

Table S3. Simulation results. (A) We simulated 100 experiments from model M2 (M2 SSD) using sample size (N), recombination fraction (r.true) and fitness (w.true). The estimated parameters (ML estimation) and their corresponding standard errors are shown. We also report the % of the time we were able to recover the correct incompatibility mode after having applied all alternative models; note that for w'=1 models M1 and M3 are equivalent to model M2; (B) We simulated 100 experiments from model M3 with biased single seed descent (M3 BSSD) using sample size (N), recombination fraction (r.true), fitness values w.true and w'.true. The estimated parameters and their corresponding standard errors are shown. We also report the % of the time we were able to recover the correct incompatibility mode after having applied all alternative models.

A

Model	N	r.true	w.true	w'.true	% correct model	w.bar	w.SEE	w'.bar	w'.SEE	r.bar	r.SEE
M2 SSD	350	0.4999	0.3	-	73	0.269	0.102	0.942	0.120	0.480	0.027
M2 SSD	350	0.3	0.3	-	67	0.228	0.133	0.915	0.135	0.300	0.036
M2 SSD	350	0.1	0.3	-	57	0.235	0.156	0.837	0.284	0.101	0.017
M2 SSD	1000	0.4999	0.3	-	64	0.272	0.096	0.941	0.096	0.485	0.022
M2 SSD	1000	0.3	0.3	-	68	0.251	0.105	0.941	0.101	0.301	0.023
M2 SSD	1000	0.1	0.3	-	62	0.270	0.124	0.919	0.124	0.099	0.011

B

Model	N	r.true	w.true	w'.true	% correct model	w.bar	w.SEE	w'.bar	w'.SEE	r.bar	r.SEE
M3 BSSD	350	0.4999	0.1	0.7	71	0.168	0.153	0.730	0.189	0.475	0.035
M3 BSSD	350	0.3	0.1	0.7	69	0.152	0.122	0.745	0.185	0.299	0.040
M3 BSSD	350	0.1	0.1	0.7	25	0.186	0.158	0.854	0.236	0.100	0.016
M3 BSSD	1000	0.4999	0.1	0.7	99	0.100	0.019	0.696	0.065	0.486	0.019
M3 BSSD	1000	0.3	0.1	0.7	93	0.110	0.053	0.718	0.091	0.298	0.026
M3 BSSD	1000	0.1	0.1	0.7	71	0.147	0.107	0.757	0.164	0.101	0.009