Ant-plant demographics in a Neotropical Mutualism

Carter Snow, Sylvia Lee, Rodolfo Probst Ph.D.

Follow me on Linkedin!

Introduction

Ant-plant mutualisms are ecological interactions that often result in specialization and coevolutionary dynamics. In many of these associations, ants defend their host plants from herbivores and parasites, which can enhance host plant fitness and promote its reproduction. In return, host plants typically provide preformed nesting structures (domatia) and nutritional rewards. However, not all mutualisms conform to this pattern. In some systems, such as the *Myrmelachista* ant and Lauraceae plant associations, host plants offer limited structural or nutritional rewards to their tenant ants, suggesting this symbiosis is still in its primordia.

The genus *Myrmelachista* is comprised of obligately arboreal ants that nest within both dead and live plant stems. Among the live-stem nesters are specialists, which exhibit associations with specific host plants; whereas others are generalists, occupying a broader range of host plant species. In the absence of direct nutritional rewards from their host, several *Myrmelachista* species associate with sap-feeding hemipterans (Coccoidea: mealybugs and soft scales) that inhabit the same stems (Figure A). These hemipterans produce an exudate called honeydew, a sugar and amino acid rich substance that serves as a nutritional resource for the ants. The resulting association represents an incipient tri-trophic mutualism, wherein ants rely on both the host plant for nesting and the Coccoiodea for food. Because Lauraceae hosts do not readily provide domatia, *Myrmelachista* colonies must excavate internal cavities within the stems, apparently without inflicting significant damage to the plant.

Our study investigates the demographic composition of live-stem specialist *Myrmelachista* colonies inhabiting Lauraceae plants. We quantified caste structure (alate queens, males, and workers), brood presence (larvae and pupae), and associated Coccoidea abundance to examine how these variables relate to host plant characteristics such as branch size and internal architecture.

Figure A. Lauraceae host plant (left) and cross section of plant branch (right), showing *Myrmelachista* ant workers and brood, as well as and mealybugs within the stem tissues.

Methods

Sampling

Samples were collected from Lauraceae host plants (n = 47) in Costa Rica during the summer months (December–March). To minimize ecological impact, only branch segments were taken from each host tree.

Because ant colonies occupy the entire host plant, these subset samples were used to extrapolate colony-level characteristics. Branches were subsequently frozen, and their internal contents were preserved in collection vials for later examination.

Quantification

For each tree, branch segments of known length and diameter were excised and processed individually.

Colony subset contents were examined under a stereomicroscope, then Categorized and separated into three main groups, subsequently divided into subgroups: adults (alate queens, males, workers), brood (larvae and pupae), and associated Coccoidea (mealybugs and soft scales).

Analysis

All data were processed and analyzed in R. Descriptive statistics were generated, and correlation models were used to examine relationships between colony demographic variables and host plant traits. For analyses involving reproductive investment, only colony subsets containing reproductive individuals were included (34 out of 47 colonies).

Results and Discussion

We examined 47 Lauraceae branch segments inhabited by *Myrmelachista* colonies. Branch lengths ranged from 23.2cm to 205cm (mean = 99.8cm) and diameters from 0.2cm to 7.0cm (mean = 1.6cm), representing understory Lauraceae species. Colony subsets averaged 1,778 individuals (±1,374; range = 109–5,805), consisting of 68% adults (alate queens, males, and workers) and 32% brood (larvae and pupae) (Figure B). Within the adult category, workers were consistently more abundant than reproductives (Figure C). Coccoidea populations averaged 43 individuals per branch (±52; range = 1-215). Distributions of colony components showed substantial overlap and variability across subsets (Figure D).

Colony size increased with branch length ($R^2 = 0.34$, $p < 0.01$; Figure E), reflecting structural feedback in which greater internal volume promotes colony expansion. Branch size corresponds to predictable increases in total colony count, indicating that spatial capacity directly constrains colony growth. Larger stems likely provide more internal nesting chambers and surface area, facilitating worker recruitment, brood rearing, and internal organization. Coccoidea abundance was also positively correlated with total adults ($r = 0.582$, $p < 0.01$) and worker counts ($r = 0.591$, $p < 0.01$). Colonies with greater Coccoidea abundance contained larger worker populations, suggesting that honeydew resources support worker maintenance and promote sustained colony growth.

Together, these relationships potentially indicate that colony structure is shaped by both the physical and nutritional constraints provided by the host plant. It is possible that when colonies are small, limited worker abundance likely reduces their ability to defend or maintain the host plant effectively, weakening mutualistic stability and affecting demographics. Conversely, when plant growth outpaces colony expansion, new tissue may remain undefended, creating a temporary imbalance in the interaction. The scaling among host architecture, colony size, and Coccoidea abundance underscores how structural and trophic feedback influence this *Myrmelachista*-Lauraceae symbiosis. Investigating this incipient association provides insight into how ecological feedback between nesting substrate and resource availability drives the emergence of early mutualistic networks.

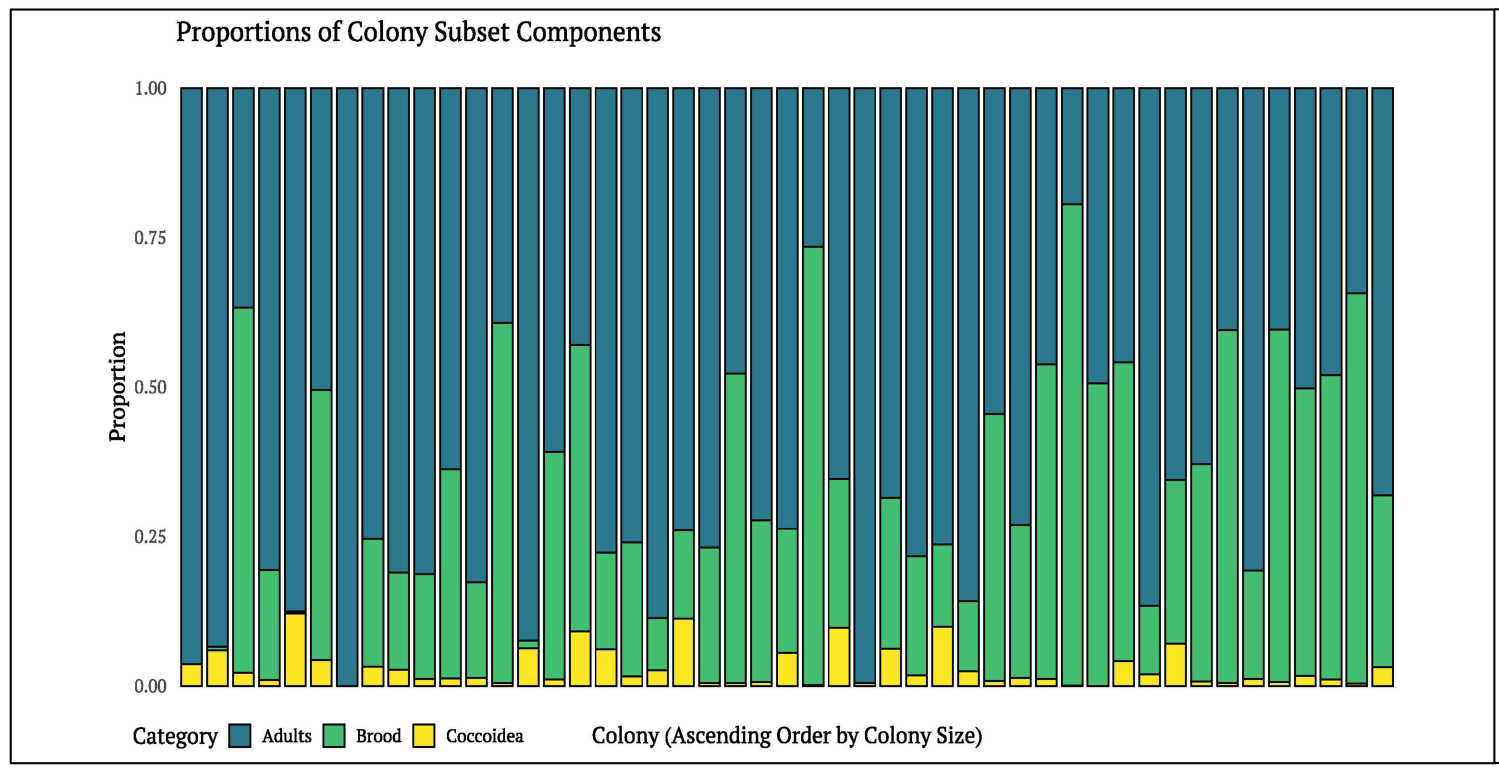

Figure B. Demographics for individual branches from *Myrmelachista* colonies (n=47), represented by the proportion of adults (workers plus reproductives), brood (larvae plus pupae), and Coccoidea. Adults corresponded to a mean proportion of 64% (± 1.9%). Brood to 33% (± 20%). In relation to colony subset total, Coccoiodea were 3% (± 3.2%).

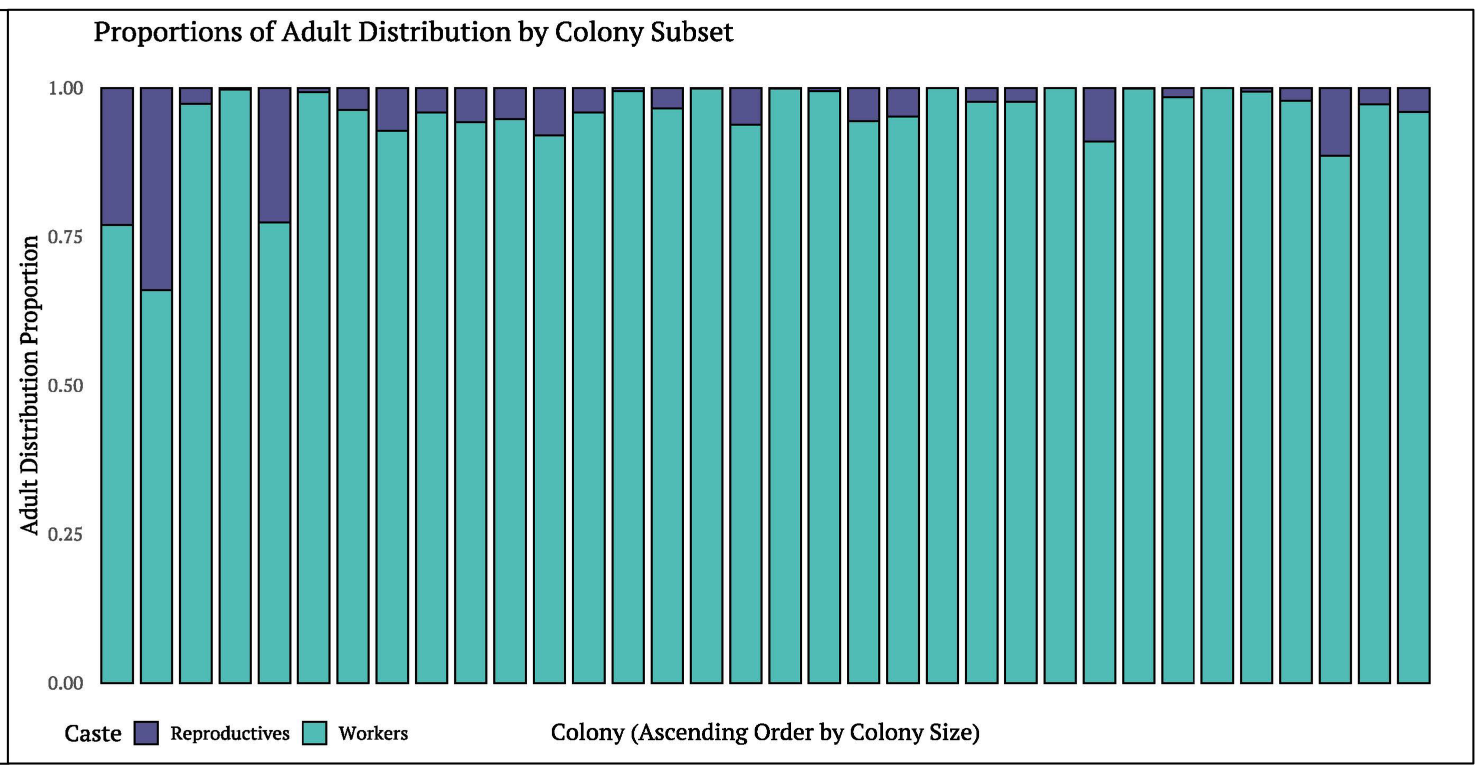

Figure C. Adult caste distribution *Myrmelachista* colonies with reproductives present. Represented in proportions of workers and reproductives (males and alate queens). Workers comprised the 94% (± 7.9%) of adults. Reproductives accounted for 6.1% (± 7.9%).

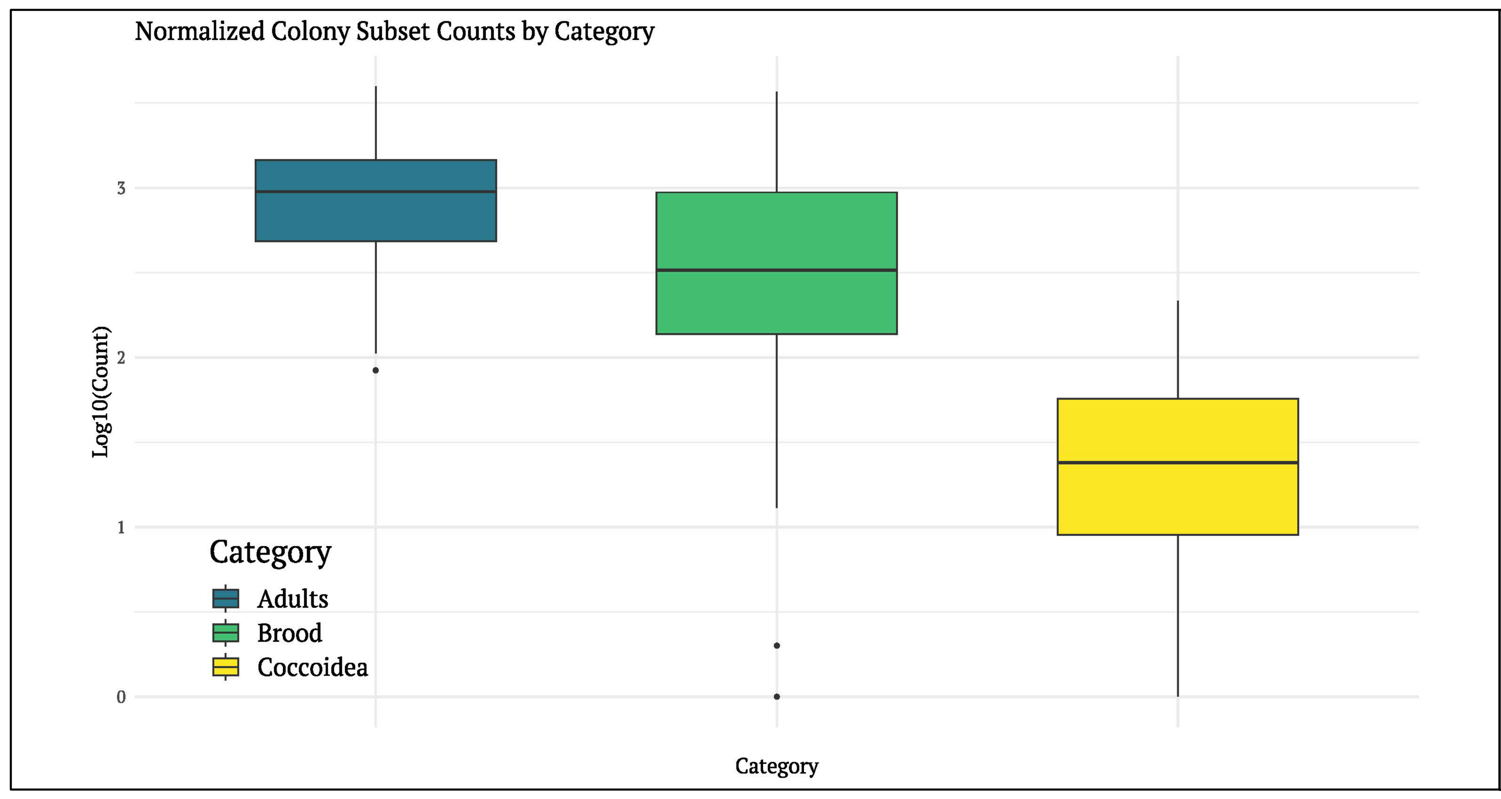

Figure D. Boxplots of colony subset counts by category. Plots illustrate variation among adults, brood, and Coccoidea across sampled branch segments. Outliers are shown as black dots. Coccoidea exhibit the greatest variation in abundance, whereas adult counts are comparatively consistent across samples.

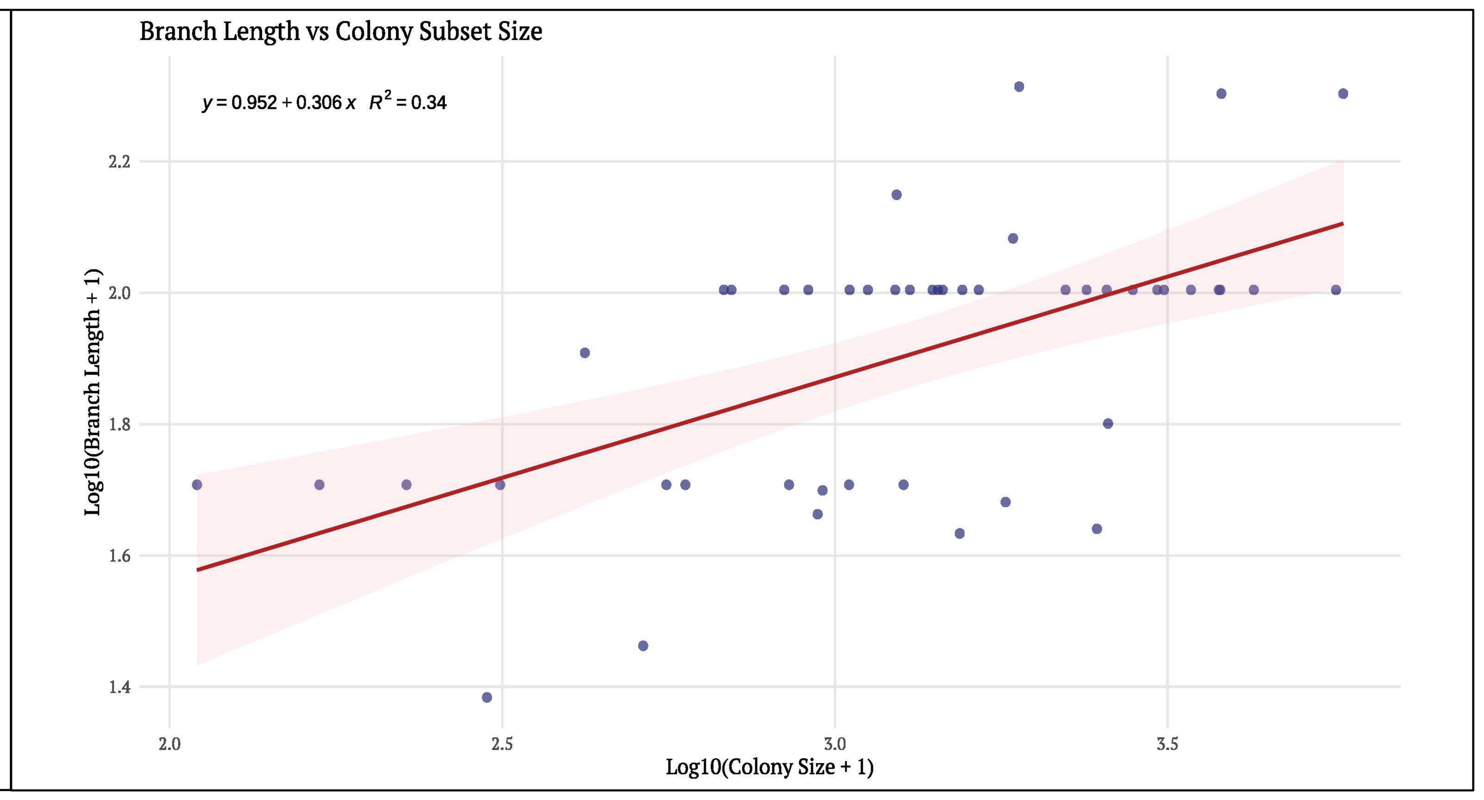

Figure E. Linear regression between colony size and branch length. The line of best fit illustrates the positive relationship between the two variables. The coefficient of determination ($R^2 = 0.34$, $p < 0.01$) indicates that a portion of the variation in colony size can be explained by branch length.

Open Questions

- Can we extrapolate colony demographics from a branch to the whole tree?
- Do seasonal changes affect colony size and branch diameter relationships?

Next Steps

Subsequent analyses will incorporate colony demographics from entire host plants and compare them to our subset counts. To evaluate the seasonal effect, colony subsets should be collected outside of the summer months in Costa Rica.

This expanded approach will generate a more complete description of colony sociometry, improving our understanding of how ant-plant-hemipteran mutualisms in the *Myrmelachista*-Lauraceae system are structured across ecological scales.

More Info

For additional information on the *Myrmelachista*-Lauraceae system, and to see where else this research has gone, check out: **Sylvia Lee's Poster Tomorrow! Poster: #125**

Acknowledgments

This work was supported by the Science Research Initiative. Open-source artificial intelligence tools were used to assist in debugging R scripts.