Within- and between- treatment beta-diversity

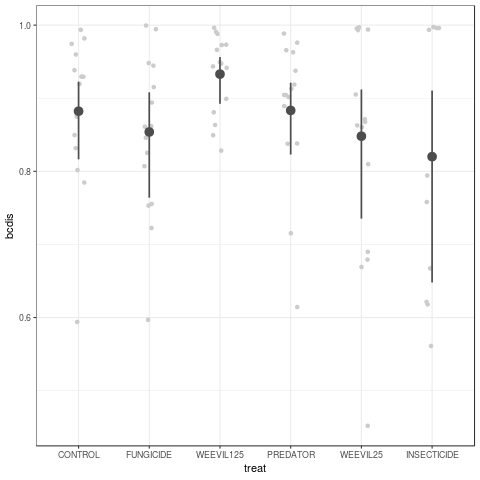
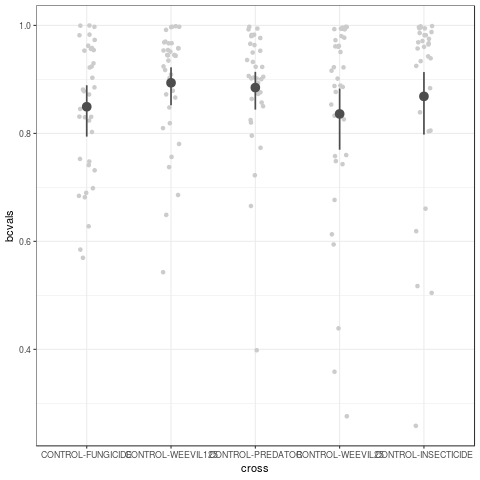


Fig X Jaccard dissimilarity for intra-treatment plant community composition. There are no statistical differences between different treatments.

Fig X. Pairwise dissimilarity of control plot and treatment plots. For each comparison 36 values were calculated.

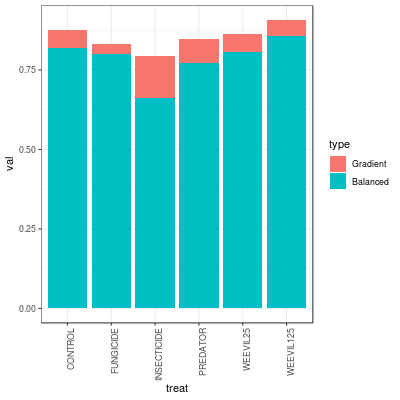
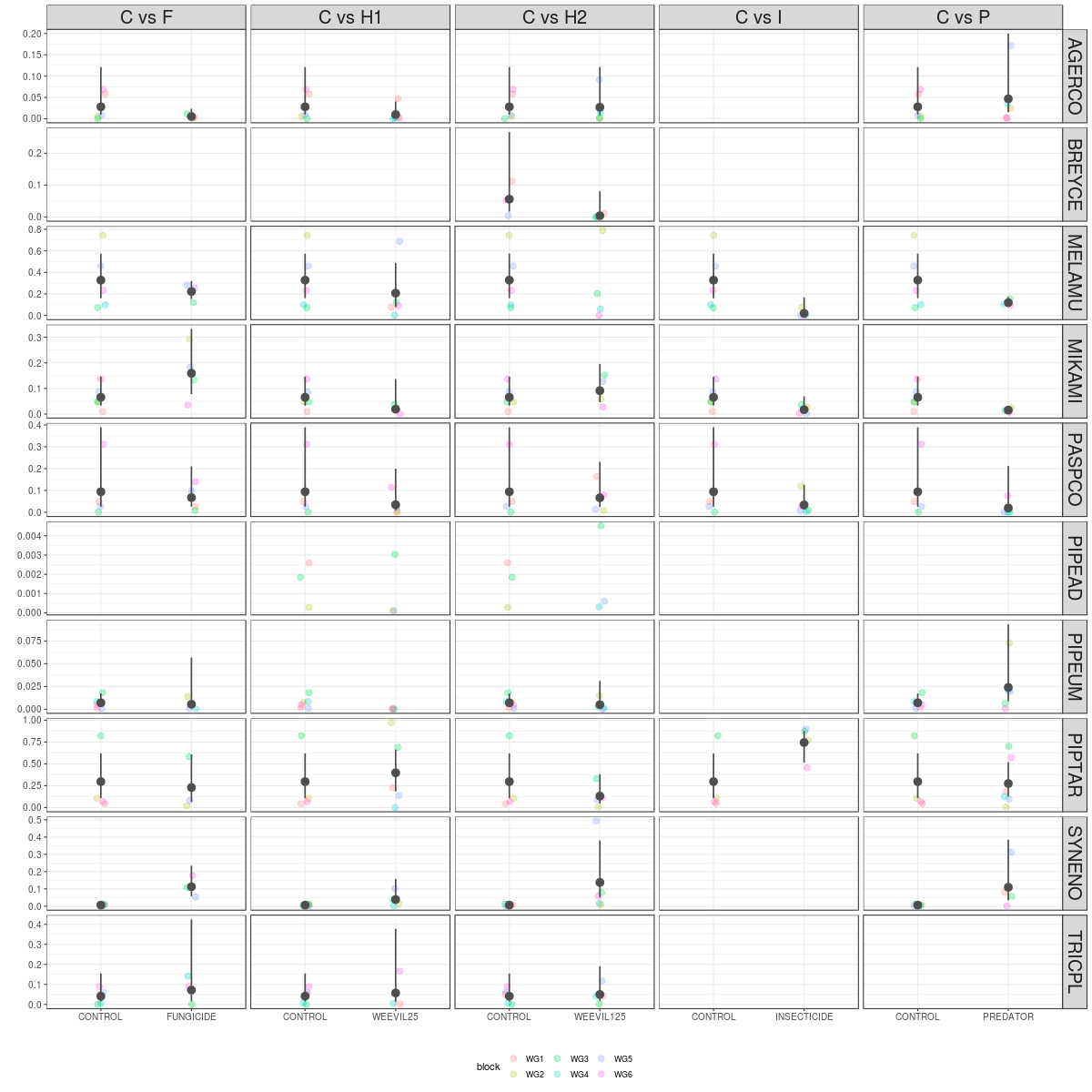


Fig X. Beta diversity partitioned into balanced beta and gradient dissimilarity (Baselga 2017). The

balanced variation component is independent or total abundance difference and yields the maximum value (1) when no species is present in more than one site. In turn, the abundance-gradient component must yield the minimum value (0) when there are no species in common, and (ii) must account for abundance differences con- ditioned to the degree to which the assemblage with lower abundance is a subset of the assemblage with higher abundance.

Most prevalent species analysis



For meaningful comparisons, we chose species which were present in control and treatment plots in at least three of the blocks, and which had an average proportion in the community higher than 0.1 [run the code and select species again]. We compared average proportions for a given species in a control and treatment combination using *betareg* function in the *betareg* package (Cribari-Neto and Zeileis 2010). To see if there were differences in trait values between species responsible for the community shifts, we built a linear mixed-effects model with trait values from the control plots as a response and garden included as a random effect. For multiple comparisons we used the *lsmeans* and *cdt* functions from the *emmeans* (Lenth 2019) package with Tukey’s multiplicity adjustment.