Ecography

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Supplementary material

Supplementary Material

Species' roles in food webs show fidelity across a highly variable oak forest

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Appendix 1 *Species distribution across sites and networks*

Species were widely distributed across the sites and interaction networks in the empirical data, with some species appearing very frequently and others rarely. Figures A1 and A2 show the presence and absence of all host and parasitoid species across all sites and networks.

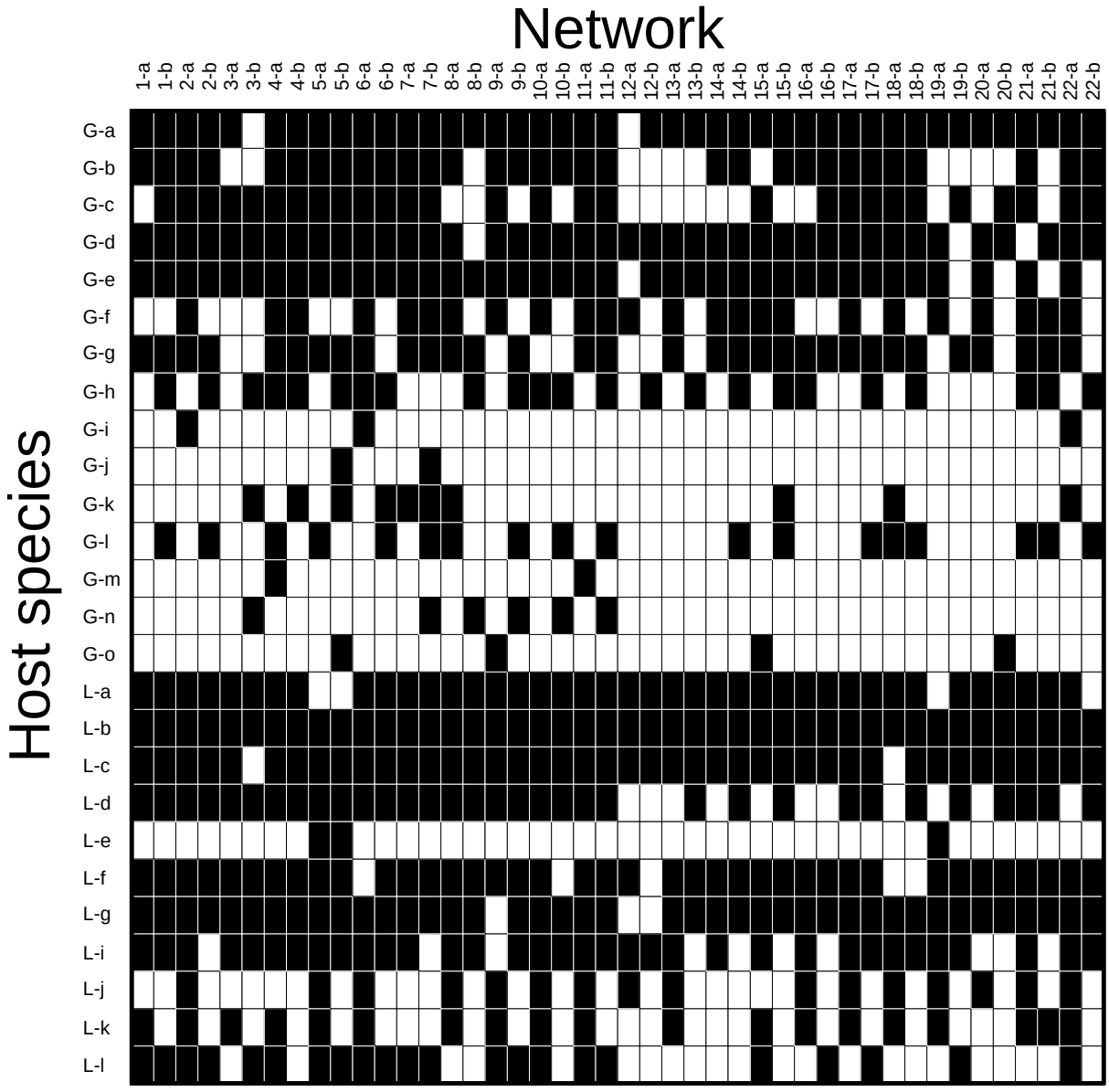

Fig. A1: Graphical representation of the distribution of each host species across all networks. Networks are labeled by site with “a” representing the 2006 network and “b” representing the 2007 network. Colors indicate the presence (black square) or absence (white square) of the host at a particular site. Host species labels are organized by guild (G for galler and L for leafminer species) and are sorted in order of decreasing abundance within each guild.

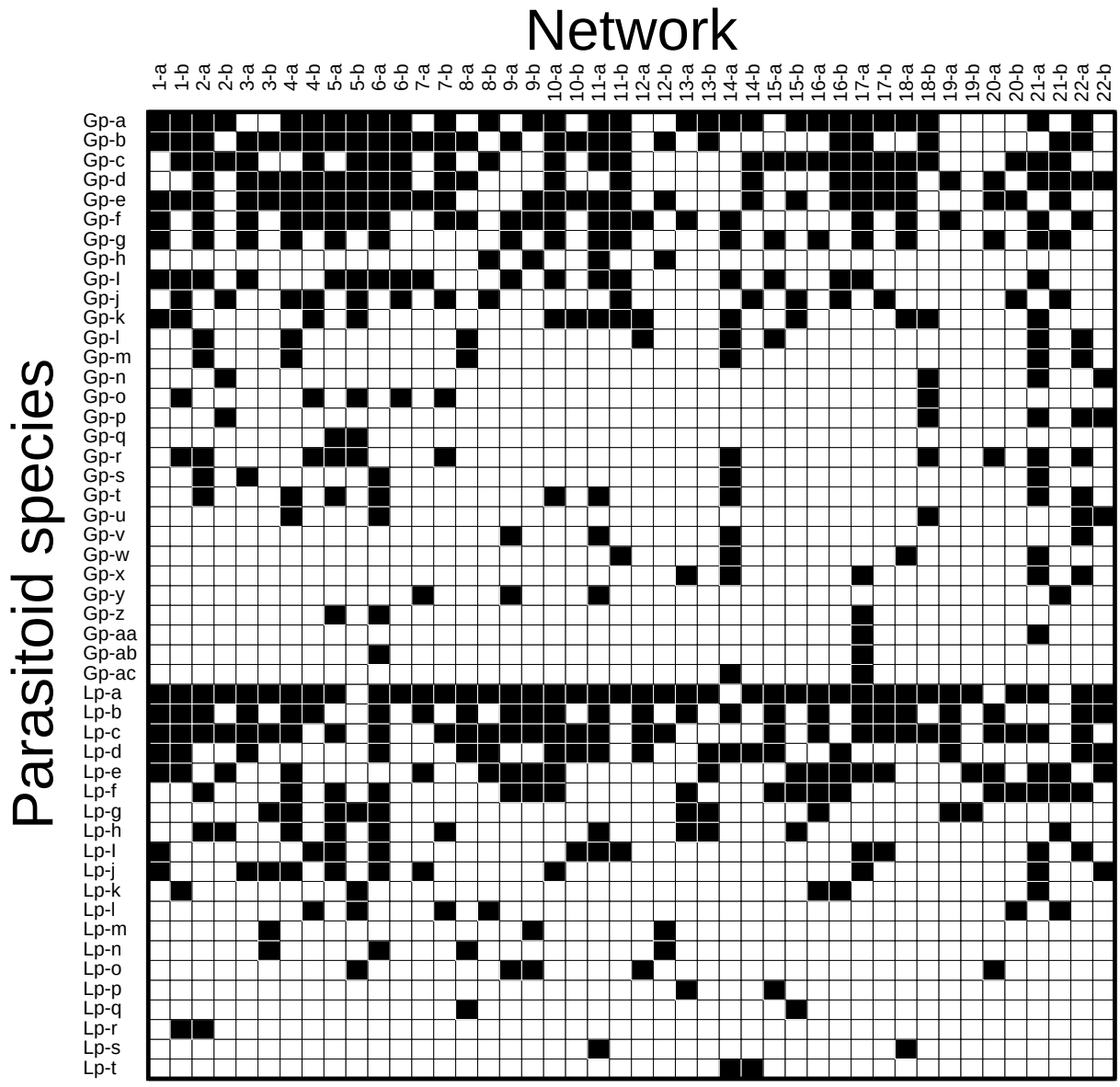

Fig. A2: Graphical representation of the distribution of each parasitoid species across all networks. Networks are labeled by site with "a" representing the 2006 network and "b" representing the 2007 network. Colors indicate the presence (black square) or absence (white square) of the parasitoid at a particular site. Parasitoid species labels are organized by guild (Gp for galler parasitoid and Lp for leafminer parasitoid species) and are sorted in order of decreasing abundance within each guild.

Appendix 2 *Robustness of our results to the use of qualitative interaction networks*

In the analysis presented in the main text, we reduced the quantitative empirical networks to their binary equivalent. By doing so, it was possible that we ended up overemphasizing the contributions of rare species to the fidelity of species' roles. To test if our fidelity analyses were indeed influenced by rare species in this way, we tested the robustness of our results by comparing them to what we would expect under a statistical resampling of the empirical quantitative networks. Rather than assume all interactions are equiprobable irrespective of their empirically-observed intensity, the resampled networks represent a weighting proportional to the actual field data.

For each empirical network, the resampling procedure works as follows. First, we randomly selected a host species i with a probability given by its observed relative abundance (compared to all host species). Next, we randomly selected a parasitoid species j with probability given by its proportional attack rate on host i (i.e., its attack rate divided by the total number of attacks on host i from all parasitoid species). We then added an interaction between host i and parasitoid j to the "resampled" network. We repeated this process until the resampled network had the exact same number of quantitative interactions as the empirical network. Throughout this process, species (and interactions) that are more abundant in the empirical network will have a higher probability of appearing in the resampled networks, and rare species (or interactions) will have a lower probability of appearing (Fig. A3- A24).

We conducted the resampling procedure 999 times for the complete set of empirical networks. For each of these, we then calculated species, network, and temporal fidelity as detailed in the main text to create a null distribution of each p-value associated with the different levels of role fidelity (D'Agostino & Stephens, 1986). To test the robustness of our original conclusions, we compared the p-values from the qualitative networks to those from the resampled distributions to assess whether the qualitative results were statistically different from results obtained from quantitative networks.

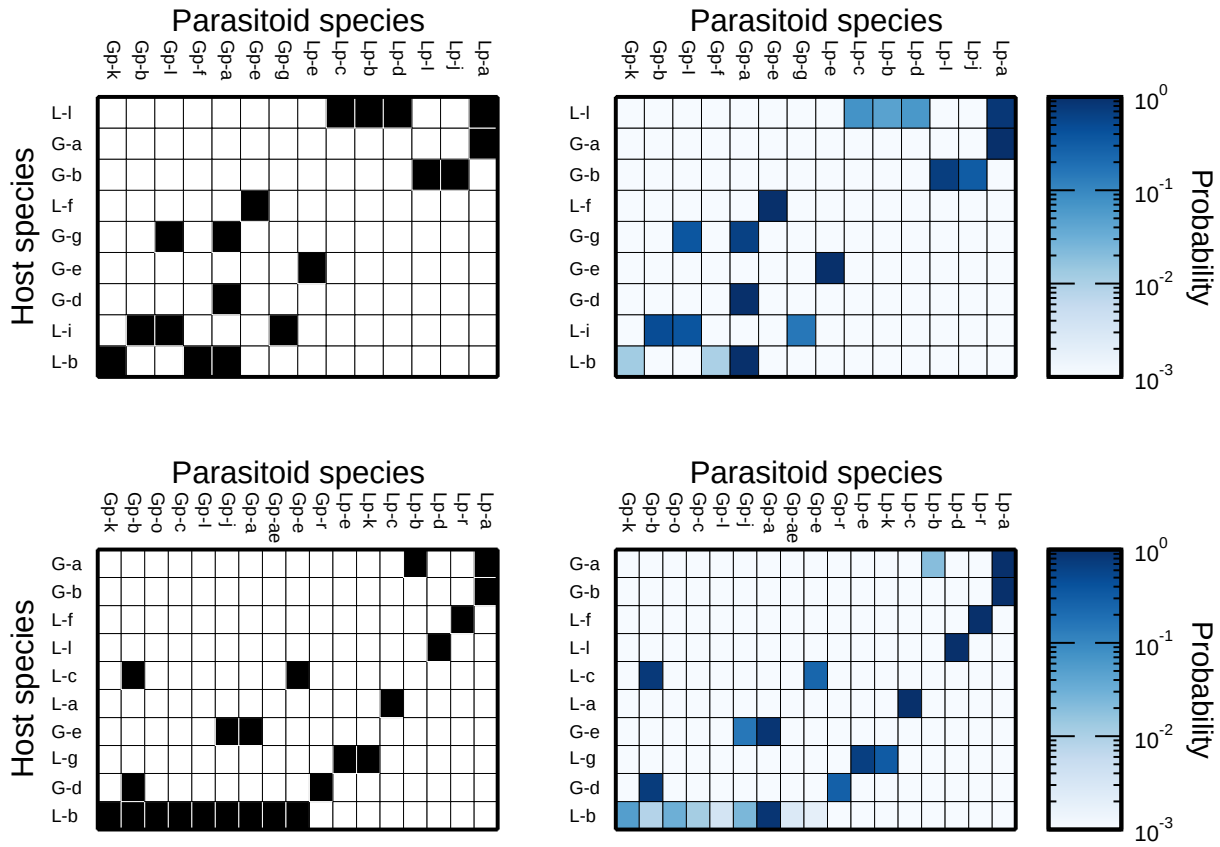

Fig. A3: Graphical representation of the qualitative interaction network (left) and the mean of all 999 resampled networks (right) for site 1 in 2006 (top) and 2007 (bottom). Each cell represents a possible interaction between a host species and parasitoid species. In the qualitative network, a black cell represents the presence of an interaction whereas white represents its absence. In the resampled network, each cell is shaded according to the probability that the interaction appeared in the resampled networks, with the colors as indicated in the colorbar at right.

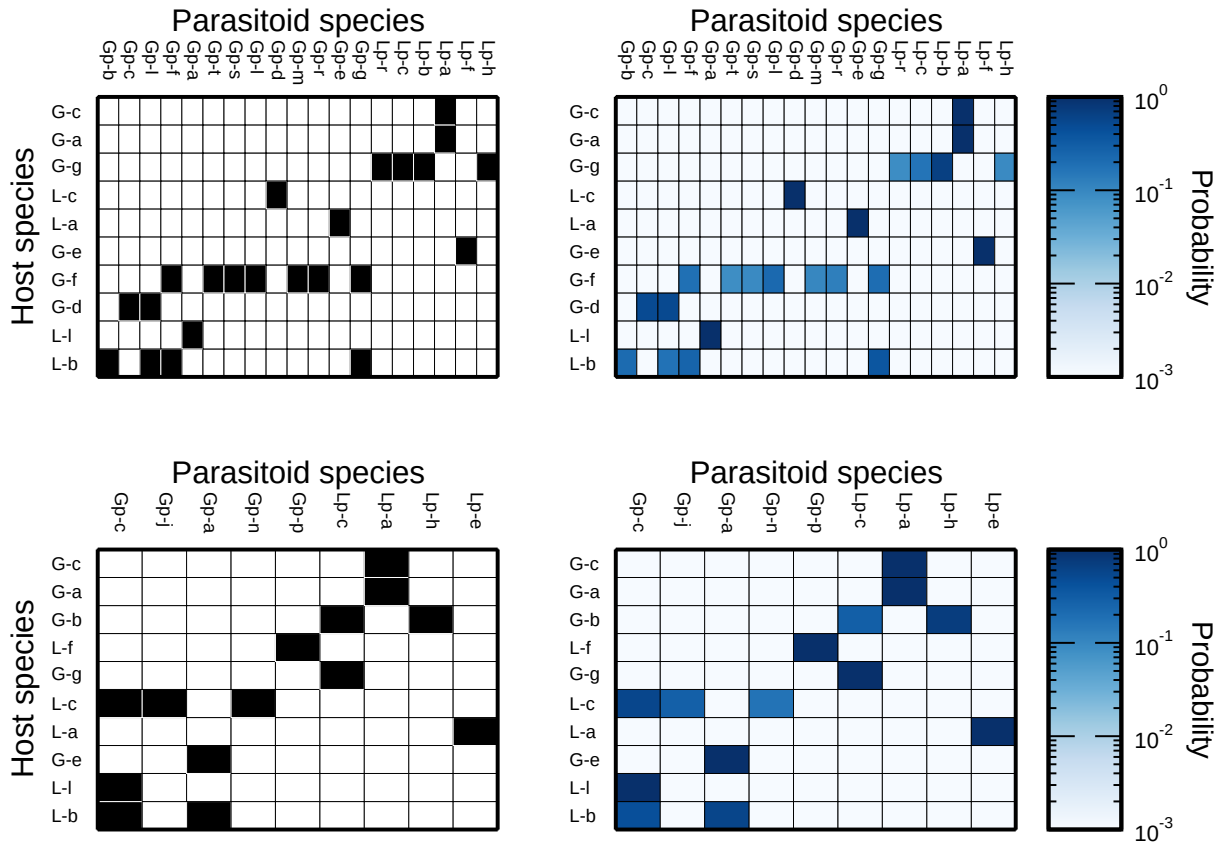

Fig. A4: Graphical representation of the qualitative interaction network (left) and the mean of all 999 resampled networks (right) for site 2 in 2006 (top) and 2007 (bottom). Each cell represents a possible interaction between a host species and parasitoid species. In the qualitative network, a black cell represents the presence of an interaction whereas white represents its absence. In the resampled network, each cell is shaded according to the probability that the interaction appeared in the resampled networks, with the colors as indicated in the colorbar at right.

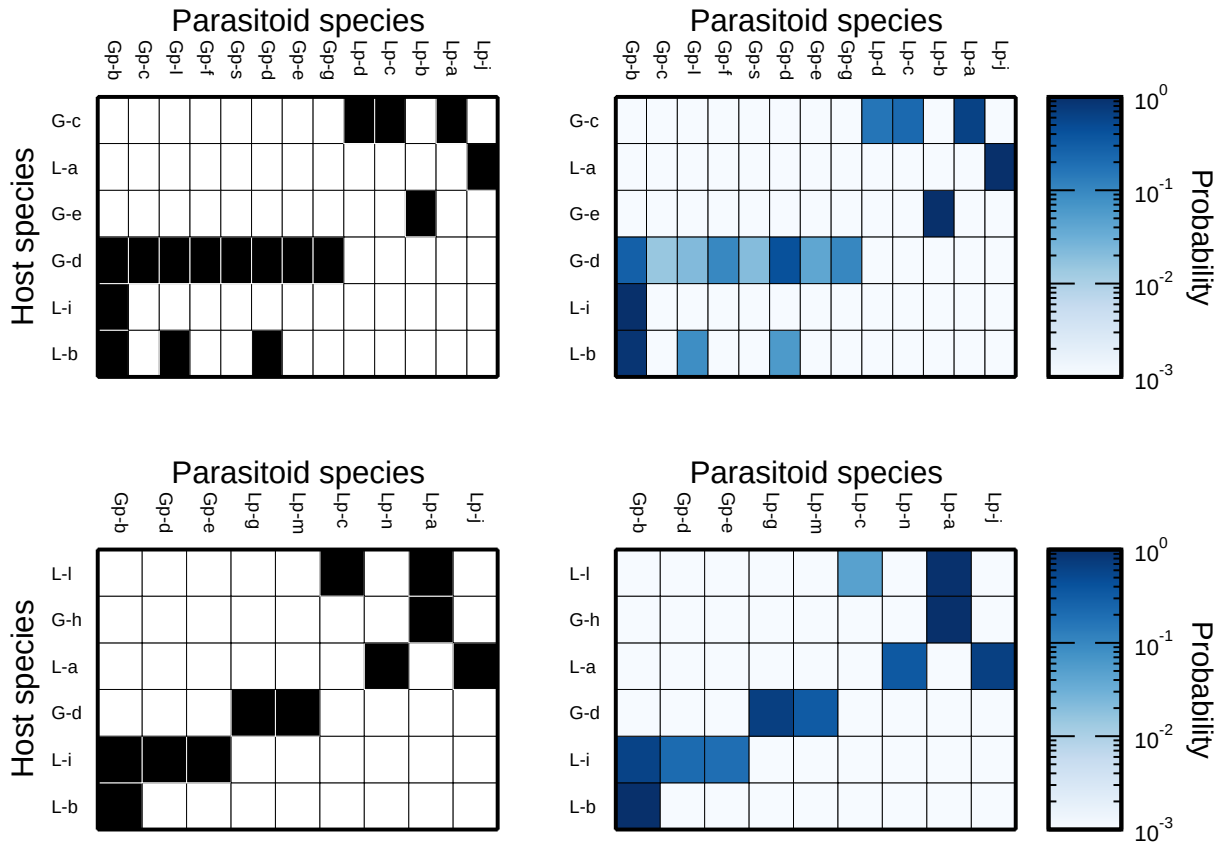

Fig. A5: Graphical representation of the qualitative interaction network (left) and the mean of all 999 resampled networks (right) for site 3 in 2006 (top) and 2007 (bottom). Each cell represents a possible interaction between a host species and parasitoid species. In the qualitative network, a black cell represents the presence of an interaction whereas white represents its absence. In the resampled network, each cell is shaded according to the probability that the interaction appeared in the resampled networks, with the colors as indicated in the colorbar at right.

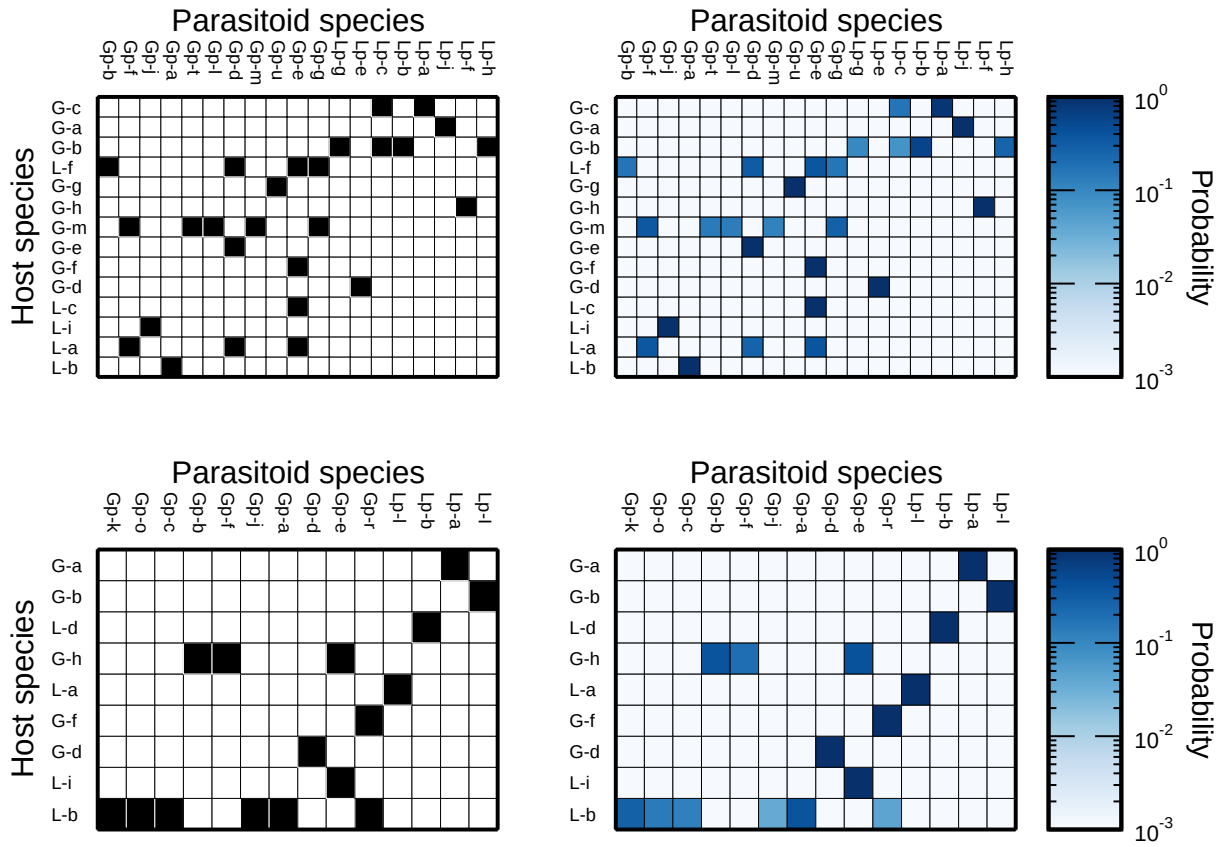

Fig. A6: Graphical representation of the qualitative interaction network (left) and the mean of all 999 resampled networks (right) for site 4 in 2006 (top) and 2007 (bottom). Each cell represents a possible interaction between a host species and parasitoid species. In the qualitative network, a black cell represents the presence of an interaction whereas white represents its absence. In the resampled network, each cell is shaded according to the probability that the interaction appeared in the resampled networks, with the colors as indicated in the colorbar at right.

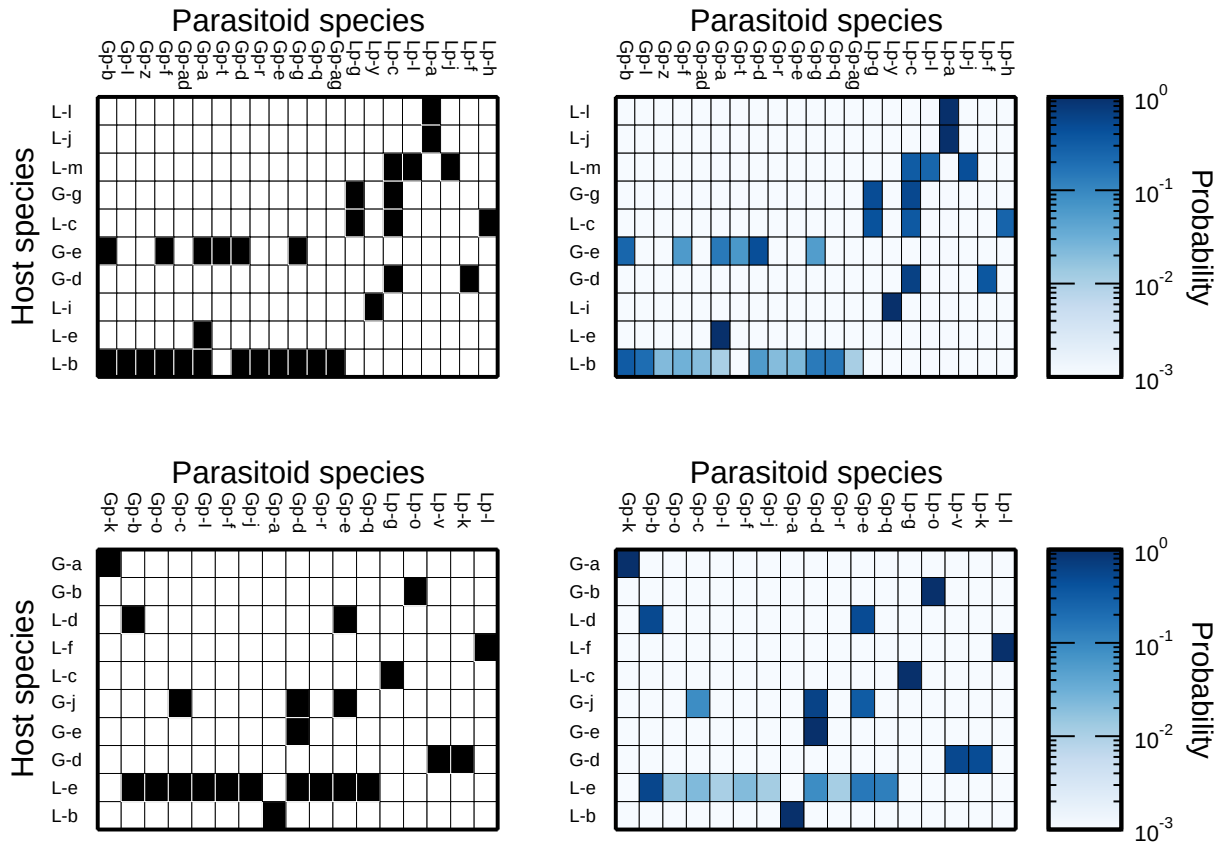

Fig. A7: Graphical representation of the qualitative interaction network (left) and the mean of all 999 resampled networks (right) for site 5 in 2006 (top) and 2007 (bottom). Each cell represents a possible interaction between a host species and parasitoid species. In the qualitative network, a black cell represents the presence of an interaction whereas white represents its absence. In the resampled network, each cell is shaded according to the probability that the interaction appeared in the resampled networks, with the colors as indicated in the colorbar at right.

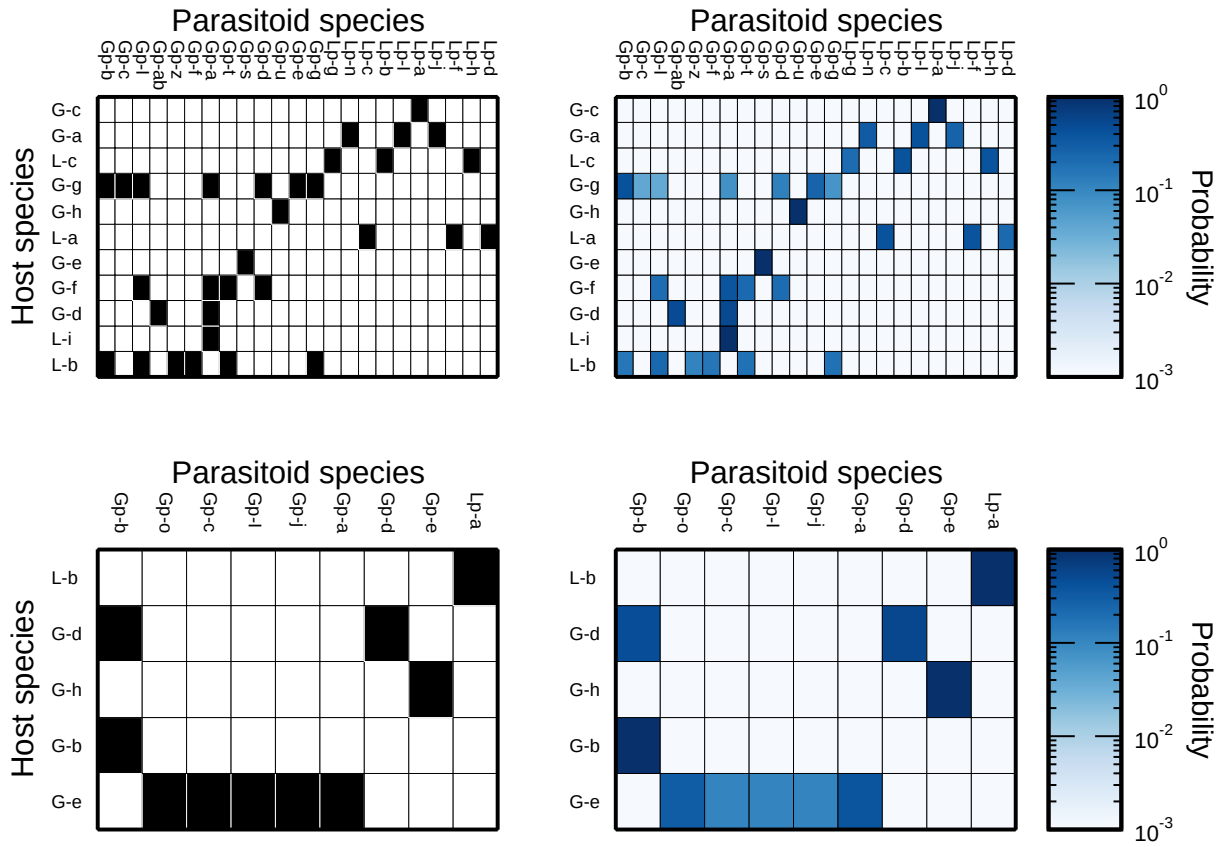

Fig. A8: Graphical representation of the qualitative interaction network (left) and the mean of all 999 resampled networks (right) for site 6 in 2006 (top) and 2007 (bottom). Each cell represents a possible interaction between a host species and parasitoid species. In the qualitative network, a black cell represents the presence of an interaction whereas white represents its absence. In the resampled network, each cell is shaded according to the probability that the interaction appeared in the resampled networks, with the colors as indicated in the colorbar at right.

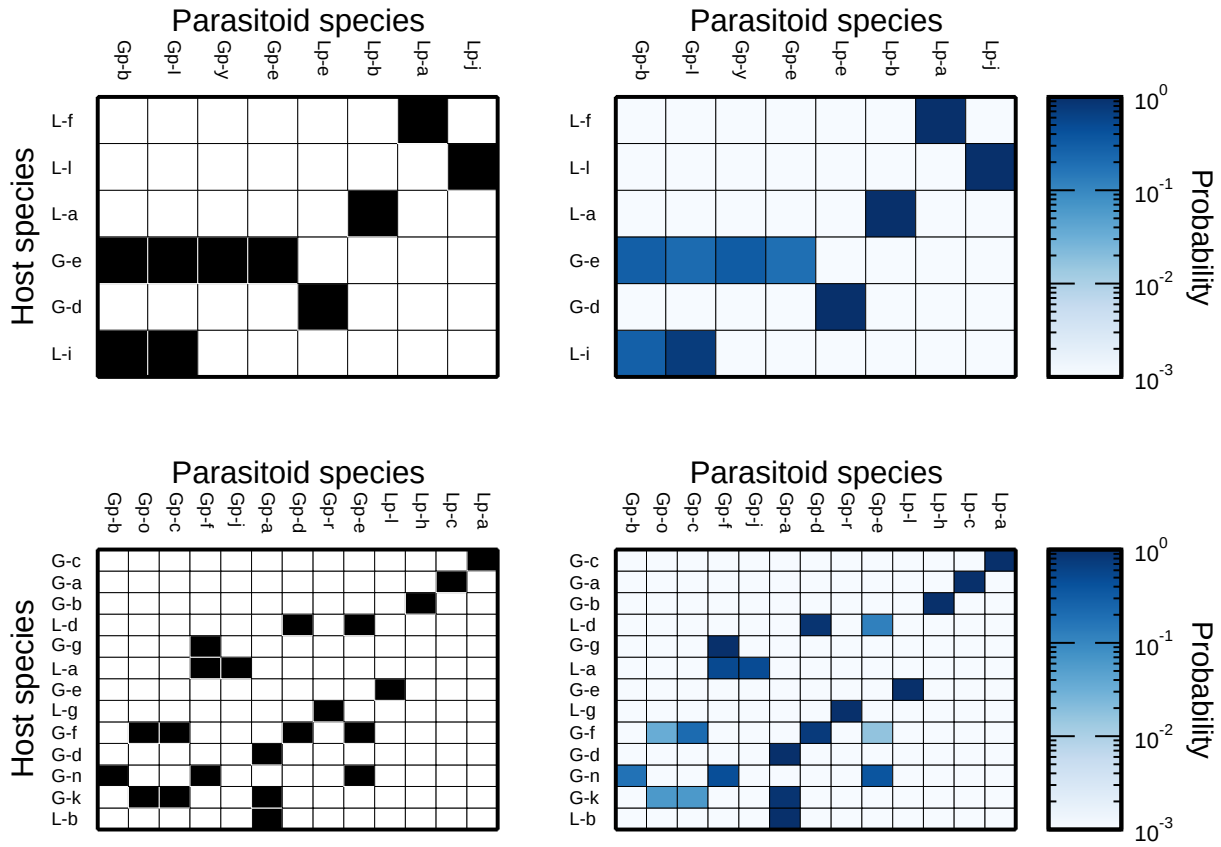

Fig. A9: Graphical representation of the qualitative interaction network (left) and the mean of all 999 resampled networks (right) for site 7 in 2006 (top) and 2007 (bottom). Each cell represents a possible interaction between a host species and parasitoid species. In the qualitative network, a black cell represents the presence of an interaction whereas white represents its absence. In the resampled network, each cell is shaded according to the probability that the interaction appeared in the resampled networks, with the colors as indicated in the colorbar at right.

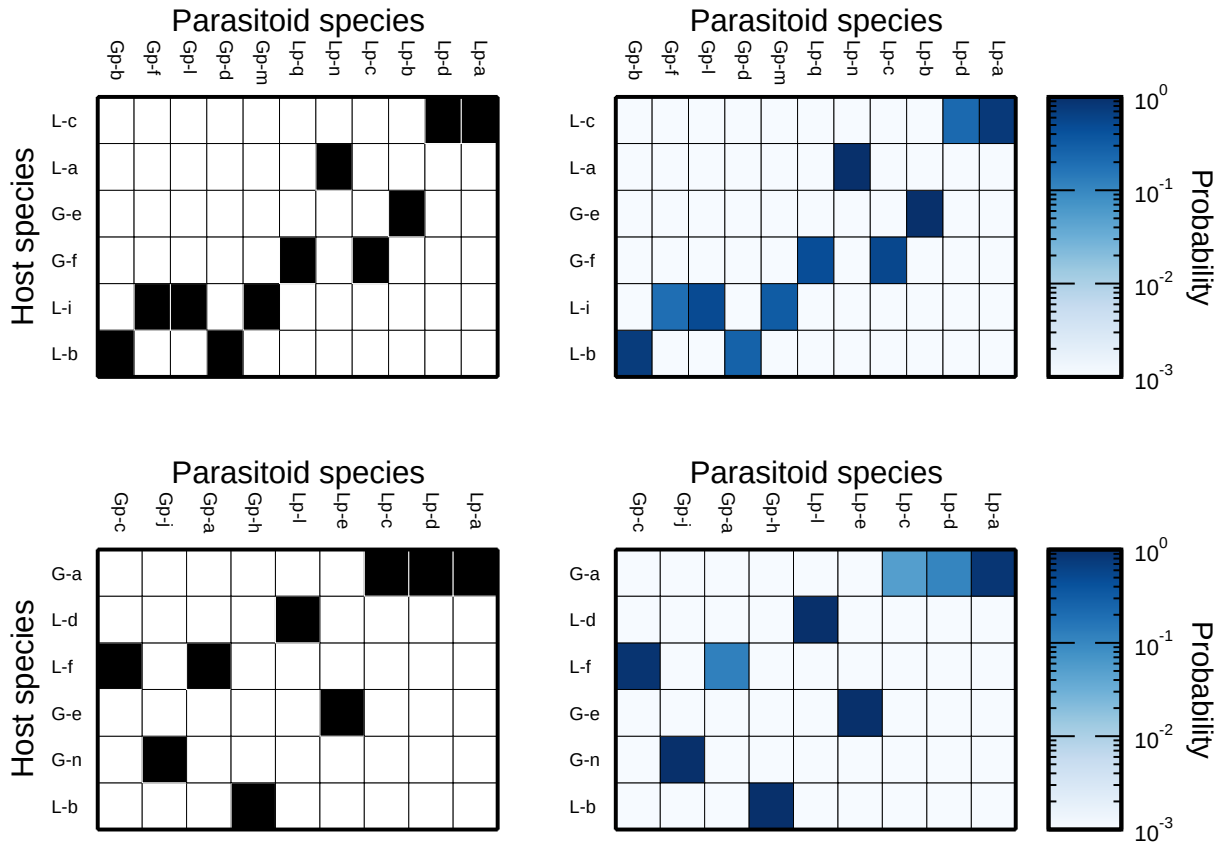

Fig. A10: Graphical representation of the qualitative interaction network (left) and the mean of all 999 resampled networks (right) for site 8 in 2006 (top) and 2007 (bottom). Each cell represents a possible interaction between a host species and parasitoid species. In the qualitative network, a black cell represents the presence of an interaction whereas white represents its absence. In the resampled network, each cell is shaded according to the probability that the interaction appeared in the resampled networks, with the colors as indicated in the colorbar at right.

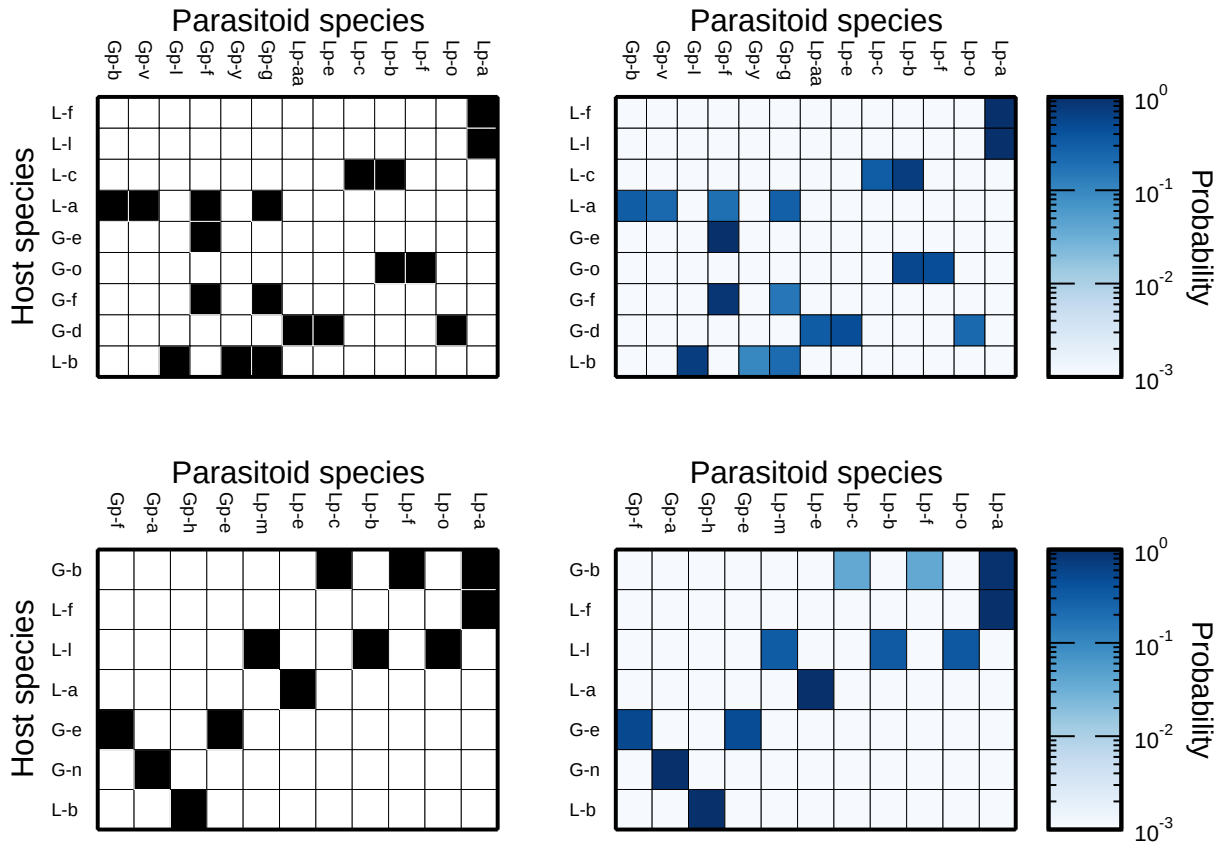

Fig. A11: Graphical representation of the qualitative interaction network (left) and the mean of all 999 resampled networks (right) for site 9 in 2006 (top) and 2007 (bottom). Each cell represents a possible interaction between a host species and parasitoid species. In the qualitative network, a black cell represents the presence of an interaction whereas white represents its absence. In the resampled network, each cell is shaded according to the probability that the interaction appeared in the resampled networks, with the colors as indicated in the colorbar at right.

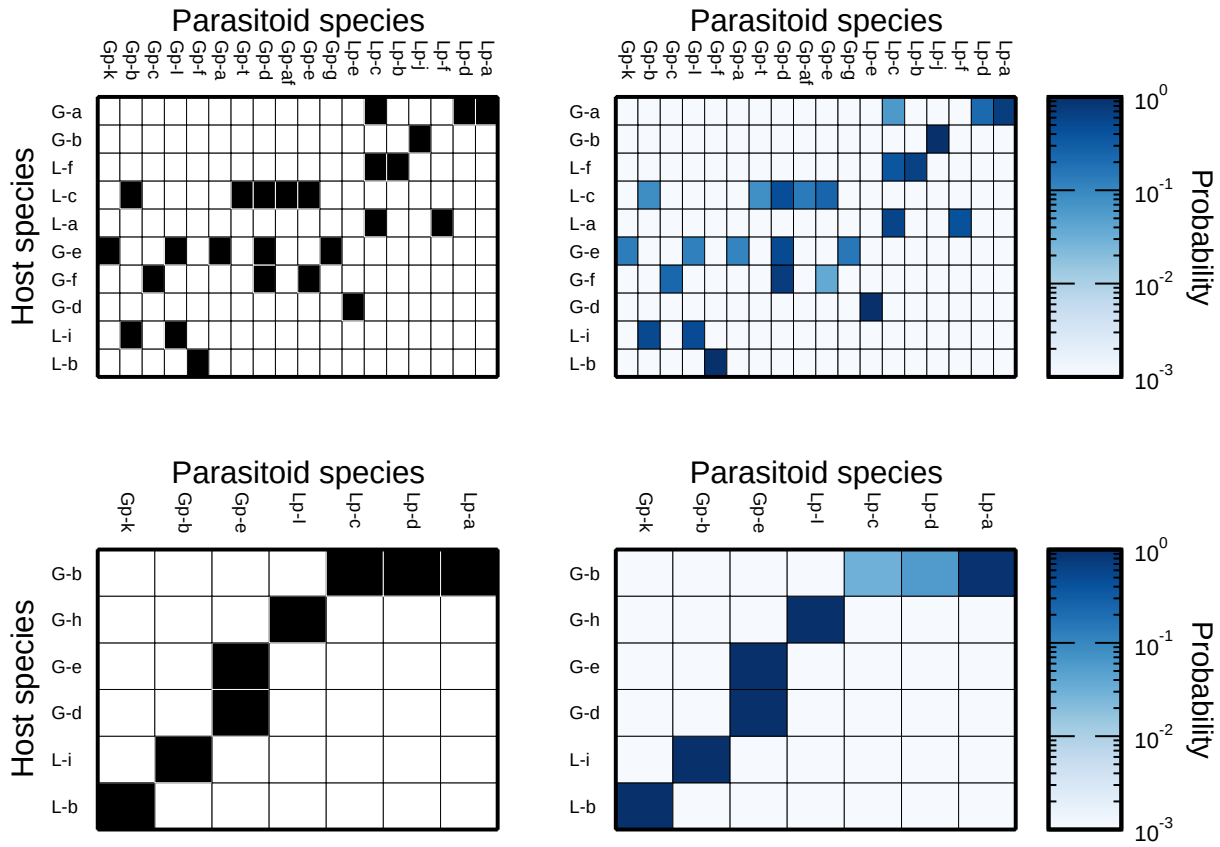

Fig. A12: Graphical representation of the qualitative interaction network (left) and the mean of all 999 resampled networks (right) for site 10 in 2006 (top) and 2007 (bottom). Each cell represents a possible interaction between a host species and parasitoid species. In the qualitative network, a black cell represents the presence of an interaction whereas white represents its absence. In the resampled network, each cell is shaded according to the probability that the interaction appeared in the resampled networks, with the colors as indicated in the colorbar at right.

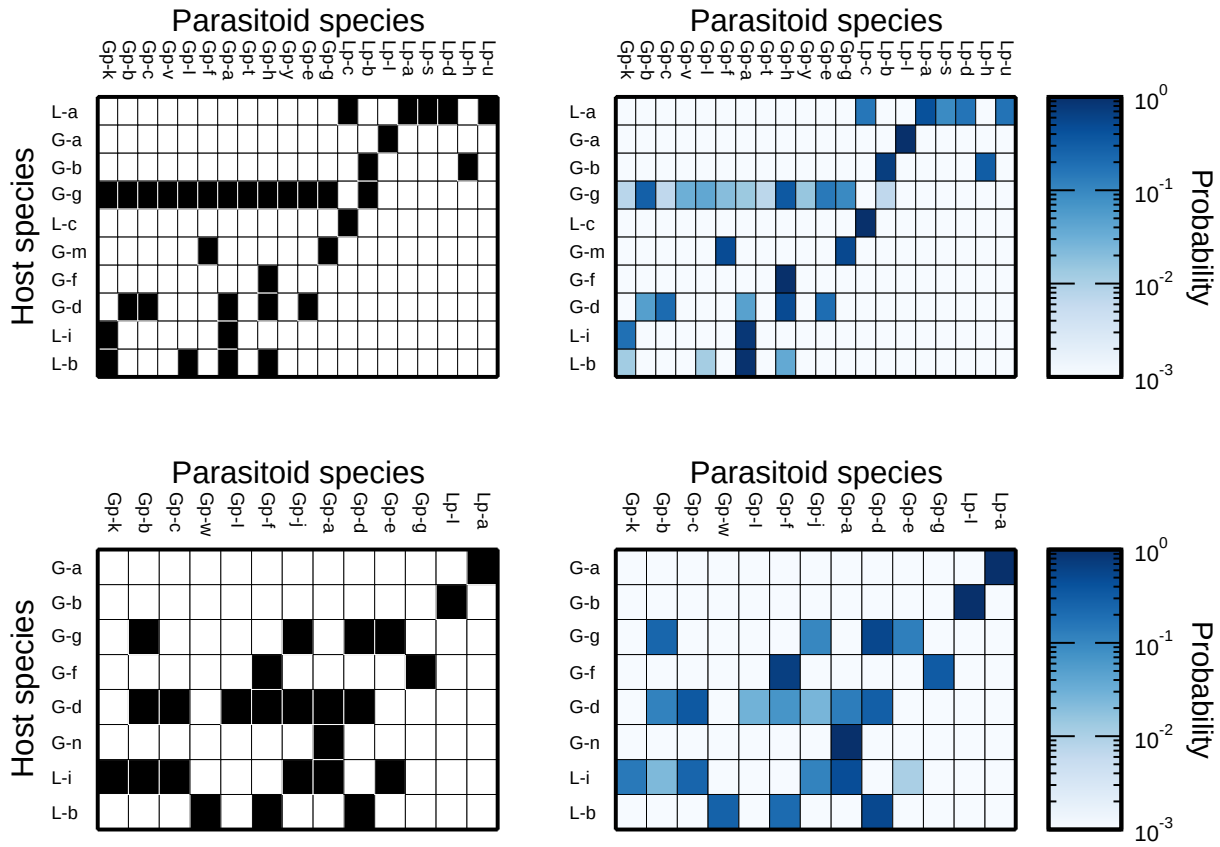

Fig. A13: Graphical representation of the qualitative interaction network (left) and the mean of all 999 resampled networks (right) for site 11 in 2006 (top) and 2007 (bottom). Each cell represents a possible interaction between a host species and parasitoid species. In the qualitative network, a black cell represents the presence of an interaction whereas white represents its absence. In the resampled network, each cell is shaded according to the probability that the interaction appeared in the resampled networks, with the colors as indicated in the colorbar at right.

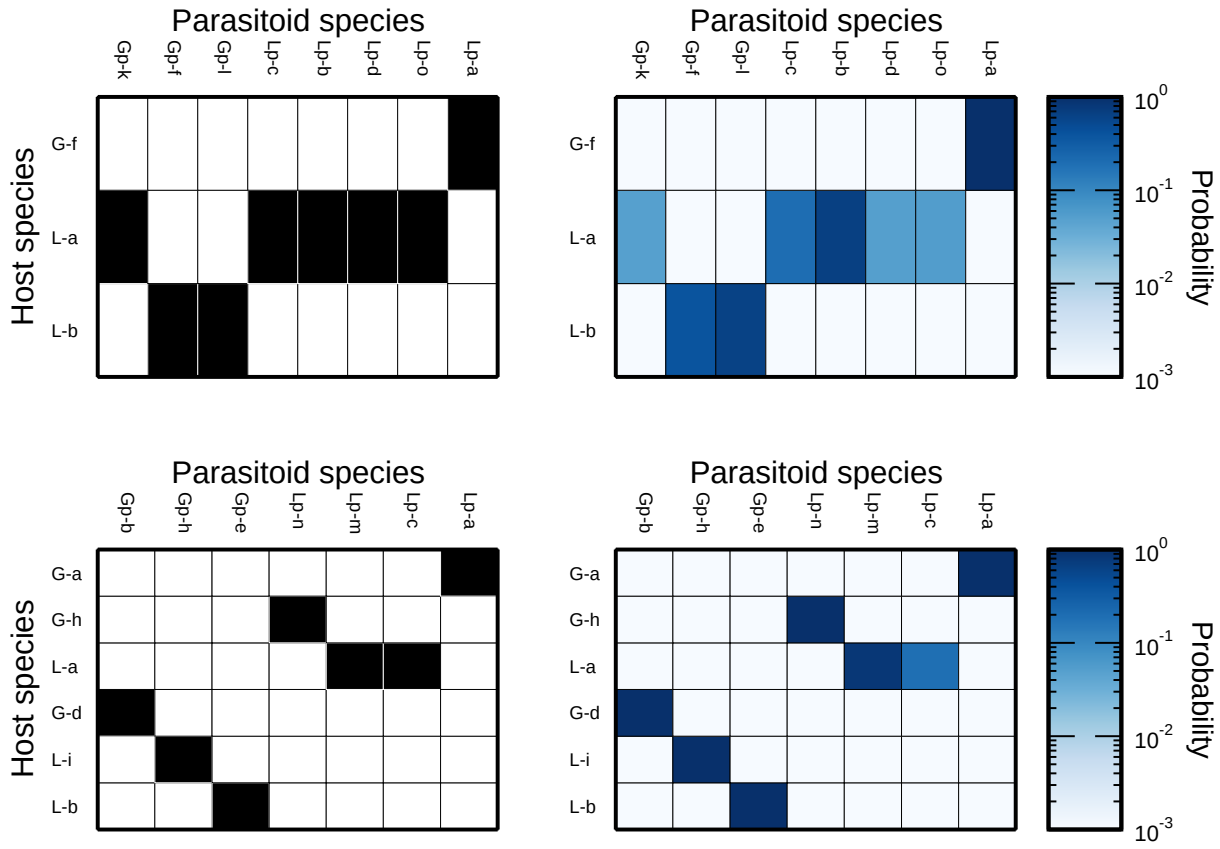

Fig. A14: Graphical representation of the qualitative interaction network (left) and the mean of all 999 resampled networks (right) for site 12 in 2006 (top) and 2007 (bottom). Each cell represents a possible interaction between a host species and parasitoid species. In the qualitative network, a black cell represents the presence of an interaction whereas white represents its absence. In the resampled network, each cell is shaded according to the probability that the interaction appeared in the resampled networks, with the colors as indicated in the colorbar at right.

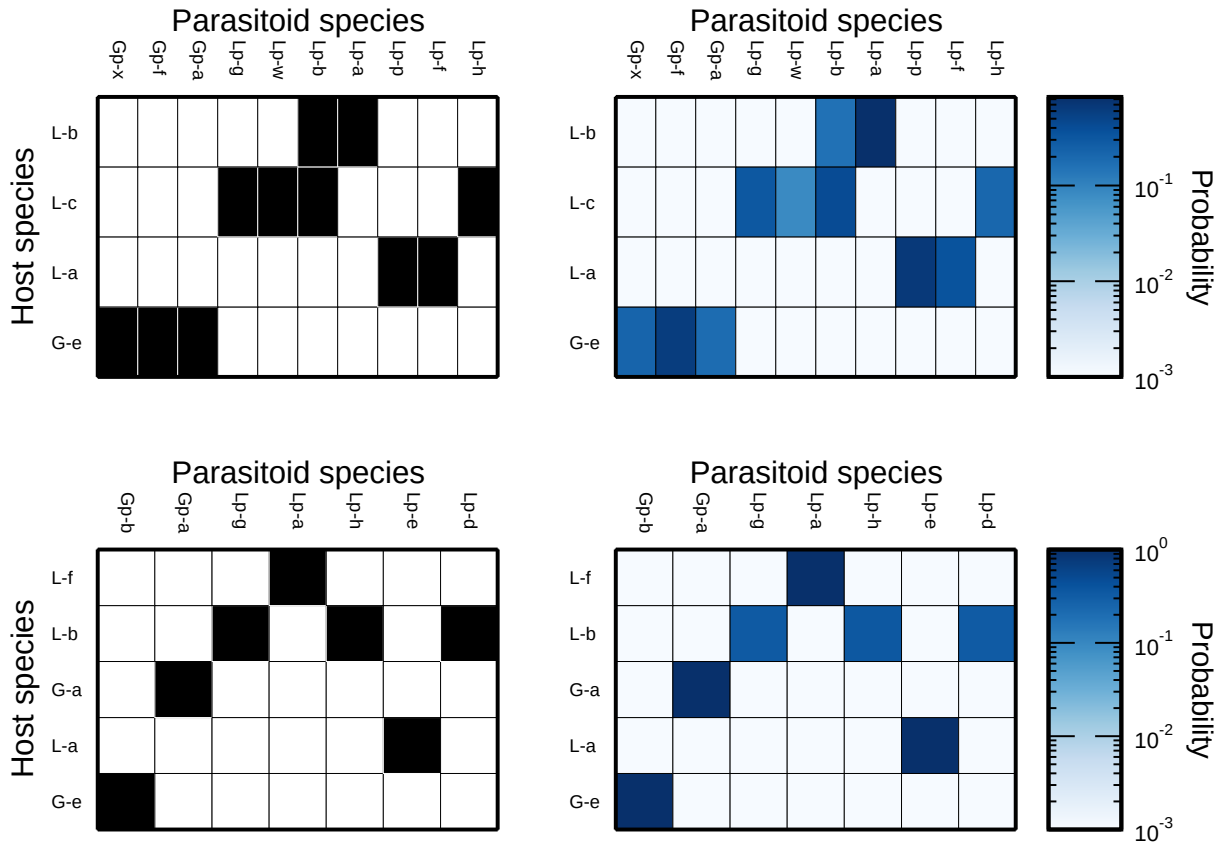

Fig. A15: Graphical representation of the qualitative interaction network (left) and the mean of all 999 resampled networks (right) for site 13 in 2006 (top) and 2007 (bottom). Each cell represents a possible interaction between a host species and parasitoid species. In the qualitative network, a black cell represents the presence of an interaction whereas white represents its absence. In the resampled network, each cell is shaded according to the probability that the interaction appeared in the resampled networks, with the colors as indicated in the colorbar at right.

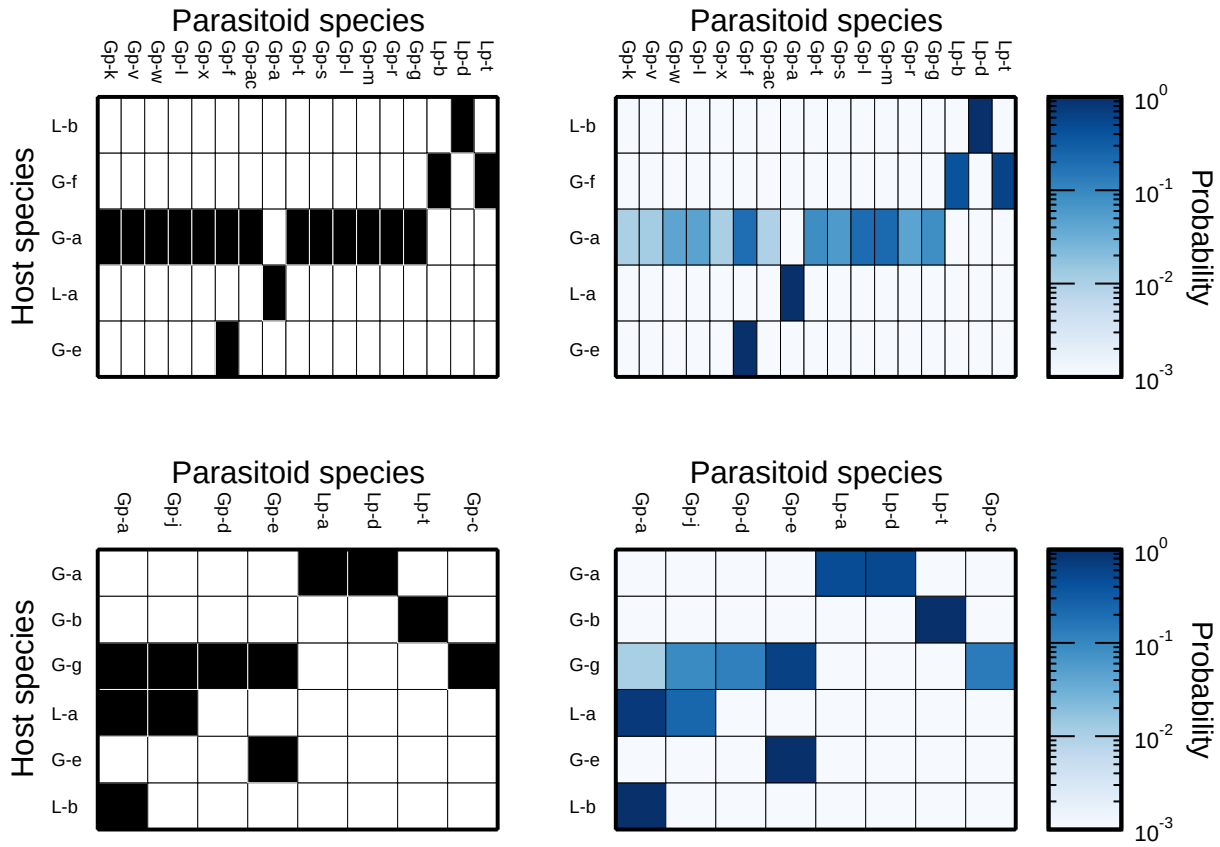

Fig. A16: Graphical representation of the qualitative interaction network (left) and the mean of all 999 resampled networks (right) for site 14 in 2006 (top) and 2007 (bottom). Each cell represents a possible interaction between a host species and parasitoid species. In the qualitative network, a black cell represents the presence of an interaction whereas white represents its absence. In the resampled network, each cell is shaded according to the probability that the interaction appeared in the resampled networks, with the colors as indicated in the colorbar at right.

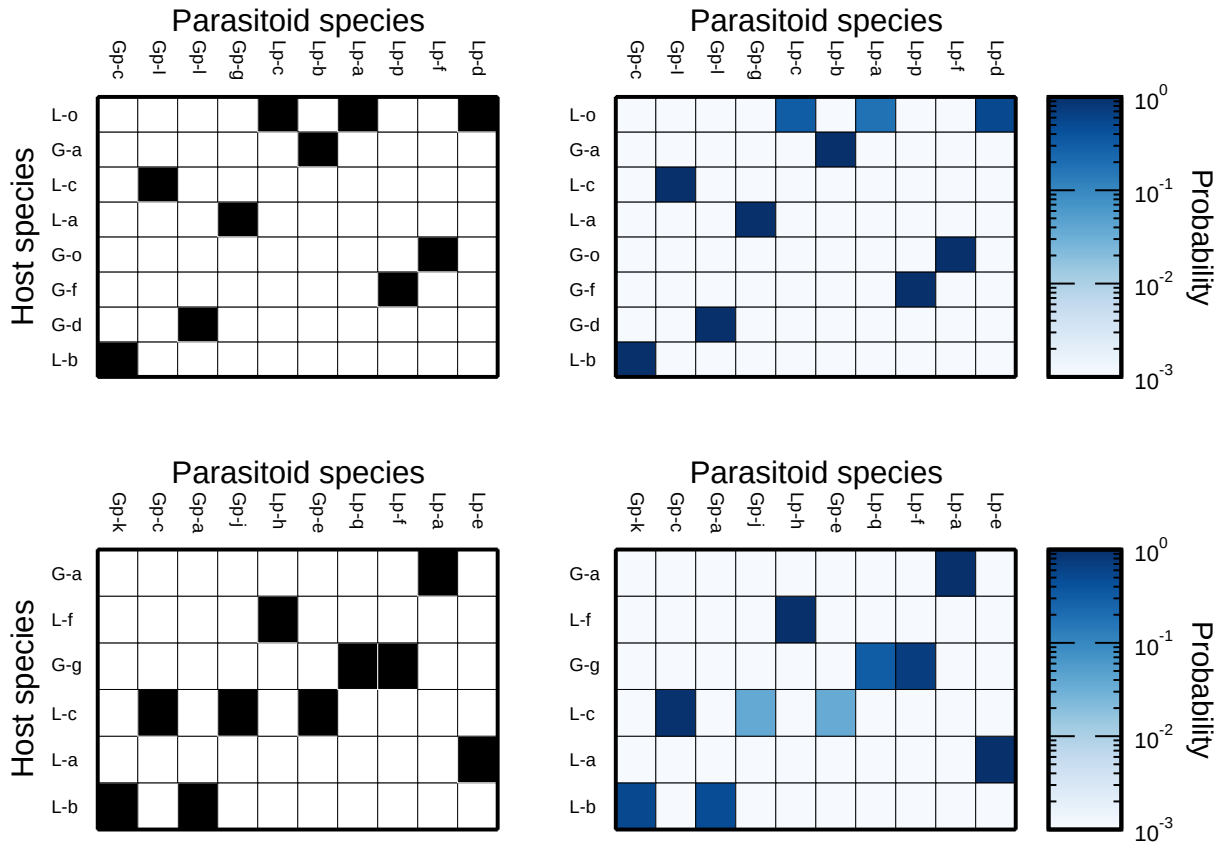

Fig. A17: Graphical representation of the qualitative interaction network (left) and the mean of all 999 resampled networks (right) for site 15 in 2006 (top) and 2007 (bottom). Each cell represents a possible interaction between a host species and parasitoid species. In the qualitative network, a black cell represents the presence of an interaction whereas white represents its absence. In the resampled network, each cell is shaded according to the probability that the interaction appeared in the resampled networks, with the colors as indicated in the colorbar at right.

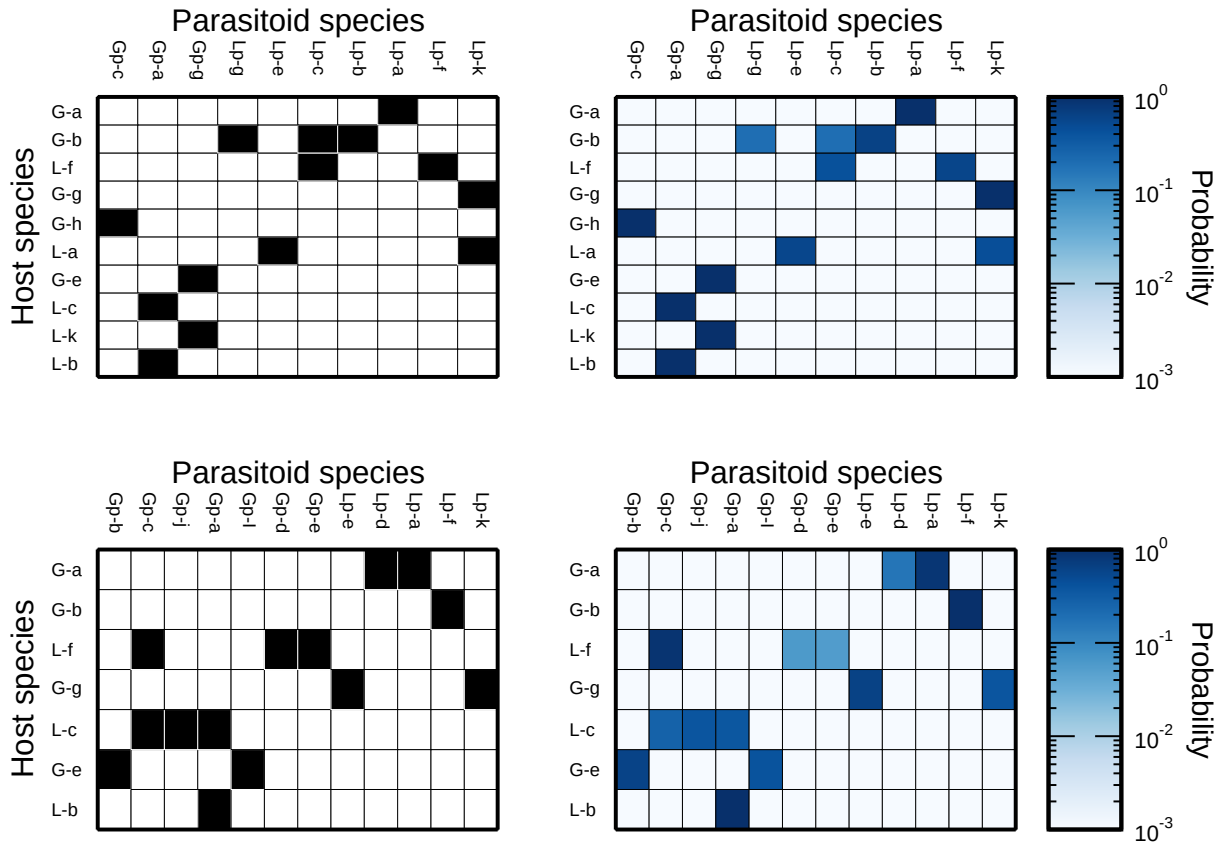

Fig. A18: Graphical representation of the qualitative interaction network (left) and the mean of all 999 resampled networks (right) for site 16 in 2006 (top) and 2007 (bottom). Each cell represents a possible interaction between a host species and parasitoid species. In the qualitative network, a black cell represents the presence of an interaction whereas white represents its absence. In the resampled network, each cell is shaded according to the probability that the interaction appeared in the resampled networks, with the colors as indicated in the colorbar at right.

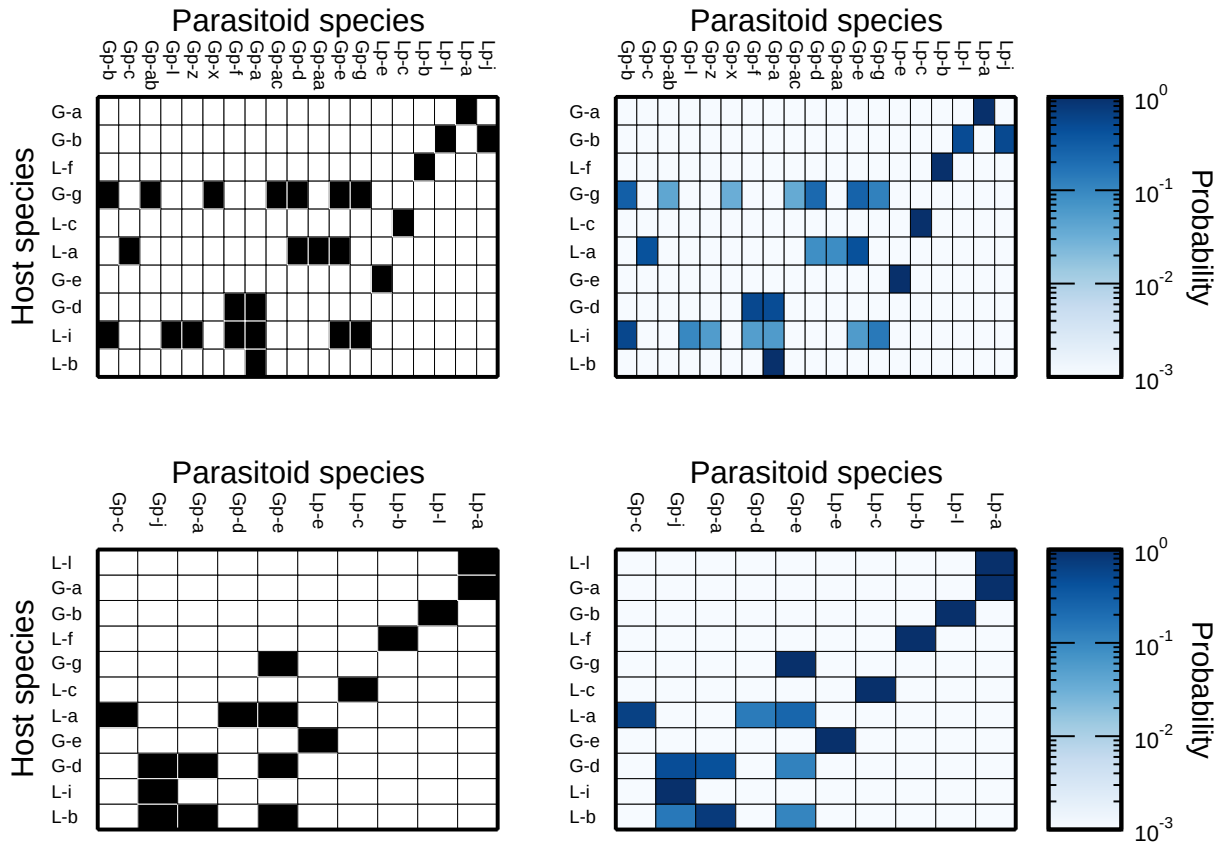

Fig. A19: Graphical representation of the qualitative interaction network (left) and the mean of all 999 resampled networks (right) for site 17 in 2006 (top) and 2007 (bottom). Each cell represents a possible interaction between a host species and parasitoid species. In the qualitative network, a black cell represents the presence of an interaction whereas white represents its absence. In the resampled network, each cell is shaded according to the probability that the interaction appeared in the resampled networks, with the colors as indicated in the colorbar at right.

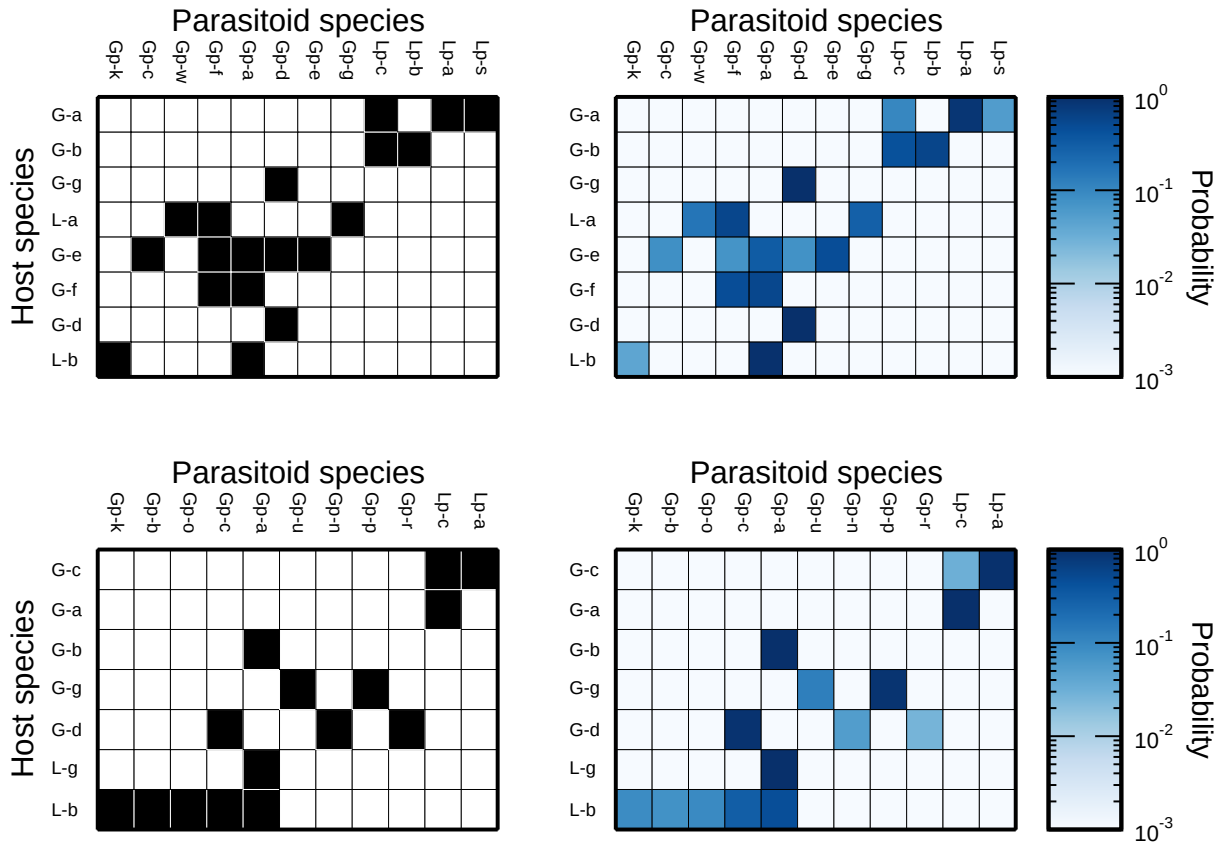

Fig. A20: Graphical representation of the qualitative interaction network (left) and the mean of all 999 resampled networks (right) for site 18 in 2006 (top) and 2007 (bottom). Each cell represents a possible interaction between a host species and parasitoid species. In the qualitative network, a black cell represents the presence of an interaction whereas white represents its absence. In the resampled network, each cell is shaded according to the probability that the interaction appeared in the resampled networks, with the colors as indicated in the colorbar at right.

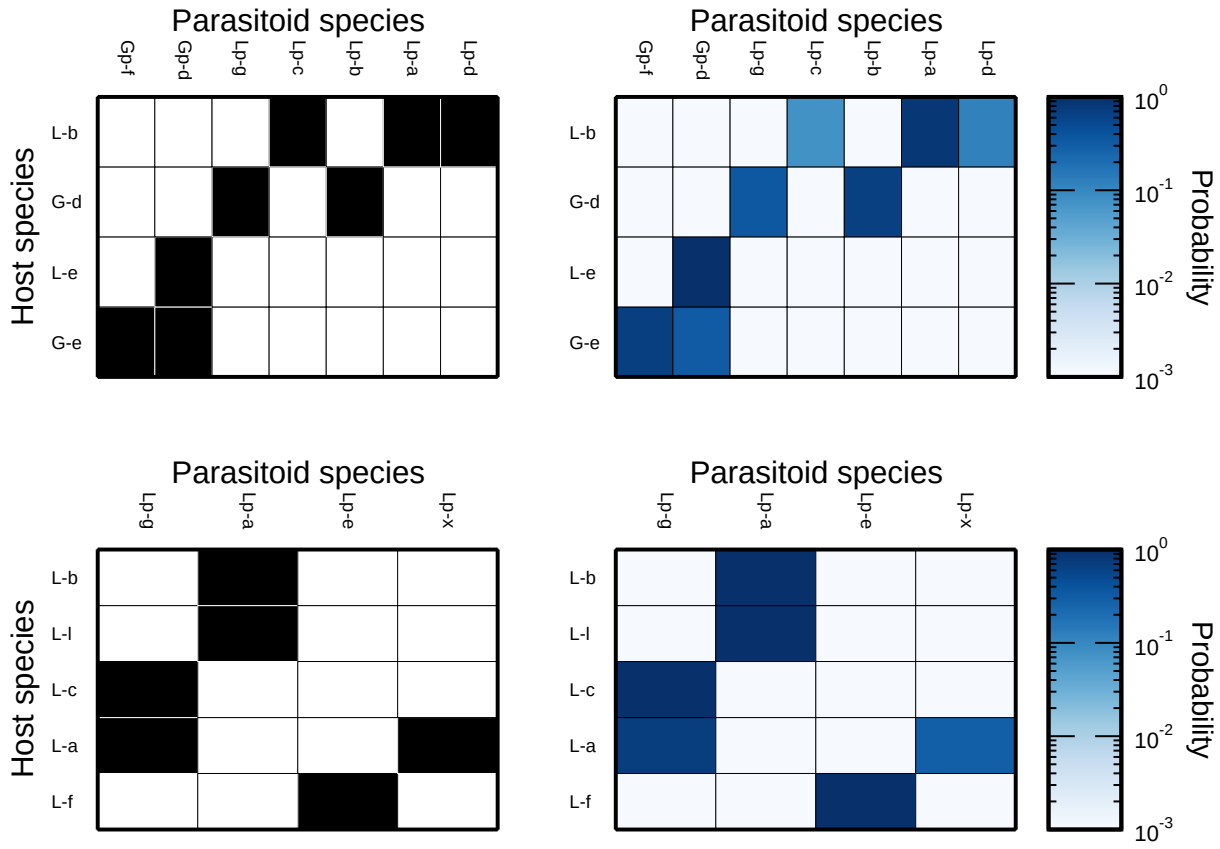

Fig. A21: Graphical representation of the qualitative interaction network (left) and the mean of all 999 resampled networks (right) for site 19 in 2006 (top) and 2007 (bottom). Each cell represents a possible interaction between a host species and parasitoid species. In the qualitative network, a black cell represents the presence of an interaction whereas white represents its absence. In the resampled network, each cell is shaded according to the probability that the interaction appeared in the resampled networks, with the colors as indicated in the colorbar at right.

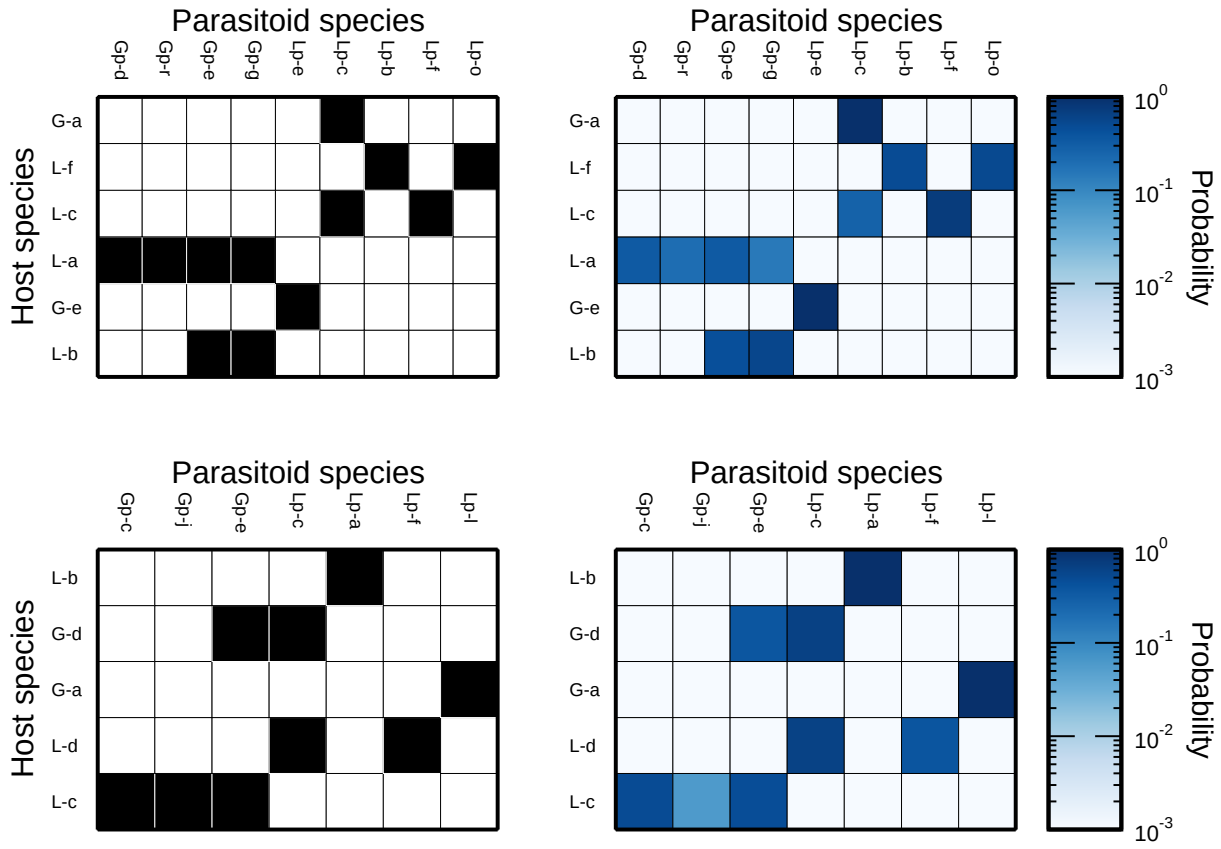

Fig. A22: Graphical representation of the qualitative interaction network (left) and the mean of all 999 resampled networks (right) for site 20 in 2006 (top) and 2007 (bottom). Each cell represents a possible interaction between a host species and parasitoid species. In the qualitative network, a black cell represents the presence of an interaction whereas white represents its absence. In the resampled network, each cell is shaded according to the probability that the interaction appeared in the resampled networks, with the colors as indicated in the colorbar at right.

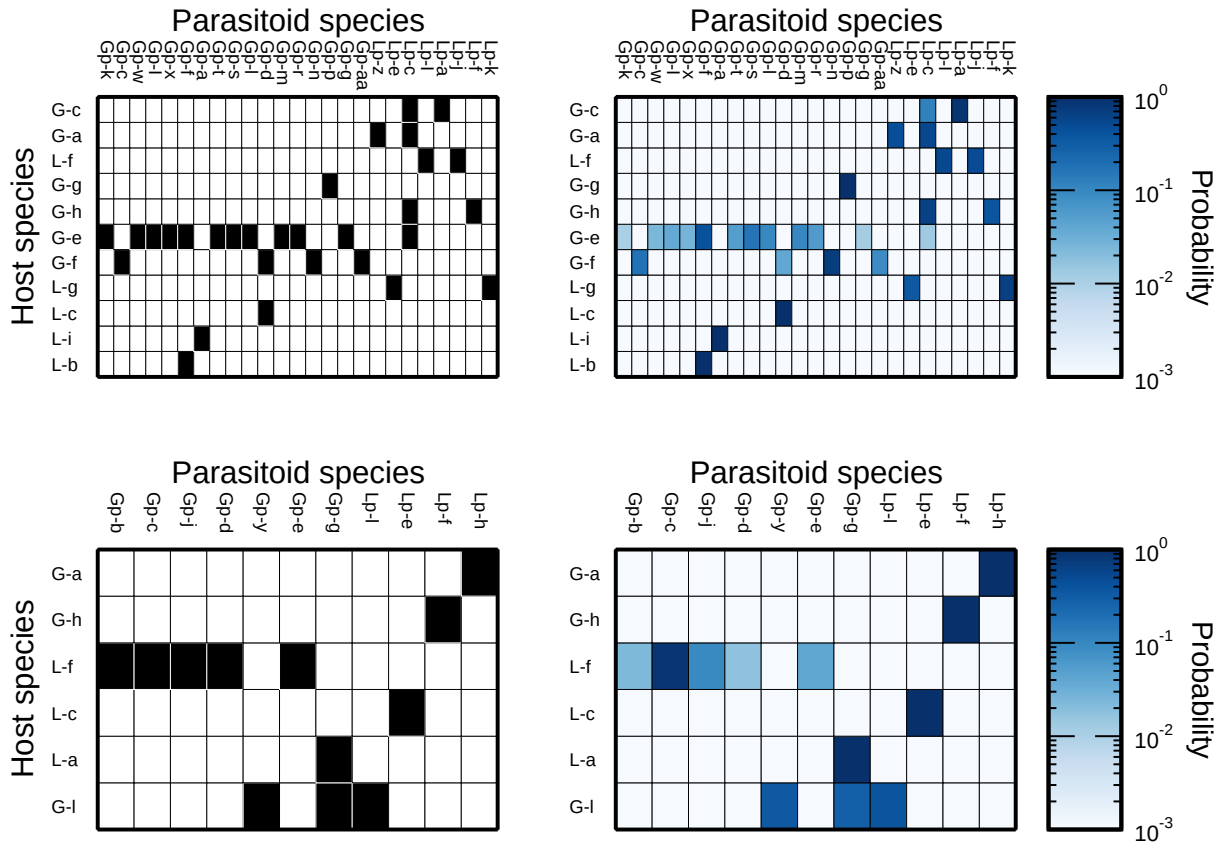

Fig. A23: Graphical representation of the qualitative interaction network (left) and the mean of all 999 resampled networks (right) for site 21 in 2006 (top) and 2007 (bottom). Each cell represents a possible interaction between a host species and parasitoid species. In the qualitative network, a black cell represents the presence of an interaction whereas white represents its absence. In the resampled network, each cell is shaded according to the probability that the interaction appeared in the resampled networks, with the colors as indicated in the colorbar at right.

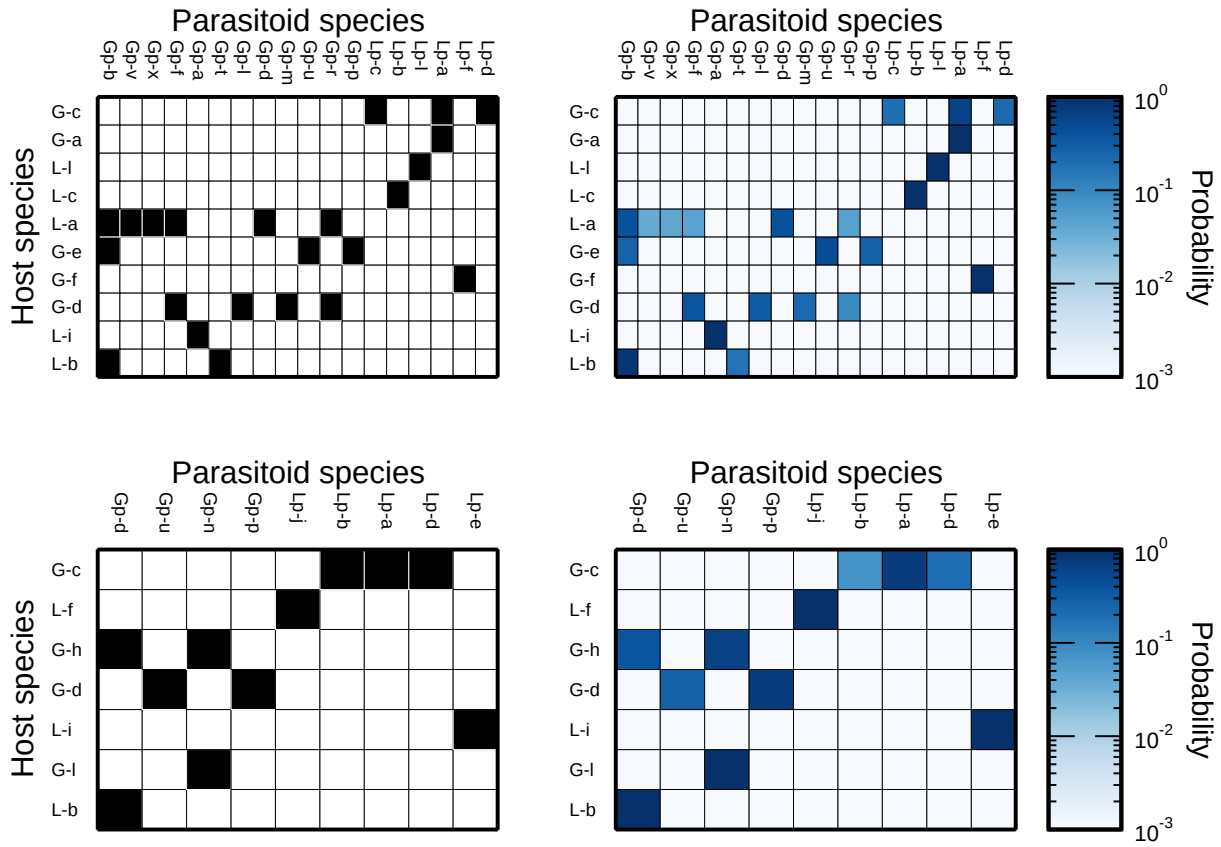

Fig. A24: Graphical representation of the qualitative interaction network (left) and the mean of all 999 resampled networks (right) for site 22 in 2006 (top) and 2007 (bottom). Each cell represents a possible interaction between a host species and parasitoid species. In the qualitative network, a black cell represents the presence of an interaction whereas white represents its absence. In the resampled network, each cell is shaded according to the probability that the interaction appeared in the resampled networks, with the colors as indicated in the colorbar at right.

Results of network resampling

Role fidelity of hosts

When examining species fidelity of host roles, 2 out of 21 host species had significantly different measures of fidelity between the results for the qualitative networks and the resampling distributions (Fig. A25). Both species belonged to the galler feeding guild and both species showed no fidelity in the main text or in the resampling analysis. As a result, our conclusion from the main text that host species show fidelity of roles does not change since 8 out of 21 species continue to show fidelity.

For network fidelity of host roles, no networks had significantly different measures of fidelity between the results for the qualitative networks and the resampling distributions (Fig. A25). For temporal fidelity of host roles, no sites had significantly different measures of temporal fidelity between the qualitative networks and resampling distributions (Fig. A25)

Role fidelity of parasitoids

When examining species fidelity of parasitoid roles, 2 out of 49 parasitoid species had significantly different measures of fidelity between the qualitative networks and the resampling distributions (Fig. A26). Of these two species, the first (a leaf-miner parasitoid) showed no fidelity in the main text and variable fidelity in the resampling analysis. The second species (a galler parasitoid) showed fidelity in the main text but showed no role fidelity in the resampling analysis. If we were to reclassify the second species, which did not show fidelity in the resampling analysis, we would end up with 15 out of 49 species showing role fidelity. As this is still

a statistically-significant proportion of parasitoids ($p < 0.001$), the conclusions from the main text about parasitoid species fidelity would not change.

For network fidelity of parasitoid roles, none of the networks had significantly different measures of fidelity between the qualitative networks and the resampling distributions (Fig. A26). For temporal fidelity of parasitoid roles, 6 out of 22 sites had significantly different measures of temporal fidelity between the qualitative networks and the resampling distribution (Fig. A26). Five sites showed highly variable measures of temporal fidelity in the resampling distributions. One site showed fidelity in the resampling analysis but did not in the main text. If we were to reclassify the site that changed in its measure of temporal fidelity, we would still be left with 8 out of 22 sites where the the fidelity of parasitoid roles were significantly different between years ($p < 0.001$). Thus, the conclusions from the main text would not change.

Summary of network resampling

The fidelity of host roles at the species, network, and temporal levels did not change significantly between the qualitative networks and the networks in the resampling analysis. For parasitoid roles, there were a greater number of differences between the qualitative networks and the resampling results for species and temporal fidelity but not for network fidelity. Nevertheless, the conclusions from the main text about parasitoid species fidelity would not change as a result of statistical resampling. Overall, the results and conclusions presented in the main text appear robust to our use of qualitative interaction networks, despite the quantitative variation observed empirically.

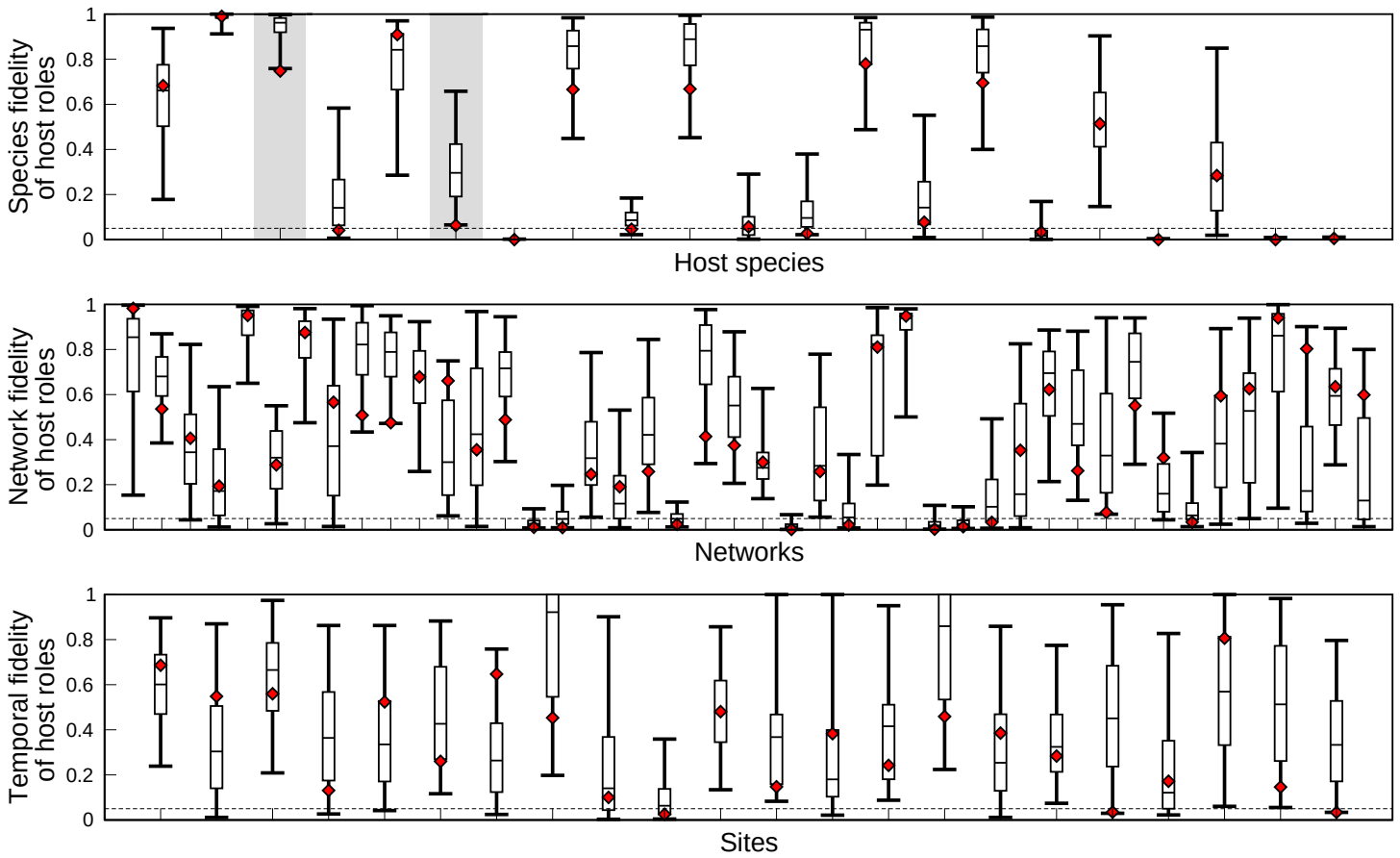

Fig. A25: Comparison of role fidelity of hosts in the main text to the p-values for the resampled networks. From top to bottom, we show species fidelity, network fidelity, and temporal fidelity. Red diamonds show the fidelity values of the qualitative networks from the main text, while white boxes indicate the lower, median, and upper quartiles for the resampled data; the error bars show the 95% confidence intervals. Gray shading represents species, networks, or sites that showed significantly different measures of fidelity between the qualitative networks and the resampled networks.Values below the dotted line represent significant species and network fidelity and, in the case of temporal fidelity, represent sites that did *not* show fidelity between years.

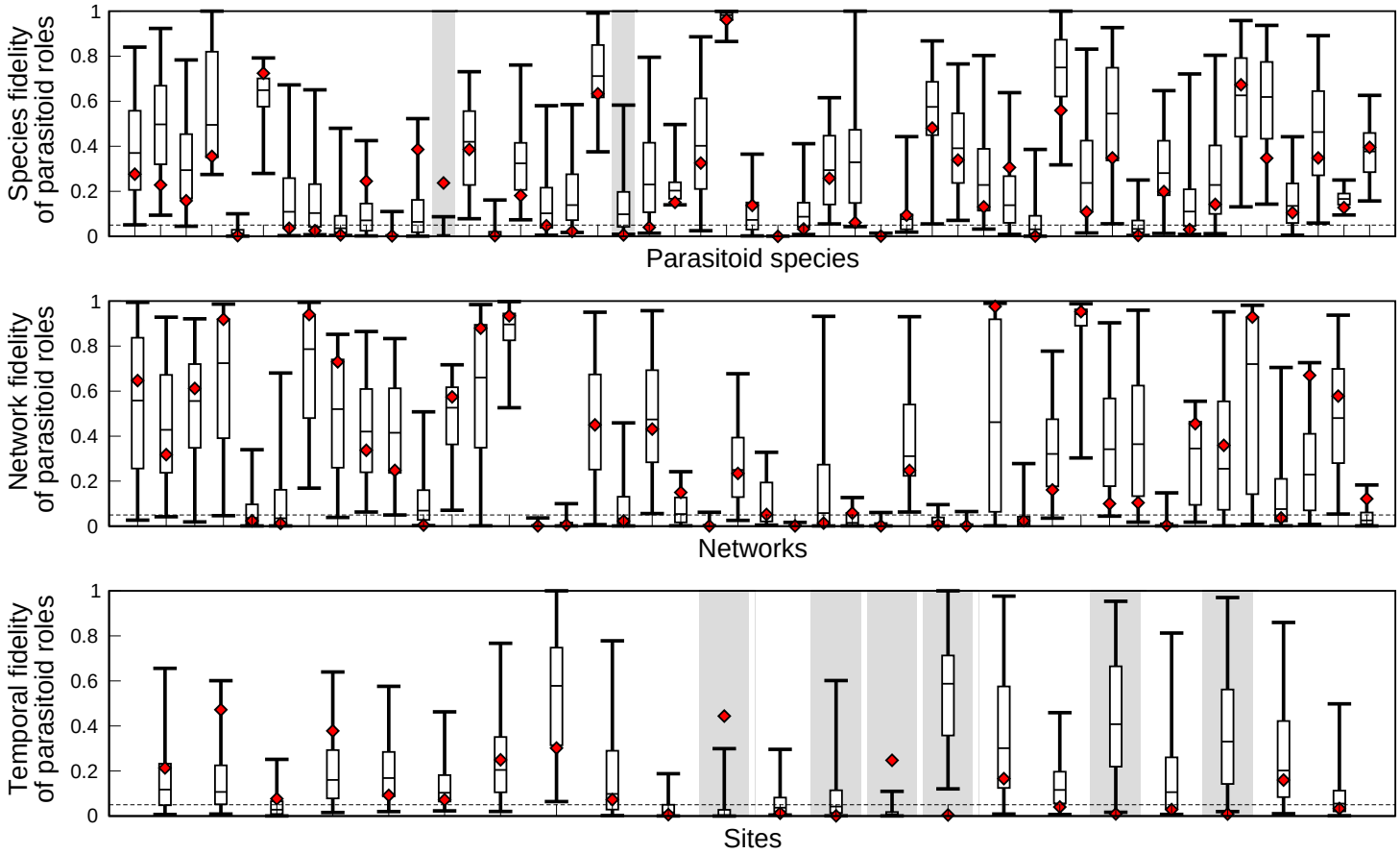

Fig. A26: Comparison of role fidelity of parasitoids in the main text to the p-values for the resampled networks. From top to bottom, we show species fidelity, network fidelity, and temporal fidelity. Red diamonds show the fidelity values of the qualitative networks from the main text, while white boxes indicate the lower, median, and upper quartiles for the resampled data; the error bars show the 95% confidence intervals. Gray shading represents species, networks, or sites that showed significantly different measures of fidelity between the qualitative networks and the resampled networks. Values below the dotted line represent significant species and network fidelity and, in the case of temporal fidelity, represent sites that did *not* show fidelity between years.

Appendix 3 *Bipartite network motifs*

In our analyses, we calculated species' roles using motifs of size two to six. These motifs are represented in Figure A27.

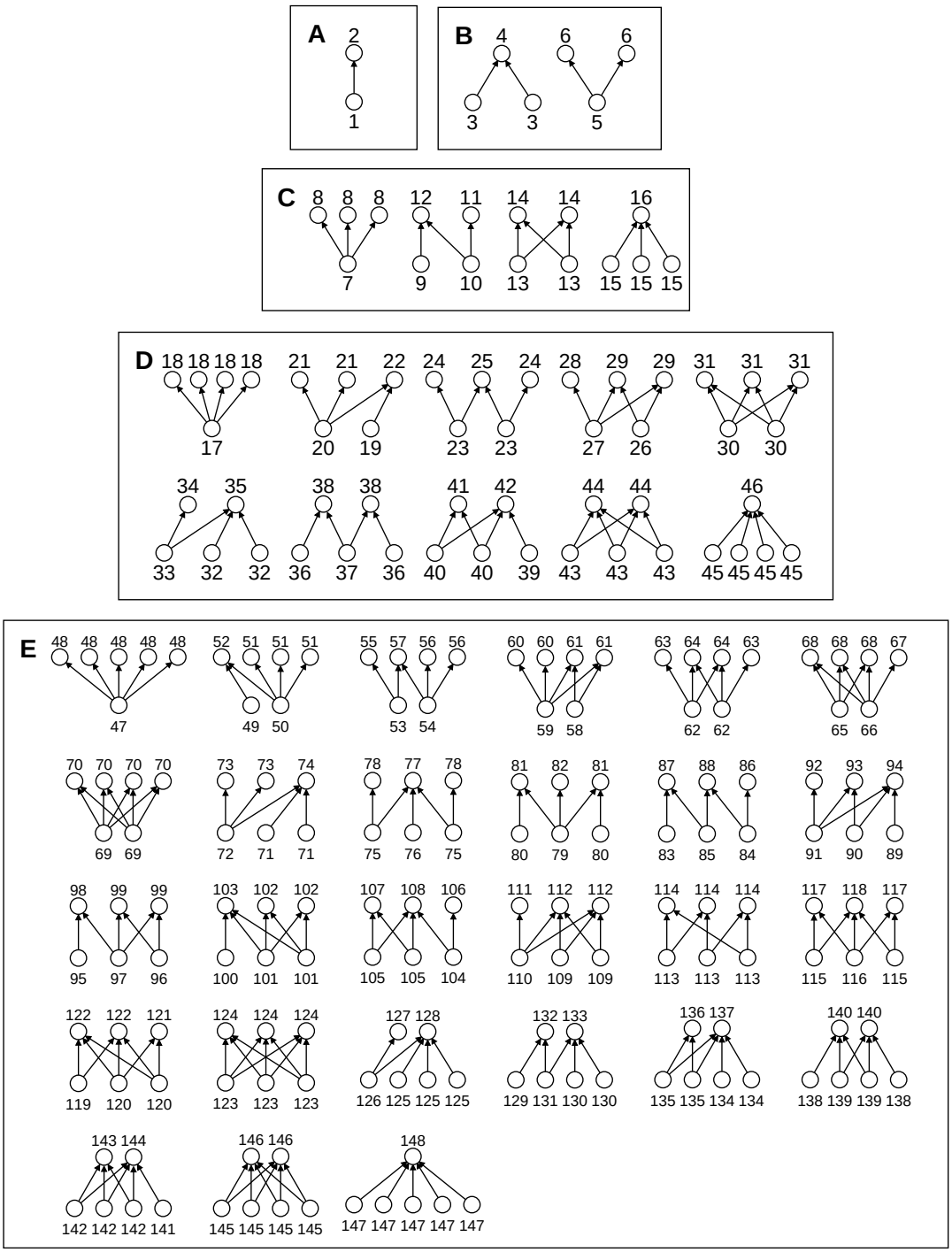

Fig. A27: All bipartite motifs made up of (**A**) two, (**B**) three, (**C**) four, (**D**) five, and (**E**) six species. Circles represent species and the arrows represent interactions between species with direction of the arrows denoting energy transfer (e.g., from host to parasitoid). The different numbers indicate all of the uniquely-identifiable positions within each motif. In total, there are 44 motifs composed of 148 unique positions.

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D'Agostino, R.B. & Stephens, M.A. (1986). Goodness-of-Fit Techniques. *Marcel Dekker, New York*.