

300 Recombinant Inbred Lines Used to Identify Genes Involved in Cowpea

Resistance to Seed Beetles

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Background and Hypothesis

- A major pest of cowpeas, an important source of dietary protein throughout the world, is the seed beetle *Callosobruchus maculatus*.
- Cowpea geneticists have performed crosses with eight cowpea cultivars to produce 300 RILs with agriculturally desirable traits¹. Previous assays of the parents revealed significant variation among each component of larval fitness².
- Here, we hypothesize that performing a similar analysis of the RILs themselves can identify genes responsible for seed beetle resistance.

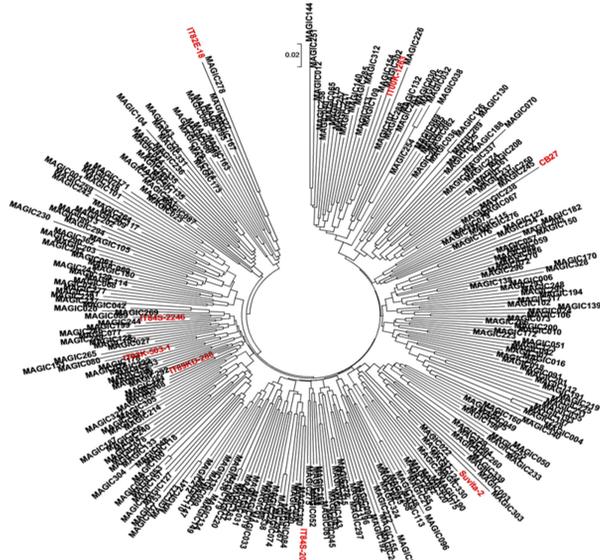
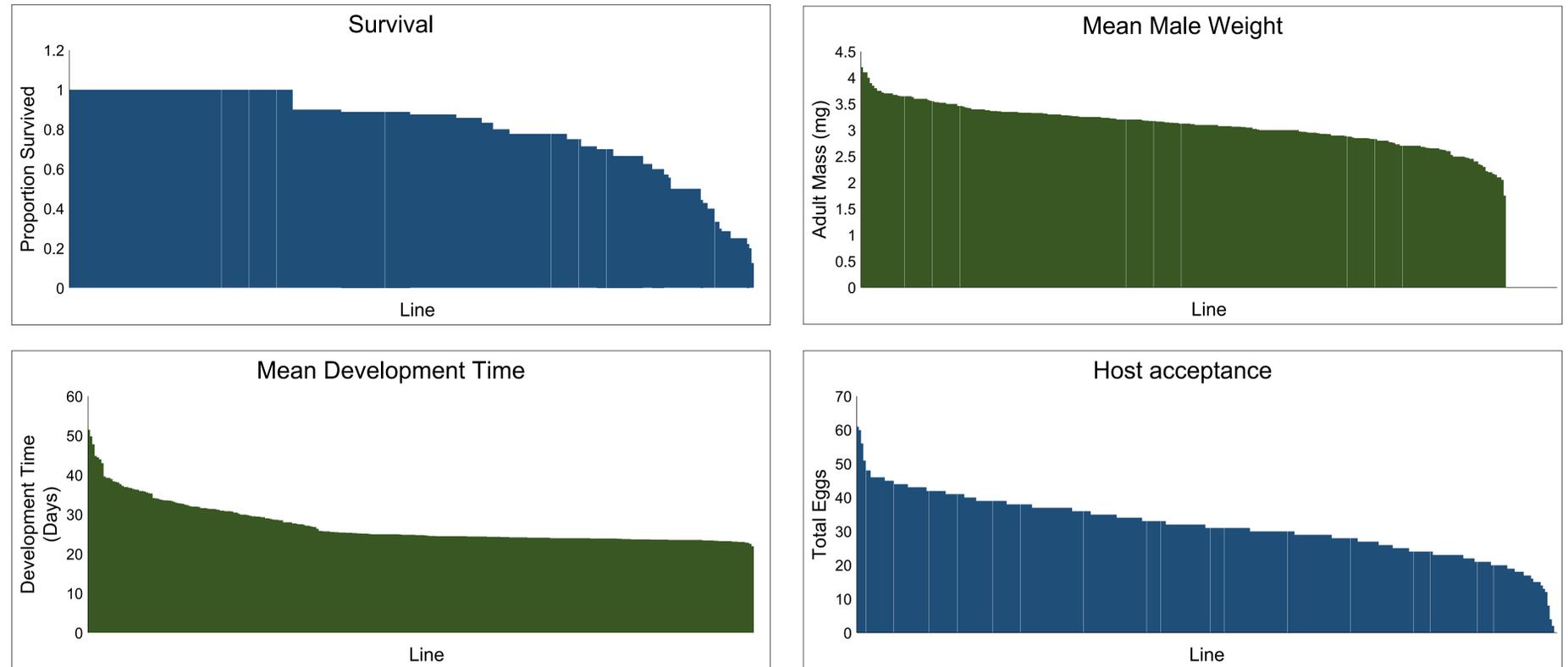


Fig. 1. Phylogenetic relationships among 8 parents (in red) and 305 recombinant inbred lines¹.

Results

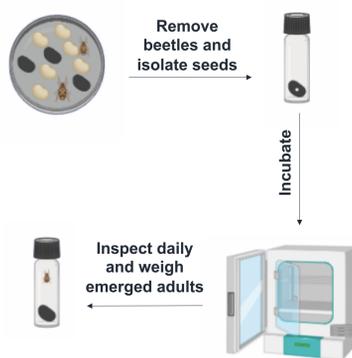
Phenotypic analysis across RILs and parents reveals variability in host acceptance, overall survival, developmental time, and weight at adult emergence.



Experimental Design

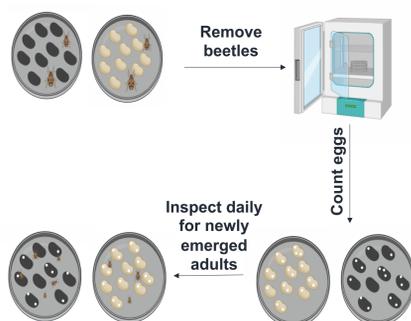
Assay 1: Development time, adult mass, survival

Beetle pairs were placed in Petri dishes containing 10 different numbered RILs. After 24 hours, cowpeas with one hatched egg were isolated into vials. Vials were inspected daily, newly emerged adults were weighed, and their development times were recorded.



Assay 2: Development time, egg laying, survival

Beetle pairs were placed in Petri dishes containing 10 seeds of the same RIL. After 24 hours, the beetles were removed. The number of eggs laid per dish was calculated. The dishes were inspected daily, and development time was calculated.



Conclusion

- Phenotypic analysis revealed significant variation among each component of larval fitness, including:
 - Assay 1: Survival, development time, and mass at adult emergence
 - Assay 2: Host acceptance, survival, and development time
- Analysis revealed negative correlations between development time vs adult weight and development time vs survival, indicating some RILs are poor for multiple fitness components.

Tab. 1: Correlations between each component of larval fitness.

	Dev. Time	♀ Weight	♂ Weight	Survival
Dev. Time				
♀ Weight	-0.63			
♂ Weight	-0.41	0.24		
Survival	-0.34	0.12	0.14	
Early Exit	-0.03	0.01	0.11	-0.58



Fig. 2: Morphological differences among RILs

Future Directions

- Genomic-wide association will eventually be used to map genomic regions and identify candidate genes associated with beetle resistance.
- Replicate results in a second beetle population from a different geographic region to determine if the level of plant resistance and its genomic basis vary among pest populations.

References

- Huynh, B. et al. 2018. A multi parent advanced generation inter-cross (MAGIC) population for genetic analysis and improvement of cowpea (*Vigna unguiculata* L. Walp.). *The Plant Journal* 93:1129-1142.
- Messina, F.J., Lish, A.M., Gompert, Z., (2019). Components of cowpea resistance to the seed beetle *Callosobruchus maculatus* (Coleoptera: Chrysomelidae: Bruchinae). *Journal of Economic Entomology*, 112, 2418-2424.
- Graphics used in experimental design were created with biorender.

Acknowledgments

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