

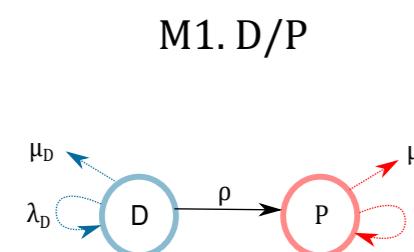
Figure S1: Ploidy and breeding system data according to three different classifications. For ploidy only models, classifications with states *D* and *P* were used (inner circle). For breeding system models classifications with states *I* and *C* were used (middle circle). For ploidy and breeding system models classifications using *ID, CD, CP* were used (outer circle). Data with missing information in one of the traits was classified simultaneously as two possible states, for example, diploids without breeding system *?D* were classified as (*CD, CP*).

Figure S2: Twenty-nine models of diversification are proposed for the study of ploidy, breeding systems, and hidden states linked to the process of diversification. We divide the models by the type of focal trait studied (ploidy only, breeding system only, or ploidy and breeding system). The contributions of the focal trait to the diversification process can be measured by comparing the models in each of the columns. That is, the focal trait only models assume that speciation and extinction rates are only linked to the trait itself, the hidden trait only models assume that the diversification rates are linked to unknown factors but not the trait of interest, and the focal trait with hidden trait models assume that both the focal trait and unknown factors are contributing to diversification. (large format figure)

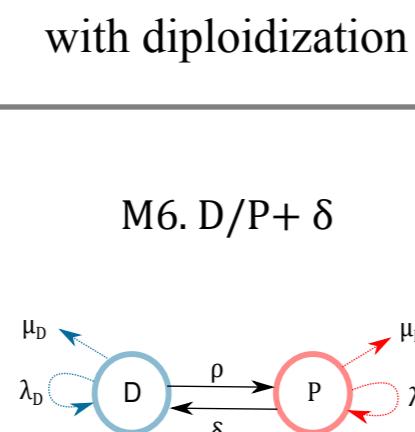
## *What is the focal trait?*

## *What affects diversification?*

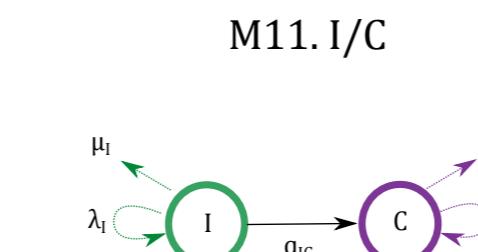
## *Focal trait only*



*only*



### *Breeding system only*



## *Ploidy and breeding system*

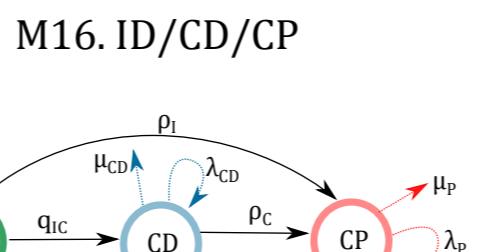
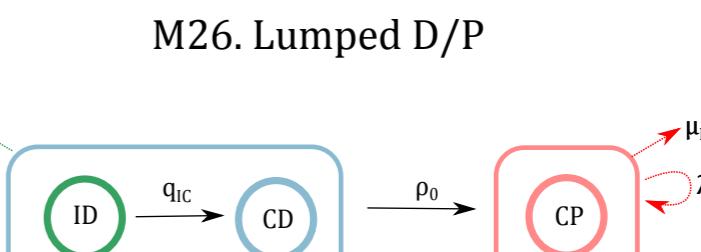
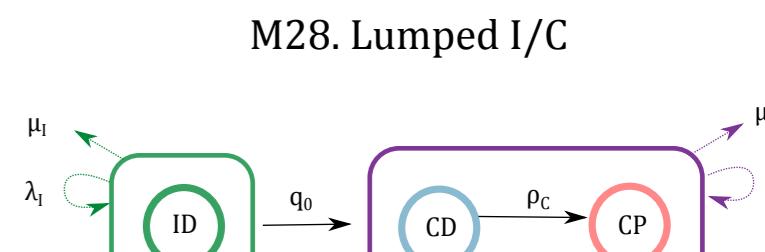


Diagram M21. ID/CD/CP +  $\delta$  illustrates a process flow involving three main stages: ID, CD, and CP. The flow starts at the green circle labeled 'ID', moves through a blue oval labeled 'CD', and ends at a red circle labeled 'CP'. A curved arrow above the flow indicates the overall progression. Below the flow, a horizontal arrow labeled  $q_{IC}$  points from ID to CD. Between the ID and CD stages, there is a vertical dashed arrow labeled  $\mu_{CD}$  pointing upwards. Between the CD and CP stages, there is a vertical dashed arrow labeled  $\lambda_{CD}$  pointing downwards. Additionally, a curved arrow labeled  $\rho_I$  points from the top of the ID stage towards the CD stage, and another curved arrow labeled  $\rho_C$  points from the bottom of the CP stage back towards the CD stage.

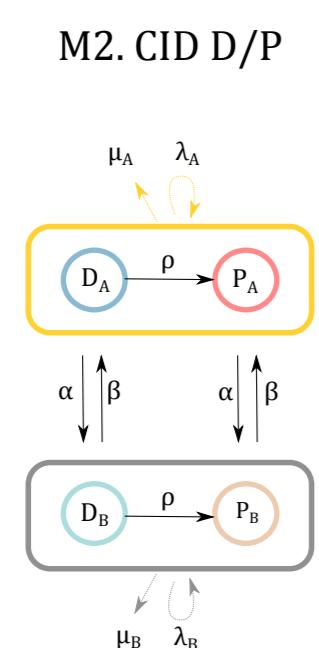
### *Ploidy only (lumped)*



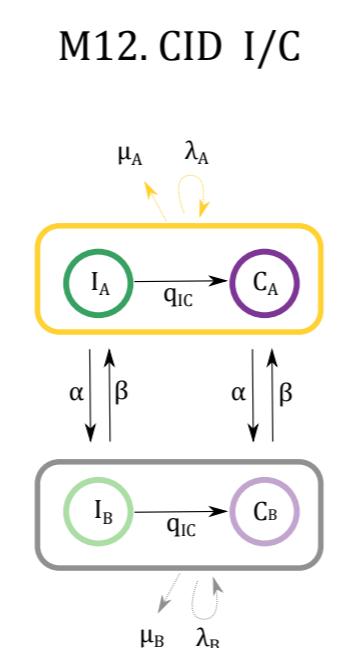
## *Breeding system only (lumped)*



## *Hidden trait only*



The diagram illustrates two coupled systems, A and B, each enclosed in a box. System A (top) consists of a blue circle labeled  $D_A$  and a red circle labeled  $P_A$ , connected by a double-headed arrow with parameters  $\rho$  and  $\delta$ . Above the boxes,  $\mu_A$  and  $\lambda_A$  are shown with arrows pointing towards the top box. System B (bottom) consists of a teal circle labeled  $D_B$  and an orange circle labeled  $P_B$ , also connected by a double-headed arrow with parameters  $\rho$  and  $\delta$ . Below the bottom box,  $\mu_B$  and  $\lambda_B$  are shown with arrows pointing towards the bottom box. The boxes are labeled M7. CID D/P + delta.

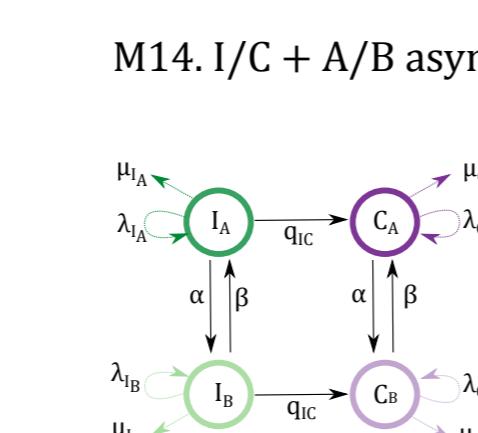
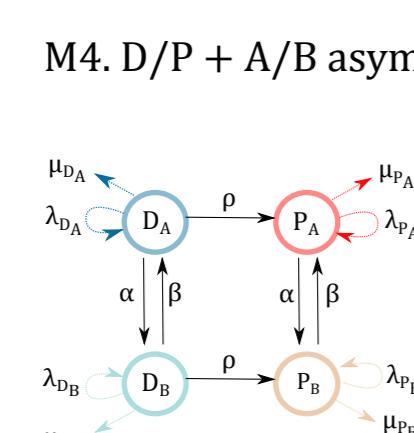


M17. CID ID/CD/CP

Diagram illustrating two coupled state-space models:

- Top Model (CID ID/CD/CP):**
  - States:  $ID_A$  (green circle),  $CD_A$  (light blue circle),  $CP_A$  (pink circle).
  - Transitions:
    - $ID_A \xrightarrow{q_{IC}} CD_A$
    - $CD_A \xrightarrow{\rho_C} CP_A$
    - $CP_A \xrightarrow{\rho_I} ID_A$
  - Self-loop on  $ID_A$ :  $\mu_A$  (with a yellow arrow).
- Bottom Model (CID ID/CD/CP):**
  - States:  $ID_B$  (green circle),  $CD_B$  (light blue circle),  $CP_B$  (orange circle).
  - Transitions:
    - $ID_B \xrightarrow{q_{IC}} CD_B$
    - $CD_B \xrightarrow{\rho_C} CP_B$
    - $CP_B \xrightarrow{\rho_I} ID_B$
  - Self-loop on  $ID_B$ :  $\mu_B$  (with a yellow arrow).

# *Focal trait and hidden trait*



4. ID/CD/CP + A/B +  $\delta$  a

M27. Lumped D/P + A/B

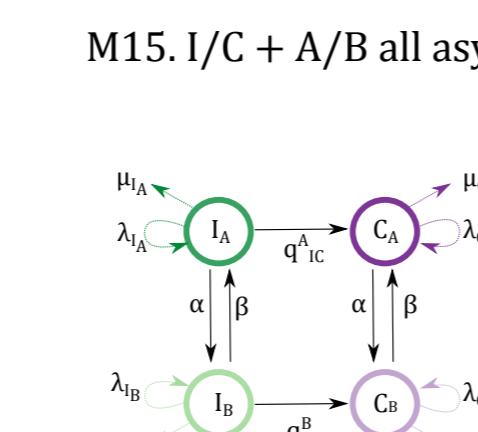
$\text{ID}_A \xrightarrow{q_{IC}} \text{CD}_A \xrightarrow{\rho_0} \text{CP}_A$   
 $\text{ID}_B \xrightarrow{q_{IC}} \text{CD}_B \xrightarrow{\rho_0} \text{CP}_B$

M29. Lumped I/C + A/B

Diagram illustrating the lumped I/C + A/B model. The system consists of two parallel paths. Each path starts with an input component (ID<sub>A</sub> or ID<sub>B</sub>) and ends with an output component (CP<sub>A</sub> or CP<sub>B</sub>). The paths are represented by purple boxes labeled CD (Controlled Device). The top path (A) has components CD<sub>A</sub> (blue) and CP<sub>A</sub> (red). The bottom path (B) has components CD<sub>B</sub> (blue) and CP<sub>B</sub> (orange). The paths are connected by a common flow q<sub>0</sub>. Each path has associated magnetic fields μ<sub>I\_A</sub>, μ<sub>C\_A</sub>, λ<sub>I\_A</sub>, and λ<sub>C\_A</sub>. Vertical arrows indicate α levels.

The diagram illustrates a two-site system labeled M5. It consists of two coupled sites, \$D\_A\$ and \$D\_B\$, represented by light blue circles. Each site has a self-loop transition labeled \$\lambda\_{D\_A}\$ and \$\lambda\_{D\_B}\$ respectively. Site \$D\_A\$ also has a transition to a state \$P\_A\$ labeled \$\rho^A\$, which is highlighted with a red circle. Site \$D\_B\$ has a transition to a state \$P\_B\$ labeled \$\rho^B\$, which is highlighted with an orange circle. Both \$P\_A\$ and \$P\_B\$ states have self-loop transitions labeled \$\lambda\_{P\_A}\$ and \$\lambda\_{P\_B}\$ respectively. Additionally, there are bidirectional transitions between \$D\_A\$ and \$D\_B\$ labeled \$\alpha\$ and \$\beta\$.

The diagram illustrates a two-player zero-sum game structure. It features two sets of nodes:  $D$  (blue circles) and  $P$  (red and orange circles). The  $D$  set includes  $D_A$  (top) and  $D_B$  (bottom), with self-loops labeled  $\mu_{D_A}$  and  $\lambda_{D_B}$ . The  $P$  set includes  $P_A$  (red top) and  $P_B$  (orange bottom), with self-loops labeled  $\mu_{P_A}$  and  $\lambda_{P_B}$ . Directed edges connect  $D_A$  to  $P_A$  (labeled  $p^A$ ) and  $D_B$  to  $P_B$  (labeled  $p^B$ ). There are also directed edges from  $P_A$  back to  $D_A$  (labeled  $\delta^A$ ) and from  $P_B$  back to  $D_B$  (labeled  $\delta^B$ ). Vertical double-headed arrows between  $D_A$  and  $D_B$  are labeled  $\alpha$  above and  $\beta$  below. Vertical double-headed arrows between  $P_A$  and  $P_B$  are also labeled  $\alpha$  above and  $\beta$  below.



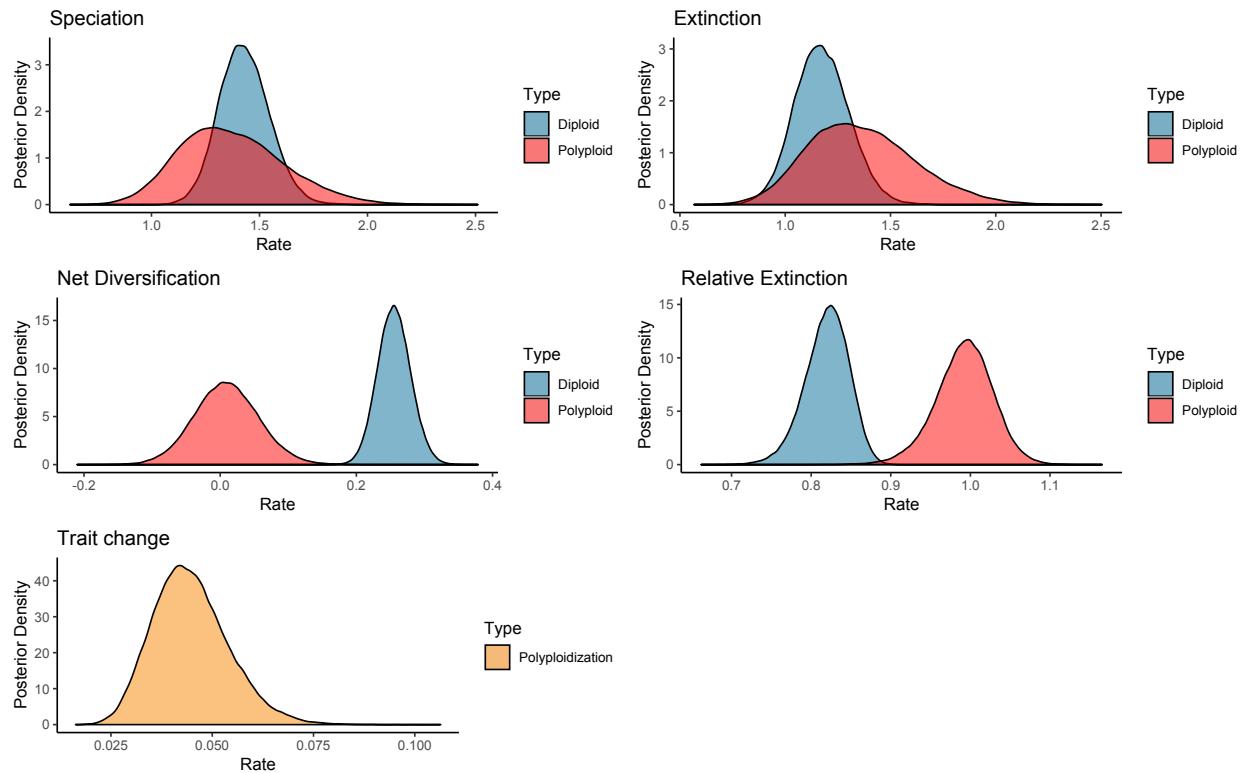


Figure S3: Posterior distributions for each of the parameters in the ploidy only model (M1). Red color represents diploid state  $D$  and blue color represents polyploid state  $P$ . (A) Speciation rates. (B) Extinction rates. (C) Net diversification rates (speciation minus extinction from panels A and B). (D) Relative extinction rates (extinction divided by speciation from panels A and B). (E) Polypliodization rate ( $\rho$ ).

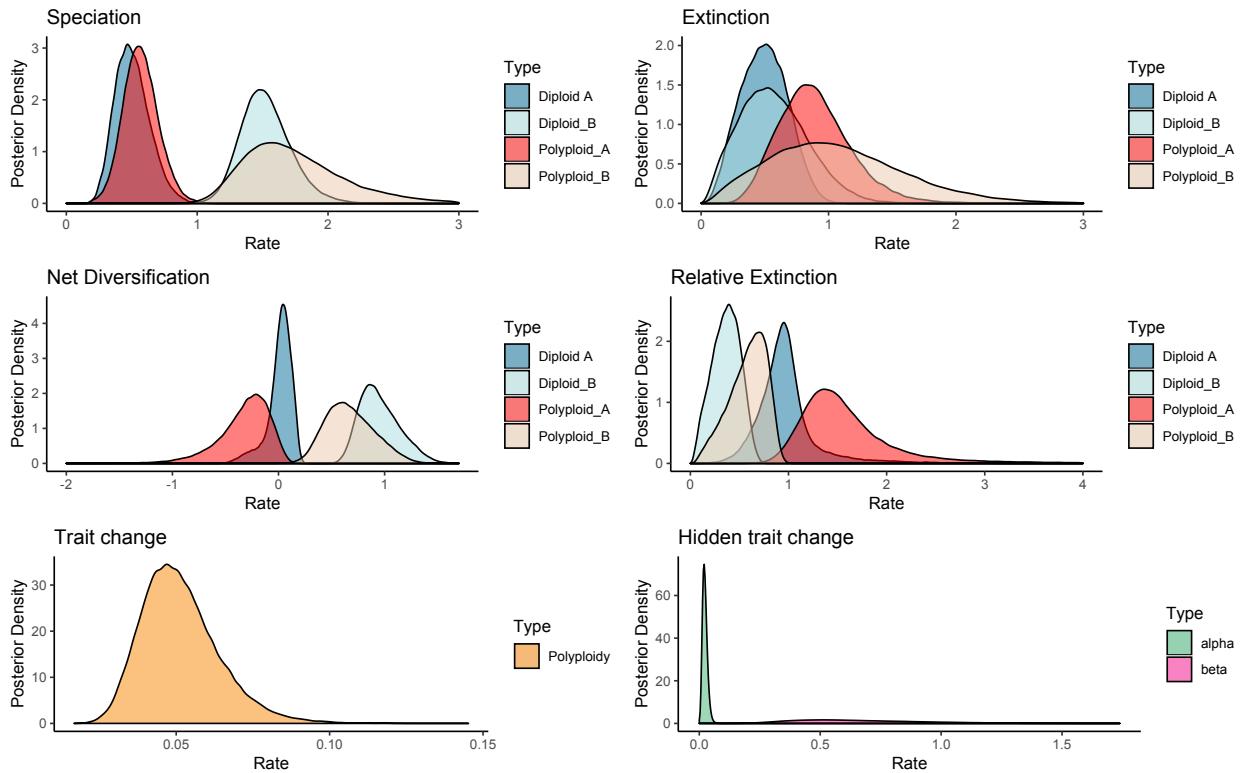


Figure S4: Posterior distributions for each of the parameters in the ploidy and hidden trait model (M4). Red color represents diploid state  $D$  and blue color represents polyploid state  $P$ . Dark colors represent hidden state  $A$  and light colors hidden state  $B$ . (A) Speciation rates. (B) Extinction rates. (C) Net diversification rates (speciation minus extinction from panels A and B). (D) Relative extinction rates (extinction divided by speciation from panels A and B). (E) Polyploidization rate ( $\rho$ ). (F) Transition rates between hidden states ( $\alpha$  and  $\beta$ ).

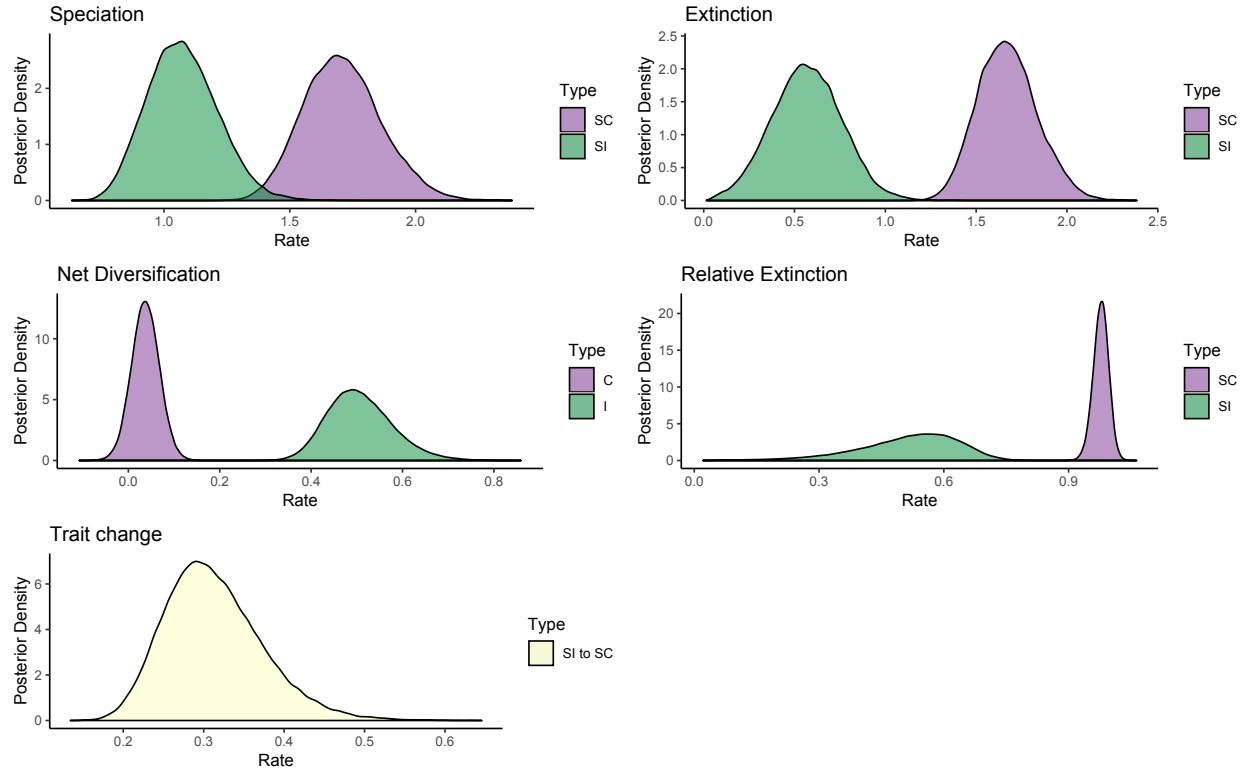


Figure S5: Posterior distributions for each of the parameters in the breeding system only model (M11). Green color represents self-incompatible state  $I$  and purple color represents self-compatible state  $C$ . (A) Speciation rates. (B) Extinction rates. (C) Net diversification rates (speciation minus extinction from panels A and B). (D) Relative extinction rates (extinction divided by speciation from panels A and B). (E) Self-incompatible to self-compatible transition rate ( $q_I C$ ).

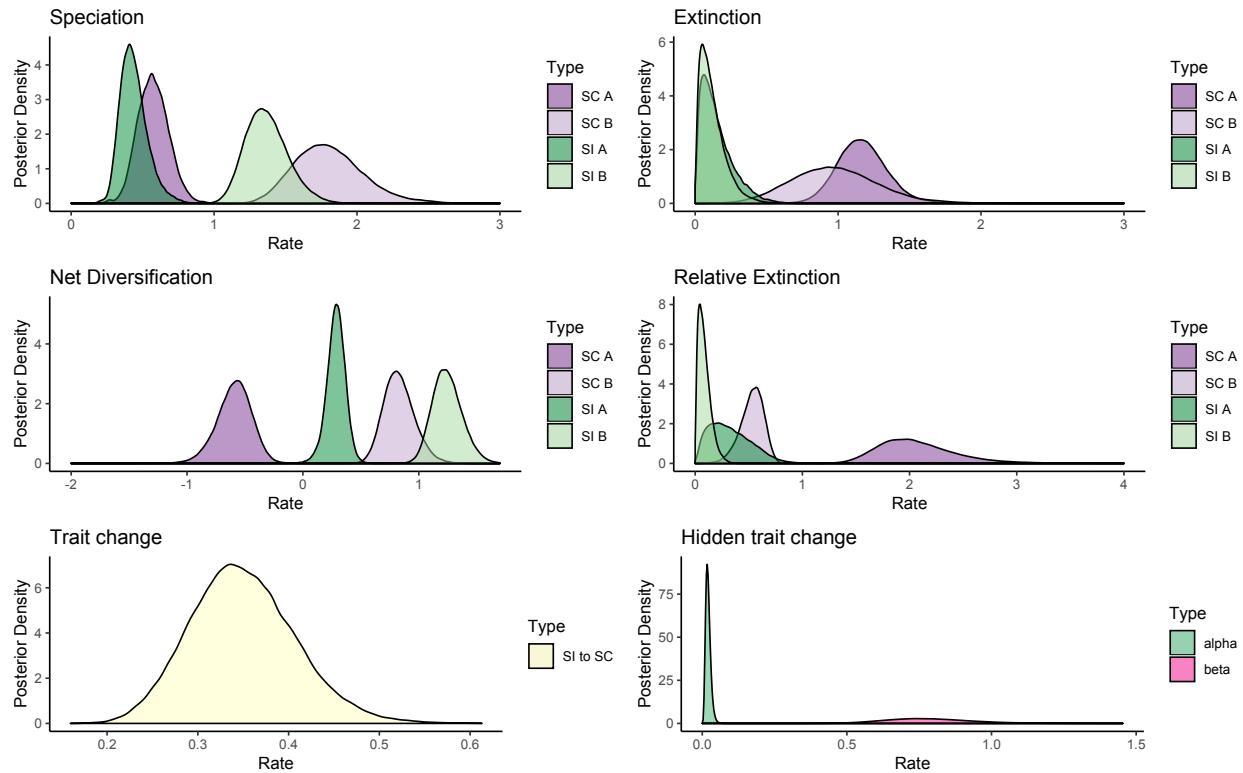


Figure S6: Posterior distributions for each of the parameters in the breeding system and hidden trait model (M14). Green color represents self-incompatible state  $I$  and purple color represents self-compatible state  $A$ . Dark colors represent hidden state  $A$  and light colors hidden state  $B$ . (A) Speciation rates. (B) Extinction rates. (C) Net diversification rates (speciation minus extinction from panels A and B). (D) Relative extinction rates (extinction divided by speciation from panels A and B). (E) Self-incompatible to self-compatible transition rate ( $q_I C$ ). (F) Transition rates between hidden states ( $\alpha$  and  $\beta$ ).

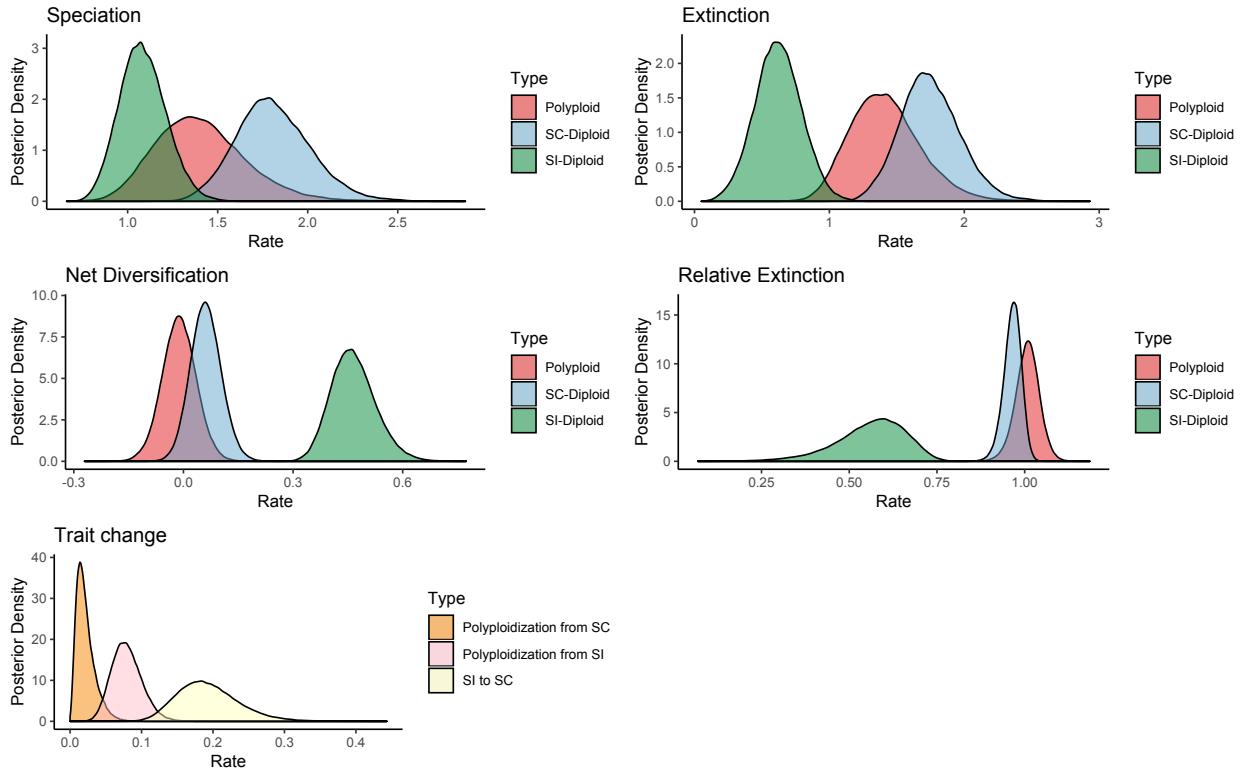


Figure S7: Posterior distribution for each of the parameters in the ploidy and breeding system model (M16). Green color represents self-incompatible diploid state  $ID$ , blue color is the self-compatible and diploid state  $CD$  and pink represents self-compatible polyplloid state  $CP$ . (A) Speciation rates. (B) Extinction rates. (C) Net diversification rates (speciation minus extinction from panels A and B). (D) Relative extinction rates (extinction divided by speciation from panels A and B). (E) Self-incompatible to self-compatible transition rate ( $q_{IC}$ , yellow), polyploidization rate from self-incompatible ( $\rho_I$ , light pink), and polyploidization from self-compatible ( $\rho_C$ , orange).

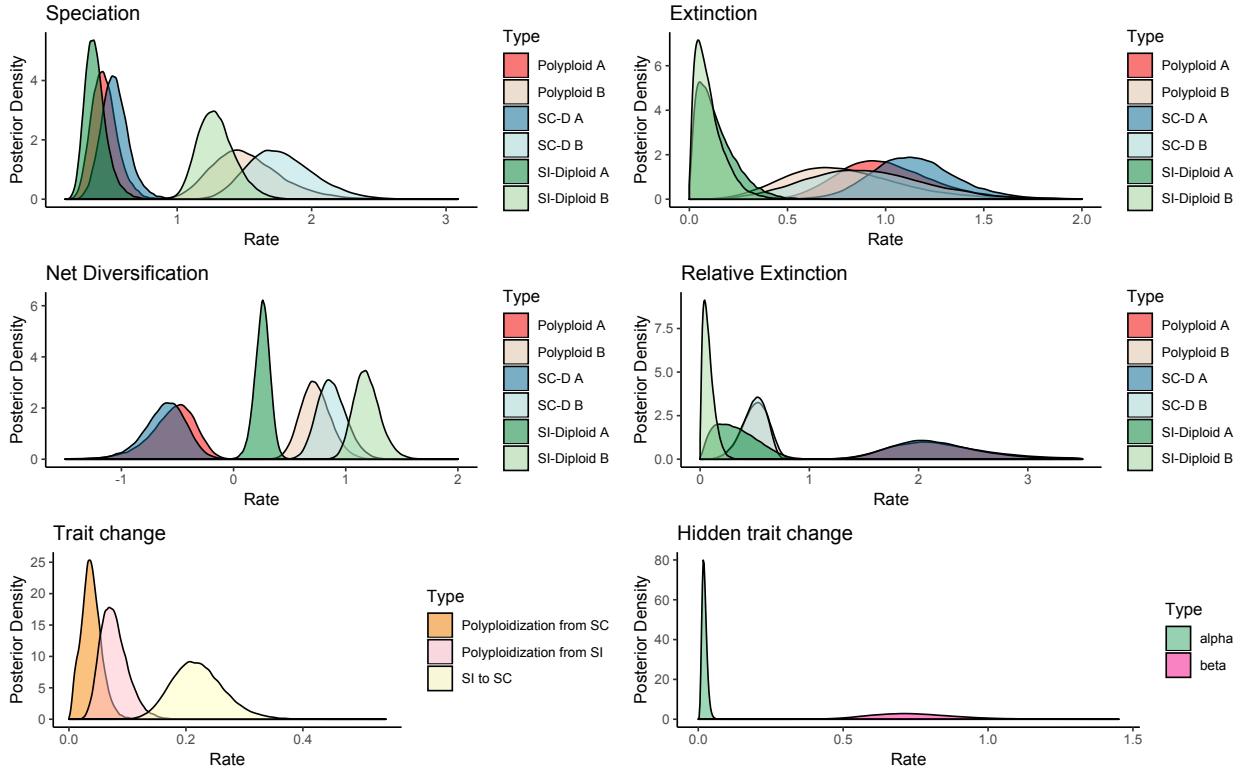


Figure S8: Posterior distribution for each of the parameters in the ploidy, breeding system, and hidden trait model (M19). Green color represents self-incompatible diploid state  $ID$ , blue color is the self-compatible and diploid state  $CD$  and pink represents self-compatible polypliod state  $CP$ . Dark colors represent hidden state  $A$  and light colors hidden state  $B$ . (A) Speciation rates. (B) Extinction rates. (C) Net diversification rates (speciation minus extinction from panels A and B). (D) Relative extinction rates (extinction divided by speciation from panels A and B). (E) Self-incompatible to self-compatible transition rate ( $q_I C$ , yellow), polypliodization rate from self-incompatible ( $\rho_I$ , light pink), and polypliodization from self-compatible ( $\rho_c$ , orange). (F) Transition rates between hidden states (  $\alpha$  and  $\beta$  ).

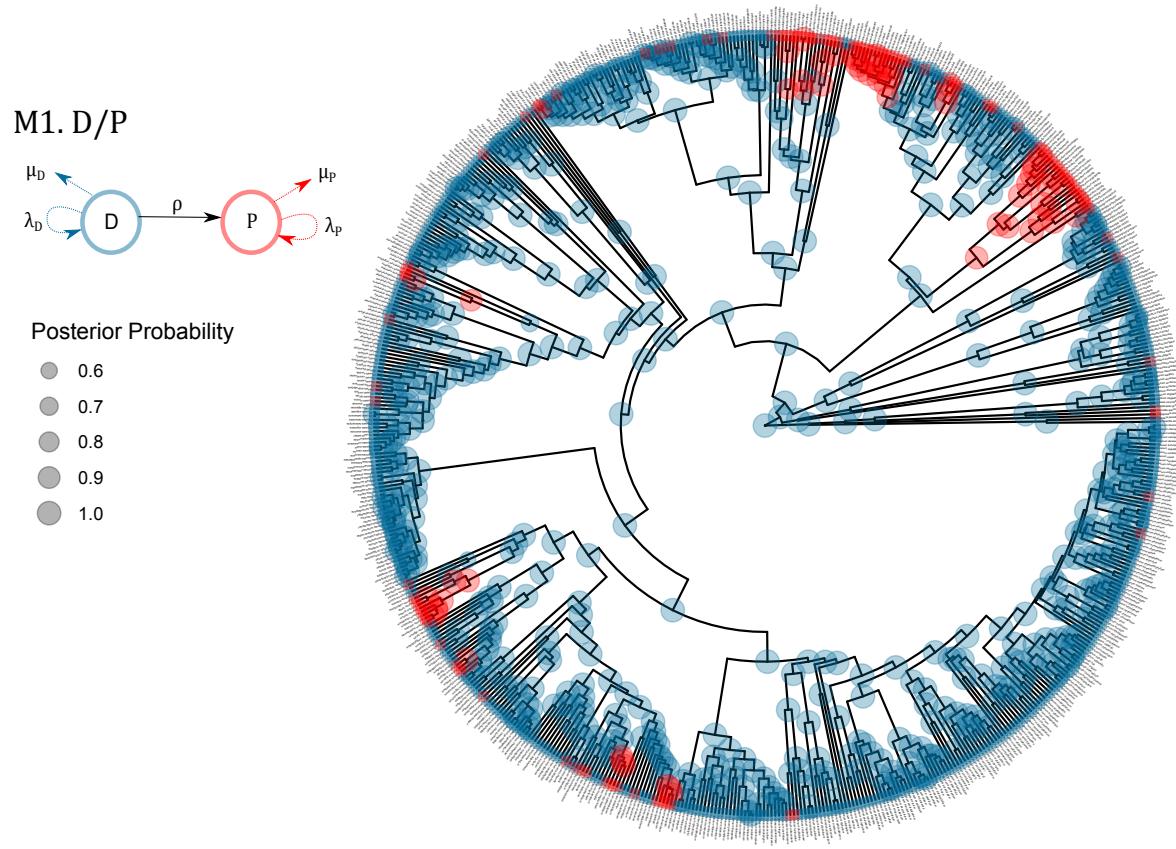
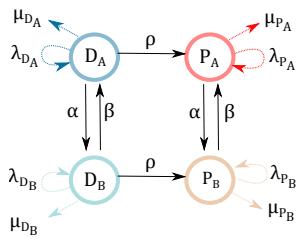


Figure S9: Ancestral state estimation showing the maximum *a posteriori* estimates of the marginal probability distributions for each of the 650 internal nodes under the ploidy only model (M1).

#### M4. D/P + A/B asym



Posterior Probability

- 0.5
- 0.6
- 0.7
- 0.8
- 0.9
- 1.0

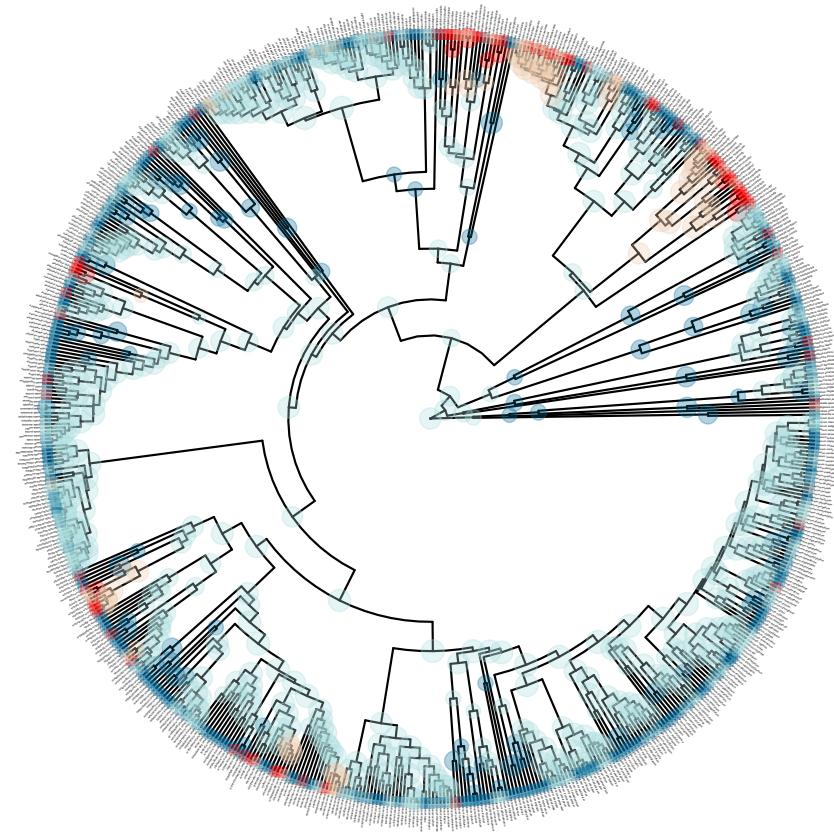


Figure S10: Ancestral state estimation showing the maximum *a posteriori* estimates of the marginal probability distributions for each of the 650 internal nodes under the ploidy and hidden states model (M4).

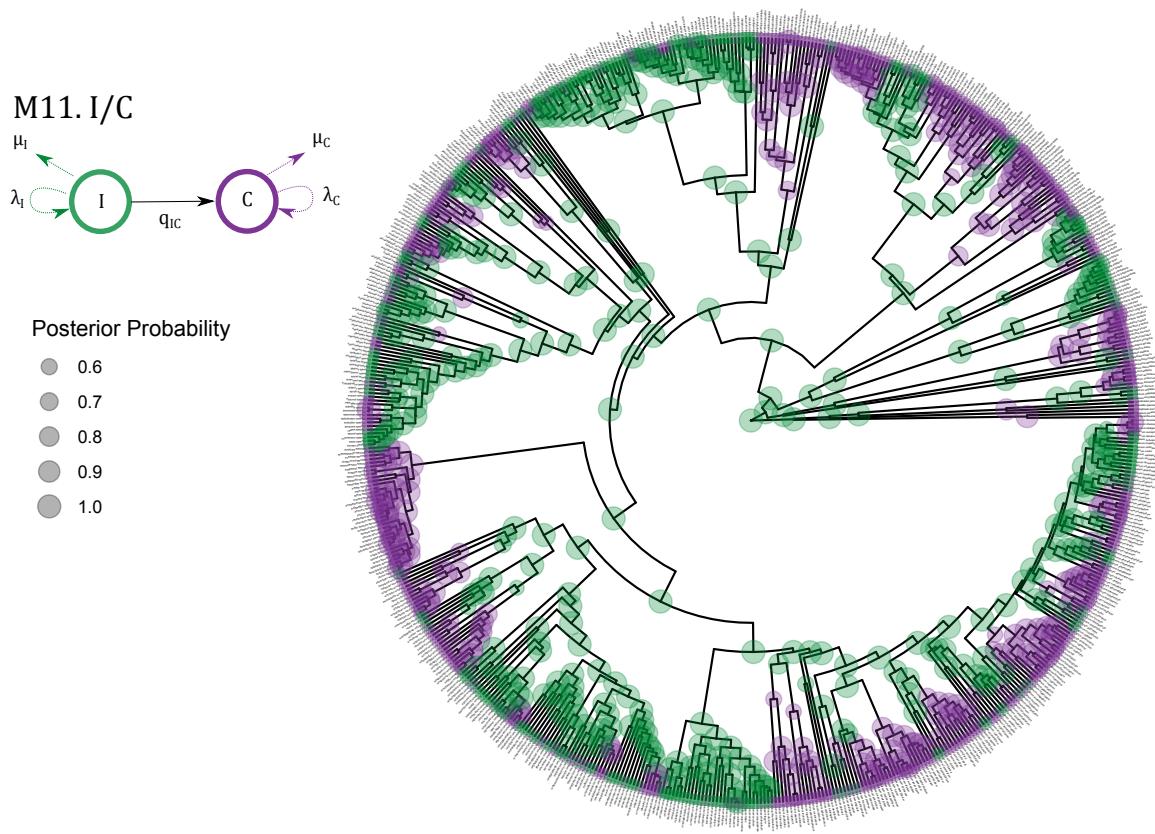
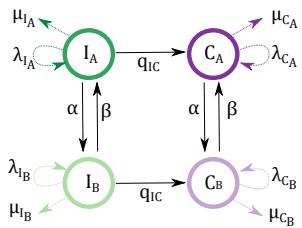


Figure S11: Ancestral state estimation showing the maximum *a posteriori* estimates of the marginal probability distributions for each of the 650 internal nodes under the breeding system only model (M11).

### M14. I/C + A/B asym



Posterior Probability

- 0.4
- 0.6
- 0.8
- 1.0

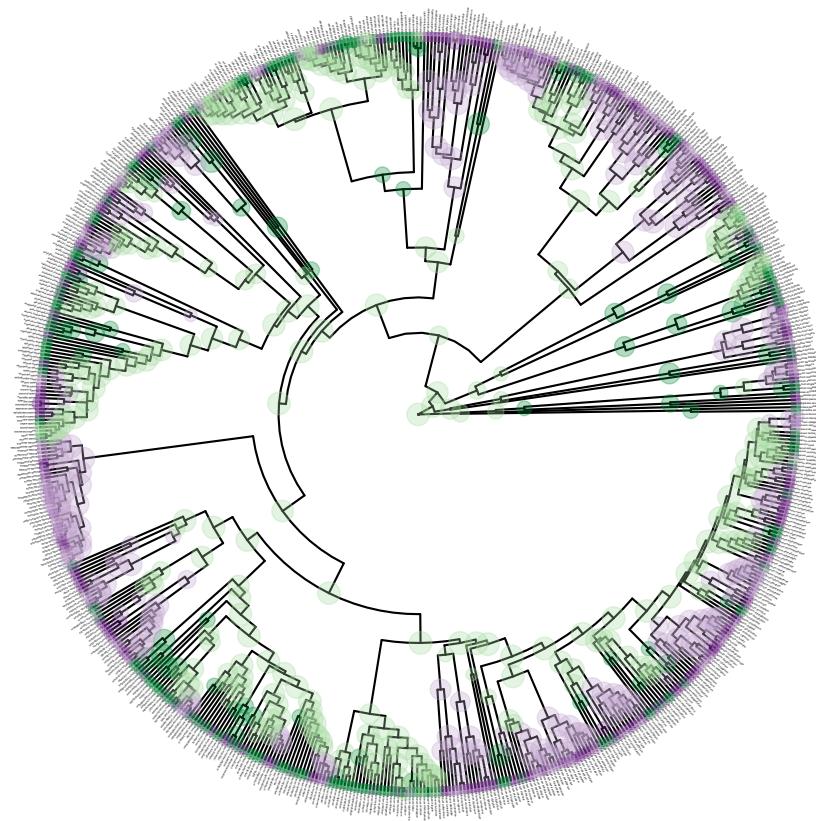


Figure S12: Ancestral state estimation showing the maximum *a posteriori* estimates of the marginal probability distributions for each of the 650 internal nodes under the breeding system and hidden states model (M14).

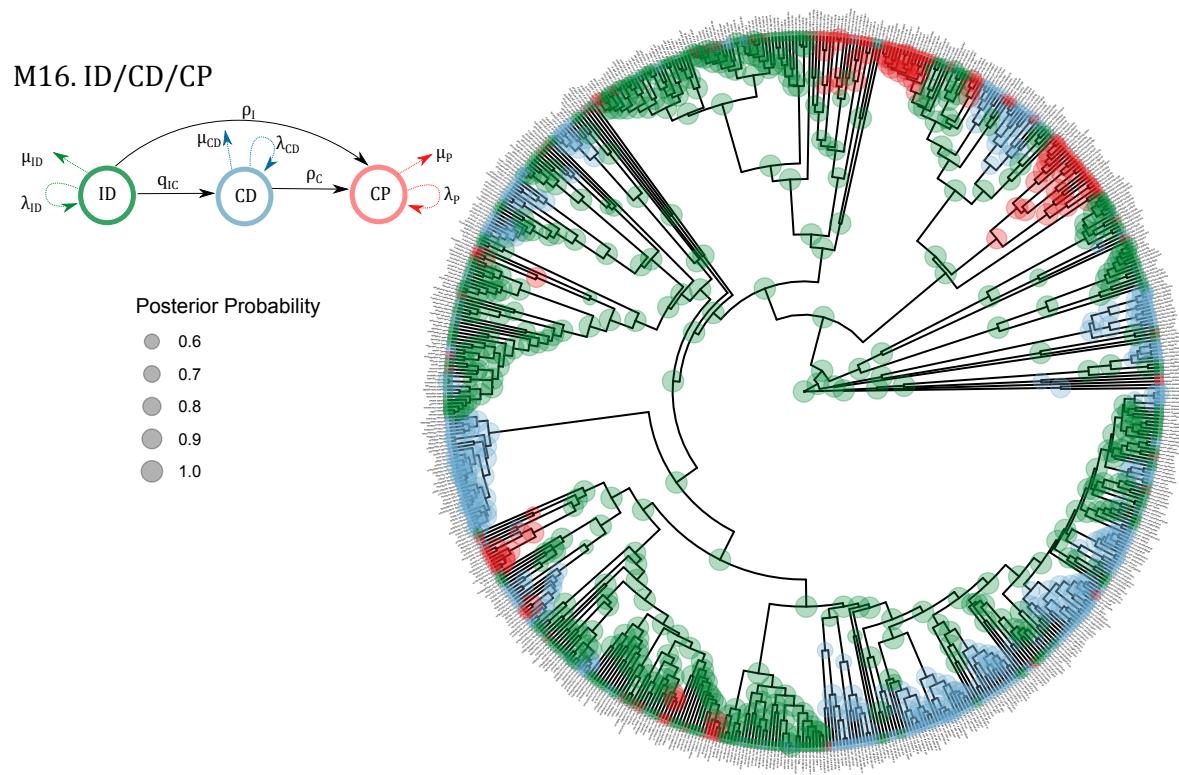


Figure S13: Ancestral state estimation showing the maximum *a posteriori* estimates of the marginal probability distributions for each of the 650 internal nodes under the ploidy and breeding system model (M16).

### M19. ID/CD/CP + A/B asym

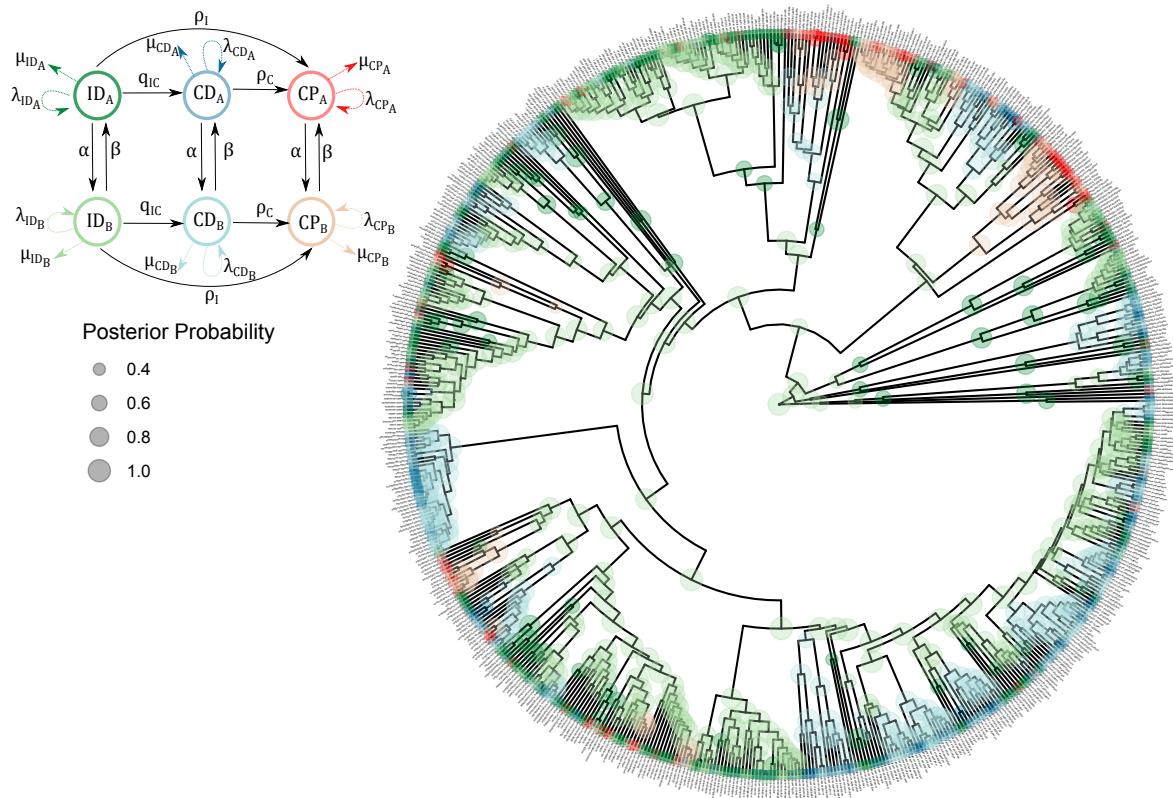


Figure S14: Ancestral state estimation showing the maximum *a posteriori* estimates of the marginal probability distributions for each of the 650 internal nodes under the ploidy, breeding systems, and hidden states model (M19).

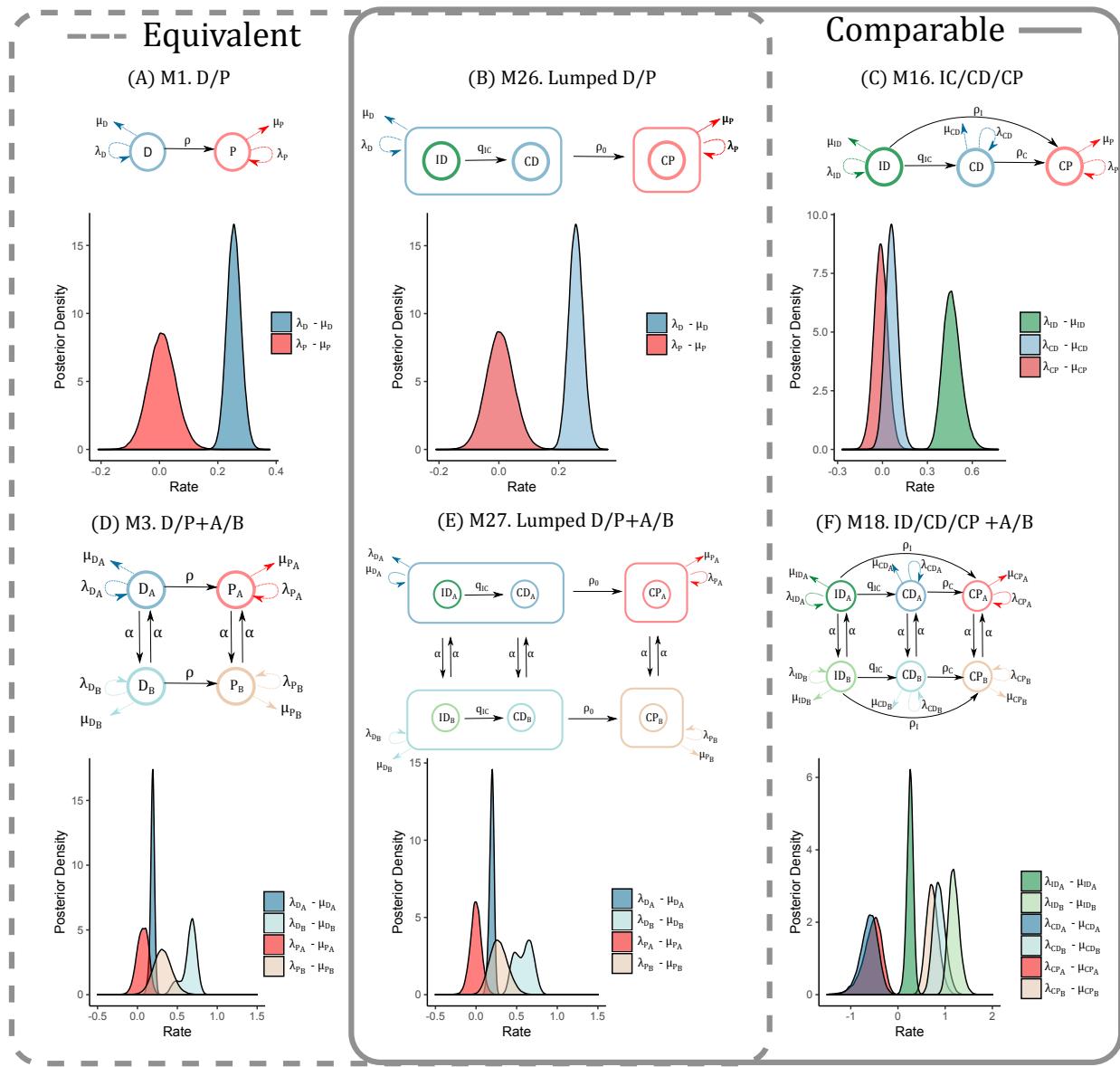


Figure S15: Testing the addition of breeding system to ploidy models. (A) Ploidy only model (M1) where data enter as binary  $D$  and  $P$ . (B) Lumped model for ploidy (M26) where data are the three-state values ( $ID, CP, CD$ ) but results are equivalent to model M1. (C) Ploidy and breeding system model (M16) where data enter as the three-state values. Models M26 and M16 are comparable whereas M1 and M16 are not. (D) Ploidy and hidden state model (M3) where data enter as binary  $D$  and  $P$ . (E) Lumped model for ploidy and hidden state (M27) where data are the three-state values ( $ID, CP, CD$ ) but results are equivalent to model M3. (F) Ploidy, breeding system, and hidden state model (M18) where data enter as the three-state values. Models M27 and M18 are comparable whereas M3 and M18 are not. Bayes factors comparing the models are shown in Table 3.

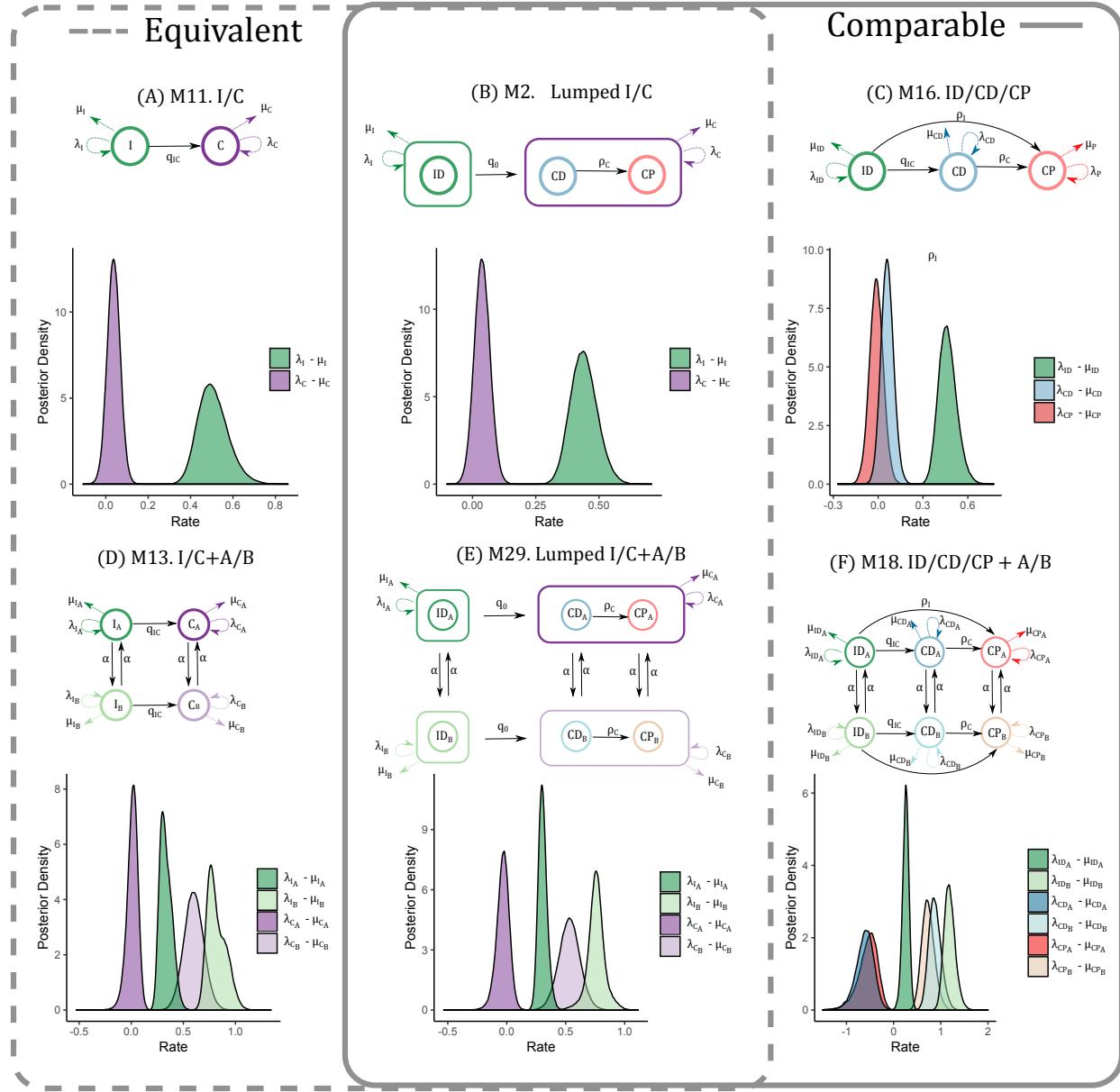


Figure S16: Testing the addition of ploidy to breeding system models. (A) Breeding system only model (M11) where data enter as binary  $I$  and  $C$ . (B) Lumped model for breeding system (M28) where data are the three-state values ( $ID, CP, CD$ ) but results are equivalent to model M11. (C) Ploidy and breeding system model (M16) where data enter as the three-state values. Models M28 and M16 are comparable whereas M11 and M16 are not. (D) Breeding system and hidden state model (M13) where data enter as binary  $I$  and  $C$ . (E) Lumped model for breeding system and hidden state (M29) where data are the three-state values ( $ID, CP, CD$ ) but results are equivalent to model M13. (F) Ploidy, breeding system, and hidden state model (M18) where data enter as the three-state values. Models M29 and M18 are comparable whereas M13 and M18 are not. Bayes factors comparing the models are shown in Table 3.

## Preferred Models

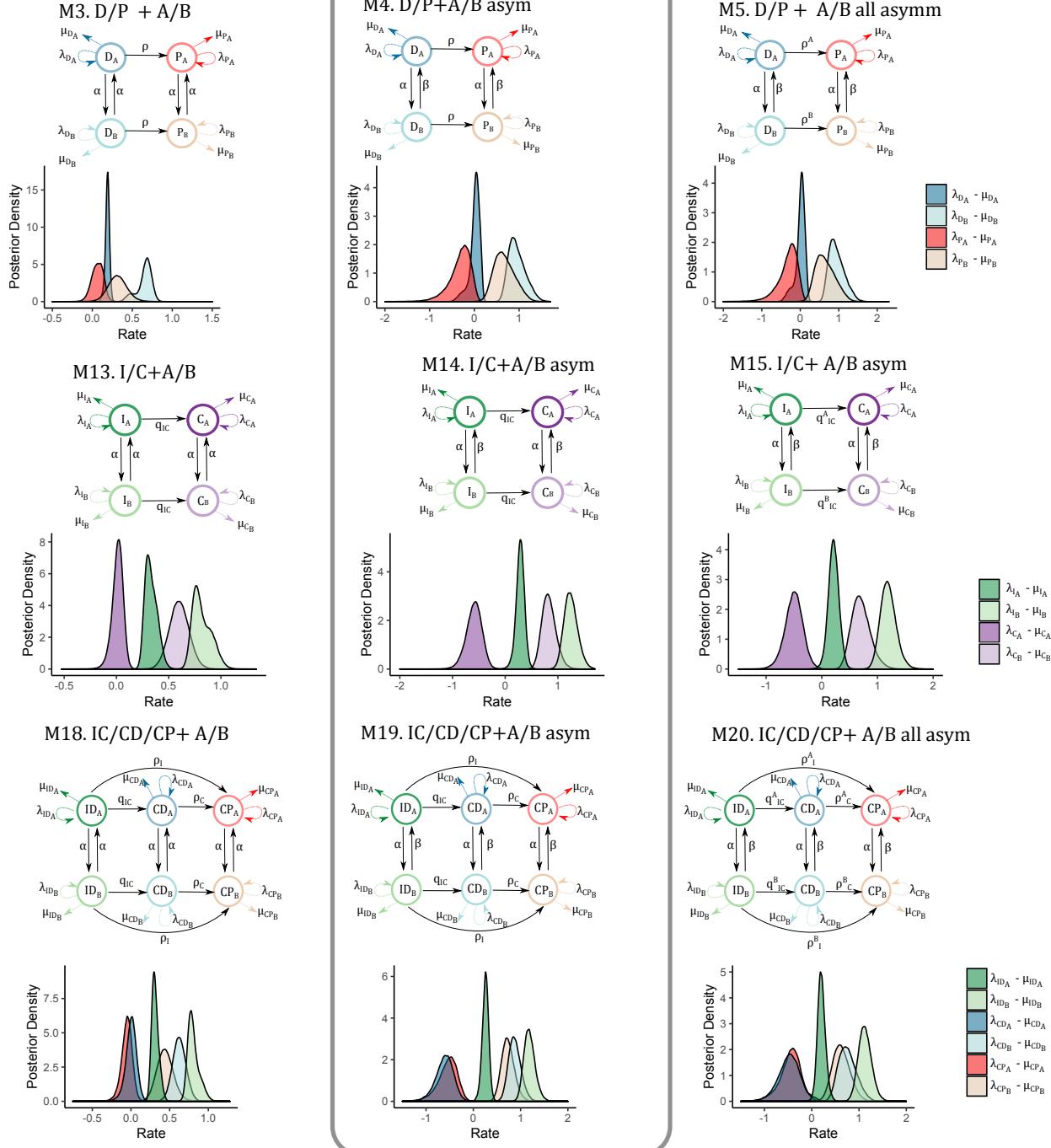


Figure S17: Effect of asymmetric rates in hidden models. First column models M3, M13, and M18 assume that the rates between hidden states are equal. The models in the second column (M4, M14, M19) assume that the rates between hidden states are different. Column three models assumes that the rates between hidden state are asymmetric and that the transition rates within each hidden states are also different. Bayes factors in Table S5 strongly preferred models with asymmetric rates between states (second column) over models with equal rates in hidden states (first column). Models in the second column are moderately or

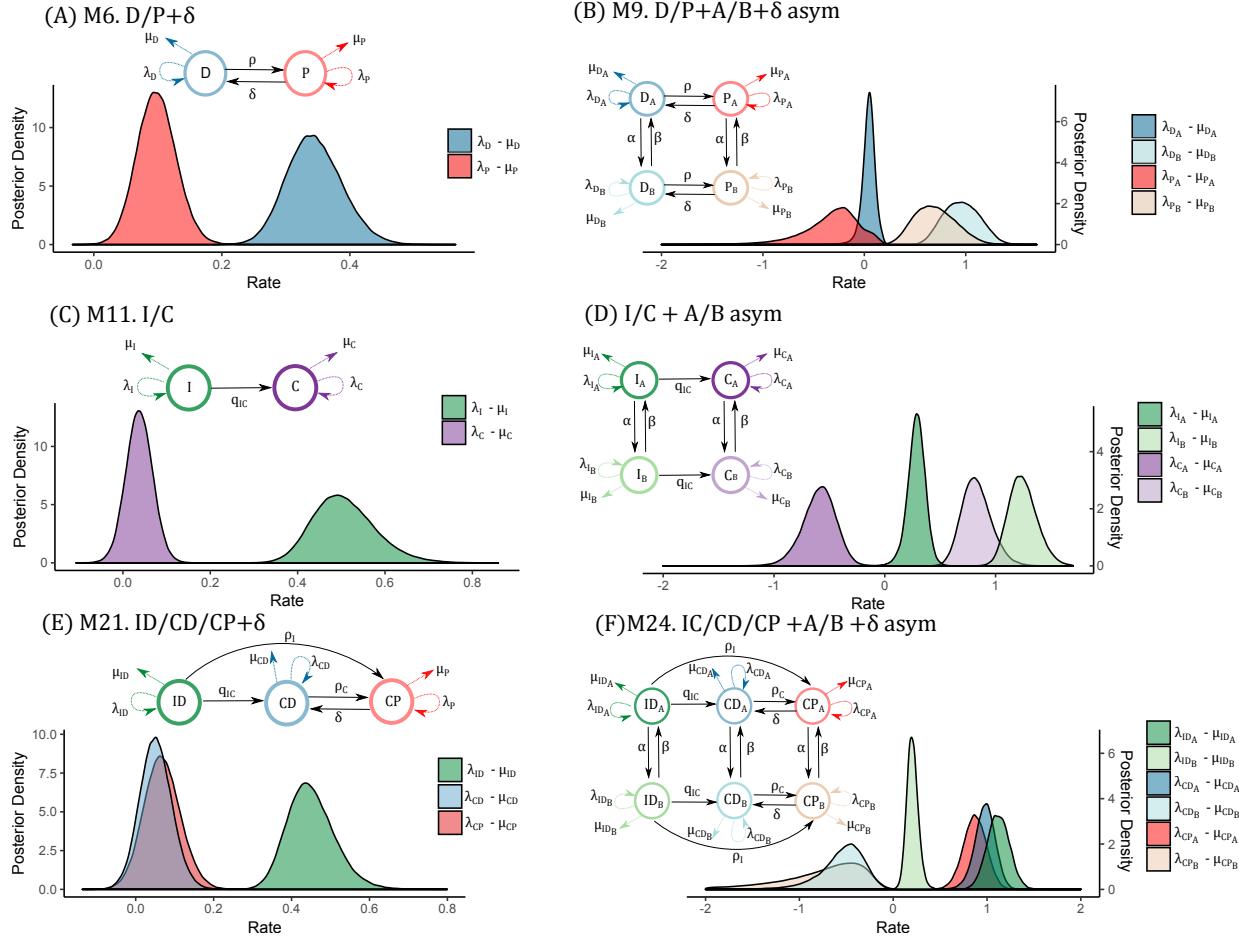


Figure S18: Posterior distributions for the net diversification rates of the preferred models with diploidization. Red color represents diploid state  $D$ , blue color represents polyploid state  $P$ , green color represents self-incompatible  $I$ , purple color represents self-compatible  $C$ , dark colors represent hidden state  $A$  and light colors represent hidden state  $B$ . (A) Ploidy only model M6. (B) Ploidy and hidden states model M9. (C) Breeding systems only model M11. (D) Breeding systems and hidden state model M14. (E) Ploidy and breeding systems model M21. (F) Ploidy, breeding systems, and hidden states model M24.

Model	Marginal log-likelihood	M7	M8	M9	M10	Evidence
M6. D/P+ $\delta$	-1268.83	55.41	42.78	53.37	52.85	Every model strongly preferred over M6
<b>M7. CID D/P+<math>\delta</math></b>	<b>-1212.42</b>		-12.62	-2.04	-2.04	Model M7 moderately preferred over M9 and M10
M8. D/P+A/B $\delta$	-1214.46			10.58	10.07	Asymmetric rates strongly preferred over symmetric
M9. D/P+A/B + $\delta$ asym	-1214.46				-0.51	No evidence
M10. D/P+A/B + $\delta$ all asym	-1214.97					

Table S1: Bayes factors in log-scale of ploidy only models with diplodization. Results indicate that a character independent model (M7) is strongly preferred over model M6 (BiSSE). Model M7 (bold) is also moderately preferred over any of the HiSSE models with asymmetric hidden rates (M9, M10).

Model	Marginal log-likelihood	M18	M19	M20	Evidence
M16. ID/CP/CD	-1459.11	45.11	65.91	63.98	Every model strongly preferred over M16
M17. CID ID/CP/CD	*				
M18. ID/CP/CD+A/B	-1414		20.79	18.87	Asymmetric rates strongly preferred over symmetric
<b>M19. ID/CP/CD +A/B asym</b>	<b>-1393.20</b>			-1.92	Asymmetric hidden rates moderately preferred over all asymmetric
M20. ID/CP/CD +A/B all asym	-1393.12				

Table S2: Bayes factors of ploidy and breeding system without diploidization in log-scale. Results indicate that the model with asymmetric hidden rates (M19, bold) is strongly preferred over M16 and M18 and moderately preferred over the MuHiSSe with all rates asymmetric (M20). \*Marginal log-likelihood for M17 could not be calculated within allotted computer time.

Model	Marginal log-likelihood	M22	M23	M24	M25	Evidence
M21. ID/CP/CD+ $\delta$	-1454.68	55.48	46.031	67.94	65.15	Every model strongly preferred over M21
M22. CID ID/CP/CD+ $\delta$	-1399.201		-9.452	12.45	9.675	Model M24 strongly preferred over M22
M23. ID/CP/CD+A/B $\delta$	-1408.65			21.91	19.12	Asymmetric rates strongly preferred over symmetric
<b>M24. ID/CP/CD +<math>\delta</math> asym</b>	<b>-1386.74</b>				-2.78	Asymmetric hidden rates preferred over all asymmetric
M25. ID/CP/CD + $\delta$ all asym	-1389.52					

Table S3: Bayes factors of ploidy and breeding system with diploidization in log-scale. Results indicate that the MuHiSSE model with asymmetric hidden rates (M24, bold) is strongly preferred over M21-M23 and moderately preferred over the MuHiSSe with all rates asymmetric (M25).

Model	Marginal log-likelihood	Comparison	$K = \log(BF(M1, M2))$	Preferred Model (Evidence)
M1. D/P <b>M4. D/P+A/B asym</b>	-1238.76 <b>-1223.28</b>	M1 vs. M4	60.47	M4 (Strong)
M11. I/C <b>M14. I/C+A/B asym</b>	-1309.07 <b>-1247.72</b>	M11 vs. M14	61.35	M14 (Strong)
M16. ID/CD/CP <b>M19. ID/CD/CP+A/B asym</b>	-1459.11 <b>-1393.20</b>	M16 vs. M19	65.90	M19 (Strong)
M6. D/P+ $\delta$ <b>M9. D/P+A/B+<math>\delta</math> asym</b>	-1283.76 <b>-1214.46</b>	M6 vs. M9	69.3	M9 (Strong)
M21. IC/CD/CP+ $\delta$ <b>M24. IC/CD/CP+A/B+<math>\delta</math> asym</b>	-1454.68 <b>-1386.20</b>	M21 vs. M24	68.48	M24 (Strong)

Table S4: Test for addition of hidden states in models via Bayes factors (in log-scale). Models with hidden states (M4, M14, M19, M9, M24, bold) are strongly preferred over simpler models that do not include hidden s

Model	Marginal log-likelihood	Comparison	K=log(BF(M1,M2)	Preferred Model (Evidence)
M3. D/P+A/B	-1234.52	M3 vs. M4	11.239	M4 (Strong)
<b>M4. D/P+ A/B asym</b>	-1223.28	M4 vs. M5	-1.658	M4 (Moderate)
M5. D/P+A/B all asym	-1224.93			
M13. I/C+ A/B	-1270.47	M13 vs. M14	22.75	M14 (Strong)
<b>M14. I/C+ A/B asym</b>	<b>-1247.72</b>	M14 vs. M15	0.05	No evidence
M15. I/C+ A/B all asym	-1247.67			
M18. IC/CD/CP+A/B	-1414.00	M18 vs. M19	20.79	M19 (Strong)
<b>M19. IC/CD/CP+ A/B asym</b>	<b>-1393.21</b>	M19 vs. M20	-1.919	M19 (Moderate)
M20. IC/CD/CP+ A/B all asym	-1395.129			
M8. D/P +A/B+ $\delta$	-1225.05	M8 vs. M9	10.58	M9 (Strong)
<b>M9. D/P+ A/B+ <math>\delta</math> asym</b>	<b>-1214.46</b>	M9 vs. M10	-0.52	M10 (Moderate)
M10. D/P+A/B+ $\delta$ all asym	-1214.98			
M23. IC/CD/DP+A/B+ $\delta$	-1408.65	M23 vs M24	21.91	M24(Strong)
<b>M24. IC/CD/DP+ A/B+<math>\delta</math> asym</b>	<b>-1386.74</b>	M24 vs M25	-2.78	M24 (Moderate)
M25. IC/CD/DP+A/B+ $\delta$ all asym	-1389.52			

Table S5: Test for asymmetry of the hidden trait transition rates via Bayes factors. For all models, asymmetric transition rates between hidden trait states are preferred over models with equal rates (bold). Adding more complexity by assuming asymmetry in all rates within both hidden states is not preferred over models with just asymmetry between hidden states.

Model	Marginal log-likelihood	Comparison	$K=\log(BF(M1,M2))$	Preferred Model (Evidence)
<b>M1. D/P</b>	-1238.76	M1 vs. M6	65.92	M6 (Strong)
<b>M6. D/P+<math>\delta</math></b>	<b>-1267.84</b>			
<b>M4. D/P+A/B asym</b>	-1223.28	M4 vs. M9	8.81	M9 (Moderate)
<b>M9. D/P+A/B+<math>\delta</math> asym</b>	<b>-1214.46</b>			
<b>M16. ID/CD/CP</b>	-1459.11	M16 vs. M21	4.41	M21 (Moderate)
<b>M21. ID/CD/CP+<math>\delta</math></b>	<b>-1454.68</b>			
<b>M19. IC/CD/CP +A/B asym</b>	-1393.20	M19 vs. M24	6.46	M24 (Moderate)
<b>M24. IC/CD/CP+A/B+<math>\delta</math> asym</b>	<b>-1386.20</b>			

Table S6: Test for inclusion of a diploidization rate via Bayes factors. Models with diploidization are moderately preferred over models that do not include a diploidization rate (**bold**).