

1 Effects of genome size on pollen performance

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5 How does genome size affect the evolution of pollen tube growth rate, a haploid

6 performance trait?

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## ABSTRACT

**Premise of the Study** – Male gametophytes of most seed plants deliver sperm to eggs via a pollen tube. Pollen tube growth rates (*PTGRs*) of angiosperms are exceptionally rapid, a pattern attributed to more effective haploid selection under stronger pollen competition. Paradoxically, whole genome duplication (WGD) has been common in angiosperms but rare in gymnosperms. Pollen tube polyploidy should initially accelerate *PTGR* because increased heterozygosity and gene dosage should increase metabolic rates, however polyploidy should also independently increase tube cell size, causing more work which should decelerate growth. We asked how genome size changes have affected the evolution of seed plant *PTGRs*.

**Methods** - We assembled a phylogenetic tree of 451 species with known *PTGRs*. We then used comparative phylogenetic methods to detect effects of neo-polyploidy (within-genus origins), DNA content, and WGD history on *PTGR*, and correlated evolution of *PTGR* and DNA content.

**Key Results** - Gymnosperms had significantly higher DNA content and slower *PTGR* optima than angiosperms, and their *PTGR* and DNA content were negatively correlated. For angiosperms, 89% of model weight favored Ornstein-Uhlenbeck models with a faster *PTGR* optimum for neo-polyploids, but *PTGR* and DNA content were not correlated. In comparisons of within-genus and intraspecific-cytotype pairs, *PTGRs* of neo-polyploids  $\leq$  paleo-polyploids.

**Conclusions** – Genome size increases should negatively affect *PTGR* when genetic consequences of WGDs are minimized, as found in intra-specific autopolyploids (low heterosis) and gymnosperms (few WGDs). But in angiosperms, the higher *PTGR* optimum of neo-polyploids and non-negative *PTGR*-DNA content correlation suggest that recurrent WGDs have caused substantial *PTGR* evolution in a non-haploid state.

45        **Keywords:** DNA content, evolution of development, gametophyte, macroevolution, pollen  
46        competition, pollen tube growth rate, polyploidy, whole genome duplication.

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## INTRODUCTION

50           In seed plants, the male gametophyte is a highly-reduced, haploid organism that develops  
51 within the pollen grain and completes its life cycle after pollination by growing a pollen tube that  
52 invades female reproductive tissues. The pollen tube functions to attach the male gametophyte  
53 and to absorb nutrients from female tissues, and in most seed plants (conifers, Gnetales, and  
54 angiosperms), it has the novel function of transporting the sperm cells to the egg-bearing female  
55 gametophyte (siphonogamy) (Friedman, 1993). Pollen tube growth rate (*PTGR*) is a central  
56 aspect of male gametophyte performance that can evolve due to changes in the time between  
57 pollination and fertilization, and due to changes in the intensity of pollen tube competition.  
58 Strikingly, angiosperms are known to have much shorter reproductive cycles (Williams and  
59 Reese, 2019), much higher potential for pollen competition (Mulcahy, 1979), and orders of  
60 magnitude faster *PTGRs* (Williams, 2012) relative to gymnosperms. The pattern of exceptionally  
61 fast angiosperm *PTGRs* is thought to have evolved rapidly via haploid selection on pollen-  
62 expressed genes (Mulcahy, 1979; Arunkumar et al., 2013; Otto et al., 2015), which constitute a  
63 large portion of the genome (Tanksley et al., 1981; Rutley and Twell, 2015; Hafidh et al., 2016).

64           If the dramatic and rapid acceleration of *PTGRs* in angiosperms has been driven by  
65 haploid selection on pollen performance genes, then one might expect polyploidy to be rare in  
66 angiosperms. Evolution above the haploid level is expected to reduce the efficiency of selection  
67 on pollen (Otto et al., 2015). Yet, the opposite is true – ancient whole genome duplications  
68 (WGDs), recent polyploids, and speciation by polyploidy have been especially common in  
69 angiosperms, whereas in gymnosperms genome size has evolved largely by other processes  
70 (Wood et al., 2009; Mayrose et al., 2011; Leitch & Leitch, 2012, 2013; Landis et al., 2018). In  
71 fact, large changes genome size can have a number of immediate effects on *PTGR*. First, *PTGR*

72 might be faster in a neo-diploid pollen tube since increases in gene number cause: 1) heterosis,  
73 due to sheltering of deleterious pollen-expressed alleles and/or new allelic interactions upon loss  
74 of haploidy (Lande and Schemske, 1985; Husband and Schemske, 1997; Comai, 2005; Birchler  
75 et al. 2010; Husband, 2016), and 2) gene dosage effects, due to increased capacity for protein  
76 synthesis and hence the possibility for higher metabolic rates (Stebbins, 1974; Comai, 2005;  
77 Conant and Wolfe, 2008). On the other hand, substantial increases in DNA content (whether by  
78 WGD or other processes) are known to increase nuclear size, cell size, and the duration of the  
79 cell cycle, independent of the effects of genes (Bennett, 1971, 1972; Cavalier-Smith, 1978; Price  
80 1988; Cavalier-Smith, 2005). The phenotypic effects of increased bulk DNA, hereafter referred  
81 to as “nucleotypic” effects (Bennett, 1971; Snodgrass et al, 2016; Doyle & Coate, 2019), cause  
82 more work for the growing pollen tube cell and should therefore negatively affect *PTGR*,  
83 counteracting the positive “genotypic” effects of heterozygosity and gene dosage.

84 As shown in Figure 1, if genome size expansion occurs without increasing the number of  
85 genes, then nucleotypic effects will predominate and slower *PTGRs* should evolve. But if  
86 genome size increase occurs by WGD, then altered gene expression patterns (due to dosage and  
87 heterozygosity effects) should counteract nucleotypic effects in the stabilized neo-polyploid (Fig.  
88 1). In the latter case, the balance of nucleotypic and genotypic effects varies depending on the  
89 magnitude of potential heterosis, which depends directly on the amount of standing genetic  
90 variation (Birchler et al. 2010). In general, at inception tetraploid sporophytes are expected to  
91 have higher heterozygosity than their diploid progenitors, irrespective of mode of  
92 polyploidization (auto- to allo-polyploidy) or mating system (Lande and Schemske 1985; Soltis  
93 and Soltis 2000). Thus, at inception, autopolyploids that arise from outcrossing progenitors and

94 allopolyploids will have a higher potential for heterosis, relative to autopolyploids that arose  
95 from selfing ancestors (Fig. 1).

96         After the initial effects of WGD, genotypic effects continue to evolve under both  
97 stabilizing and directional selection on *PTGR*, mediated by shifts in mating system and  
98 phenomena such as genome downsizing, biased gene retentions, recombination, and ultimately  
99 the return to disomic inheritance (Conant and Wolfe, 2008; De Smet et al. 2013; Conant et al.,  
100 2014; Freeling et al., 2015; Dodsworth et al., 2016; Panchy et al. 2016; Wendel et al., 2018).  
101 Nucleotypic effects by definition can only evolve by changes in genome size, which after WGD  
102 tend to be biased to small losses relative to the size of the WGD (Dodsworth et al. 2016). Hence,  
103 with time, genotypic effects are predicted to overwhelm nucleotypic effects, irrespective of  
104 initial effects and the direction of *PTGR* evolution.

105         In this study, we used model-based comparative phylogenetic analyses to determine if  
106 polyploidy, DNA C-value, and WGD history have affected the evolution of *PTGRs* in seed  
107 plants, and whether genome size effects have occurred predominantly during polyploid periods  
108 of history or during subsequent periods of more or less diploid evolution. Because all seed plants  
109 have at least one WGD in their history, we defined neo-polyploids as having a higher  
110 chromosome multiple than the base chromosome number of their genus, and paleo-polyploids  
111 (hereafter, “diploids”) as having similar chromosome number as the genus base number (as in  
112 Wood et al. 2009; Mayrose et al. 2011). This allowed us to determine if, 1) neo-polyploids have  
113 faster *PTGRs* than diploids, as predicted if WGDs generally produce strong initial genotypic  
114 effects that persist in the polyploid condition, or 2) neo-polyploids have slower *PTGRs* than  
115 diploids, as predicted if nucleotypic effects initially outweigh genotypic effects and if fast  
116 *PTGRs* generally evolve after diploidization (eg. in paleopolyploids). We also predict an

117 underlying negative correlation between *PTGR* and genome size due to nucleotypic effects,  
118 which should be most apparent in intraspecific neo-polyploids and in lineages with little history  
119 of WGD.

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## 121 MATERIALS AND METHODS

122 ***Tree Construction and Dating*** – GenBank accessions for 16 gene regions (*rbcL*, *matK*, *trnL-F*,  
123 *18s\_rDNA*, *atpB*, *ndhF*, *adh*, *trnL*, *rpl32*, *trnT-L*, *psbA-trnH*, *rpl32-trnL*, *ITS*, *5.8s\_rRNA*, *rps16*,  
124 and *26s\_rDNA*) for 451 seed plant species with pollen tube growth rate data were retrieved,  
125 cleaned, and assembled into a multiple gene alignment (length – 9263 base pairs, 16 partitions,  
126 69.6% missing data) using PHLAWD and phyutility (Smith and Donoghue, 2008; Smith and  
127 Dunn, 2008). Tree inference was performed using maximum likelihood in RAxML version 8  
128 (Stamatakis, 2014) on CIPRES. A pruned version of the seed plant tree from Magallón et al.  
129 (2015) was used as a guide tree to enforce topology of major clades. The resulting maximum  
130 likelihood estimate of the tree was rooted and ultrametricized using the *ape* (Paradis et al., 2004)  
131 and *geiger* packages in R (Harmon et al., 2008). Time-calibration was performed with the  
132 Congruification method (Eastman et al., 2013), using the Magallón et al. (2015) phylogeny as the  
133 reference tree.

134 ***Data collection and character scoring*** – Data on *PTGRs* were taken from Williams  
135 (2012) and more recent literature (cited in Appendix S1; see the Supplementary Data with this  
136 article). The *PTGR* value used for each species represents an estimate of maximum sustained  
137 growth rate, which is consistent with other comparative analyses of physiological traits, and with  
138 the fact that researchers almost always measure *PTGRs* from the longest pollen tube(s). Thus,  
139 *PTGR* values for each species represent an average of maximum in vivo growth rates, or if there

140 was more than one report for a species the average of those values (as in Williams, 2012).  
141 *PTGRs* were taken exclusively from within-ploidy level crosses (i.e., never from inter-ploid  
142 crosses), in keeping with our overall goal of finding mechanisms underlying the pattern of *PTGR*  
143 evolution within stabilized polyploids.

144 DNA content was analyzed using 1C-value: the amount of nuclear DNA in the  
145 unreplicated gametic nucleus, irrespective of ploidy level (Swift, 1950; Bennett and Leitch,  
146 2012). As we were primarily interested in the nucleotypic effects of bulk DNA amount, we use  
147 the terms C-value, DNA content, and genome size interchangeably throughout. C-value data was  
148 collected from the Kew Royal Botanic Gardens Plant C-value Database (Bennett and Leitch,  
149 2012). Chromosome counts were obtained from the Index to Plant Chromosome Numbers  
150 (IPCN). To examine the effect of recent polyploidy (defined as occurring at or within the genus  
151 level; Wood et al., 2009; Mayrose et al., 2011) on *PTGR*, we scored taxa as “neo-polyploid” if  
152 their chromosome counts were  $\geq 1.5$  times that of their generic 1x base count (from Wood et al.,  
153 2009) and “diploid” (paleo-polyploid) if  $< 1.5$  times that value ( $N = 206$  angiosperms, 23  
154 gymnosperms). To examine the effect of ancient (deeper than genus-level) duplication events on  
155 *PTGR*, the number of WGDs in each genus-to-root lineage was counted for each angiosperm  
156 (found in Appendix S1 of Landis et al. 2018) and gymnosperm (Li et al. 2015).

157 ***Phylogenetic Comparative Analyses*** - To visualize changes in DNA content and *PTGR*  
158 along tree branches and to generate estimates of node states, ancestral state reconstructions were  
159 performed and plotted using the contMap function in *phytools* (Felsenstein, 1985; Revell,  
160 2012)(Appendix S2). Given many known biological differences between gymnosperms and  
161 angiosperms in pollen tube growth (Friedman, 1993; Williams, 2008) and in mechanisms of  
162 genome size change (see Discussion) (Ohri and Khoshoo, 1986; Leitch et al., 1998), all



163 comparative analyses were performed on gymnosperms only, angiosperms only, and the full  
164 dataset (all spermatophytes). C-value and *PTGR* were log<sub>10</sub>-transformed for all analyses.

165 Model-based analyses were used to examine patterns of *PTGR* and C-value evolution  
166 separately. The *OUwie* function was implemented in R (Beaulieu and O'Meara, 2014), and the  
167 following models were tested: single- and multi-rate Brownian motion (BM1, BMS,  
168 respectively), single-regime Ornstein-Uhlenbeck (OU1), and multi-regime OU models with  
169 either one global  $\alpha$  and  $\sigma^2$  estimate (OUM), one  $\alpha$  and multiple  $\sigma^2$  (OUMV), or multiple  $\alpha$  and  
170 one  $\sigma^2$  (OUMA). In all models,  $\sigma^2$  represents the rate of random evolution and  $\alpha$ , the strength of  
171 attraction to an optimum,  $\theta$ . The single- and multiple-regime models were compared to test  
172 whether or not, 1) angiosperms and gymnosperms evolve around different *PTGR* or C-value  
173 optima, and 2) diploids and neo-polyploids (within all three groups) evolve around different  
174 *PTGR* or C-value optima. For all analyses, AICc values were used to calculate model weights  
175 and the weighted average of parameter values was then calculated using all models that  
176 contributed > 1% of the model weight (Burnham & Anderson, 2002). Unless otherwise noted, all  
177 measures of uncertainty around parameter estimates are standard errors.

178 Since each *PTGR* value represents a species mean obtained from multiple measurements,  
179 we attempted to incorporate error into phylogenetic comparative analyses. Since species means  
180 were log<sub>10</sub>-transformed for analysis, log<sub>10</sub>-transformed *SEs* are also required. As there is no  
181 reliable way to calculate the log<sub>10</sub>-transformed *SE* from the literature without the original data for  
182 each species, we took the following approach. First, we assumed all species had similar *SEs* in  
183 *PTGR*, and we applied an empirically-determined *SE* from an exemplar species to all. *Magnolia*  
184 *grandiflora* has an average *PTGR* of  $828 \pm 141 \mu\text{m h}^{-1}$  ( $N = 25$  outcrosses), close to the  
185 angiosperm median of  $587 \mu\text{m h}^{-1}$  (Williams, 2012 and this study) (Appendix S3). The standard

186 deviation (*SD*) of log<sub>10</sub>-transformed data was calculated and divided by the mean of the log<sub>10</sub>-  
187 transformed data to acquire a coefficient of variation (*CV*) of 0.0237. We then multiplied the  
188 log<sub>10</sub>-transformed mean *PTGR* of each species by 0.0237 to provide an estimate of the log<sub>10</sub>  
189 taxon-specific standard deviation. The standard deviation (*SD*) was used as a conservative  
190 estimate of error because sample sizes were generally not available for calculating *SE*. Secondly,  
191 we performed a sensitivity analysis by evaluating each evolutionary model in *OUwie* with *SDs*  
192 calculated from hypothetical global *CVs* of 0.00, 0.05, 0.10, 0.25, and 0.50 (Appendix S4).

193 The association between recent polyploidy and *PTGR* was also assessed among 10  
194 diploid-polyploid near-relative pairs (appearing as sister taxa on the tree at the within-genus  
195 level). Only polyploid taxa with a single diploid sister on the tree were used. The *PTGRs* of 11  
196 intraspecific diploid-autopolyploid pairs from the literature were also compared. A two-tailed  
197 binomial (sign) test was used to test significance in both.

198 The cumulative effect of ancient polyploid events was explored with phylogenetic  
199 generalized least squares (*PGLS*) regression using the *phylolm* package in R (Ho & Ane, 2014).  
200 The number of ancient duplication events in the history of each tip taxon (inferred from Landis et  
201 al., 2018) was used as the predictor variable with *PTGR* as the response variable.

202 The relationship between pollen tube growth rate and gametophytic DNA content was  
203 also assessed with *PGLS* regression. Gametophytic DNA content was used as the predictor  
204 variable and *PTGR* the response variable. BM (Grafen, 1989) and OU (Martins and Hansen,  
205 1997) models were both used, in addition to Pagel's lambda, kappa, and delta models (Pagel,  
206 1997, 1999). To examine the effect of ploidy and the interaction between ploidy and C-value on  
207 *PTGR*, a phylogenetic ANCOVA was implemented with C-value as the covariate in *phylolm*.

208 Shifts among convergent *PTGR* and C-value optima were determined with a maximum  
209 likelihood approach to detect multiple optima within seed plants, using *SURFACE* in R (Ingram  
210 and Mahler, 2013). Using an OU model with a global  $\alpha$  and  $\sigma^2$ , a single-optimum model was  
211 subdivided into multiple-optima models in a stepwise fashion until adding another optimum  
212 decreased the model likelihood by  $\Delta\text{AIC} > -2$ . Separate optima were then collapsed (i.e. two  
213 regimes were assigned the same optimum) in a pairwise fashion until further collapses decreased  
214 model likelihood. Shifts in *PTGR* and C-value optima that occurred at the same node, or within  
215 two nodes of each other, were identified manually. Nodes with *PTGR* or C-value regime shifts  
216 were also manually compared to the Landis et al. (2018) WGD map to see if a WGD had  
217 occurred at that node or up to two nodes *prior* to the regime shift.

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## RESULTS

220 ***PTGR evolution and C-value evolution in angiosperms versus gymnosperms*** – The *PTGR* tree  
221 comprised 451 seed plants, with 28 species from 7 of 8 gymnosperm orders (Christenhusz et al.  
222 2011) including Cycads, *Ginkgo*, conifers and Gnetales; and 423 species from 38 of 64 (59%) of  
223 angiosperm orders (APG IV 2016), including representatives from all three ANA grade lineages,  
224 Chloranthaceae, eumagnoliids, and a broad distribution of both monocots and eudicots (full tree  
225 in Appendix S2). Gymnosperm *PTGR*s ranged from  $< 1$  to  $19 \mu\text{m h}^{-1}$  (mean  $\pm$  *SD* =  $3.29 \pm 4.34$ ,  
226 median =  $1.49 \mu\text{m h}^{-1}$ ), whereas angiosperm *PTGR*s ranged from  $< 5$  to  $> 30,000 \mu\text{m h}^{-1}$  (mean  $\pm$   
227 *SD* =  $1744 \pm 3576 \mu\text{m h}^{-1}$ , median =  $587 \mu\text{m h}^{-1}$ ). The maximum likelihood (ML) reconstruction  
228 indicated that ancestral  $\log_{10}$  *PTGR* of extant angiosperms was  $2.44 \mu\text{m h}^{-1}$  (95% CI: 1.09-3.69)  
229 versus  $0.215 \mu\text{m h}^{-1}$  (95% CI: -1.48-1.92) for extant gymnosperms (Appendix S2).

230 Model-based analyses of seed plant *PTGRs* and C-values favored OU models with  
231 separate optima for angiosperms and gymnosperms, accounting for > 99.9 % of the model  
232 weight in both analyses (Appendix S5, S6).  $\log_{10}$  *PTGR* optima were more than an order of  
233 magnitude faster in angiosperms ( $2.69 \pm 0.048 \mu\text{m h}^{-1}$ ) than in gymnosperms ( $0.187 \pm 0.123 \mu\text{m}$   
234  $\text{h}^{-1}$ ).

235 The C-value tree included 183 species from the *PTGR* tree for which DNA content data  
236 could be obtained. The resulting  $\log_{10}$  C-value optimum for angiosperms ( $0.184 \pm 0.051 \text{ pg}$ ) was  
237 more than a magnitude of order smaller than that of gymnosperms ( $1.231 \pm 0.041 \text{ pg}$ ). Ancestral  
238  $\log_{10}$  DNA content was also smaller for angiosperms than for gymnosperms,  $0.29 \text{ pg}$  (95% CI: -  
239  $0.45$ - $1.04$ ) versus  $1.10 \text{ pg}$  (95% CI:  $-0.28$ - $2.47$ ), consistent with larger comparative analyses of  
240 DNA content (see Leitch and Leitch, 2013).

241 ***Joint evolution of PTGR and ploidy*** – In model-based analyses of angiosperms using the  
242 empirical error rate, 89% of the model weight favored a separate and higher optimum for neo-  
243 polyploids ( $N = 68$ ) than for diploids ( $N = 138$ ) (model averaged  $\log_{10}$  *PTGR* =  $3.2 \pm 0.23$  vs.  $2.8$   
244  $\pm 0.08 \mu\text{m h}^{-1}$ ; Table 2). In the sensitivity analysis, OU models with separate and faster *PTGR*  
245 optima for neo-polyploids than diploids received > 50% of model weight when the error  
246 calculated from CVs ranged from 0 to 25 %, but above 25% single-regime and BM models had  
247 the majority of the weight (Appendix S4). These are conservative results, since *SDs*, not *SEs*,  
248 were used to model error on the tree. The gymnosperm-only analysis was not performed due to  
249 low sample size (2 of 23 species were polyploid).

250 A survey of intraspecific cytotypes found autopolyploids had slower *PTGR* than diploids  
251 in 9 of 11 pairs and no difference in the remaining two (Binomial test,  $P = 0.002$ ; Appendix  
252 S7b). In the nearest-relative comparisons, within-genus polyploids had slower *PTGR* than

253 diploids in four pairs, faster *PTGR* in five, and no difference in one (Two-tailed binomial test,  $P$   
254 = 0.623)(Appendix S7a).

255 The historical effect of number of ancient genome duplications on *PTGR* was non-  
256 significant, whether or not recent (within-genus) WGDs were included (kappa model weight >  
257 99.9%,  $N = 451$ ;  $P > 0.3$  in both analyses).

258 ***Joint evolution of PTGR, DNA content and ploidy*** - For seed plants, ordinary least  
259 squares (*OLS*) regression showed a significant negative correlation between DNA content and  
260 *PTGR* ( $N = 183$ ,  $P < 0.0001$ ), but that result was clearly driven by the large DNA contents and  
261 slow *PTGRs* of gymnosperms relative to angiosperms (Fig. 2), because the *PGLS* regression was  
262 non-significant (Table 1). Taking these two clades separately, DNA content was negatively  
263 correlated with *PTGR* in gymnosperms in the *PGLS* regression ( $N = 23$ ; model-averaged slope: -  
264  $1.09 \pm 0.49 \log_{10} PTGR$ ; Table 1). In angiosperms, a positive correlation using *OLS* ( $N = 161$ ;  
265  $P = 0.0005$ ), was non-significant using *PGLS* (Table 1). The patterns of *PTGR* and C-value  
266 evolution in seed plants can be visualized in Figure 3. In a smaller phylogenetic ANCOVA  
267 analysis, after controlling for C-value, the effect of ploidy on *PTGR* was non-significant in  
268 angiosperms ( $N = 100$ ) and seed plants ( $N = 118$ ) (non-significant ploidy x C-value interaction  
269 removed; Appendix S8).

270 ***Coincident regime shifts in PTGR and DNA content*** – Maximum likelihood analysis of  
271 convergent evolution of *PTGRs* detected 13 distinct optima ( $N = 451$  taxon tree), with 51 shifts  
272 (22 to faster and 29 to slower optima). For C-value, there were 9 distinct optima ( $N = 184$  taxon  
273 tree), with 4 shifts to larger and 7 shifts to smaller optima. Regime shifts in both traits were  
274 coincident at only two nodes: a *PTGR* acceleration (from  $\theta = 0.147$  to  $\theta = 2.47 \log_{10} \mu\text{m h}^{-1}$ ) and  
275 genome downsizing ( $\theta = 2.71$  to  $\theta = 0.702 \log_{10} \text{pg}$ ) in the CA of extant angiosperms; and a

276 *PTGR* slowdown ( $\theta = 2.78$  to  $\theta = 2.47 \log_{10} \mu\text{m h}^{-1}$ ) and genome size decrease ( $\theta = 0.209$  to  $\theta =$   
277  $-0.386 \log_{10} \text{pg}$ ) in the CA of rosids and Saxifragales (i.e. superrosids; Fig. 4). When the search  
278 was relaxed to include adjacent nodes, an additional coincidence occurred, with shift to higher  
279 *PTGR* followed by a shift to higher C-value near the base of monocots. Ancient WGDs  
280 coincided with the shifts in *PTGR* and C-value at the CA of angiosperms (above) and with a  
281 decrease in C-value in the CA of eudicots.

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283

## DISCUSSION

284 The impact of genome size on *PTGR* is determined by the magnitudes of conflicting nucleotypic  
285 and genotypic effects. Such effects depend on the mechanism of genome size change.

286 Nucleotypic effects decelerate *PTGR* and are always present irrespective of mode of genome size  
287 change, whereas large-scale genetic effects are only possible after WGD. We predicted that  
288 angiosperms and gymnosperms should have different patterns of *PTGR* evolution based on their  
289 contrasting patterns of genome size change. Gymnosperm *PTGRs* should be most susceptible to  
290 nucleotypic effects because they have evolved large genomes sizes and WGDs have been rare. In  
291 contrast, angiosperms have evolved smaller genome sizes despite recurrent WGDs and  
292 widespread present-day polyploidy. Thus, gene duplication and sorting have played a much  
293 greater role in the evolution of angiosperm *PTGRs*, allowing genotypic effects to counterbalance  
294 or overwhelm nucleotypic effects. Below we discuss our findings in light of these expected  
295 patterns.

296

297 *The evolution of PTGR in angiosperms versus gymnosperms* - We found that seed plant  
298 *PTGRs* best fit an OU model, indicating less *PTGR* variation among lineages than expected

299 under a Brownian motion evolutionary model, with a faster optimum for angiosperms than for  
300 gymnosperms. Phylogenetic half-lives were similar (5.6 and 5.7 MY, respectively) and very  
301 short (only 3.9% and 2.3 % of their respective crown ages), indicating a strong attraction to their  
302 optimum values. Such a pattern is consistent with stabilizing selection on *PTGR* imposed by  
303 slower evolution of linked sporophytic traits, such as the timing of stigma receptivity relative to  
304 egg receptivity, pollen tube pathway length, or maternal provisioning. Gymnosperm *PTGRs* may  
305 have been constrained by a hard boundary such as by biophysical or physiological limitations, or  
306 a soft boundary, such as by lack of selection for fast rates. Angiosperms have clearly not been  
307 bound by those same limitations, given their much higher *PTGR* optimum, the convergent  
308 evolution of extremely fast *PTGRs* in many unrelated derived lineages of monocots and eudicots,  
309 and occasionally large within-genus differences in *PTGR*.

310 Our results suggest that most of the accelerations of angiosperm *PTGR*, and their higher  
311 *PTGR* variance relative to gymnosperms, have largely evolved *after* the origin of angiosperms  
312 and their novel pollen tube cell biology. First, estimates of angiosperm ancestral *PTGR* and  
313 ancestral optimum under OU (275 and 295  $\mu\text{m h}^{-1}$ , respectively) are slower than the angiosperm-  
314 wide OU optimum of 490  $\mu\text{m h}^{-1}$  and the angiosperm median of 587  $\mu\text{m h}^{-1}$ . Secondly, the higher  
315 among-lineage variance is due to many transitions to both faster and slower *PTGR* optima within  
316 extant angiosperms. Transitions to slower rates within angiosperms are concentrated on lineages  
317 that have evolved delayed fertilization, such Fagales, orchids and others, or high selfing rates,  
318 which suggests relaxation of directional selection on *PTGR* (Williams and Reese, 2019). In  
319 contrast, gymnosperm *PTGRs* were likely ancestrally slow (Figure 4).

320 There are several non-mutually exclusive hypotheses for what triggered the evolution of  
321 fast *PTGRs* in angiosperms. First, Mulcahy (1979) invoked a shift to much higher intensity of

322 pollen competition in angiosperms as a driver of the origin and continued evolution of faster  
323 growth rates. Notably, no other type of tip-growing cell in land plants (whether gametophytic or  
324 sporophytic) has evolved comparably fast tip-growth rates and none of those cell types, including  
325 gymnosperm pollen tubes, experience intense competition for resources (Williams et al., 2016).  
326 Secondly, gymnosperm *PTGRs* may be slow because they lack novel biophysical or  
327 physiological attributes of pollen tubes and/or those attributes enabled faster *PTGRs* to evolve in  
328 angiosperms (Hoekstra, 1983; Derksen et al., 1999; Fernando et al., 2005; Williams, 2008,  
329 2009). Thirdly, with or without pollen competition, rapid *PTGRs* may have been necessary as  
330 angiosperm sporophytes transitioned to a much faster reproductive cycle (Stebbins, 1974;  
331 Williams, 2012; Williams and Reese, 2019). Finally, our results suggest a new possibility, that  
332 strong differences in genome-level processes have impacted the evolution of angiosperm *PTGRs*  
333 relative to their living and extinct seed plant relatives.

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335 ***Mechanisms of genome size change and PTGR evolution within seed plants*** – A major finding  
336 of this study is that angiosperm neo-polyploids evolved around a much faster *PTGR* optimum  
337 ( $1648 \mu\text{m h}^{-1}$ ) than diploids ( $595 \mu\text{m h}^{-1}$ ), despite several sources of variation in the data. First,  
338 neo-polyploids were by definition derived within genera, and their smaller sample size and  
339 shorter branch lengths reduced the power to estimate parameters relative to diploids, as reflected  
340 by the larger standard error around the neo-polyploid optimum. Nevertheless, the proportion of  
341 neo-polyploids in our data set (33% of angiosperms) is almost exactly that found in the full  
342 Wood et al. (2009) data set and similar to that in other studies (Mayrose et al., 2011; Barker et  
343 al., 2016; Landis et al., 2018).



344           There was also biological variability in our dataset. In our taxon sampling, we were  
345 agnostic to variation in mating systems and modes of polyploid origins, since our interest was in  
346 how *PTGR* has evolved in natural stabilized polyploids. In retrospect, our sample does seem  
347 representative. Of 14 angiosperm polyploids whose mode of origin has been studied, seven were  
348 autopolyploid and seven allopolyploid, similar to the nearly-equal proportions found by Barker  
349 et al. (2016). Furthermore, among 16 polyploids for which mating system has been studied, eight  
350 were fully outcrossing, seven were self-compatible (two autogamous, two mixed mating, and  
351 three unknown), and one was apomictic – a not unusual distribution (Goodwillie et al., 2005;  
352 Gibbs, 2014; Ashman et al., 2014). Thus, our taxon sampling seems not to have been greatly  
353 biased. Even with such information, predicting the magnitude of genetic variation in polyploids  
354 is not so simple. For example, autotetraploids originate with a subset of the genetic variation in  
355 the diploid progenitor population but they often outcross and hybridize, whereas allopolyploids  
356 can be highly heterozygous when they originate, but often are highly selfing (Stebbins, 1974;  
357 Soltis and Soltis, 1999; Barringer 2007; Whitney et al., 2010). Hence, despite several sources of  
358 heterogeneity, the faster *PTGR* optimum of neo-polyploids indicates that *PTGR* acceleration  
359 evolves either at the time of WGDs or during the time period in which the descendant species  
360 retain a polyploid chromosome number.

361           The closest approximation of the initial effect of polyploidy on *PTGR* is the comparison  
362 of diploids with their intraspecific, autopolyploid cytotypes. In all 11 pairs, *PTGR*s of  
363 autopolyploid cytotypes were slower than or equal to those of their intraspecific diploid  
364 progenitors. We should re-emphasize that all studies involved in vivo crosses among diploid  
365 sporophytes (1x pollen on 2x pistils) compared to crosses among tetraploid sporophytes (2x  
366 pollen on 4x pistils), in keeping with our goal of generalizing effects on *PTGR* in stabilized

367 polyploids. Nucleotypic effects acting to slow *PTGR* should be most apparent in autopolyploids  
368 at inception, because there is lower potential for heterosis. Thus, the lack of any examples of  
369 faster *PTGR* in neo-autotetraploid cytotypes than in their diploid progenitors suggests that  
370 increased gene dosage by itself generally does not initially fully offset nucleotypic effects.

371 Nucleotypic effects on *PTGR* could be substantial. Tube size affects *PTGR* in a linear  
372 fashion, because larger tubes must make more tube wall per unit time, and since tube diameter is  
373 constant during growth, the rate of wall production is directly proportional to tip extension rate  
374 (Williams et al., 2016). Kostoff & Prokofieva (1935) reported in vivo pollen tubes to be 39%  
375 larger in diameter in an allotetraploid *Nicotiana* relative to the mean of its presumed diploid  
376 progenitors, and Iyengar (1938) found 8-53% larger tube diameters in tetraploid versus diploid  
377 species of *Gossypium*.

378 Taken together our results suggest that nucleotypic effects are strong and act as a brake  
379 on *PTGR* at inception (intraspecific polyploid analysis), but as neo-polyploids become stabilized  
380 and persist over time, nucleotypic effects are more than offset by genotypic effects (within-genus  
381 pairs and model-based analyses) which often produce faster *PTGRs* in angiosperms.

382 We found that DNA content has evolved around a significantly lower optimum in  
383 angiosperms than in gymnosperms, even though angiosperms have a broad range of DNA C-  
384 values that encompass the entire range of seed plant genome sizes (Fig. 3; see Leitch and Leitch,  
385 2013 for a larger survey). Angiosperms also have great variation in ploidy level, a history of  
386 speciation by polyploidy, and much evidence of past genome duplication (Ahuja, 2005; Wood et  
387 al., 2009; Husband et al., 2013; Van de Peer et al., 2017; Landis et al., 2018). There were at least  
388 1-7 WGDs in the lineages leading from the seed plant root to each of the tips in our *PTGR* tree,  
389 and 33% of taxa (68/206 angiosperms versus 2/23 gymnosperms) were identified as neo-

390 polyploids. The often low DNA content and high ploidy levels of angiosperms are not surprising  
391 given that genome duplication is commonly followed by rapid loss of DNA sequences, gene  
392 fractionation by large-scale deletions, biased retention of genes with beneficial dosage effects,  
393 and ultimately a return to an apparent diploid state in sporophytes (Conant and Wolfe, 2008;  
394 Conant et al., 2014; Freeling et al., 2015; Dodsworth et al., 2016; Wendel et al., 2018). Thus, one  
395 explanation for the much faster *PTGRs* of angiosperms relative to gymnosperms is that  
396 widespread gene duplication by WGDs have often enabled transgressive evolution of faster  
397 *PTGRs* leading to the observed pattern of convergent evolution of extremely fast *PTGRs* in many  
398 unrelated lineages of monocots and eudicots.

399 WGDs have been rare in gymnosperms (Ahuja, 2005; Leitch et al., 2005; Wood et al.,  
400 2009; Soltis et al., 2009; Husband et al., 2013; Leitch and Leitch, 2013; Lee and Kim, 2014) and  
401 their high DNA contents are thought to be due mainly to high transposon activity without  
402 repeated rounds of genome duplication (Leitch & Leitch, 2013; Lee and Kim, 2014). Hence,  
403 gymnosperms may have experienced the nucleotypic effects of higher DNA content on pollen  
404 tube dimensions, which is predicted to reduce *PTGR*, without the potential for counter-balancing  
405 effects, such as initially higher gene dosage and heterozygosity followed by gene sorting during  
406 the diploidization process. Our finding of a negative correlation between *PTGR* and DNA  
407 content in gymnosperms, but not in angiosperms supports that hypothesis.

408 Though gymnosperm *PTGRs* are likely affected by tube sizes, nucleotypic effects do not  
409 account for the magnitude of the difference in their slow *PTGRs* relative to those of angiosperms.  
410 Gymnosperm pollen tubes can range up to 300  $\mu\text{m}$  in diameter (Coulter and Chamberlain, 1928;  
411 Gifford and Foster, 1989), but many species of siphonogamous conifers and Gnetales have  
412 angiosperm-like pollen tube diameters in the 10 to 20  $\mu\text{m}$  range. Yet no gymnosperm has

413 evolved a *PTGR* faster than  $20 \mu\text{m h}^{-1}$ . It has been argued that their pecto-cellulosic wall  
414 structure is a limitation relative to angiosperm pollen tube walls, which use the plasma  
415 membrane-bound enzymes callose synthase and pectin-methylesterase in a novel way to more  
416 rapidly synthesize a strong and durable tube cell wall and callose plugs (Derksen, 1999,  
417 Abercrombie et al., 2012; Wallace and Williams, 2017). However, other types of pecto-cellosic  
418 tip-growing cells, such as root hairs, grow faster than gymnosperm pollen tubes (Williams et al.,  
419 2016). Thus, it seems likely that the extremely slow growth rates of gymnosperm pollen tubes  
420 reflect an ancestrally antagonistic relationship between maternal tissues and pollen tubes that  
421 functioned as invasively growing rhizoids, coupled with a lack of selection for faster growth rate  
422 due to the absence of pollen competition and a long period between pollination and fertilization.  
423 Our results also suggest a lack of opportunity for genotypic effects to evolve due to the rarity of  
424 WGDs.

425

426 **Conclusions** - Studies across the tree of life have consistently shown that ploidy level and DNA  
427 content are correlated with cell size and metabolic rate (Cavalier-Smith, 1978; Gregory, 2001;  
428 Cavalier-Smith, 2005). Pollen tube dimensions and energetics affect the amount of cell wall  
429 material produced per unit of growth and the rate at which cell wall is produced, which together  
430 determine *PTGR*. In gymnosperms, *PTGR* was negatively correlated with genome size, but in  
431 angiosperms, where the effects of WGDs are much more prevalent, there was no such  
432 correlation, and neo-polyploids evolved around a higher *PTGR* optimum than diploids. These  
433 results support the expectation that genome size increases incur nucleotypic effects that act as a  
434 brake on growth rate. The degree to which genotypic effects counterbalance nucleotypic effects  
435 depends on the historical nature and time since genome size increase in any particular lineage.

436 Understanding causal relationships between genome size, ploidy and *PTGR* will involve  
437 mechanistic studies of tube cell dimensions and wall synthesis rates in haploid and polyploid  
438 gametophytes. On the other hand, there appears to be great variation in the tug of war between  
439 genotypic and nucleotypic effects, and there are likely to be deeper evolutionary patterns  
440 underlying that variation.

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449

450

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452 J.B.R. collected data on genome sizes and ploidy levels, constructed the phylogenetic tree and  
453 performed all comparative analyses; J.H.W. collected data on *PTGRs* and diploid-autopolyploid  
454 *PTGRs*.

455

456 **Data Accessibility Statement:** Scripts written during the creation of this manuscript are  
457 available on GitHub: <https://github.com/jbr1848/PTGR.genome.evolution>. The phylogenetic tree  
458 created during this study can be found on TreeBase:  
459 <http://purl.org/phylo/treebase/phylovs/study/TB2:S24291>.

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677 **Table 1:** Phylogenetic generalized least squares regression of  $\log_{10} PTGR$  as a function of  $\log_{10}$   
 678 C-value. Only models contributing more than 1% of total weight are included. *P* values are for  
 679 the slope of the regression. Gymnosperm averaged model:  $\text{Log}_{10} PTGR = 1.46 (\pm 0.62) - 1.09 (\pm$   
 680  $0.49) * (\log_{10} \text{C-value})$ .

681  
 682

Seed plants ( <i>N</i> = 183)			Angiosperms ( <i>N</i> = 161)			Gymnosperms ( <i>N</i> = 23)		
Model	Weight	<i>P</i>	Model	Weight	<i>P</i>	Model	Weight	<i>P</i>
kappa	0.999	0.463	kappa	0.975	0.284	OU	0.265	0.020
			lambda	0.024	0.221	delta	0.257	0.006
						kappa	0.193	0.445
						BM	0.121	0.001
						lambda	0.119	0.327
						EB	0.044	0.001

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689 **Table 2: Parameter estimates for angiosperm *PTGR* analyses under different evolutionary**  
 690 **models.** Note that OU1 is a single optimum model, and the rest specify separate “diploid”  
 691 (paleo-polyploid) and neo-polyploid optima. BM1 and BMS models contributed <1% model  
 692 weight and were excluded.

693

694

<b>Model</b>	<b><math>\Delta AICc</math></b>	<b>Model weight</b>	<b>Diploid <math>\sigma^2</math></b>	<b>Polyploid <math>\sigma^2</math></b>	<b>Diploid <math>\alpha</math></b>	<b>Polyploid <math>\alpha</math></b>	<b>Diploid optimum</b>	<b>Polyploid optimum</b>
<b>OUMA</b>	[332.76]	0.373	0.099		0.077	0.074	2.776	3.285
<b>OUMV</b>	0.23	0.333	0.099	0.057	0.077		2.768	3.262
<b>OUM</b>	1.53	0.174	0.090		0.080		2.760	3.263
<b>OU1</b>	2.26	0.120	0.089		0.077		2.812	
<b>AVERAGED MODEL</b>		~1.0	0.096 ± 0.177	0.082 ± 0.220	0.078 ± 0.213	0.077 ± 0.217	2.775 ± 0.079	3.217 ± 0.231

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697

## FIGURE LEGENDS

698 **Figure 1. Predicted initial effects of large increases in genome size on pollen tube growth**

699 **rate (*PTGR*).** The dashed line indicates an ancestral haploid (1x) *PTGR*. Upon transition to a

700 larger (> 1x) genome size, nucleotypic effects should act to decrease *PTGR* regardless of

701 mechanism of change. Genotypic effects are only present after WGD or large-scale gene

702 duplications and are predicted to increase *PTGR* via increased gene dosage and heterozygosity.

703 The magnitude of heterosis due to initial increase in heterozygosity is expected to scale with

704 genetic variation in the descendent taxon. The ancestral haploid *PTGR* can only be conserved

705 when genotypic and nucleotypic effects perfectly offset each other.

706

707 **Figure 2: Relationship between pollen tube growth rate (*PTGR*) and DNA content (1C-**

708 **value) in seed plants.** The model- averaged slope of the PGLS regression is shown for

709 gymnosperms (green points,  $N = 161$ ), whereas slopes for seed plants (all points,  $N = 183$ ) and

710 angiosperms (purple points,  $N = 23$ ) were non-significant. Optima (with standard error bars) for

711 each group (from model-based analyses in Tables S3, S4) are included for illustrative purposes.

712

713 **Figure 3: Inferred pattern of pollen tube growth rate (*PTGR*) and genome size changes in**

714 **seed plants.** Contour plot comparing *PTGR* evolution (left,  $\mu\text{m h}^{-1}$ ) and C-value evolution (right,

715 picograms) ( $N = 183$ ). Scale bar at the bottom of each phylogeny indicates 100 million years.

716 GYM = gymnosperms; ANA = Amborellales, Nymphaeales, Austrobaileyales, Chloranthales,

717 eumagnoliids; MONO = monocots.

718

719 **Figure 4: Coincident evolution of pollen tube growth rate (*PTGR*) and DNA content (C-**  
720 **value).** Paired *SURFACE* plot showing regime shifts in *PTGR* (left) versus DNA content (right)  
721 ( $N = 183$ ). Nodes which have experienced a regime shift along the stem leading to it are marked  
722 with magenta diamonds (not all *PTGR* shifts are shown, since *PTGR* tree has been pruned to  
723 match C-value tree). Branch colors: *gray* = seed plant ancestral optimum (*PTGR*  $\theta = 0.147$ ; C-  
724 value  $\theta = 2.71$ ); *green* = ancestral optimum for angiosperms (*PTGR*  $\theta = 2.47$ ; C-value  $\theta =$   
725  $0.702$ ); *red* = derived lineages following a shift to a higher optimum than previously; *blue* =  
726 derived lineages following a shift to a lower optimum than previously. Black arrows indicate  
727 instances where shifts in *PTGR* and C-value coincide. Scale bar at the bottom of each phylogeny  
728 indicates 100 million years. GYM = gymnosperms; A = Amborellales, Nymphaeales,  
729 Autrobaileyales, Chloranthales, eumagnoliids; MONO = monocots.

730

731 **Additional Supporting Information may be found online in the supporting information**  
732 **section at the end of the article:**

733

734 **Appendix S1: 119 additional *PTGR* values and references not reported in Williams 2012.**

735

736 **Appendix S2: Pollen tube growth rate (*PTGR*) evolution across Spermatophytes.**

737

738 **Appendix S3: Summary statistics for pollen tube growth rate (*PTGR*) of *Magnolia***  
739 ***grandiflora*.**

740

741 **Appendix S4: Sensitivity analysis for the magnitude of  $\log_{10}$  *PTGR* error estimates.**

742

743 **Appendix S5: *PTGR* evolution in gymnosperms vs. angiosperms.**

744

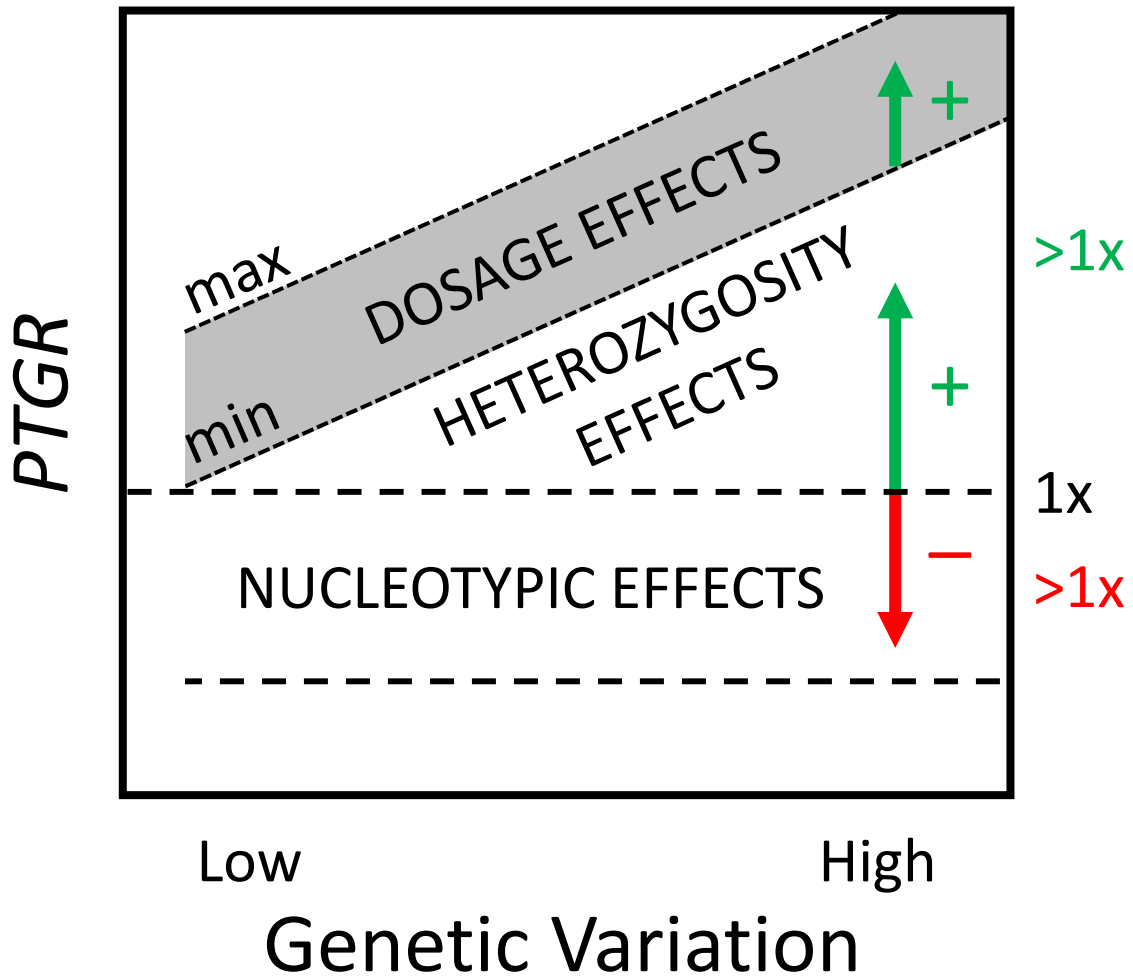
745 **Appendix S6: C-value evolution in gymnosperms vs. angiosperms.**

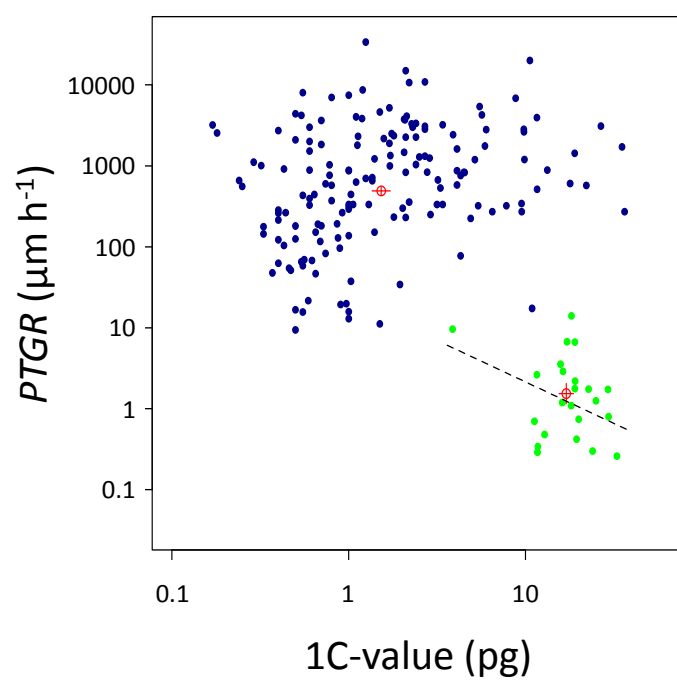
746

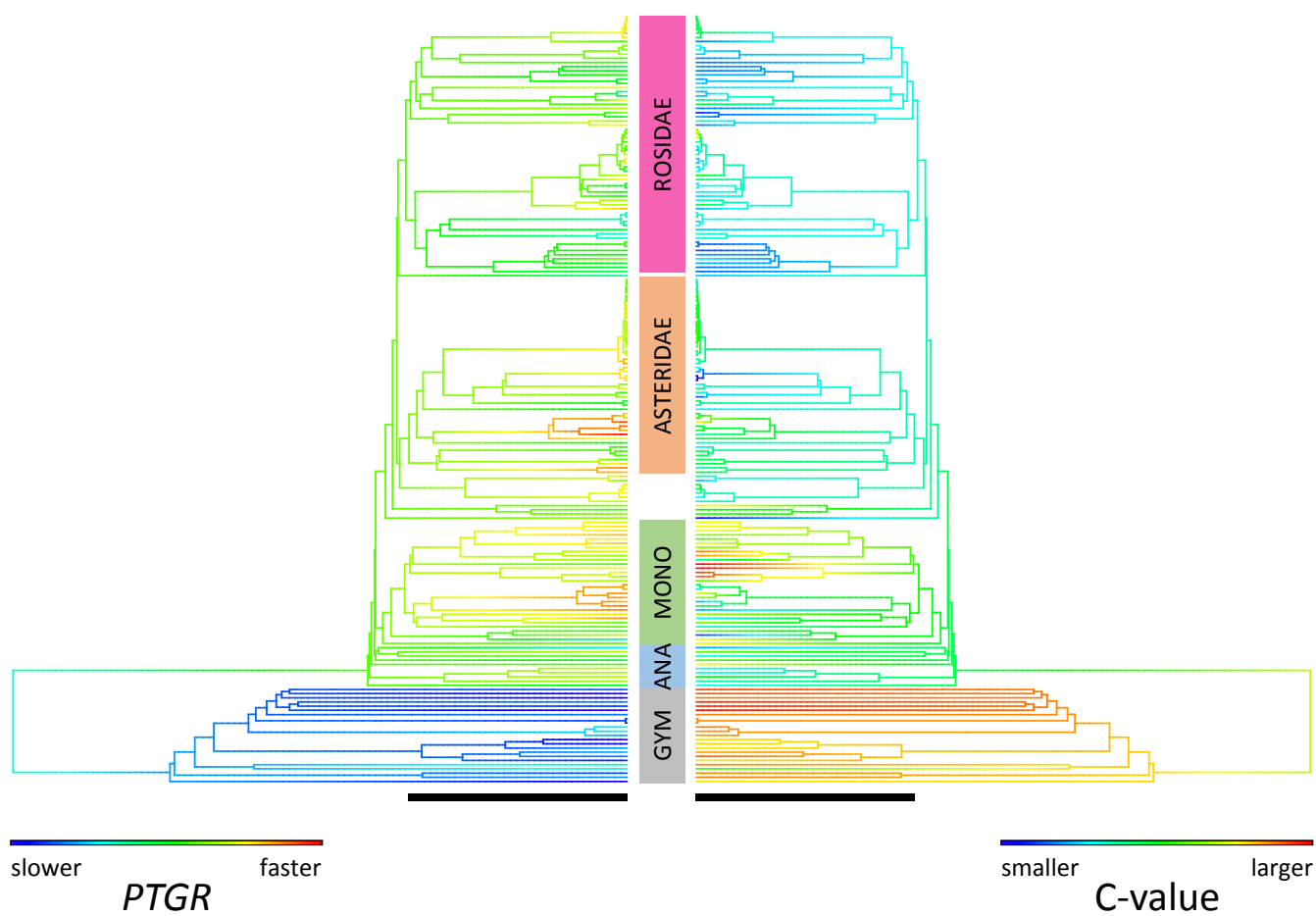
747 **Appendix S7: Closely-related taxon analyses.**

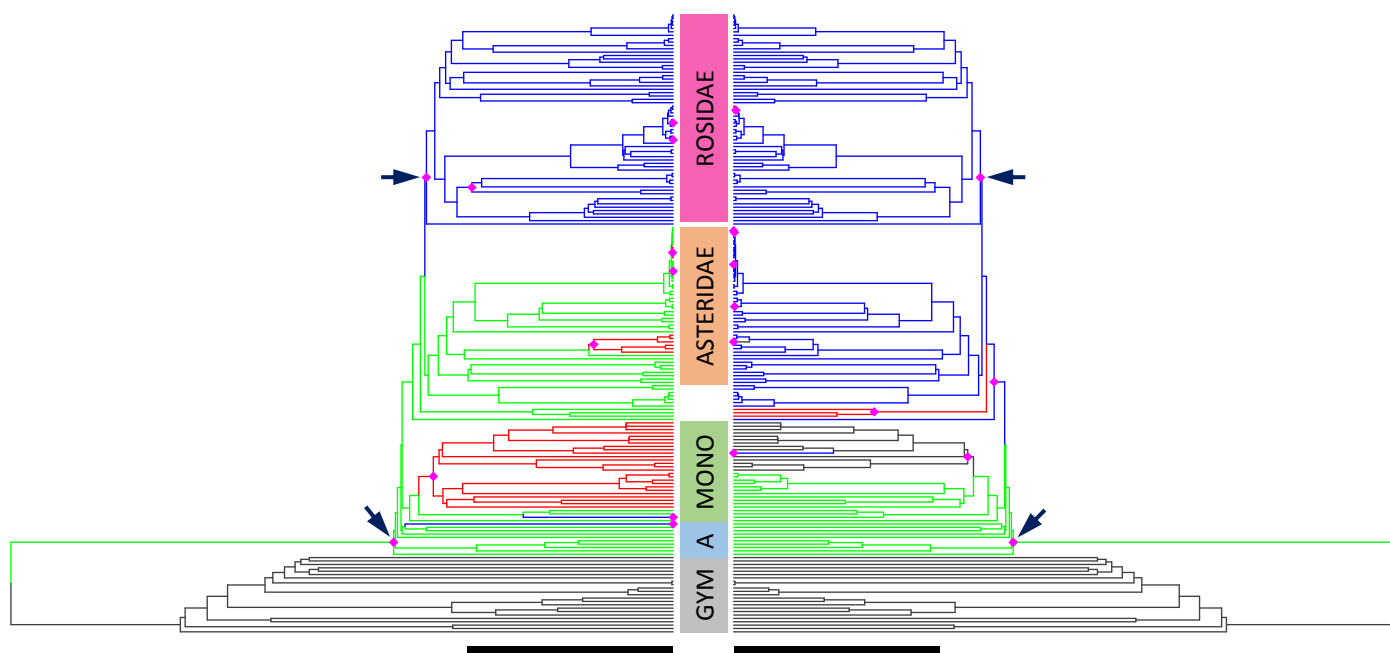
748

749 **Appendix S8: Phylogenetic ANCOVA results.**











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**Appendix S1:** 119 additional *PTGR* values and references not reported in Williams 2012.

<b>Taxon</b>	<b><i>PTGR</i> (<math>\mu\text{m h}^{-1}</math>)</b>	<b>Reference</b>
<i>Abelmoschus esculentus</i>	5217	Patil et al 2013
<i>Abutilon x hybridum</i>	1292	Cited in Sears 1937
<i>Acacia mangium</i>	46.5	Ngheim et al 2013
<i>Acacia_auriculiformis</i>	116	Ngheim et al 2013
<i>Acer rubrum</i>	182	van Ryn et al 1988, Radford et al 1968
<i>Aegle marmelos</i>	181	Bhardwaj and Tandon 2013
<i>Albuca canadensis</i>	1000	Johnson et al 2012
<i>Albuca setosa</i>	2477	Johnson et al 2012
<i>Alstroemeria aurea</i>	3091	Aizen and Raffaele 1998, De Jeu et al. 1996
<i>Alstroemeria pelegrina</i>	574	De Jeu et al. 1996
<i>Anathallis</i>	4320	Gontijo et al 2010
<i>Antirrhinum controversum</i>	131	Cario and Guemes 2014
<i>Antirrhinum valentinum</i>	160	Cario and Guemes 2014
<i>Aureolaria pedicularia</i>	15.2	Ramstetter and Mulcahy 1986
<i>Bertholletia excels</i>	800	Moritz and Ludders 1993
<i>Betula papyrifera</i>	11.1	Williams unpubl.
<i>Boswellia serrata</i>	182	Sunnichan et al 2005
<i>Brassica rapa</i>	371	Hiroi et al 2013
<i>Calluna vulgaris</i>	387	Behrend et al 2012, Mahy and Jacquemart 1999
<i>Cambessedesia</i>	587	dos Santos et al 2012
<i>Camellia oleifera</i>	338	Gao et al 2015
<i>Carica papaya</i>	214	Traub and O'Rork 1939
<i>Ceiba pentandra</i>	2500	Gribel et al 1999
<i>Ceratonia siliqua</i>	152	Von Haselberg et al. 2004
<i>Chamaecrista fasciculata</i>	637	Tucker 1996, Fenster and Sork 1988
<i>Citrullus lanatus</i>	1151	Sedgley and Buttrose 1978
<i>Citrus maxima</i>	58.3	Distefano et al 2012
<i>Citrus medica</i>	122	Distefano et al 2012
<i>Citrus reticulata</i>	51.3	Distefano et al 2012
<i>Clarkia xantiana</i>	630	Hove and Mazer 2013
<i>Commiphora wrightii</i>	42.4	Geetha et al 2013
<i>Cornus florida</i>	70.8	Reed 2004
<i>Corylus heterophylla</i>	62.5	Liu et al 2014
<i>Cucumis anguria</i>	774	Matsumoto et al. 2012
<i>Cucumis melo</i>	870	Matsumoto et al. 2012
<i>Cucumis metulifer</i>	1009	Matsumoto et al. 2012
<i>Cybistax antispyhilitica</i>	583	Bittencourt et al 2010

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<i>Cyrtandra kauaiensis</i>	261	Johnson et al 2015
<i>Cyrtandra longifolia</i>	221	Johnson et al 2015
<i>Cyrtandra platyphylla</i>	305	Johnson et al 2015
<i>Cytisus multiflorus</i>	4.48	Valtueña et al 2010
<i>Cytisus striatus</i>	19.8	Rodriguez-Riaño et al 1999
<i>Dalzellia zeylanica</i>	1159	Sehgal et al 2011
<i>Dianthus caryophyllus</i>	3002	Larsen et al 1995
<i>Downingia bacigalupii</i>	853	Kaplan 1969
<i>Echium vulgare</i>	590	Melser et al 1997
<i>Eruca vesicaria</i>	275	Cited in Sears 1937
<i>Eucalyptus globulus</i>	58.3	Gore et al 1990
<i>Faramea occidentalis</i>	2183	Travers 1999
<i>Ficus carica</i>	47.6	Beck and Lord 1988
<i>Fumana</i>	273	Carrío and Guemes 2013
<i>Guihaiothamnus acaulis</i>	188	Xie et al 2013
<i>Haberlea rhodopensis</i>	152	Bogacheva-Milkoteva 2013
<i>Handroanthus ochraceus</i>	1617	Oliveira, pers. comm.
<i>Handroanthus serratifolius</i>	1617	Oliveira, pers. comm.
<i>Hedyosmum brasiliense</i>	97.2	Williams and Edwards, unpubl.
<i>Hedyotis acutangula</i>	991	Wu et al 2010
<i>Helleborus foetidus</i>	514	Vesprini and Pacini 2000
<i>Heuchera micrantha</i>	181	Rabe and Soltis 1999
<i>Hippophae rhamnoides</i>	20.9	Mangla et al 2013
<i>Hymenaea</i>	1667	Gibbs et al 1999
<i>Ipomoea purpurea</i>	7450	Shu-Mei Chang, pers. comm. 2014
<i>Ipomopsis aggregata</i>	2409	Sage et al 2006, Wolf et al 2001
<i>Jathropa curcas</i>	915	Abdelgadir et al 2012
<i>Lactoris fernandeziana</i>	40	Bernardello et al 1999
<i>Lactuca sativa</i>	3085	Einset 1944
<i>Lagerstroemia indica</i>	1175	Pounders et al 2006
<i>Lathyrus chloranthus</i>	271	Herrick et al 1993
<i>Lathyrus odoratus</i>	321	Herrick et al 1993
<i>Limnocharis</i>	467	Hall 1902
<i>Linaria</i>	392	Cited in Sears 1937
<i>Lupinus arizonicus</i>	442	Wainwright 1978
<i>Magnolia grandiflora</i>	828	Edwards, Rankin, and Williams, unpubl. 2014
<i>Medicago rigidula</i>	82.2	Sangduen et al 1983
<i>Medicago sativa</i>	192	Barnes and Cleveland 1963
<i>Morinda parvifolia</i>	957	Liu et al 2012
<i>Mussaenda kwangtungensis</i>	963	Luo et al 2015
<i>Mussaenda shikokiana</i>	816	Chen et al 2014
<i>Nemesia strumosa</i>	333	Sears 1937

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<i>Nivenia corymbosa</i>	873	Goldblatt and Bernhardt 1990
<i>Nivenia stokeii</i>	1217	Goldblatt and Bernhardt 1990
<i>Nuphar advena</i>	835	Taylor and Williams, unpubl.
<i>Nyctanthes arbor tristis</i>	526	Bhatnagar and Uma 1969
<i>Orchis anthropophora</i>	357	Luca et al 2015
<i>Orchis italica</i>	357	Luca et al 2015
<i>Oreocharis acaulis</i>	1318	Guo et al 2013
<i>Oroxylum indicum</i>	3000	Gautam et al 2009
<i>Paeonia brownii</i>	20.8	Bernhardt et al 2013
<i>Parthenium</i>	1333	Gerstel and Riner 1950
<i>Passiflora edulis</i>	2174	Rego et al 2000
<i>Phalaenopsis</i>	208	Zhang and O'Neill 1993
<i>Phoenix dactylifera</i>	315	Reuveni et al 1986
<i>Platanthera</i>	462	Stickler et al 2013 (poster)
<i>Plumbago zeylanica</i>	12741	Russell 1985
<i>Polypleurum stylosum</i>	153	Khosla et al 2000
<i>Potamogeton intortusifolius</i>	267	Zhang et al 2010
<i>Potamogeton perfoliatus</i>	1585	Zhang et al 2010
<i>Potamogeton wrightii</i>	1483	Zhang et al 2010
<i>Pseudopiptadenia</i>	39	Pires and Freitas 2008
<i>Restrepia</i>	99	Millner et al 2015
<i>Schisandra sphenanthera</i>	88.9	Du et al 2012
<i>Silene vulgaris</i>	2323	Glaeti 2006
<i>Solanum chacoense</i>	396	Liu et al 2012
<i>Solanum laxum</i>	333	Lewis and Crowe 1958
<i>Sorghum bicolor</i>	3638	Heslop-Harrison et al 1984, Hodnett et al 2005
<i>Spathodea campanulata</i>	4028	Bittencourt et al 2003
<i>Sporobolus anglicus</i>	8943	Li et al 2008
<i>Thryptomene calycina</i>	320	Beardsell et al 1993
<i>Ticodendron incognitum</i>	382	Sogo and Tobe 2008
<i>Torenia baillonii</i>	3200	Kikuchi et al 2007
<i>Torenia concolor</i>	1900	Kikuchi et al 2007
<i>Trimezia</i>	2000	Bystedt and Vennigerholz 1991
<i>Vaccinium corybosum</i>	191	Knight and Scott 1964
<i>Vaccinium myrtillus</i>	67.1	Jacquemart and Thompson 1996
<i>Vaccinium uliginosum</i>	54.3	Jacquemart and Thompson 1996
<i>Vaccinium vitis idaea</i>	98.6	Jacquemart and Thompson 1996
<i>Zeyheria montana</i>	2554	Bittencourt and Semir 2004
<i>Zeylanidium lichenoides</i>	354	Chaudhary et al 2014, Sehgal et al 2014

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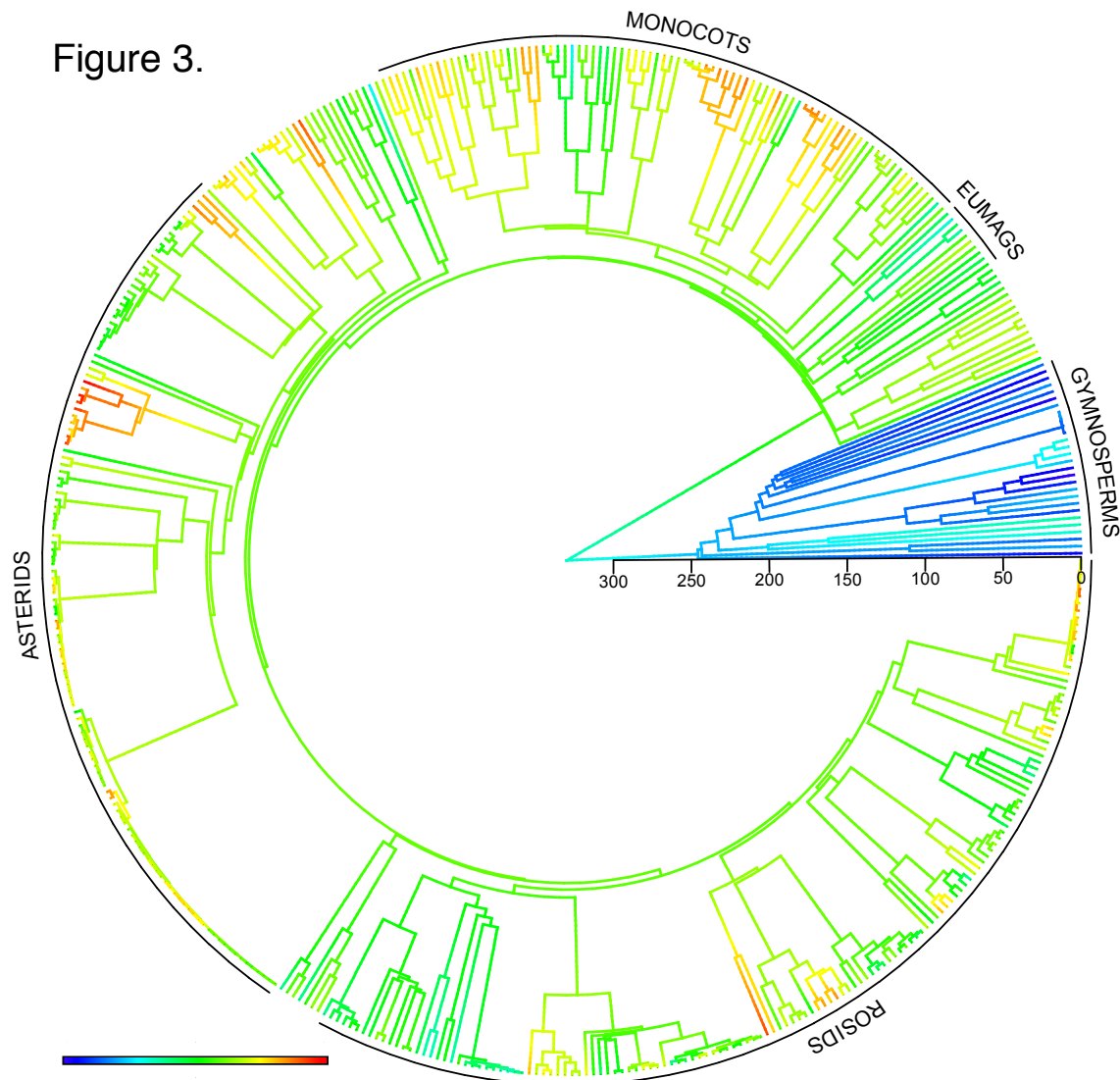
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**Appendix S2: Pollen tube growth rate (PTGR) evolution across Spermatophytes.** Contour plot showing reconstructed history of *PTGR*. Cool colors indicate *PTGR*s closer to the minimum value in seed plants while warm colors indicate *PTGR*s closer to the maximum value in seed plants. Scale bar indicates millions of years before present.



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**Appendix S3: Summary statistics for pollen tube growth rate (*PTGR*) of *Magnolia grandiflora*.**

<b>Statistic</b>	<b><i>PTGR</i></b>
raw mean ( $N = 25$ crosses)	827.6 $\mu\text{m h}^{-1}$
raw SD ( $N = 25$ )	141.3 $\mu\text{m h}^{-1}$
raw CV	0.1708
Log(10) mean	2.912 $\mu\text{m h}^{-1}$
transformed SD	0.0689 $\mu\text{m h}^{-1}$
transformed CV	0.0237

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**Appendix S4: Sensitivity analysis for the magnitude of  $\log_{10}$  *PTGR* error estimates.** Values in each column represent model weights from separate analyses of angiosperm diploids ( $N = 138$ ) vs. polyploids ( $N = 68$ ). Column headings indicate the coefficient of variation (CV), ranging from zero to 0.50, used to calculate estimated species-specific standard deviations around *PTGRs* in each analysis. The best-fitting model at each CV is indicated in bold. <sup>a</sup>, Empirically-determined CV of *Magnolia grandiflora*.

Model	Coefficient of Variation					
	0.00	0.0237 <sup>a</sup>	0.05	0.10	0.25	0.50
OUMV	<b>0.376</b>	<b>0.373</b>	<b>0.459</b>	<b>0.461</b>	0.119	0.045
OUMA	0.363	0.333	0.307	N/A	0.172	0.070
OUM	0.157	0.174	0.137	0.309	0.212	0.080
OU1	0.104	0.120	0.097	0.230	<b>0.390</b>	0.188
BM1	1.74E-31	1.77E-25	3.20E-20	4.58E-14	0.089	<b>0.528</b>
BMS	5.45E-32	5.52E-26	4.81E-24	1.30E-12	0.017	0.089

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**Appendix S5: *PTGR* evolution in gymnosperms vs. angiosperms.** Selective regime 1 represents gymnosperms ( $N = 28$ ) and selective regime 2 represents angiosperms ( $N = 423$ ). Models representing <1% of the model weight are excluded.

model	$\Delta AIC_c$	model weight	sigma sq1	alpha1	sigma sq2	alpha2	optimum1	se1	optimum2	se2
<b>OUMV</b>	(822.1)	0.338	0.091	0.122	0.139	0.122	0.187	0.123	2.690	0.048
<b>OUM</b>	0.040	0.332	0.137	0.124	0.137	0.124	0.188	0.150	2.690	0.047
<b>OUMA</b>	0.051	0.330	0.091	0.120	0.091	0.123	0.187	0.123	2.690	0.048
<b>AVERAGED MODEL</b>		~1	0.106	0.122	0.122	0.123	0.187	0.132	2.690	0.048

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**Appendix S6: C-value evolution in gymnosperms vs. angiosperms.** Selective regime 1 represents gymnosperms ( $N = 23$ ) and selective regime 2 represents angiosperms ( $N = 161$ ). Models representing <1% of the model weight are excluded.

model	$\Delta AICc$	model weight	sigma sq1	alpha1	sigma sq2	alpha2	optimum1	se1	optimum2	se2
<b>OUMV</b>	(172.4)	0.502	0.007	0.095	0.005	0.095	1.231	0.041	0.184	0.051
<b>OUMA</b>	0.02	0.498	0.006	0.085	0.006	0.096	1.231	0.042	0.184	0.051
<b>AVERAGED MODEL</b>		~1	0.007	0.09	0.005	0.095	1.231	0.041	0.184	0.051

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### Appendix S7: Closely-related taxon analyses.

#### Appendix S7a. Closely-related species pairs extracted from ploidy dataset. *PTGRs* in $\mu\text{m h}^{-1}$ .

Binomial test ( $P = 0.623$ ;  $N = 10$ ).

DIPLOID TAXON	POLYPLOID TAXON	DIPLOID <i>PTGR</i>	POLYPLOID <i>PTGR</i>	FASTER TAXON
<i>Anagallis arvensis</i>	<i>Anagallis monelli</i>	233.33	105.56	diploid
<i>Hemerocallis thunbergii</i>	<i>Hemerocallis fulva</i>	4166.67	6266.67	polyploid
<i>Ipomoea purpurea</i>	<i>Ipomoea batatas</i>	7450	4625	diploid
<i>Iris mandshurica</i>	<i>Iris pseudacorus</i>	278.65	4255.50	polyploid
<i>Lythrum junceum</i>	<i>Lythrum salicaria</i>	722.22	493.60	diploid
<i>Medicago rigidula</i>	<i>Medicago sativa</i>	82.23	192.17	polyploid
<i>Prunus avium</i>	<i>Prunus domestica</i>	260.88	177.5	diploid
<i>Tabebuia rosea</i>	<i>Tabebuia chrysotricha</i>	1111.11	1342.45	polyploid
<i>Trifolium pratense</i>	<i>Trifolium polymorphum</i>	103.89	444.44	polyploid
<i>Ulmus pumila</i>	<i>Ulmus americana</i>	56.25	56.25	equivocal

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**Appendix S7b. Intraspecific diploid-polyploid cytotypes taken from the literature.** All are autopolyploids. Binomial test,  $N = 11$ ,  $P = 0.0020$ . Percent difference is calculated relative to the diploid.

REF.	TAXON	DIPLOID PTGR	POLYPLOID PTGR	POLYPLOID +/- (% DIFF)
1	<i>Beta vulgaris</i> 2x,4x	241.2 $\mu\text{m/h}$	142.7 $\mu\text{m/h}$	slower (-69%)
2	<i>Cucumis melo</i> 2x,4x	“no difference”		equivocal
3	<i>Datura stramonium</i> 2x,4x	2953.7 $\mu\text{m/h}$	2812.5 $\mu\text{m/h}$	slower (-4.8%)
4	<i>Lactuca sativa</i> 2x,4x	“faster”	“slower”	slower
5	<i>Malus domestica</i> 2x,4x	3.8 units/96 h	3.1 units/96 h	slower (-18.4%)
6	<i>Malus domestica</i> 2x,3x	682 $\mu\text{m/h}$	465 $\mu\text{m/h}$	slower (-31.8%)
7	<i>Secale cereale</i> 2x,4x	12.24 units/h	12.08 units/h	slower (-1.3%)
8	<i>Solanum sp.</i> 2x,4x	“faster”	“slower”	slower
9	<i>Trifolium pratense</i> 2x,4x	2322 $\mu\text{m/h}$	1950 $\mu\text{m/h}$	slower (-16%)
10,11	<i>Zea mays</i> 2x,4x	Slower pollen germination and pollen tube growth rate in 4x		slower

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**Appendix S8: Phylogenetic ANCOVA results.** Models comprising <1% of the model weight are excluded.

**Appendix S8a: Angiosperms only ( $N = 100$ ).**

<b>Full model</b>				
<u>Model</u>	<u>Weight</u>	<u><math>P_{C\text{-value}}</math></u>	<u><math>P_{\text{ploidy}}</math></u>	<u><math>P_{\text{interaction}}</math></u>
kappa	0.688	0.028	0.565	0.334
OU	0.287	0.005	0.679	0.414
lambda	0.025	0.076	0.867	0.626

Model averaged slope for C-value:  $0.399 \pm 0.167$

<b>No interaction</b>			
<u>Model</u>	<u>Weight</u>	<u><math>P_{C\text{-value}}</math></u>	<u><math>P_{\text{ploidy}}</math></u>
kappa	0.652	0.046	0.748
OU	0.313	0.006	0.895
lambda	0.035	0.083	0.979

Model averaged slope for C-value:  $0.344 \pm 0.153$

<b>C-value only</b>		
<u>Model</u>	<u>Weight</u>	<u><math>P_{C\text{-value}}</math></u>
kappa	0.642	0.045
OU	0.322	0.005
lambda	0.036	0.079

Model averaged slope for C-value:  $0.344 \pm 0.153$

**Appendix S8b: All seed plants ( $N = 118$ ).**

<b>Full model</b>				
<u>Model</u>	<u>Weight</u>	<u><math>P_{C\text{-value}}</math></u>	<u><math>P_{\text{ploidy}}</math></u>	<u><math>P_{\text{interaction}}</math></u>
kappa	0.998	0.080	0.486	0.624

Slope for C-value:  $0.288 \pm 0.163$

<b>No interaction</b>			
<u>Model</u>	<u>Weight</u>	<u><math>P_{C\text{-value}}</math></u>	<u><math>P_{\text{ploidy}}</math></u>
kappa	0.997	0.092	0.562

Slope for C-value:  $0.263 \pm 0.155$

<b>C-value only</b>		
<u>Model</u>	<u>Weight</u>	<u><math>P_{C\text{-value}}</math></u>
kappa	0.997	0.090

Slope for C-value:  $0.264 \pm 0.154$