

Supplementary Information for

## Evolution and seed dormancy shape plant genotypic structure through a successional cycle

Anurag A. Agrawal, Amy P. Hastings, and John L. Maron

Email: agrawal@cornell.edu

## This PDF file includes:

Figures S1 to S3 Tables S1 to S2

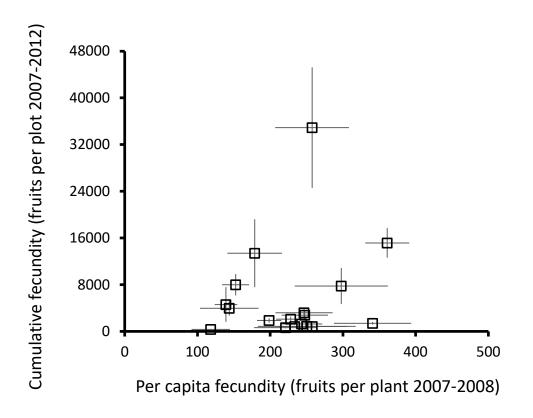
Figure S1. Per capita fecundity of the original genotypes planted in this experiment and their cumulative fecundity.

Figure S2. Predicting long-term fitness of common evening primrose (*Oenothera biennis*) genotypes in field populations with ambient insects versus insects suppressed by regressing against genotype-specific trait values.

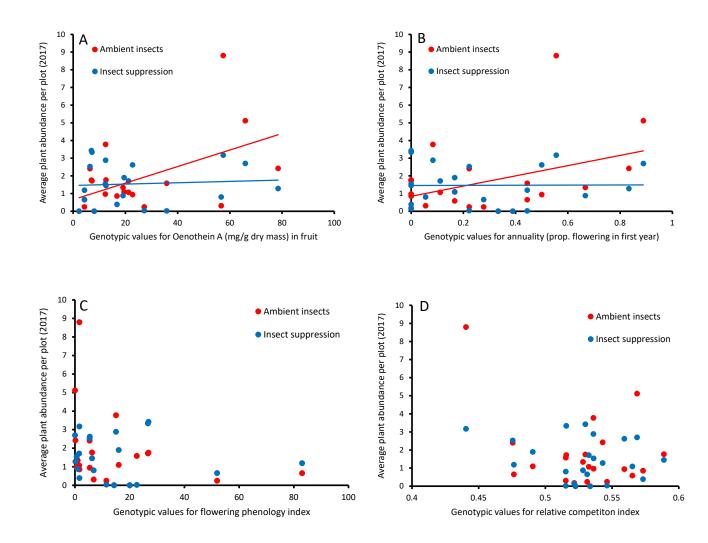
Figure S3. Proportional recruitment per *Oenothera biennis* genotype.

Table S1. Four trait-based genotypic analyses for predicting long-term fitness of *Oenothera biennis.* 

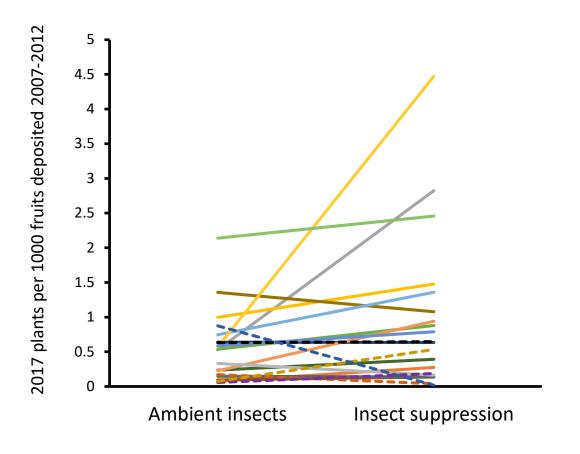
Table S2. Genetic correlations between the four traits studied to predict long-term fitness of *Oenothera biennis*.



**Figure S1**. Per capita fecundity of the original 18 genotypes planted in this experiment (2007) and their cumulative fecundity (2007-2012). Shown are means ± SE from eight control plots. Note the difference in magnitude of variation on the X and Y axis.



**Figure S2**. Predicting long-term fitness of common evening primrose (*Oenothera biennis*) genotypes in field populations with ambient insects versus insects suppressed by regressing against genotype-specific trait values: A) fruit chemical defense, B) annual reproduction, C) flowering phenology, and D) competitive ability. Genotypic values on the X axis are based on those reported Ref. 1. Plant abundance in 2017 is after disturbance to the soil and is the average of eight populations with ambient insects suppression. Each point is a genotype. Statistics are provided in Table S1. Slopes are shown where they are significantly different.



**Figure S3**. Proportional recruitment per *Oenothera biennis* genotype. The proportion of established plants per 1000 fruits deposited (2007-2012) after soil disturbance in 2016 is shown on the Y axis as a function of the two treatments. Each line is a genotype with at least three replicates in each environment. The dashed lines represent outcrossed genotypes.

Table S1. Four trait-based genotypic analyses for predicting long-term fitness of *Oenothera biennis* (measured as abundance of genotypes after resurrection in 2017, averaged across the 8 control or 8 insect suppression populations). Genotype was included as a random effect in each model (and was significant in each case). Genotypic values of Oenothein A and the index of flowering phenology were based on field estimates, while annuality and competitive tolerance were estimated from a rooftop common garden (all data from Ref. 1). Field estimates lacked values for two genotypes which were absent due to extirpation.

	DF	F	Р
Insect suppression (IS)	1,19	0.555	0.466
Oenothein A (OA)	1,19	3.378	0.082
IS X OA	1,19	10.361	0.005
Insect suppression (IS)	1, 21	0.390	0.539
Probability of being annual (PI)	1, 21	1.771	0.198
IS X PI	1, 21	7.184	0.014
Insect suppression (IS)	1,19	0.391	0.539
Flowering phenology index (FI)	1,19	1.248	0.278
IS X FI	1,19	1.722	0.205
Insect suppression (IS)	1, 21	0.318	0.579
Competitive tolerance (CT)	1, 21	2.612	0.121
IS X CT	1, 21	1.969	0.175

Table S2. Genetic correlations (based on means for each genotypic clone, shown is Pearson's r) between the four traits studied to predict long-term fitness of *Oenothera biennis*. Genotypic values of fruit chemical defense (Oenothein A) and the index of flowering phenology were based on field estimates, while annuality and competitive tolerance were estimated from a rooftop common garden (all data from Ref. 1). N=21 genotypes for which we had data on all traits. \*p<0.05, \*\*p<0.01.

	Annual reproduction	Chemical defense	Flowering phenology
Annual reproduction			
Chemical defense	0.583**		
Flowering phenology	-0.062	-0.445*	
Competitive tolerance	-0.097	-0.002	-0.310

## References

1. Agrawal AA, Hastings AP, Johnson MTJ, Maron JL, & Salminen JP (2012) Insect herbivores drive real-time ecological and evolutionary change in plant populations. *Science* 338(6103):113-116.