Figure S1. Phylogenetic signal for each of 48 study units used in this study. Regression lines reflect best fit line $RI = b_{\bullet 0} +$ $b_{\bullet 1}\log_{10}(PD + 1)$, where RI is the relative impact on the host or enemy compared to the most severely affected species in the study, and PD is the phylogenetic distance from that host to the most severely affected species, in units of millions of years of independent evolution. See Table S1 for sources and Table S2 for coefficients and statistics. Figures are grouped by Type of Interaction and impacted partner: S1A. Herbivore Impacts on Host Plants, S1B. Pathogen Impacts on Host Plants, S1C. Plant Impacts on Herbivore Behavior, and S1D. Plant Effects on Herbivore or Pathogen Development.
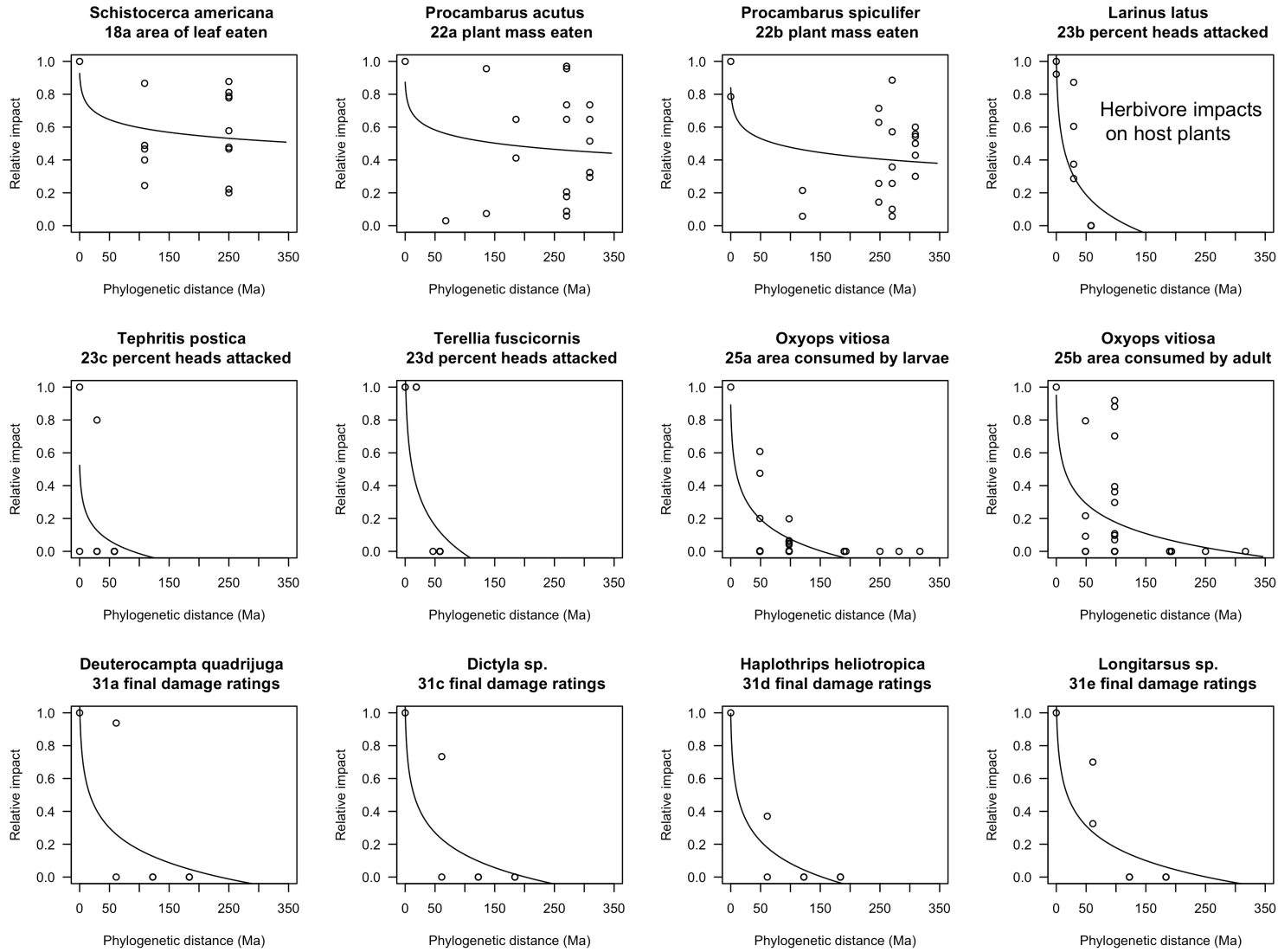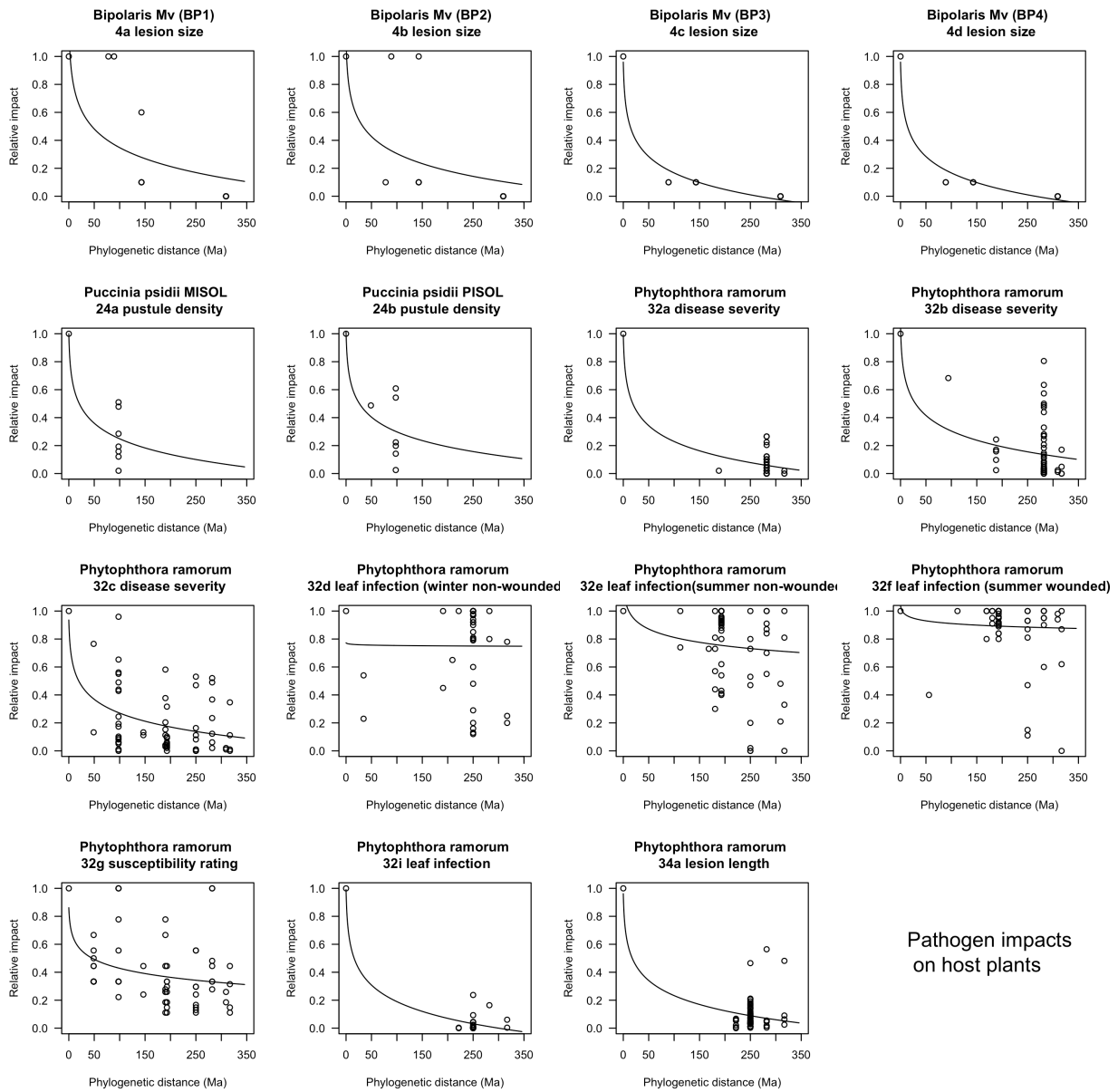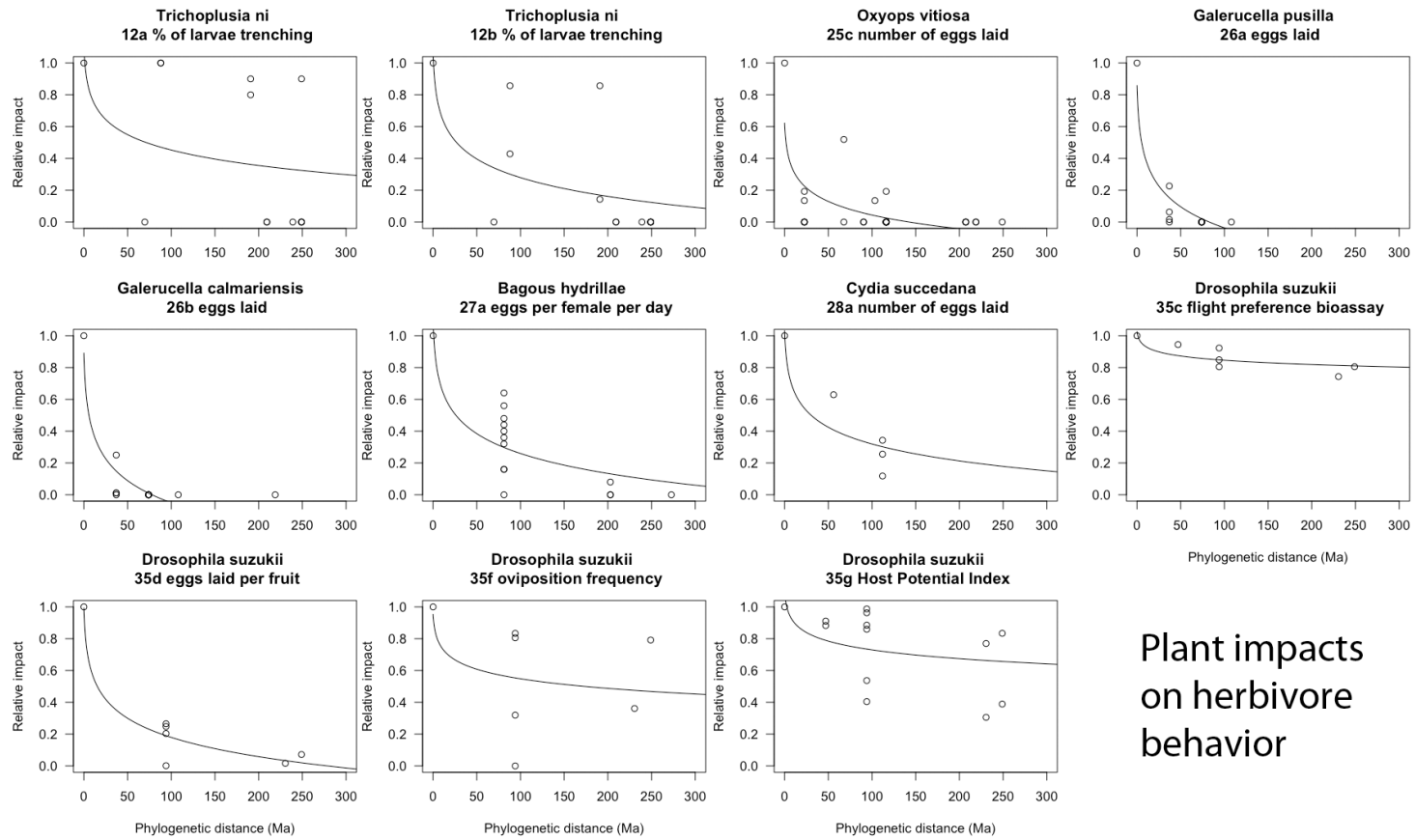
Figure 1A. Herbivore Impacts on Host Plants

Figure 1B. Pathogen Impacts on Host Plants

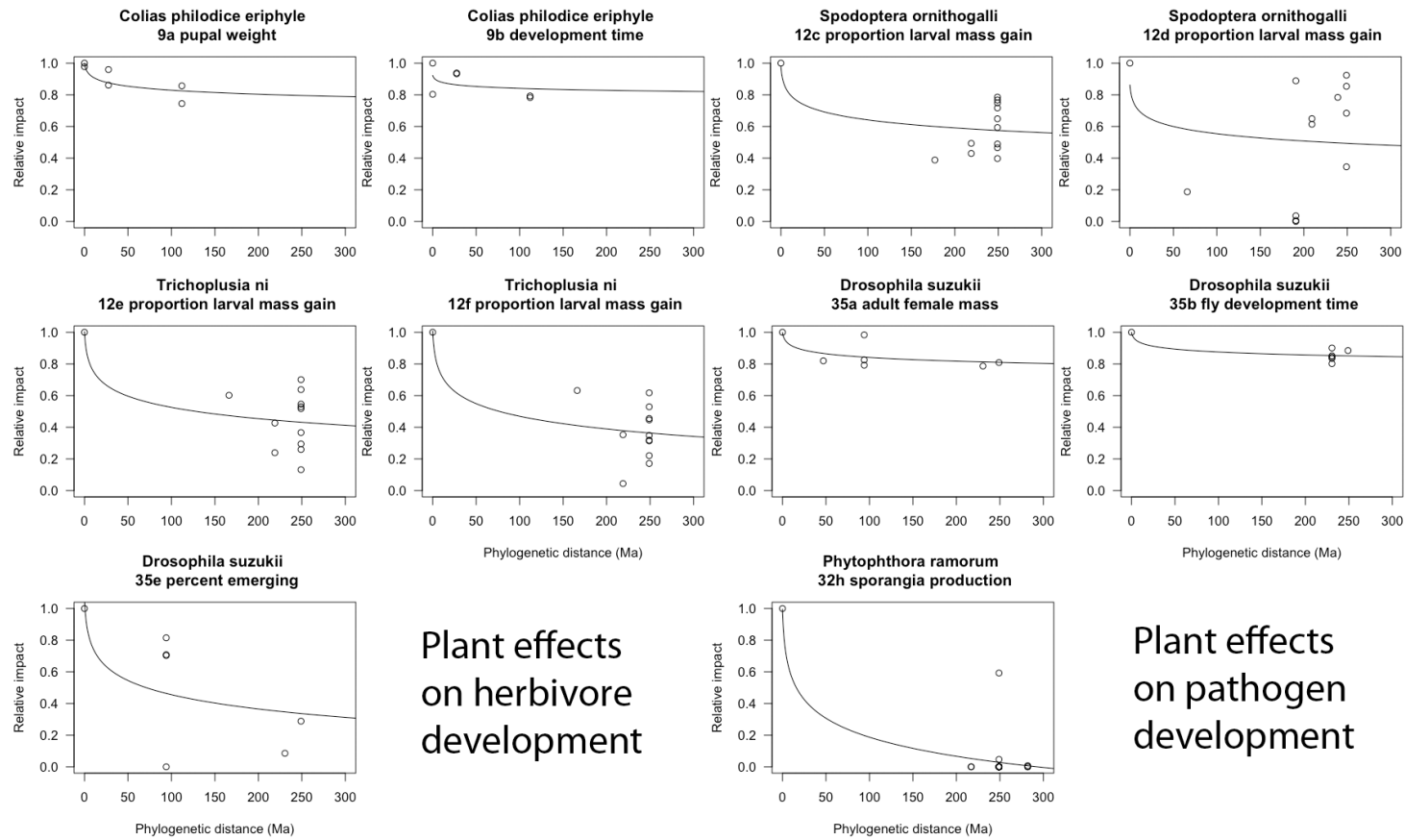**Figure S1C. Plant Impacts on Herbivore Behavior**

Figure S1D. Plant Effects on Herbivore or Pathogen Development