodyAnnualShortHermaphrodismSelfingN
AngiospermPoaceaePanicumPanicum halliiwildHerbnon_woodyPerennialLongHermaphrodismSelfingN
AngiospermPoaceaePanicumPanicum virgatumwildHerbnon_woodyPerennialLongHermaphrodismOut
AngiospermPoaceaeSecaleSecale cerealecultivatedHerbnon_woodyAnnualShortHermaphrodismOutcr
AngiospermPoaceaeSetariaSetaria italicacultivatedHerbnon_woodyAnnualShortHermaphrodismSelfing
AngiospermPoaceaeSorghumSorghum bicolorcultivatedHerbnon_woodyAnnualShortHermaphrodismSel
AngiospermPoaceaeTriticumTriticum aestivumcultivatedHerbnon_woodyAnnualShortHermaphrodismSel
AngiospermPoaceaeTriticumTriticum dicoccoideswildHerbnon_woodyAnnualShortHermaphrodismSelfi
AngiospermPoaceaeTriticumTriticum turgidumcultivatedHerbnon_woodyAnnualShortHermaphrodismSel
AngiospermPoaceaeTriticumTriticum urartuwildHerbnon_woodyAnnualShortHermaphrodismSelfingNAI
AngiospermPoaceaeZeaZea mayscultivatedHerbnon_woodyAnnualShortMonoecyOutcrossingNA0.972
AngiospermPoaceaeZoysiaZoysia japonicawildHerbnon_woodyPerennialLongHermaphrodismOutcross
AngiospermPoaceaeZoysiaZoysia matrellawildHerbnon_woodyPerennialLongHermaphrodismOutcross
AngiospermPolygonaceaeFagopyrumFagopyrum esculentumcultivatedHerbnon_woodyAnnualShortHe
AngiospermRhamnaceaeZiziphusZiziphus jujubacultivatedTreewoodyPerennialLongHermaphrodismOut
AngiospermRosaceaeEriobotryaEriobotrya japonicacultivatedTreewoodyPerennialLongHermaphrodism
AngiospermRosaceaeFragariaFragaria x ananassacultivatedHerbnon_woodyPerennialLongHermaphro
AngiospermRosaceaeFragariaFragaria iinumaewildHerbnon_woodyPerennialLongHermaphrodismMixe
AngiospermRosaceaeMalusMalus domesticacultivatedTreewoodyPerennialLongHermaphrodismOutcrc
AngiospermRosaceaeMalusMalus pumilawildTreewoodyPerennialLongHermaphrodismOutcrossingSIN
AngiospermRosaceaeMalusMalus sieversiawildTreewoodyPerennialLongHermaphrodismOutcrossingSI
AngiospermRosaceaePrunusPrunus armeniacacultivatedTreewoodyPerennialLongHermaphrodismOut
AngiospermRosaceaePrunusPrunus aviumcultivatedTreewoodyPerennialLongHermaphrodismOutcross
AngiospermRosaceaePrunusPrunus dulciscultivatedTreewoodyPerennialLongHermaphrodismOutcross
AngiospermRosaceaePrunusPrunus mume cultivatedTreewoodyPerennialLongHermaphrodismOutcross
AngiospermRosaceaePrunusPrunus persicacultivatedTreewoodyPerennialLongHermaphrodismOutcro
AngiospermRosaceaePrunusPrunus salicinawildTreewoodyPerennialLongHermaphrodismOutcrossing
AngiospermRosaceaePyrusPyrus communiscultivatedTreewoodyPerennialLongHermaphrodismOutcro
AngiospermRosaceaeRosaRosa chinensis cultivatedHerbnon_woodyPerennialLongHermaphrodismOut
AngiospermRosaceaeRubusRubus idaeuscultivatedShrubwoodyPerennialLongHermaphrodismOutcro
AngiospermRosaceaeRubusRubus occidentaliswildShrubwoodyPerennialLongHermaphrodismOutcro
AngiospermRubiaceaeCoffeaCoffea arabica cultivatedTreewoodyPerennialLongHermaphrodismMixedS
AngiospermRubiaceaeCoffeaCoffea canephora cultivatedTreewoodyPerennialLongHermaphrodismOut
Angiosperm RutaceaeCitrusCitrus x clementina cultivatedTreewoodyPerennialLongHermaphrodismOutc

AngiospermRutaceaeCitrusCitrus sinensis cultivatedTree woodyPerennial LongHermaphrodismOutcross
AngiospermSalicaceaePopulusPopulus adenopoda wildTree woodyPerennial LongDioecyOutcrossingNA
AngiospermSalicaceaePopulusPopulus alba wildTree woodyPerennial LongDioecyOutcrossingNANA219
AngiospermSalicaceaePopulusPopulus deltoides wildTree woodyPerennial LongDioecyOutcrossingNAN
AngiospermSalicaceaePopulusPopulus nigra wildTree woodyPerennial LongDioecyOutcrossingNANA219
AngiospermSalicaceaePopulusPopulus simonii wildTree woodyPerennial LongDioecyOutcrossingNANA2
AngiospermSalicaceaePopulusPopulus tremula wildTree woodyPerennial LongDioecyOutcrossingNANA
AngiospermSalicaceaeSalixSalix purpurea wildTree woodyPerennial LongDioecyOutcrossingNANA2193
AngiospermSolanaceaeCapsicumCapsicum annuum cultivatedHerb non_ woody Annual ShortHermaphrodism
AngiospermSolanaceaeCapsicumCapsicum baccatum cultivatedHerb non_ woody Perennial LongHermaphrodism
AngiospermSolanaceaeNicotianaNicotiana tabacum cultivatedHerb non_ woody Annual_Perennial ShortH
AngiospermSolanaceaePetuniaPetunia axillaris wildHerb non_ woody Annual ShortHermaphrodism Mixed
AngiospermSolanaceaeSolanumSolanum lycopersicum cultivatedHerb non_ woody Annual ShortHermaphrodism
AngiospermSolanaceaeSolanumSolanum virginianum cultivatedHerb non_ woody Annual ShortHermaphrodism
AngiospermSolanaceaeSolanumSolanum pennellii wildHerb non_ woody Perennial LongHermaphrodismC
AngiospermSolanaceaeSolanumSolanum pimpinellifolium wildHerb non_ woody Biannual ShortHermaphrodism
AngiospermSolanaceaeSolanumSolanum tuberosum cultivatedHerb non_ woody Perennial LongHermaphrodism
AngiospermTheaceaeCamelliaCamellia sinensis cultivatedShrub woody Perennial LongHermaphrodismO
AngiospermUrticaceaeBoehmeriaBoehmeria nivea cultivatedShrub woody Perennial Long Monoecy Outcrossing
AngiospermVitaceaeVitisVitis amurensis wildLiana woody Perennial Long Dioecy Outcrossing NANA21911
AngiospermVitaceaeVitisVitis cinerea wildLiana woody Perennial Long Dioecy Outcrossing NANA219115
AngiospermVitaceaeVitisVitis rotundifolia wildLiana woody Perennial Long Dioecy Outcrossing NANA22021
GymnospermCupressaceaeCryptomeriaCryptomeria japonica wildTree woody Perennial Long Dioecy Outcrossing
GymnospermPinaceaeLarixLarix kaempferi wildTree woody Perennial Long Monoecy Outcrossing NANA21
GymnospermPinaceaePiceaPicea abies wildTree woody Perennial Long Monoecy Outcrossing NA0.94212
GymnospermPinaceaePinusPinus balfouriana wildTree woody Perennial Long Monoecy Outcrossing NANA
GymnospermPinaceaePinusPinus koraiensis wildTree woody Perennial Long Monoecy Outcrossing NA0.88
GymnospermPinaceaePinusPinus lambertiana wildTree woody Perennial Long Monoecy Outcrossing NA0.9
GymnospermPinaceaePinusPinus massonianawildTree woody Perennial Long Monoecy Outcrossing NAN
GymnospermPinaceaePinusPinus pinaster wildTree woody Perennial Long Monoecy Outcrossing NA0.872
GymnospermPinaceaePinusPinus radiata wildTree woody Perennial Long Monoecy Outcrossing NA0.9212
GymnospermPinaceaePinusPinus taeda wildTree woody Perennial Long Monoecy Outcrossing NA0.99212

ISI_statusoutcrossing_rateploidynb_chromosomegenetic_map_cmgenome_size_Mbtipn_markersn_processingNANA22934451408.32Actinidia chinensisNA9429https://doi.org/10.1007/s11295-015-0941-35827
yOutcrossingNANA2161288616.14Amaranthus hybridus4804616https://doi.org/10.3835/plantgenome20
1OutcrossingSINA295551222.5Beta vulgaris284929https://doi.org/10.1007/s00122-007-0609-y1821223
tHermaphrodismselfingNANA41814041447.44Chenopodium quinoa51112818https://doi.org/10.3835/pl
OutcrossingNANA26433.61007.3Spinacia oleracea2833356https://doi.org/10.1007/s10681-015-1618-6
OutcrossingSCNA2980816381.5Allium cepa1435968https://doi.org/10.1186/s12864-021-07803-y162163
smOutcrossingSINA4203148.28440.1Mangifera indica659417320https://doi.org/10.3389/fpls.2016.0131
itcrossingNA0.9629635.1421.539Daucus carota4311889https://doi.org/10.1007/s11032-013-9979-9182
phrodisismixedSC0.66261790.42376.5Catharanthus roseusNANA6NANANA2372396.08333333333329
crossingNANA2151023.54694.4Anthurium andraeanum2284315https://doi.org/10.1016/j.scienta.2014.0
1627393107.106Cocos nucifera7049416https://doi.org/10.1007/s11295-008-0168-73223472194.19412
jNANA2161499.51535.18Elaeis guineensis1755NA16NA322183995.9487593.718750.9767584257220
NA21614851402.73Elaeis oleifera36213416https://doi.org/10.1007/s11295-013-0629-5NANANA87.670
ngNANA2181293929.1Phoenix dactylifera11998518https://doi.org/10.1186/1471-2164-15-28536292951
irodismMixedSCNA212959.441369.2Carthamus tinctorius11789612https://doi.org/10.1534/g3.115.0266
odismOutcrossingSINA2914131278.75Cichorium intybus19951989https://doi.org/10.3389/fpls.2019.002
dismOutcrossingSCNA2171251.151075.8Cynara cardunculus7089417https://doi.org/10.1007/s00122-01
dismOutcrossingSINA21724722376.54Helianthus annuus95359317https://doi.org/10.1007/s11032-016-
selfingSCNA2929742591.7Lactuca sativa137882139https://doi.org/10.1534/g3.112.0049291822592287.9
Taraxacum kok-saghyz518948https://doi.org/10.1038/srep31031NANANA177.5111.76250.6296478873
142489.71369.2Betula pendula5928014https://doi.org/10.1007/s11032-010-9436-yNANANA97.8177.83
dismOutcrossingNANA28567234.72Arabidopsis halleri851998https://doi.org/10.1534/genetics.106.0644
dismSelfingNA0.00325422.5123.5Arabidopsis thaliana6761005https://doi.org/10.1371/journal.pgen.0020
aphrodismOutcrossingNANA28889167.352Barbarea vulgaris1311298https://doi.org/10.1016/j.phytochen
SelfingSCNA27499.637185.68Boechera strictaNA1597https://doi.org/10.1038/s41559-017-0119NANA2
OutcrossingSINA210973.3567.24Brassica campestris6141279https://doi.org/10.1016/S1673-8527(08)6
ismMixedSC0.341720481545.24Brassica carinata403118517https://doi.org/10.1007/s00122-014-2321-
ismMixedSC0.241815791496.34Brassica juncea332916818https://doi.org/10.1186/s12864-015-2343-1
ismOutcrossingNANA4191917.91124.7Brassica napus182620019https://doi.org/10.1038/srep33113384
odismOutcrossingSINA29890.01762.8Brassica oleracea1776799https://doi.org/10.3389/fpls.2016.00334
mOutcrossingSINA210858.98782.4Brassica rapaNANA10NA20278278.2485.8981.097878323108380.1
ismSelfingSCNA6201385.6641.356Camelina sativa16018720https://doi.org/10.1139/g06-117NANANA3
dismSelfingNANA4161064.4391.2Capsella bursa-pastorisNANA16https://doi.org/10.1006/anbo.2000.13
lfingNANA28381.8263122.04Capsella rubella7685508https://doi.org/10.1038/ng.266916221515.25547.7
NANA291067.8024268.73Draba nivalisNANA8https://doi.org/10.1371/journal.pgen.101014116230829.8
odismOutcrossingSINA291538978Raphanus sativus2637939https://doi.org/10.1007/s00122-014-2426-
itcrossingSINA212890.4489Sinapis alba26415012https://doi.org/10.1186/1471-2229-13-14224348940.7
dismOutcrossingSINA2252113537.9Ananas comosus74113525https://doi.org/10.1016/j.scienta.2013.0
aphrodismOutcrossingNANA2111801600Chimonanthus praecox1656411https://doi.org/10.1016/j.scient
singNANA210745.92836.2Humulus lupulusNANA10https://doi.org/10.1007/s10681-011-0403-4NANA28
NA2181069.9372Carica papaya707549https://doi.org/10.1534/genetics.107.08146318236720.66666666
phrodisismOutcrossingSINA215978.3616.14Dianthus caryophyllus4129115https://doi.org/10.1186/1471-2
jNANA212671.12640.6Silene latifolia4078712https://doi.org/10.1534/genetics.113.1507552422641220.0
hrodisismOutcrossingSINA6908184.5837Ipomoea batatas207720245https://doi.org/10.1007/s11032-013-
SINA2711751545.24Cornus florida271947https://doi.org/10.1007/s10681-008-9802-6NANANA220.7485
dNA0.762111096440.1Citrullus lanatusNANA11NANANA40.0090909090999.63636363636362.49
nMixedSCNA2121150929.1Cucumis melo35415912https://doi.org/10.1007/s11032-010-9421-5NANA92
edNANA271061.19195.669Cucumis sativus30771537https://doi.org/10.3389/fpls.2016.0043714288027
MixedSCNA2202533.8449.88Cucurbita maxima45818620https://doi.org/10.1186/s12864-015-2312-8401
yMixedSCNA2201936420.54Cucurbita moschata1829420https://doi.org/10.1139/G08-07240NA41621.0
edSCNA2202817.6537.9Cucurbita pepo771812020https://doi.org/10.1111/pbi.1286040NA53826.89514
NANA2131436.12831.3Luffa acutangula17718613https://doi.org/10.3389/fpls.2016.00980NANANA63.94
cyOutcrossingNANA2111551.702291.58Momordica charantiaNANA11https://doi.org/10.1073/pnas.1921
utcrossingNANA4212820.263606.68Dioscorea alata583718920https://doi.org/10.1007/s00122-019-0331
rodismMixedSCNA2121621655.26Vaccinium corymbosum785NA12https://doi.org/10.1007/s11032-016-0

herodismOutcrossingSINA2121112414.622Vaccinium macrocarpon484936212https://doi.org/10.1186/s12
essingNANA2172133723.72Eucommia ulmoides70615217https://doi.org/10.3390/ijms150220533427244;
nOutcrossingSINA21841602102.7Hevea brasiliensis1232614918https://doi.org/10.1371/journal.pone.01
3mMixedSC0.682111655.8420.54Jatropha curcas120819011https://doi.org/10.1111/tpj.1276122241638
lismMixedNANA21824121222.5Manihot esculenta22403348018https://doi.org/10.1534/g3.114.0150087
ingNANA2101551508.56Ricinus communis33619010https://doi.org/10.1016/j.indcrop.2016.10.026NANA
gSC0.97213966635.7Acacia mangium24917513https://doi.org/10.1007/s00122005152126263648.974.3
SelfingSCNA4201446.72806.86Arachis hypogaea176516620https://doi.org/10.1186/1471-2164-15-351
MixedSCNA2111059860.64Cajanus cajan33918811https://doi.org/10.1007/s00122-012-1916-522285678
igSC0.01281083.93929.1Cicer arietinum66981298https://doi.org/10.1038/srep13387162929116.137513
gSC0.052202445.81105.14Glycine max21478200520https://doi.org/10.1186/s12864-015-2344-040211C
SC0.05272429.614107.6Lens culinaris689797https://doi.org/10.3389/fpls.2016.016041424108586.8347
IANA26508.5469.44Lotus japonicus1588946https://doi.org/10.1093/dnares/dsn02212246578.2484.751.
ingSC0.052252169586.8Lupinus albus4419626https://doi.org/10.1270/jsbbs.63.292NANA58723.47286.
lfingSC0.12201629.91153Lupinus angustifolius82449420https://doi.org/10.1371/journal.pone.00647994
mOutcrossingSCNA43221331276.29Medicago sativa359138416https://doi.org/10.1534/g3.114.012245
elfingNA0.03281215469.44Medicago truncatula1881778https://doi.org/10.1534/g3.112.0032691624655
ismSelfingSC0.052111042.2586.8Phaseolus vulgaris704026711https://doi.org/10.1534/g3.115.0205942
1282377.18543232.97Pisum fulvum12058847https://doi.org/10.3389/fpls.2018.001671424597404.1212
dSC0.32712554772.64Pisum sativum64263487https://doi.org/10.1186/s12864-016-2447-21424768681.
itcrossingSINA272084528.12Trifolium pratense21531557https://doi.org/10.1038/srep3035814241875.4
crossingSINA41612741095.36Trifolium repens110918416https://doi.org/10.1186/1471-2164-14-3883241
SelfingSCNA281701.7547.68Trifolium subterraneum3431888https://doi.org/10.1007/s11032-011-9612-
A261216.817622.582Vicia faba1103956https://doi.org/10.1016/j.plantsci.2013.11.014122130322937.09
ngSCNA2111628.15537.9Vigna angularis203215311https://doi.org/10.1038/srep3952322253848.9148.C
SCNA2111865.1537.9Vigna mungo42810411https://doi.org/10.1139/G08-05022253848.978.6454545454
SC0.04211732.9894.87Vigna radiata56020111https://doi.org/10.1016/j.cj.2016.06.010NANA51381.3518
herodismSelfingSC0.05211852.4586.8Vigna unguiculata226NA11https://doi.org/10.1139/g11-078222587
0.4211973.9567.24Vigna vexillata8230011https://doi.org/10.1371/journal.pone.013894222256251.5672
ossingSINA212743833.241Castanea mollissima139633712https://doi.org/10.1007/s11295-012-0579-3N
OutcrossingNANA213613.75000Gentiana scabra2639313https://doi.org/10.1186/1471-2164-13-672NA
mOutcrossingNANA2183774.71985.34Primulina eburnea23218918https://doi.org/10.1007/s12041-016-
gNA0.982162457.82606.36Juglans regia25778416https://doi.org/10.1186/s12864-015-1822-8NANA606
nOutcrossingNANA281516615Salvia miltiorrhiza5164968https://doi.org/10.1038/srep24070NANANA76.
kedNA0.52121087.4909.54Persea americana16371512https://doi.org/10.1007/s11295-009-0208-y2429C
SelfingNANA2151151684.6Linum usitatissimum77041115https://doi.org/10.1007/s00122-012-1953-030
edNANA281141704.16Punica granatum1092768https://doi.org/10.1007/s11295-015-0936-016270488.0
rtHermaphrodismSelfingSC0.1272016586.8Corchorus capsularis768NA7https://doi.org/10.1007/s11032
tHermaphrodismSelfingNANA27358.5909.54Corchorus olitoriusNANA7NA142449129.93428571428651.2
herodismMixedSCNA4265115.62694.39Gossypium barbadense229213526https://doi.org/10.1111/jpb.1
dismMixedSCNA4264071.982347.2Gossypium hirsutum643413726https://doi.org/10.1186/s12864-016-
ismMixedSCNA4263320.82386.32Gossypium tomentosum12049326https://doi.org/10.1007/s12041-013
tHermaphrodismSelfingNANA2184924.81496.34Hibiscus cannabinus39618018https://doi.org/10.1111/j.1
mOutcrossingSINA210852.8420.5Theobroma cacao352645910https://doi.org/10.1186/s12864-016-2411
1MixedNANA2111197472.231Musa acuminataNA26811https://doi.org/10.1186/1471-2229-10-652226114
smOutcrossingNA0.952111236606.36Eucalyptus camaldulensis1689211NA22260155.12363636364
crossingSC0.842111107591.5922Eucalyptus grandis4101195011https://doi.org/10.1186/1471-2164-13-
MixedNANA2111241.4586.8Eucalyptus tereticornis58513211https://doi.org/10.1371/journal.pone.01451
itcrossingSINA2111208.5595.602Eucalyptus urophylla70013211https://doi.org/10.1371/journal.pone.01
1MixedSC0.528494.3948.66Nelumbo lutea4098518https://doi.org/10.1186/1471-2164-15-37216294411
lismOutcrossingSC0.9828581.3234.72Nelumbo nucifera8971968https://doi.org/10.1371/journal.pone.01
ngNA0.9922330491907.1Olea europaea56431213https://doi.org/10.1007/s10528-016-9721-54621907
dismOutcrossingNANA2131035.855603.94Vanilla tahitensis225NA16https://doi.org/10.2135/cropsci201
dismSelfingSCNA2162981.28948.66Sesamum indicum3019312013https://doi.org/10.1038/srep315562
mOutcrossingNA0.782141750450Mimulus guttatus307348014https://doi.org/10.1534/g3.113.010124NA
xedNANA278186894.9Aegilops sharonensis4011797https://doi.org/10.1139/gen-2013-0065142689598C

:rossingSINA27577.24110.19Aegilops speltoides1371747https://doi.org/10.1007/s00122-005-0035-y142
NANA271374.44327.21Aegilops tauschii718511027https://doi.org/10.1073/pnas.1219082110NANANA6
fingNANA27948.724938.9Aegilops umbellulata54041547https://doi.org/10.1534/g3.117.0399661424939
0.1321945843828720.1519078297864950.1770936979867420.475136273556178MediumOutcrossing
rossingSINA41411564000.02Agrostis capillaris32227114https://doi.org/10.2135/cropsci2008.12.071428
tcrossingSINA41414243423Agrostis stolonifera35318114https://doi.org/10.1007/s11032-014-0029-zNAN
IA0.05621284312938.94Avena sativa7202NA21https://doi.org/10.3835/plantgenome2015.10.01024261
nrodismSelfingNANA251597.992268.43Brachypodium distachyon5584765https://doi.org/10.1007/s0012
dismOutcrossingNANA27462.1531560.42Cenchrus americanus4601907https://doi.org/10.1186/s12870-
ossingSINA21414102018Cenchrus purpureus191318514https://doi.org/10.1038/s41598-018-32674-xN
:crossingSINA41810551110.03Cynodon dactylon770913018https://doi.org/10.1038/s42003-020-1086-yI
crossingSINA27715.774303.2Dactylis glomerata172NA7https://doi.org/10.1139/G10-1111423227614.74
crossingNANA41425748244.54Elymus lanceolatus51538714https://doi.org/10.1139/g11-045284824058
odismOutcrossingSINA29623.6811.74Eremochloa ophiuroides89899https://doi.org/10.1016/j.scienta.20
utcrossingSINA6211417.54185.84Festuca arundinaceaNA19521https://doi.org/10.3835/plantgenome20
SelfingNA0.0227927.075418.1Hordeum vulgare18321287https://doi.org/10.1186/s12863-016-0438-614:
smOutcrossingSINA27488.82660.16Lolium multiflorum192887https://doi.org/10.1111/grs.12055142266
singSI0.927952.62365.782Lolium perenne103521697https://doi.org/10.1093/aob/mcw0811422695337.9
nOutcrossingNANA2191605.52591.7Miscanthus sinensis318226119https://doi.org/10.1111/gcbb.12275
?2121058368.4Oryza nivara107013112https://doi.org/10.1038/srep2742524245530.788.1666666666667:
A0.372121596.8449.88Oryza rufipogon15323112https://doi.org/10.1016/S2095-3119(16)61465-X24244:
ANA2121650489Oryza sativa930318712https://doi.org/10.1186/s12284-016-0125-224248940.75137.53
NANA29976.0097517.72Panicum hallii1519NA9https://doi.org/10.1038/s41467-018-07669-xNANANA57
crossingSINA4182085.21792.674Panicum virgatum49913918https://doi.org/10.1534/g3.111.001503364
rossingNA0.922715938097.84Secale cereale40485647https://doi.org/10.1371/journal.pone.0028495142
jNANA291318.8518.34Setaria italica10351679https://doi.org/10.1186/s12864-016-2628-z18251357.593
elfingNA0.121021581188.27Sorghum bicolor224613010https://doi.org/10.1186/s12864-016-3430-7202:
elfingNA0.036212875.316948.74Triticum aestivum1081619121https://doi.org/10.3389/fpls.2016.016174
ingNANA4161727.9310290.76Triticum dicoccoides265044514https://doi.org/10.3389/fpls.2017.0179828
elfingNANA4143058.613000Triticum turgidum189876814https://doi.org/10.1007/s00122-012-1939-y284
NA271444.7094940Triticum urartu45064757https://doi.org/10.1038/s41586-018-0108-01424817705.71:
?2101545.652669.9Zea mays418331410https://doi.org/10.1186/s12864-016-2555-z2022665266.99154.5
singNANA4201337.2420.54Zoysia japonica222816220https://doi.org/10.1111/tpj.1284240442121.02766:
singNANA4201824.95563.439Zoysia matrella35639520https://doi.org/10.1186/s12864-016-2969-7NAN/
ermaphrodismOutcrossingSINA281574.31359.4Fagopyrum esculentum88841788https://doi.org/10.1270-
utcrossingSINA2121456.53437.754Ziziphus jujuba254014512https://doi.org/10.1007/s11295-016-1032-:
nOutcrossingSINA2171036762.84Eriobotrya japonica9609617https://doi.org/10.1016/j.scienta.2019.02.0
odismMixedSCNA27451.7199.628Fragaria ananassaNANANANANANANA28.518285714285764.52857
edSCNA27416.2214.373Fragaria iinumae41731097https://doi.org/10.3835/plantgenome2015.08.0071N.
SCNA8281820697.762Fragaria vescaNANANANA14224124.9200714285714652.608339233148270.16
ossingSINA21712671874.77Malus domestica15417158617https://doi.org/10.1038/hortres.2016.57NAN/
IA2171299.67733.5Malus pumilaNANA17NANA275343.147058823529476.45117647058821.77187457
INA2171481.72753.06Malus sieversiiNANA17NA34273444.297647058823587.161.967598863304390.
:crossingSINA28522.69293.4Prunus armeniaca357678https://doi.org/10.1007/s11295-007-0125-x16229
singSI0.9528849342.3Prunus avium7181008https://doi.org/10.1371/journal.pone.0141261NANA34242:
singSINA28591.4240Prunus dulcis157938https://doi.org/10.1186/1471-2164-11-5511623233073.9252.4
singSINA281550.62234.03Prunus mume80073878https://doi.org/10.1093/dnares/dsv003NANANA29.2:
ssingSINA28389.2273.84Prunus persica1839NA8https://doi.org/10.1007/s11295-015-0911-916226934.
SINA29639.491222.57Prunus salicina14411378https://doi.org/10.1371/journal.pone.0208032NANANA2:
issingSINA2172243.4537.9Pyrus communis314310217https://doi.org/10.1093/jxb/eru311NANA53831.6-
tcrossingSINA271027.425515.12Rosa chinensis22131527https://doi.org/10.1038/s41598-019-42428-y1
ssingSINA27462.7311.982Rubus idaeus4521717https://doi.org/10.1186/1471-2164-14-2NANA29344.56:
singSINA27309293.4Rubus occidentalis4381007https://doi.org/10.1007/s00122-015-2541-x14229341.9
SCNA42238001173.6Coffea arabica33827822https://doi.org/10.1007/s11295-015-0927-1444117453.34:
crossingSINA2111349.203583.04Coffea canephora30399311https://doi.org/10.1111/pbi.13066NA2807:
crossingSINA291084.1301.365Citrus clementina9612969https://doi.org/10.1186/1471-2164-13-593NAN.

ingSINA29976.58490.956Citrus sinensis122979https://doi.org/10.1007/s11295-007-0083-318261154.5t
NA2192178.5508.56Populus adenopoda21218919https://doi.org/10.1007/s10681-009-0085-3NANANA
3027.1508.56Populus alba32214119https://doi.org/10.1007/s11295-010-0297-7NANA50926.76631578
A2194067.16500Populus deltoides201215019https://doi.org/10.1186/s12864-016-3003-9NANANA26.3'
92278.5514.0368Populus nigra18816519https://doi.org/10.1007/s11295-007-0085-1NANA52827.05456
2194067.16394.51Populus simonii143015019https://doi.org/10.1186/s12864-016-3003-9NANANA20.76
2191542.35469.44Populus tremula3446119https://doi.org/10.1007/s11295-009-0204-238244024.70736
466405.53Salix purpureaNANA19https://doi.org/10.1093/aob/mcz04738246021.3436842105263182.42
dismMixedNANA21213723090.48Capsicum annuum257812012https://doi.org/10.1093/dnares/dsv0382
hrodismSelfingSCNA21210563628.38Capsicum baccatum395NA12https://doi.org/10.1007/s11032-016
ermaphrodismSelfingSCNA4242662.435066.04Nicotiana tabacum440910024https://doi.org/10.1007/s1
SC0.62279701369.2Petunia axillaris2073497https://doi.org/10.1139/g10-1161421369195.6138.571428f
hrodismSelfingNA0.032121297.3823.786Solanum lycopersicum197410012https://doi.org/10.1186/1471-
odismSelfingSC0.082121285.5958.44Solanum melongena95218312https://doi.org/10.1007/s00122-012
OutcrossingSINA212789.7926.426Solanum pennellii20813112https://doi.org/10.1111/jipb.12449NANAN
odismMixedSCNA2121567.5688.247Solanum pimpinellifolium44012012https://doi.org/10.1371/journal.p
hrodismOutcrossingSINA212883860.64Solanum tuberosum226417812https://doi.org/10.1007/s00122-0
OutcrossingSINA21512183814.2Camellia sinensis11245415https://doi.org/10.1270/jsbbs.62.2633023817
ossingNANA2142265.1716Boehmeria nivea13214714https://doi.org/10.1007/s11032-014-0082-7NANAI
23489Vitis amurensis2289419NA38248925.736842105263259.10526315789472.296523517382410.15
98489Vitis cinerea23518819https://doi.org/10.1007/s00122-009-1107-138248925.736842105263260.84
163.108417.44Vitis rotundifolia234634420https://doi.org/10.1007/s00122-019-03302-7NANANA20.8721
1929.13446.946Vitis vinifera719914919https://doi.org/10.3389/fpls.2015.0039338241623.52347368421
crossingNANA2111266.210758Cryptomeria japonica320519011https://doi.org/10.1186/s12864-018-458
12546.59291Larix kaempferi21014512https://doi.org/10.1111/jipb.13265NANANA774.2545.5416666666
1889.218190.8Picea abies68624712https://doi.org/10.1371/journal.pone.0101049NANANA1515.9157.4
2121572.829281.32Pinus balfourianaNANA12https://doi.org/10.1007/s11295-015-0866-xNANANA2440
8212857.4627579.6Pinus koraiensis1229412https://doi.org/10.1007/s00468-010-0438-5NANANA2298.1
99212123127602.7Pinus lambertiana3999412https://doi.org/10.1007/s11295-010-0347-1NANANA2300
A212195625134.6Pinus massoniana25112012https://doi.org/10.1515/sg-2014-0001NANANA2094.5516
12170823814.3Pinus pinaster35717712https://doi.org/10.1186/1471-2164-12-368NANANA1984.52514
106021936.54Pinus radiata7878612https://doi.org/10.1007/s00468-014-1090-2NANANA1828.04588.33
230521516Pinus taeda3856125112https://doi.org/10.1534/g3.115.019588NANANA1793192.083333333

genyhaploid_chromosome_numberdoi_originalkew.nchromosomeskew.ploidykew.Cvaluechrom_sizechi
5848.5627586206896118.7931034482762.446177005226080.239792893303610.2803438329199510.
010.12.0027NANA68538.5087580.52.090433992274480.187555412956620.2204911507234250.48047
135.83333333333361.66666666666670.453987730061350.1550855354126190.1810135988186390.46
antgenome2012.06.0011364144780.413333333333780.9699883933012770.1835404046676670.2156
1221002167.88333333333372.26666666666670.4304576590886530.1740044959222660.2041685642
3821820.1666666666789.77777777777780.04932393248481520.2017416721516790.2372718502340.
040444022.005157.4147.153556009997730.2789266018374980.3212299920341450.4889463300918
.97846.837666666666770.56666666666671.506622163073880.171085957701350.2006211161428230
08.40.7533768146433830.3604442820654040.3954019254384260.476740713677567MediumMixeddip
8.017NANA4690312.9668.2333333333330.2180257327880030.1670099060914870.1956502050738
5171.18750.881527698121660.2904515808876930.3325840871414070.486903223805481LongMixed
650.207445645184670.2439177071850490.481715352824042LongOutcrossingdiploid-0.15061196036
062592.81251.058649918373460.2061502571611880.2424138274433150.481634391072574LongOut
.616666666666771.8333333333331.391669357442690.173264596957320.2032702034384760.4818
0902421364114.179.9533333333330.700730353491090.1866846856057930.2194503482082790.473
76NANANA142.083333333331571.10498533724340.2785627410947740.3208664761040560.47539
09-1159-2NANANA63.282352941176573.59705882352941.162994980479640.1762589940489670.20
-0558-83422372139.796470588235145.4117647058821.040167638667980.2679302307678790.31010
966666666667330.4444444444441.147509356792840.3715528938860050.4045341775458110.48572
0239440.2313604164698670.2710668914190040.466420052058733MediumOutcrossingdiploid-0.02146
57142857141.818361086765990.295636169240610.337591718092830.485402583517186LongOutc
08516223529.3470.8752.415644171779140.1716184713378370.2012691416097690.45895230891723
014410215624.784.53.421052631578950.1938064059406220.2279275257288240.4387612811881245
n.2010.11.007NANANA20.919111.1255.312156412830440.2305726811918290.2701921089016190.46
23526.525714285714371.37671428571432.690849849202930.1724819547329890.2023192155152080
01040-X18256256.72497.331.715852196601090.2125135110568310.2497697554611840.47125135110
z344154090.8964705882353120.4705882352941.325360461805290.2417379062038050.2824606696
364149183.1387.722222222221.055241455818860.1986923060655870.2336942130229570.48326
1112559.1947368421053100.9421052631581.705254734595890.2174363580766690.2554049584359
4NANA75884.755555555555598.891.166767173571050.2146572162844740.2522297470498080.4682
1959422979749970.2304535561841820.4695942297975ShortOutcrossingdiploid-0.22218378718691N.
02.067869.282.160422604606490.1688484627759130.1978946910779680.483442423138796ShortSel
00832439124.4566.5252.720858895705520.1639730590281560.1919350846937060.47899831618926
72828753.128697967879380.1273632447671010.146676466636740.453420405595888ShortSelfingdip
0858888888889118.6447111111113.973513935920810.2396196217063240.2801548334454970.4710
4182538108.666666666667170.8888888888891.572597137014320.2902131671520380.33235232882
7574.21.820858895705520.1772723260574270.2081279731705420.473106027171452ShortOutcrossir
4.018NANA53821.51684.523.928239449711840.1938371381367290.2279639265641280.4877534855
ta.2009.12.008NANANA54.54545454545163.7272727272733.001666666666670.284346223859425
836283.6274.590.2629927367604540.1779250052477940.2089171129371170.467792500524779Long
366666759.4388888888892.87607526881720.150881915579340.1758267610316070.4806045508655
164-14-734NANA61141.07665.221.587788489628980.1616226629195260.1890534973302550.47744
0555.9250.2541467848216310.1440810999282040.1674137790145350.470340091660684MediumDip
-9908-y60414679.390.93888888888899.778375149342890.2034414338980890.2392586896271680.46
571428571167.8571428571430.7603996790142630.287764784289410.3299647090007260.4696806
90343103840040.2156733292647410.2533925134708160.474152120842249ShortMixeddiploid-0.0226
2977.42595.8333333333331.237756969109890.2104312073637270.2473713818089610.4758692672
1.9527142857143151.5985714285715.423393588151420.2737163402627770.3159949606519890.467
NA45022.494126.695.632168578287540.2487350311157390.2900036274106730.487436751555787S
02796.84.60360488895230.2117790161343820.248924760585820.485588950806719ShortMixeddiplo
0.885.238148354712770.2635243774582380.3055691279836280.488176218872912ShortMixeddiplo
461538461538110.4707692307691.727559244556720.2297601621695820.2692883612575130.47921
1016117222200526.5072727272727141.063818181815.321702448727620.2637059399465060.3057
11-640456228.8895238095238134.2982380952384.648682995978110.2568587074669220.29861749
0443-524265054.605135.083333333332.473827183102890.2576709699449950.2994702279076350.

?864-016-2802-3NANANA34.551833333333392.66666666666672.681960918619850.20594090513678
2.5717647058824125.4705882352942.947272425800030.2473891397821380.2885615837456840.481
1219613622103116.816666666667231.111111111111.97840871260760.3299993615091270.3692860
1.2309090909091150.5272727272733.93731868549960.2727327597183420.3149995229132390.4793
'2280767.9166666666671341.973006134969330.2565489036875870.2982918490081760.486474939
450950.856155.13.049787635677210.2768791256294020.3191804052619760.47768791256294LongC
30769230769231.519584709768760.1774527702506150.2083462009271630.475188674634663LongC
4042807140.34372.3350.5154158027119270.1741209214533310.204309862553040.48370604607266
8.2496.27272727272731.230479643056330.2110451598463390.2480794233855470.47373137816784
35.491251.166645140458510.2580911350846240.2999107144832980.469761391885578ShortSelfingC
0055.257122.292.213113270716830.2438193318011960.2847163229610360.48719096659006ShortS
'.0871428571430.5914913818288050.3766760426169140.4086819278415870.482382291802416Shoi
.083205521472390.1941901901209640.2283819852474520.449031698353494MediumSelfingdiploid-0
.763.696319018404910.1972469496310160.2319926375586030.487889877985241ShortSelfingdiploid
10290557.6581.4951.413616652211620.1891299979013190.222370276727680.484456499895066Shc
;16284139.884062566.656251.671250264438330.1642079769931770.1922228030250090.489506499.
58.68151.8752.588190184049080.2739689138090350.3162502104261860.471746114226129ShortSel
22258753.345454545454594.74545454545451.77607361963190.2089016684425650.2456042018635
5297.1481750.7352946052700770.3599729997043640.3950101156067860.482496624963045ShortMi
.805714285714179.2857142857140.2629571893124140.2967363593004280.3386464735610790.4709
457142857143297.7142857142863.946072862228280.3601865022406760.395187660471090.480026
109368.4679.6251.163087934560330.1861597866996480.2188223573616680.480384986668728Medi
.816254368.46212.71253.10710633946830.3194089066086610.3597856902617970.47742611332608
17202.80.06904777063883150.3131850497516930.3540938816860590.468864174958615ShortMixedC
0136363636363.026863729317720.2703950432314730.3126244514316390.479126822111952ShortS
45451.608291503997030.1845851394736910.216935926273280.471325921770335ShortSelfingdiploic
818181818266.62727272727270.8190016426967050.1641561350183930.1921593136655080.469468
753.345454545454577.49090909090911.452624403544650.1827123521076790.2146875009769640.
72727272788.53636363636361.716909949933010.1999062643681880.2351204931317660.47271875
NANANA69.4367561.91666666666670.8916988002270650.1555521452600250.1815885975216160.4
.NANA384.61538461538547.20769230769230.122740.126259209839410.1453067401414550.471250
-0650-1NANANA110.2966666666667209.7055555555561.901286429528440.3175615901946980.35810
637.8975153.613754.053400620093670.2755462421073190.3178408470789290.485971640131707Lc
.875189.52.46504065040650.304192702511740.3457230494326170.475524087813967MediumOutrc
0575.79590.61666666666671.195549398597090.20297135723930.2387097566526140.47524761310
1268545.6476.73333333333331.681273736488460.1814734960504920.2131973483199680.47876489
12142.6251.620370370370.2652381573202940.3073394331969760.470654769665037LongMixeddd
?-015-0311-814224583.82857142857142883.435582822085890.3564347297092480.39205671272023
21428571428570.394155287288080.1346237875697650.1556866125244350.447803398224252Short
22882622450103.630384615385196.7538461538461.898611559573780.309192542350780.35039907
-3269-y524234790.2769230769231156.6146153846151.734824471710970.2782230731222060.32052
3-0286-3262238191.7815384615385127.7230769230771.391598779711020.2498655721987570.2912
439-0523.2011.01879.x36NA149183.13273.63.291230602670520.3505081284989890.387062048501
5-x20241642.0585.282.028061831153390.1950011719698240.2293414884462780.469500117196982
2.9300909090909108.81818181822.534776412391390.2276890115432060.2669780710947250.47
112.3636363636362.038393033841280.2320996202960380.2718865233110170.475645420026913Lo
-24022261153.7811090909091100.6363636363641.87122142584030.2170252013498480.2549362096
4422258753.3454545454545112.8545454545452.115541922290390.2327007045378040.272552108E
4514422262654.1456363636364109.8636363636362.029039526395140.229002387565250.2684441E
8.582561.78750.5210507452617380.1553111913537770.181291692308350.456913898919222Medi
1222316223729.3472.66252.476567825494210.1746779663449810.2049856780917450.4593347457
'82.9173913043478132.5652173913041.598762519007920.2550488156246750.2967118356399510.4
0.11.0634NANANA431.07230769230879.68076923076920.1848431639168160.1862490461769670.21
16294959.29125186.333.142622225033210.3019323038549190.3435909215082340.48762076899093
1436232.14285714285711253.8888888888890.2468664002201760.2880003599797490.481919028
4.985714285714116.8571428571430.1186384139001290.2375166657206460.2778555238045490.462

25037587.1782.45714285714290.140431464238880.1906401212968430.2241687600825240.4558057
318.172857142857196.3428571428570.317618049505340.3089154934246650.3501414039435530.47
9705.557142857143135.5314285714290.1920913563749010.2581324513008640.2999540064484440
diploid-0.715452725257670.143734256926952CommelinidsViridiplantaeEukaryotaMagnoliopsida
343447285.71571428571482.57142857142860.2889985550072250.1908186891115860.22438118180
NA3423244.5101.7142857142860.4160093485246860.2184702891567910.2565821624719420.47989
12934616.14135.3809523809520.2197243359966120.2579776510629650.2997917828804220.488475
?2-011-1598-410235553.686319.59845.953105092575350.3679881218617630.4016247544772030.47
-018-1267-8NANANA222.91714285714366.02185714285710.2961721844118890.1630700222558680
ANANA144.142857142857100.7142857142860.6987115956392470.2171300857806390.25505581890
NANA78261.668333333333358.61111111111110.9504247632946860.1492988188000270.173870511
42857142857102.2528571428570.1663343558282210.2191876401707320.2573976060318350.45988
38.895714285714183.8571428571430.3122066240202610.3001359267880440.3418883558667460.48
113.03.03018281290.193333333333369.28888888888890.7682262793505310.168864005757220.1979
14.07.00322844181199.32571428571467.50.3386417063241790.16571179114080.194063312594515
25428774.014285714286132.4385714285710.171106107306990.2549156319737230.2965712994702
1380.02285714285769.82857142857140.1837483459641530.1698054566286270.199061501705243C
968857142857136.0857142857140.4026575567824930.2587011765081540.3005495182321220.4655
3822592136.40526315789584.50.6194775629895440.1938064059406220.2279275257288240.48388
2.871878393051030.1993560264155050.2344743461719230.474946335534625ShortSelfingdiploid-0.
537.49133.0666666666673.549390948697430.2555749152303520.2972665702605740.47963124293
3.374233128834360.2601417704189480.3020545412736880.480011814201579ShortSelfingdiploid0.2
.5244444444444108.4455222222221.885207641196010.2272182243234870.2664516110045910.469
1132099.593115.844444444441.163178581270210.236312311111690.2765341838125490.48535068
280931156.83428571429227.5714285714290.1967191251000270.3280524081161240.367556575179
33333333333146.5333333333332.544275957865490.2689984076970220.3111993307641010.474333
734118.827215.81.816085569777910.3212701886026130.3614720414175810.482127018860261Sho
42616944807.082857142857136.9190476190480.1696468292038230.259551834961250.3014388149
3412005643.1725107.9956250.1679108248564730.2266480115341150.2658133186516940.48291550
112005928.571428571429218.4714285714290.2352769230769230.32285231049680.3628998232087
4285714286206.3870.2924512145748990.3154821315391450.3562041565490780.473640304505592
650.5789168133637960.2764009522664710.3187003186165680.477640095226647ShortOutcrossing
6.863.179721310695770.1645721291857140.1926686947930660.483228606459286MediumOutcrossi
ANA28.1719591.24753.238948670574810.2038904876834730.2397826876523480.485194524384174
/jsbbs.64.291NANANA169.925196.78751.158084449021630.3092151960510090.3504201383931710.
9NANANA36.4795121.37753.327279705039820.2427790524628290.2835902158509120.4785649210
06534275844.872941176470660.94117647058821.358082953174980.1537256368071120.179336919
7142857142.26270863806680.1603664856286380.1875113311973810.451480926518377MediumMixe
|ANANA30.624714285714359.45714285714291.941475838841650.1509166954652790.175869722446
612237911041350.1885639694644830.487900849682291MediumMixedpolyploid-0.413671911145396
ANA110.28058823529474.52941176470590.6758162334579710.1778237511035710.2087947260788
73960460.1810100480474140.2126393274799010.48123588517926LongOutcrossingdiploid-0.293286
1978491915660370.2327020885297180.482226423033296LongOutcrossingdiploid-0.16420070396778
9336.67565.336251.781492842535790.1618331219095740.1893117312384630.457729140238697Lon
7875106.1252.480280455740580.2242552273425530.2631271401504940.465531903417819LongOut
464166666666670.1768107952747660.2075696056332050.459601349409346LongOutcrossingdiploid-
5375193.82756.625731743793530.3072037783467070.34854568764870.475900472293338LongOutc
.2348.651.421267893660530.1293052255099770.1490861909551710.453663153188747LongOutcro
24.7371.05455555555562.873212921777420.1719279263781350.2016455691903870.4635475473753
411764705882131.9647058823534.170663692136080.254416184485970.2960439073261390.485553
14256273.5885714285714146.7751.994535253921420.2692274365459340.3114333472079870.46703
38857142857166.11.483098383881120.1632105316083910.1910008006053490.451887218801199Lo
914285714285744.14285714285711.053169734151330.119652707282220.1371164377846740.44566
54545454545172.7272727272733.237900477164280.2916732676428480.3337696190289080.490530
53.0036363636364122.65481818182.314083081778270.2442332070615720.2851636489436030.47
|ANA33.485120.4555555555563.597298956414980.2417205873321820.2824418591300970.47130228

506666666667108.5088888888891.989139556294250.2272983743174060.2665412733968970.46969
126.7663157894737114.6578947368424.283663677835460.2348890967860220.2749684890340450.4
94737159.3210526315795.952296680824290.2805890577638310.3228869199955730.488452055671
157894736842214.0610526315798.134320.3202262467649320.3605271012418620.49053822351394
384210526119.9210526315794.432562026687580.2411034938397270.2817711676605890.486373868
36842105263214.06105263157910.30939646650280.3202262467649320.3605271012418620.4905386
38421052681.17631578947373.285510395364690.1886271141997410.2217705559137280.483611951
10526315798.54683993785910.2990791045802820.3408833430748040.489425216030541LongDioec
1423090257.54114.333333333330.4439439828117320.2344975048769160.2745368918524610.4778
3-0485-82423628302.365880.2910389760719660.1991074174124970.2341822249454690.474925618
11032-016-0514-74845061211.085110.934583333330.525544606832950.2303366247953390.269929
5714290.7084428863569970.2612231506439520.3031810593253320.465889021520565ShortMixeddi
-2164-15-1152NANANA68.648833333333108.108333333331.574802193773630.226791051785853
2-1815-924295479.87107.1251.34124201827970.2255387757016410.2645696170336130.4771282313
IA77.202166666666765.8083333333330.8524156273679710.1626855959457990.1903573006649450
none.0096417NANANA57.353916666667130.6252.277525365166870.2529945285856680.29453949
16-2673-724285671.7273.5833333333331.025980665551220.1762358654860980.206873655041420
7254.2881.20.3193330187195220.188664534230970.2218151955122560.479244302282065LongOutc
NA51.1428571428571161.7928571428573.163547486033520.2827109839977290.3249923862058320
502452595169770.1750402126619540.481591855764051LongDioecy diploid-0.5111995878008930.466
4105263157892.36396728016360.1535372772776470.1791045807795250.481765119856718LongDio
08.15545.181841701801460.2268507472511060.2660403410151350.486342537362555LongDioecydi
05101.5331578947374.316248495343960.2182283385042430.256306884121820.485169912552855L
1-5NANANA978115.1090909090910.1176984569622610.235431835150340.2755661019512610.4759
66670.05882036379291790.122690803118060.1408812949526560.468557566926505LongOutcrossing
1333333333330.1038546957802850.2789435677649650.3212469342975550.48157863064708LongOut
0.11131.0666666666670.05371342548764880.253464790404690.2950376564975330.4794553992003
371.4550.0310903711438890.1726163540775480.2024825768831160.472718029506462LongOutcros
0.225102.583333333330.04459708651689870.2196262879398610.2578957040082230.47663552399
630.07782101167315180.2837340135103360.3260037209549080.481977834459195LongOutcrossing
2.3333333333330.07172161264450350.2649532286014280.3070455888874530.480412769050119Lo
3333333333330.04832120288796680.199604292801220.23476595403680.474967024400102LongOut
33330.1071295779884740.3060003837617440.3474200001095050.483833365313479LongOutcrossin

rom_genmaprecPrec_intra_HPrec_intra_KPrec_interlongevity2mating_system2ploidy2resmarker_densi
49102734114841Long Dioecy diploid 0.138424055388539NA Superasterids Viridiplantae Eukaryota Magnoliopsida
72213309789 Short Outcrossing diploid -0.2330047685771450.779043723829 Superasterids Viridiplantae Eukaryota Magnoliopsida
61676170601402 Short Outcrossing diploid -0.5956865688395380.232310838445808 Superasterids Viridiplantae Eukaryota Magnoliopsida
6822793321940.482418911370426 Short Selfing polyploid -0.3207258026504820.35303708616592 Superasterids Viridiplantae Eukaryota Magnoliopsida
2653280.445667415987044 Short Dioecy diploid -0.453228668492660.280949071776035 Superasterids Viridiplantae Eukaryota Magnoliopsida
490.466860185794631 Short Outcrossing diploid -0.4180873128067840.0875988157372646 Lilioids + Alii
75 Long Outcrossing polyploid 0.48031099659338114.9829584185412 Superrosids Viridiplantae Eukaryota Magnoliopsida
0.46345399530015 Short Outcrossing diploid -0.3796420202291951.02244394943291 Superrosids Viridiplantae Eukaryota Magnoliopsida
0.899358395213941 NA Superasterids Viridiplantae Eukaryota Magnoliopsida
390.477800660406099 Medium Outcrossing diploid -0.5581729718936310.0485685071574642 Lilioids + Alii
diploid 0.3980606602430150.226577400320427 Commelinids Viridiplantae Eukaryota Magnoliopsida
45141.14318842090178 Commelinids Viridiplantae Eukaryota Magnoliopsida
crossing diploid -0.153445372469490.258068195590028 Commelinids Viridiplantae Eukaryota Magnoliopsida
48033164296 Long Dioecy diploid -0.3692634897094961.29049617909805 Commelinids Viridiplantae Eukaryota Magnoliopsida
1890390467149 Short Mixed diploid -0.3226853723384430.860356412503652 Superasterids Viridiplantae Eukaryota Magnoliopsida
15860121642 Medium Outcrossing diploid 0.3353837402064491.56011730205279 Superasterids Viridiplantae Eukaryota Magnoliopsida
169016604124060.480956411414645 Short Outcrossing diploid -0.360552254270630.658114891243726 Superasterids Viridiplantae Eukaryota Magnoliopsida
062518689650.486348837103993 Short Outcrossing diploid 0.2599453197921524.01213528911779 Superasterids Viridiplantae Eukaryota Magnoliopsida
8099320667 Short Selfing diploid 1.025682127215315.32006019215187 Superasterids Viridiplantae Eukaryota Magnoliopsida
65076767680.364788732394366 NANANANA
ossing diploid 0.4884919833441970.432369266725095 Superrosids Viridiplantae Eukaryota Magnoliopsida
Medium Outcrossing diploid -0.3395980841414620.362133605998637 Superrosids Viridiplantae Eukaryota Magnoliopsida
Short Selfing diploid -0.1506309209720185.47368421052632 Superrosids Viridiplantae Eukaryota Magnoliopsida
66321585148979 Short Outcrossing diploid 0.1359486448868270.782781203690425 Superrosids Viridiplantae Eukaryota Magnoliopsida
0.453211707818998 Medium Selfing diploid -0.32485118838196 NA Superrosids Viridiplantae Eukaryota Magnoliopsida
05683 Short Outcrossing diploid -0.07270311644732021.0824342430012 Superrosids Viridiplantae Eukaryota Magnoliopsida
022010.484808112129636 Short Mixed polyploid 0.1046222188426052.60865626051617 Superrosids Viridiplantae Eukaryota Magnoliopsida
068367031 Short Mixed polyploid -0.205794192296322.22476175200823 Superrosids Viridiplantae Eukaryota Magnoliopsida
180.485128229372456 Short Outcrossing polyploid -0.03951593190696021.62354405619276 Superrosids Viridiplantae Eukaryota Magnoliopsida
29524625383 Short Outcrossing diploid -0.08743875292503132.32826428945988 Superrosids Viridiplantae Eukaryota Magnoliopsida
ASuperrosids Viridiplantae Eukaryota Magnoliopsida
fing polyploid -0.3691419043951420.249471432402597 Superrosids Viridiplantae Eukaryota Magnoliopsida
Short Selfing polyploid -0.38902852757553 NA Superrosids Viridiplantae Eukaryota Magnoliopsida
diploid -0.6850938610367226.29301868239921 Superrosids Viridiplantae Eukaryota Magnoliopsida
168846856258 Medium Selfing diploid 0.174280116519618 NA Superrosids Viridiplantae Eukaryota Magnoliopsida
78820.476690351905782 Short Outcrossing diploid 0.4406073217736822.69631901840491 Superrosids Viridiplantae Eukaryota Magnoliopsida
ng diploid -0.318813613952740.539877300613497 Superrosids Viridiplantae Eukaryota Magnoliopsida
525469 Medium Outcrossing diploid -0.1398656104340781.37757947573898 Commelinids Viridiplantae Eukaryota Magnoliopsida
50.3266077655093730.480395111259948 Long Outcrossing diploid 0.4503794770767240.275 Magnoliids Viridiplantae Eukaryota Magnoliopsida
g Dioecy diploid -0.46158963008649 NA Superrosids Viridiplantae Eukaryota Magnoliopsida
19 Long Dioecy diploid -0.4888324933948431.9005376344086 Superrosids Viridiplantae Eukaryota Magnoliopsida
1510861302 Medium Outcrossing diploid -0.4484194937391520.668679196286558 Superasterids Viridiplantae Eukaryota Magnoliopsida
Dioecy diploid -0.7302233920251840.154131636749224 Superasterids Viridiplantae Eukaryota Magnoliopsida
9670490482109 Medium Outcrossing polyploid -0.002674485309577262.48148148148 Superasterids Viridiplantae Eukaryota Magnoliopsida
83546992 Long Outcrossing diploid 0.3686365679568010.175377287670524 Superasterids Viridiplantae Eukaryota Magnoliopsida
6506944872326 NA Superrosids Viridiplantae Eukaryota Magnoliopsida
280311 Short Mixed diploid -0.1119348950600540.381013884404262 Superrosids Viridiplantae Eukaryota Magnoliopsida
673762894682 Short Mixed diploid 0.42441554845951315.7255364927505 Superrosids Viridiplantae Eukaryota Magnoliopsida
hort Mixed diploid 0.2614980830972161.0180492575798 Superrosids Viridiplantae Eukaryota Magnoliopsida
id -0.002452914573336870.432776905882912 Superrosids Viridiplantae Eukaryota Magnoliopsida
d 0.35403080671195214.3483918944042 Superrosids Viridiplantae Eukaryota Magnoliopsida
2320166891 Short Mixed diploid 0.04479754887127520.212919523637676 Superrosids Viridiplantae Eukaryota Magnoliopsida
570083873260.478518721813319 Short Dioecy diploid 0.356442583631654 NA Superrosids Viridiplantae Eukaryota Magnoliopsida
7837390.488421843212711 Medium Dioecy polyploid 0.3007275696522299.62121711610734 Lilioids + Alii
.479805914162083 Long Mixed diploid 0.257986037684421.19799774135458 Superasterids Viridiplantae Eukaryota Magnoliopsida

?31613835ShortOutcrossingdiploid-0.4168327976680630.0333317924475511CommelinidsViridiplantae
?2702213346381ShortSelfingdiploid0.4468254674412141.66042322882412CommelinidsViridiplantaeEuk
).465447493042981ShortSelfingdiploid0.06607944947426721.09417076676993CommelinidsViridiplant
62410.477915620650828MediumOutcrossingpolyploid-0.3604940148243920.0804995975020125Com
?0734939771MediumOutcrossingpolyploid-0.1401052006873460.103125912941864CommelinidsViridip
?126241094ShortSelfingpolyploid0.07530703517836590.556614374902426CommelinidsViridiplanta
?3597624372353ShortSelfingdiploid1.120454276015452.07875423760384CommelinidsViridiplanta
?1.1908285808888310.451867146036553ShortOutcrossingdiploid-0.5652366578110640.2947924276797
?021820.479795006127189LongOutcrossingdiploid-0.1096723258086190.94796828543112Commelinids
?9244160.480516601044446MediumOutcrossingpolyploid-0.5862619785368776.94485734619785Com
?3948595819MediumOutcrossingdiploid-0.2051637094995350.0399702546941811CommelinidsViridipl
?35723994770575MediumOutcrossingpolyploid0.3848236896933610.062465583282997CommelinidsViri
?9136499783350.463207111750802MediumOutcrossingdiploid-0.4479064132249470.10964101805997
?0.484081513863848MediumOutcrossingpolyploid-0.534561007221033NACommelinidsViridiplanta
?420.464987947424818ShortSelfingdiploid0.03593007057176410.338125911297318CommelinidsViridi
?0.452829350946947ShortOutcrossingdiploid-0.5498752819593730.0721761097076868CommelinidsVir
?28739501165MediumOutcrossingdiploid0.1263136327018314.37572016356537CommelinidsViridiplant
?4547681085MediumOutcrossingdiploid-0.2809991219595351.22776555928541CommelinidsViridiplant
?1247436980020752.90445168295331CommelinidsViridiplantaEukaryotaMagnoliopsida
?5863MediumMixeddiploid0.2716337615656610.340090690850894CommelinidsViridiplantaEukaryotaM
?9804615298055119.0245398773006CommelinidsViridiplantaEukaryotaMagnoliopsida
?690913813721MediumSelfingdiploid0.03436853057784692.93401838831801CommelinidsViridiplanta
?33950649MediumOutcrossingpolyploid0.05849410511538730.27835512759152CommelinidsViridiplanta
?910.475436058302303ShortOutcrossingdiploid0.5466175849761810.499886389456942CommelinidsVi
?15641078ShortSelfingdiploid0.3352822085606261.99675888413011CommelinidsViridiplantaEukaryot
?rtSelfingdiploid0.6671266367520811.89014281266042CommelinidsViridiplantaEukaryotaMagnoliopsic
?512040.488550087379107ShortSelfingpolyploid0.06600928988796150.638159532803028Commelinids
?0720882ShortSelfingpolyploid-0.1539707638495970.257512564669665CommelinidsViridiplantaEuka
?380.487346593606914ShortSelfingpolyploid0.5225770721683880.146CommelinidsViridiplantaEukary
?2ShortSelfingdiploid0.4866119482249780.912145748987854CommelinidsViridiplantaEukaryotaMagno
?diploid0.2716284581282711.56672534551856CommelinidsViridiplantaEukaryotaMagnoliopsida
?ingpolyploid-0.3724990278639165.29795025443477CommelinidsViridiplantaEukaryotaMagnoliopsida
?IMediumOutcrossingpolyploid-0.08384092997534576.32366591591991CommelinidsViridiplantaEukary
?476151899506376ShortOutcrossingdiploid0.5476106207765936.53523613358835SuperasteridsViridip
?038569LongOutcrossingdiploid0.1817735885687925.80234560963464SuperrosidsViridiplantaEukaryo
?2384910.479630919812183LongOutcrossingdiploid-0.5230215494956541.25845524618531Superrosic
?eddiplloid-0.431240607304915NASuperrosidsViridiplantaEukaryotaMagnoliopsida
?61940.45013095649504MediumMixeddiploid-0.51852957716895419.4660708204858SuperrosidsViridi
?NASSuperrosidsViridiplantaEukaryotaMagnoliopsida
?580.481048455947269LongOutcrossingdiploid-0.3903371603760618.22340873813855SuperrosidsVirid
?118125525NASuperrosidsViridiplantaEukaryotaMagnoliopsida
?85NASuperrosidsViridiplantaEukaryotaMagnoliopsida
?ngOutcrossingdiploid-0.4379926880603561.21676891615542SuperrosidsViridiplantaEukaryotaMagnol
?tcrossingdiploid0.03531762798721612.09757522640958SuperrosidsViridiplantaEukaryotaMagnoliopsi
?-0.2991619211621490.654166666666667SuperrosidsViridiplantaEukaryotaMagnoliopsida
?rossingdiploid0.66667734305855534.2135623637995SuperrosidsViridiplantaEukaryotaMagnoliopsida
?singdiploid-0.7276243537182166.71560035056968SuperrosidsViridiplantaEukaryotaMagnoliopsida
?348LongOutcrossingdiploid-0.3240270902059356.47436761468302SuperrosidsViridiplantaEukaryota
?3893205057LongOutcrossingdiploid0.2762581110216495.84309351180517SuperrosidsViridiplantaEul
?32490935133MediumOutcrossingdiploid0.3182324454975994.29608634881193SuperrosidsViridiplanta
?ngOutcrossingdiploid-0.44124313115385114.491220647345SuperrosidsViridiplantaEukaryotaMagnoli
?4672468889LongOutcrossingdiploid-0.8402958218728861.49284253578732SuperrosidsViridiplantaE
?0603074675LongMixedpolyploid0.5055884377666120.288002726653033SuperasteridsViridiplantaEuk
?76748473369234LongOutcrossingdiploid0.163739017359795.21233534577387SuperasteridsViridiplanta
?87481353LongOutcrossingdiploid0.1806834638618923.18882418329932SuperrosidsViridiplantaEukal

9819368601LongOutcrossingdiploid0.03900220988245020.248494773462388SuperrosidsViridiplantaë
186046794567685LongDioecy diploid0.148441113899970.416863300298883SuperrosidsViridiplantaëE
1781LongDioecy diploid0.4774096128277920.633160295736983SuperrosidsViridiplantaëEukaryotaMag
14LongDioecy diploid0.7740445629203594.024SuperrosidsViridiplantaëEukaryotaMagnoliopsida
8096828LongDioecy diploid0.1925046756676160.365732570119493SuperrosidsViridiplantaëEukaryota
3223513944LongDioecy diploid0.7921227639009893.62474968948823SuperrosidsViridiplantaëEukaryo
3378934LongDioecy diploid-0.1907816836769750.732788002726653SuperrosidsViridiplantaëEukaryot
cy diploid0.630077141917748NASuperrosidsViridiplantaëEukaryotaMagnoliopsida
74792073076ShortMixeddiploid-0.02711886722916680.834174626595221SuperasteridsViridiplantaëE
117708MediumSelfingdiploid-0.3011418605085830.10886401093601SuperasteridsViridiplantaëEukary
96991659220.488764026033139ShortSelfingpolyploid-0.04212096934493970.870305011409306Super
iploid0.1861368136921720.151183172655565SuperasteridsViridiplantaëEukaryotaMagnoliopsida
0.2659735036746960.477232587648821ShortSelfingdiploid0.01776658297635822.39625339590622S
30847ShortSelfingdiploid-0.002921023030024780.993280747881975SuperasteridsViridiplantaëEukary
0.471890466328817MediumOutcrossingdiploid-0.4875791035953140.224518741917865Superasterids
31327190.479416210715472ShortMixeddiploid0.2206777018660750.639305365660875Superasterids
0.473019655457175MediumOutcrossingdiploid-0.3702875934896522.63060048336122SuperasteridsVi
crossingdiploid-0.3683499049945410.294688270148393SuperasteridsViridiplantaëEukaryotaMagnoliop
0.484479355999838LongOutcrossingdiploid0.4434082860990.184357541899441SuperrosidsViridiplanti
6257668711656SuperrosidsViridiplantaëEukaryotaMagnoliopsida
ecy diploid-0.482254794494740.480572597137014SuperrosidsViridiplantaëEukaryotaMagnoliopsida
iploid0.1090336334668165.61996933691069SuperrosidsViridiplantaëEukaryotaMagnoliopsida
LongDioecy diploid0.036726310266025316.1070912369727SuperrosidsViridiplantaëEukaryotaMagnolio
948348650031LongDioecy diploid-0.1221545106061260.297917828592675ConifersViridiplantaëEukary
gdiploid-1.031584427405480.0226025185663545ConifersViridiplantaëEukaryotaPinopsida
utcrossingdiploid0.157532356485310.037711370582932ConifersViridiplantaëEukaryotaPinopsida
391LongOutcrossingdiploid-0.0620807471717683NAConifersViridiplantaëEukaryotaPinopsida
ssingdiploid-0.6641511616221840.00442355944248648ConifersViridiplantaëEukaryotaPinopsida
4988LongOutcrossingdiploid-0.3026074389302470.0144551076525123ConifersViridiplantaëEukaryota
jdiploid0.1676133310093930.00998623411552203ConifersViridiplantaëEukaryotaPinopsida
ongOutcrossingdiploid0.03615145402032060.0149909928068429ConifersViridiplantaëEukaryotaPinops
tcrossingdiploid-0.4346367590474470.0358762138422924ConifersViridiplantaëEukaryotaPinopsida
ngdiploid0.3436517670014590.179215467559026ConifersViridiplantaëEukaryotaPinopsida

itycladekingdomsuperkingdomclass
opsida
:ukaryotaMagnoliopsida
olataeEukaryotaMagnoliopsida
rasteridsViridiplantaeEukaryotaMagnoliopsida
iridiplantaeEukaryotaMagnoliopsida
smatidsViridiplantaeEukaryotaMagnoliopsida
Magnoliopsida
antaeEukaryotaMagnoliopsida

AlismatidsViridiplantaeEukaryotaMagnoliopsida

ida
aryotaMagnoliopsida
:ukaryotaMagnoliopsida
taeEukaryotaMagnoliopsida
SuperasteridsViridiplantaeEukaryotaMagnoliopsida
rasteridsViridiplantaeEukaryotaMagnoliopsida
yotaMagnoliopsida

:Magnoliopsida
psida
ntaeEukaryotaMagnoliopsida
gnoliopsida
otaMagnoliopsida
diplantaeEukaryotaMagnoliopsida
otaMagnoliopsida
sViridiplantaeEukaryotaMagnoliopsida
eEukaryotaMagnoliopsida

a

psida
/iridiplantaeEukaryotaMagnoliopsida

caryotaMagnoliopsida
ViridiplantaeEukaryotaMagnoliopsida

iopsida
intaeEukaryotaMagnoliopsida
a
/iridiplantaeEukaryotaMagnoliopsida
ukaryotaMagnoliopsida

Magnoliopsida
ryotaMagnoliopsida
Ja

ryotaMagnoliopsida
ukaryotaMagnoliopsida
lismatidsViridiplantaeEukaryotaMagnoliopsida
EukaryotaMagnoliopsida

2263SuperasteridsViridiplantaeEukaryotaMagnoliopsida
ukaryotaMagnoliopsida
sidsViridiplantaeEukaryotaMagnoliopsida
otaMagnoliopsida
agnoliopsida
psida
opsida
gnoliopsida
gnoliopsida

a

da
EukaryotaMagnoliopsida
ntaeEukaryotaMagnoliopsida
yotaMagnoliopsida
ukaryotaMagnoliopsida
gnoliopsida
liopsida

yotaMagnoliopsida
eEukaryotaMagnoliopsida
yotaMagnoliopsida
ntaeEukaryotaMagnoliopsida
Magnoliopsida
uperasteridsViridiplantaeEukaryotaMagnoliopsida
oliopsida
a
iopsida
Magnoliopsida
EukaryotaMagnoliopsida

/iridiplantaeEukaryotaMagnoliopsida
dsViridiplantaeEukaryotaMagnoliopsida
osidsViridiplantaeEukaryotaMagnoliopsida
lantaeEukaryotaMagnoliopsida
gnoliopsida
liopsida
noliopsida
sViridiplantaeEukaryotaMagnoliopsida
diplantaeEukaryotaMagnoliopsida
sidsViridiplantaeEukaryotaMagnoliopsida
psida
karyotaMagnoliopsida
ntaeEukaryotaMagnoliopsida
5954Lilioids + AlismatidsViridiplantaeEukaryotaMagnoliopsida
oliopsida
ryotaMagnoliopsida
ukaryotaMagnoliopsida

›EukaryotaMagnoliopsida

ukaryotaMagnoliopsida

aeEukaryotaMagnoliopsida

melinidsViridiplantaeEukaryotaMagnoliopsida

plantaEukaryotaMagnoliopsida

ukaryotaMagnoliopsida

karyotaMagnoliopsida

727CommelinidsViridiplantaeEukaryotaMagnoliopsida

sViridiplantaeEukaryotaMagnoliopsida

imelinidsViridiplantaeEukaryotaMagnoliopsida

antaeEukaryotaMagnoliopsida

iplantaeEukaryotaMagnoliopsida

CommelinidsViridiplantaeEukaryotaMagnoliopsida

karyotaMagnoliopsida

iplantaeEukaryotaMagnoliopsida

iplantaeEukaryotaMagnoliopsida

taeEukaryotaMagnoliopsida

iaeEukaryotaMagnoliopsida

Magnoliopsida

›EukaryotaMagnoliopsida

aeEukaryotaMagnoliopsida

ViridiplantaeEukaryotaMagnoliopsida

taMagnoliopsida

da

sViridiplantaeEukaryotaMagnoliopsida

ryotaMagnoliopsida

otaMagnoliopsida

liopsida

yotaMagnoliopsida

plantaEukaryotaMagnoliopsida

taMagnoliopsida

dsViridiplantaeEukaryotaMagnoliopsida

plantaeEukaryotaMagnoliopsida

diploplantaeEukaryotaMagnoliopsida

liopsida

ida

I

Magnoliopsida

karyotaMagnoliopsida

eEukaryotaMagnoliopsida

iopsida

ukaryotaMagnoliopsida

karyotaMagnoliopsida

taeEukaryotaMagnoliopsida

ryotaMagnoliopsida

Eukaryota Magnoliopsida

Eukaryota Magnoliopsida

Magnoliopsida

Magnoliopsida

Magnoliopsida

Eukaryota Magnoliopsida

Eukaryota Magnoliopsida

rasterids Viridiplantae Eukaryota Magnoliopsida

Superasterids Viridiplantae Eukaryota Magnoliopsida

ota Magnoliopsida

: Viridiplantae Eukaryota Magnoliopsida

Viridiplantae Eukaryota Magnoliopsida

: Viridiplantae Eukaryota Magnoliopsida

sida

tae Eukaryota Magnoliopsida

ipsida

ota Pinopsida

: Pinopsida

sida

TraitPredictorANOVA.pvalue.lmAIC.lmBIC.lmANOVA.pvalue.pglssAIC.pglssBIC.pglss
chrom_genmapNull02194.12200.6702186.152189.45
chrom_genmapMating system0.0082188.42201.550.0052179.52189.4
chrom_genmapLongevity0.0232190.42203.580.012180.932190.83
chrom_genmapMating system + Longevity0.1512188.52208.270.0052179.32195.79
resNull0228.2234.830220.03223.33
resMating system0.008222.5235.740.007214.23224.12
resLongevity0.015223.7236.880.011214.8224.7
resMating system + Longevity0.035219.7239.450.008212228.49

responseDfSum.SqMean.SqF.valuePr..F.
mating_system2151.417475.70875.51770.0047
chrom_size165.871265.87124.80070.0296
nb_chromosome137.596937.59692.74010.0995
mating_system:chrom_size252.346826.17341.90750.1512
Residuals1932648.162713.7211NANA
Parametercoefficients.Estimatecoefficients.Std..Errorcoefficients.t.valuecoefficients.Pr...t..
(Intercept)112.875432.31783.49276e-04
mating_systemMixed17.929911.93231.50260.1346
mating_systemSelfing15.713212.7111.23620.2179
chrom_size0.01490.01780.84110.4014
nb_chromosome-0.9460.5213-1.81470.0711
mating_systemMixed:chrom_size0.00520.02480.20780.8356
mating_systemSelfing:chrom_size0.0690.03591.92290.056

responseDfSum.SqMean.SqF.valuePr..F.
mating_system20.00810.00415.19430.0065
longevity220.00410.00212.65260.0735
marker_density10.00360.00364.56490.0341
n_progeny1000.00180.9662
Residuals1650.12898e-04NANA
Parametercoefficients.Estimatecoefficients.Std..Errorcoefficients.t.valuecoefficients.Pr...t..
(Intercept)-0.1021730.2252014-0.45369610.6506438
mating_systemMixed0.15453910.09016311.71399490.0884075
mating_systemSelfing0.18205010.10362721.75677940.0808104
longevity2Medium-0.23480910.1024374-2.29221940.0231564
longevity2Short-0.07980590.1069734-0.74603460.4567081
marker_density0.01120280.00540362.07321490.0397066
n_progeny-3.6e-068.47e-05-0.04245940.9661838