Supplementary Information.

Links to publication containing additional details on model structure.

Wayne M. Getz, Richard Salter, Andrew J. Lyons, Nicolas Sippl-Swezey, 2015.

Panmictic and Clonal Evolution on a Single Patchy Resource Produces Polymorphic Foraging Guilds (http://journals.plos.org/plosone/article?id=10.1371/journal.pone.0133732)

Research Article | published 14 Aug | PLOS ONE | 10.1371/journal.pone.0133732.

Running the model

The model is run on the Nova Platform that can be downloaded from the Nova Software Website at https://www.novamodeler.com/ . The software platform is free, but users need to register and obtain a license to run the model under Windows, Mac OS X, and Linux operating systems. The models itself can downloaded at http://nature.berkeley.edu/getzlab/nova.html.

Additional Figures S1 and S2.

Figures S1. Genetic structure of runs listed in Table 2 are illustrated here in terms of the parameter values of α (blue), δ (red), ρ (green) and m (black) ordered along the horizontal axis according to the final biomass achieved by individuals during generation 500 of the ecological simulation. **Panels A**: random cases. **Panels B**: m-trait mating cases.

Fig. S1: Panels A.

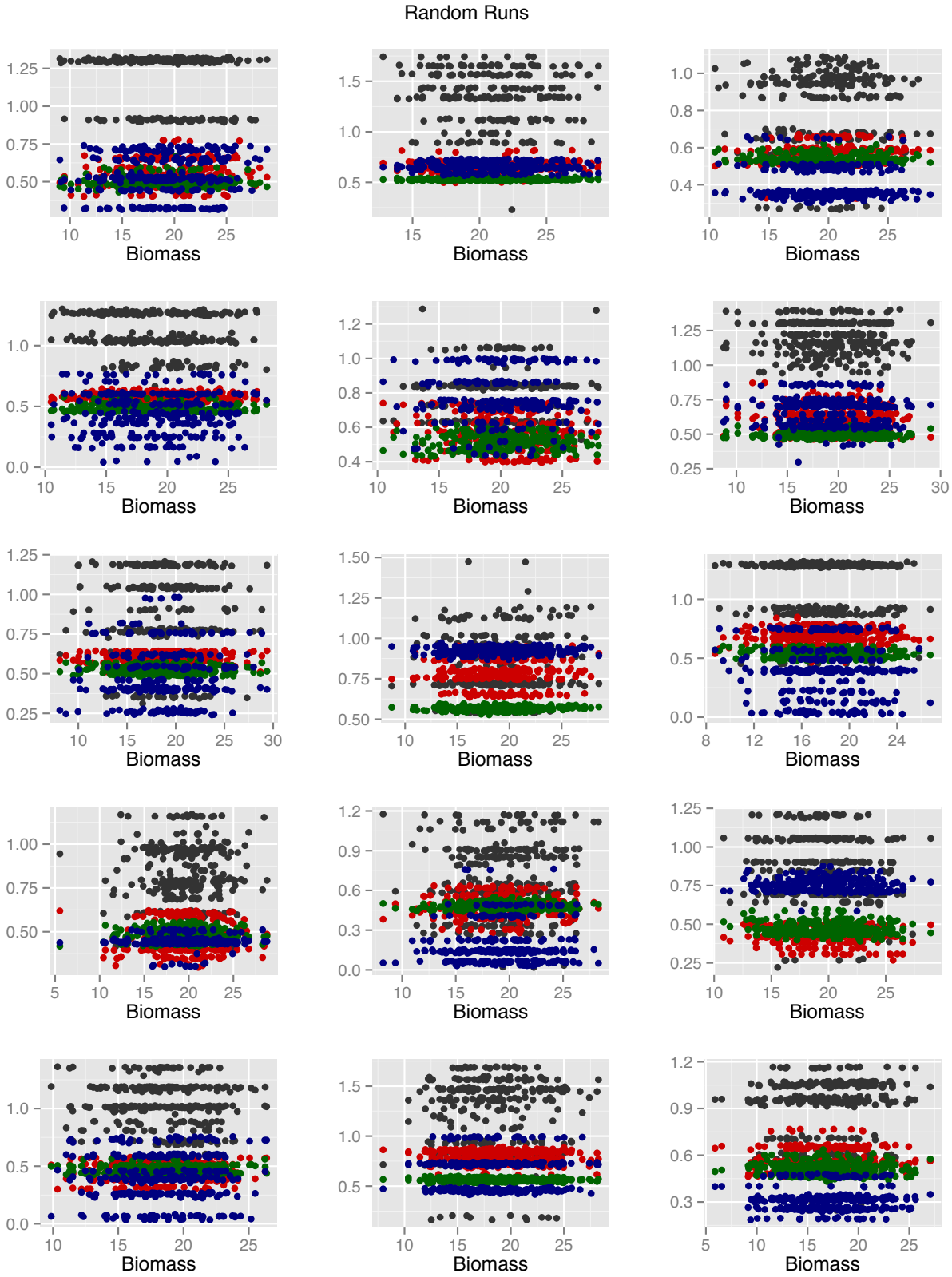
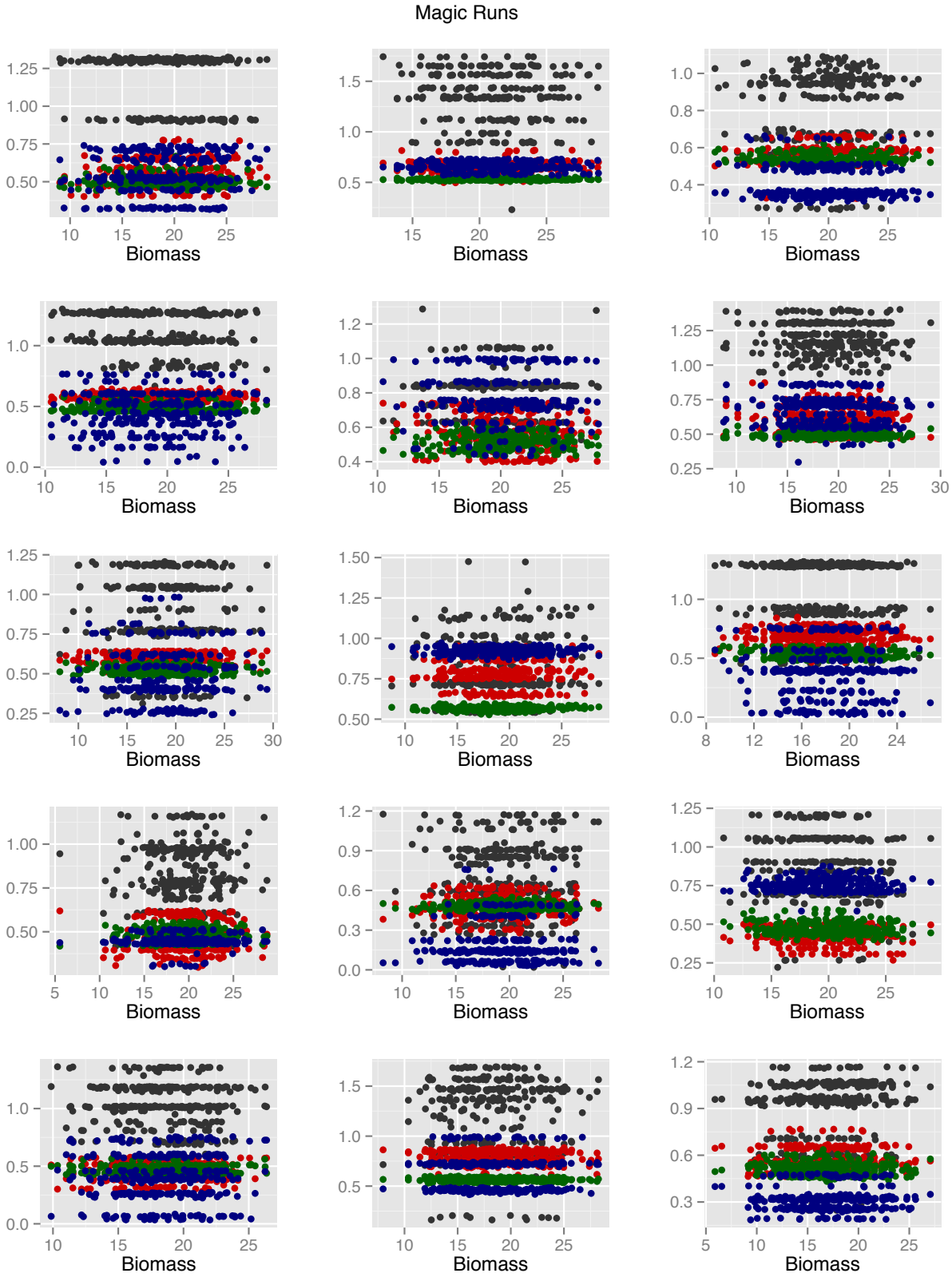


Fig. S1: Panels B.



Figures S2. Dendrograms associated with the genetic structure of runs listed in Table 2 are illustrated for all 15 random (**Panels A**) and *m*-trait mating (**Panels B**) cases.

Fig. S2: Panels A.

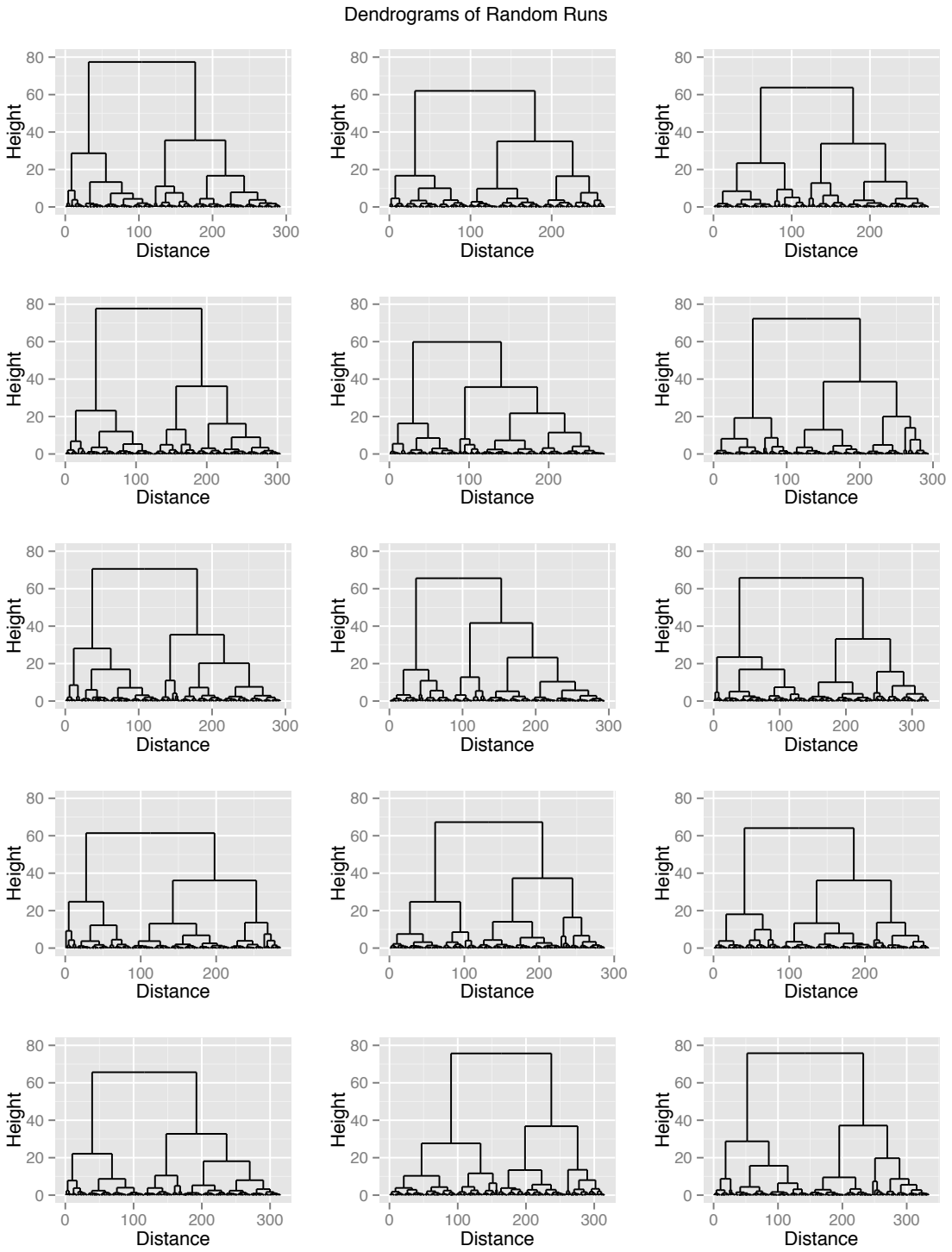


Fig. S2: Panels B.