

Supplemental Information for:

Species Identity Dominates over Environment in Driving Bacterial Community Assembly in Wild Invasive Leaf Miners

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RUNNING TITLE: Bacterial community assembly in *Liriomyza*

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Table S2 to S4;

Fig. S1 to S8.

Table S2 The alpha diversity of four leaf miner bacterial communities.

| Host species | ACE | Chao 1 | Pielou evenness | Simpson evenness | Shannon | Richness |
|------------------------|----------|----------|-----------------|------------------|------------|----------|
| <i>L. chinensis</i> | 569.71 ± | 526.96 ± | 0.57 ±0.18 | 0.034 ±0.022 | 3.27 ±1.36 | 316.42 ± |
| | 300.50 | 287.33 | | | | 190.04 |
| <i>L. huidobrensis</i> | 426.95 ± | 406.77 ± | 0.38 ±0.22 | 0.026 ±0.016 | 2.02 ±1.37 | 181.56 ± |
| | 289.73 | 272.75 | | | | 126.59 |
| <i>L. trifolii</i> | 399.31 ± | 365.67 ± | 0.46 ±0.13 | 0.029 ±0.016 | 2.39 ±0.87 | 185.07 ± |
| | 288.21 | 235.58 | | | | 101.59 |
| <i>L. sativae</i> | 428.23 ± | 385.22 ± | 0.46 ±0.14 | 0.035 ±0.038 | 2.41 ±1.01 | 193.90 ± |
| | 319.59 | 271.22 | | | | 129.73 |

Table S3 Network features of bacterial community of laboratory and wild leaf miners.

| Topological property | Laboratory | Wild |
|----------------------------|------------|----------|
| Edges | 425 | 257 |
| Positive edges | 344 | 257 |
| Negative edges | 81 | 0 |
| Vertices | 67 | 65 |
| Connectance | 0.192221 | 0.123558 |
| Average degree | 12.68657 | 7.907692 |
| Average path length | 2.435097 | 1.884861 |
| Diameter | 4.13294 | 3.859676 |
| Edge connectivity | 1 | 0 |
| Clustering coefficient | 0.716957 | 0.934223 |
| Clusters | 1 | 6 |
| Centralization degree | 0.247173 | 0.079567 |
| Centralization betweenness | 0.136181 | 0.042124 |
| Centralization closeness | 0.270383 | 0.007344 |

Table S4 Redundancy analysis (RDA) variation.

| Factors | Explained variation (%) | <i>F</i> | <i>p</i> |
|------------|-------------------------|----------|----------|
| Sex | 0.23 | 1.05 | 0.387 |
| Host plant | 1.10 | 2.61 | 0.001 |
| Location | 1.00 | 2.94 | 0.001 |
| Longitude | 2.33 | 12.70 | 0.001 |
| AMT | 1.90 | 7.83 | 0.001 |
| AP | 1.95 | 4.98 | 0.001 |
| Species | 1.17 | 3.90 | 0.001 |

AP: annual mean precipitation; AMT: annual mean temperature.

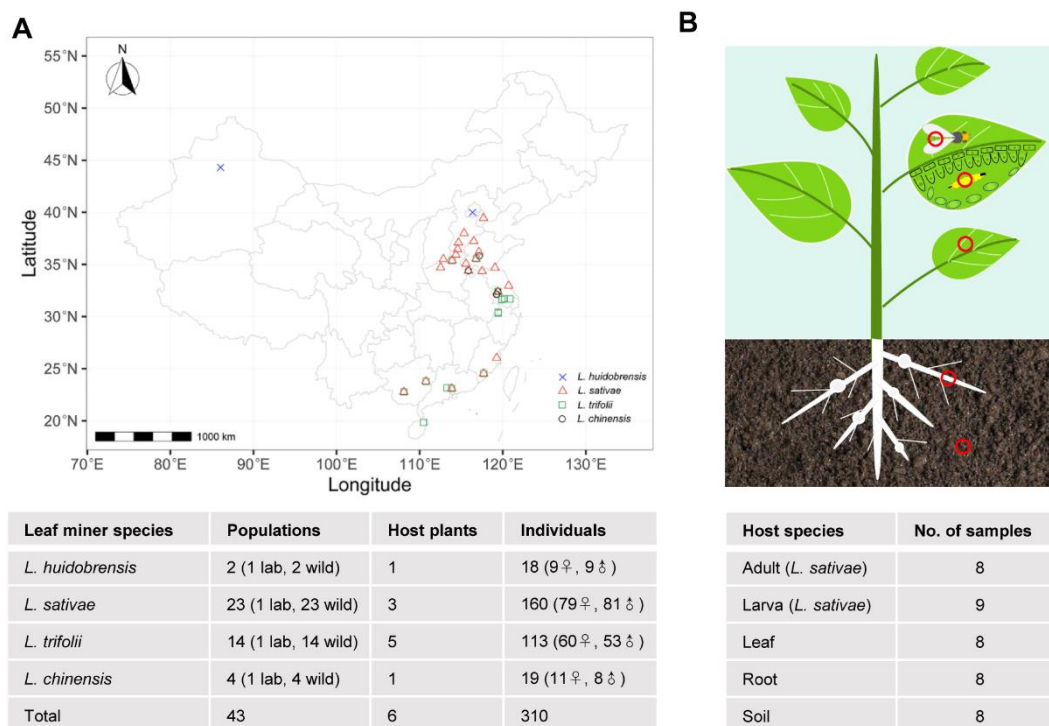


FIG S1 Experimental design. (A) Location of sampling sites across multiple geographic regions of China. A total of 310 individual samples associated with four leaf miner species, including *L. trifolii*, *L. sativae*, *L. chinensis* and *L. huidobrensis*, were collected from 43 populations and 6 host plant species. (B) Samples from the continuum of leaf miners and their associated with leaves, roots and soil. Detailed samples information corresponded in Table S1 in the Supplemental Material.

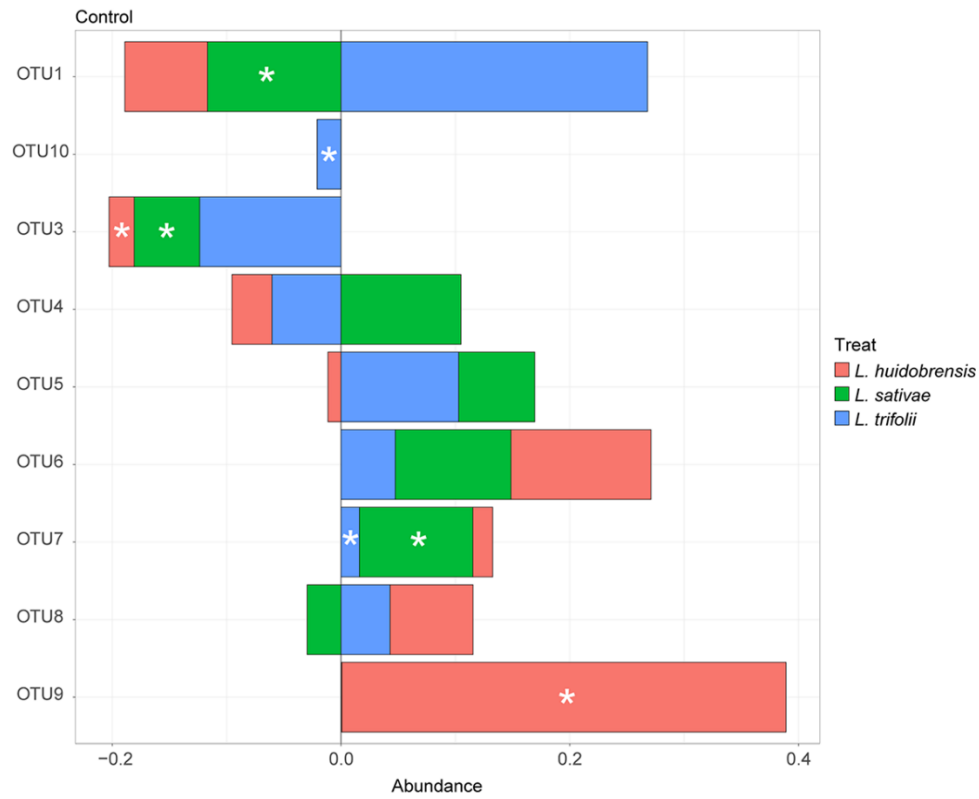


FIG S2 The significantly different OTUs between the native leaf miner *L. chinensis* and other three invasive leaf miners. “*” represents significant difference between each invasive leaf miner and the native leaf miner (Control) ($p < 0.05$).

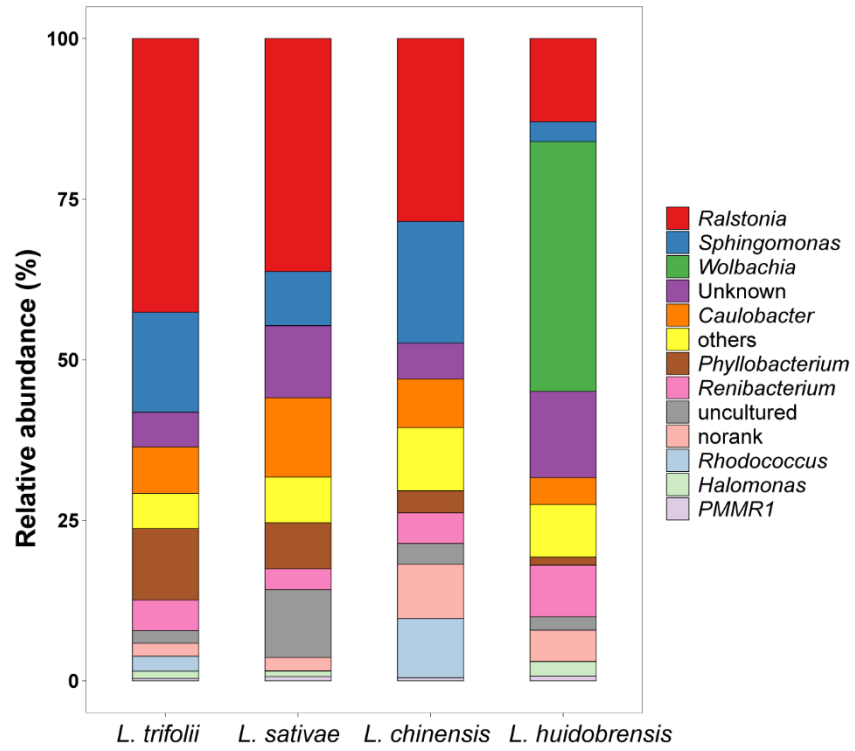


FIG S3 Relative abundance of each bacterial genus in different leaf miner species.

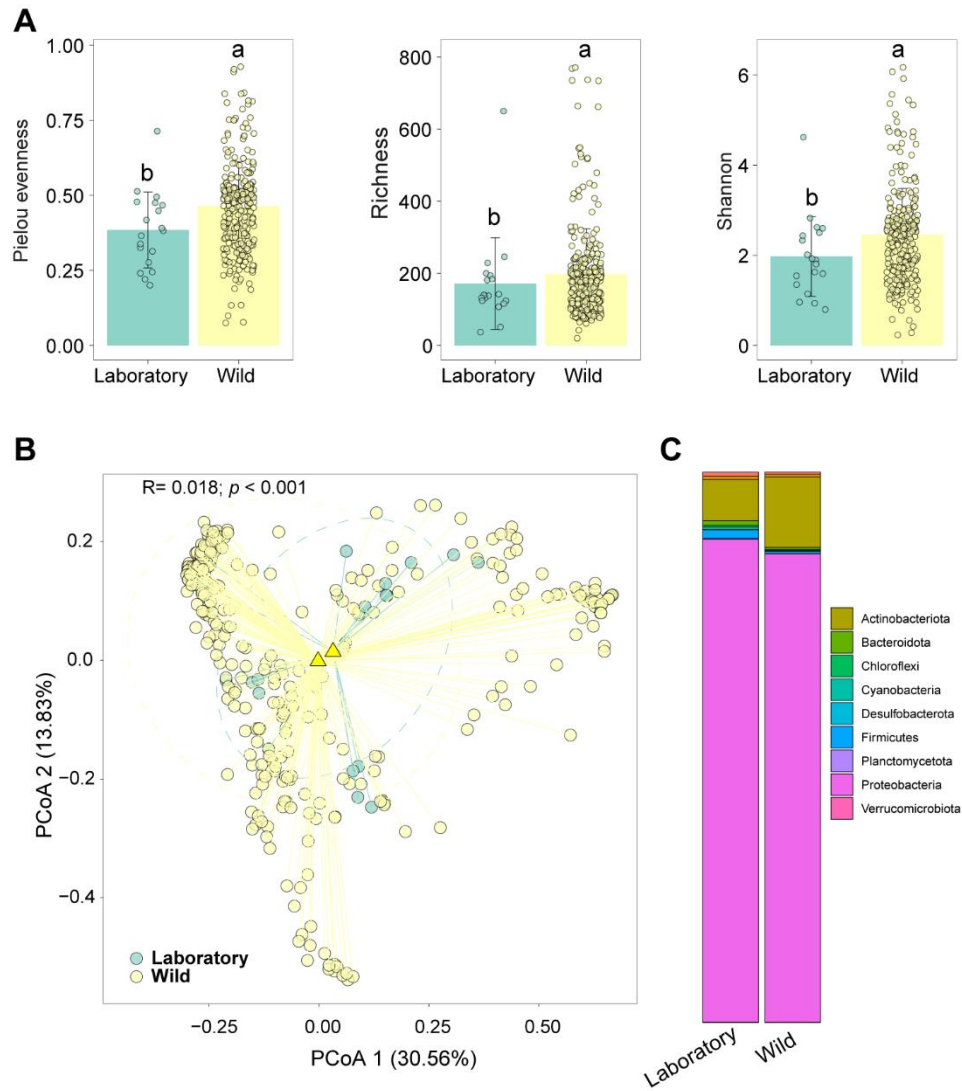


FIG S4 Comparison between the bacterial communities in laboratory-reared and wild leaf miner. (A) The alpha diversity indices (Pielou evenness, Shannon and Richness index) of the laboratory-reared and wild leaf miner bacterial communities. Different letters indicate significant differences between groups at a level of $p < 0.05$. (B) Principal coordinates analysis (PCoA) of bacterial community structure between the laboratory-reared and wild leaf miner. (C) The relative abundance of each bacterial phylum in the laboratory-reared and wild leaf miner.

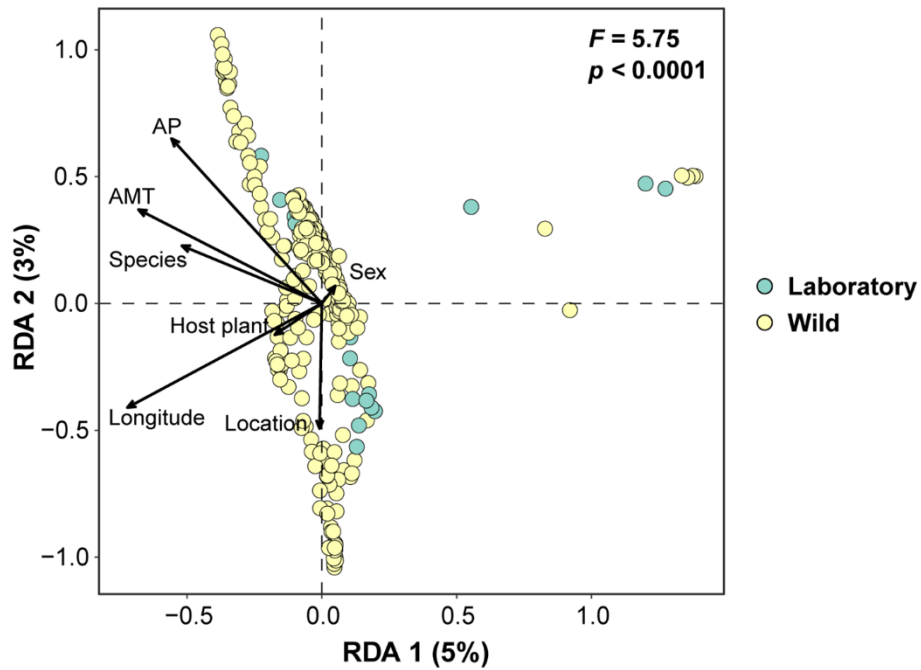


FIG S5 Redundancy analysis (RDA) highlighting correlations between multiple environmental factors and bacterial communities. AP: annual mean precipitation; AMT: annual mean temperature.

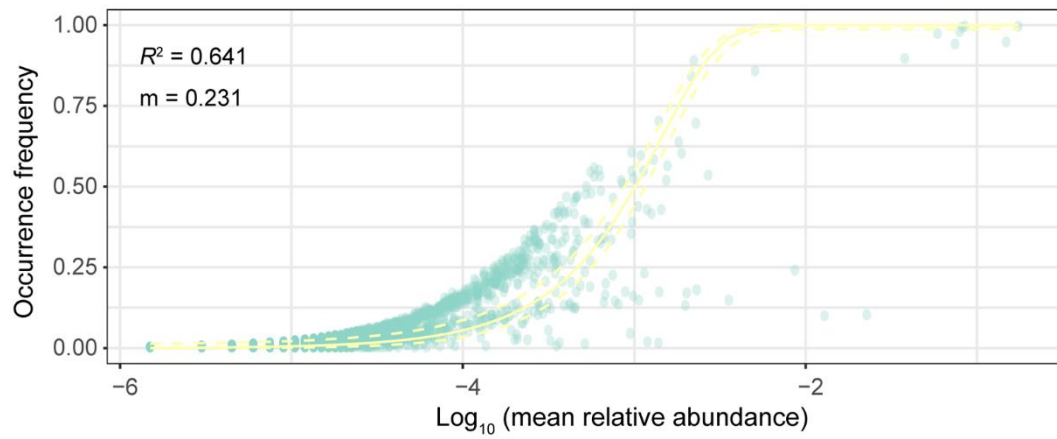


FIG S6 Fit of the neutral for 310 leaf miner samples. The yellow solid and dashed lines represent the predicted occurrence frequency and 95% confidence interval of the neutral model, respectively. m indicates the estimated migration rate and R^2 indicates the fit to the neutral model.

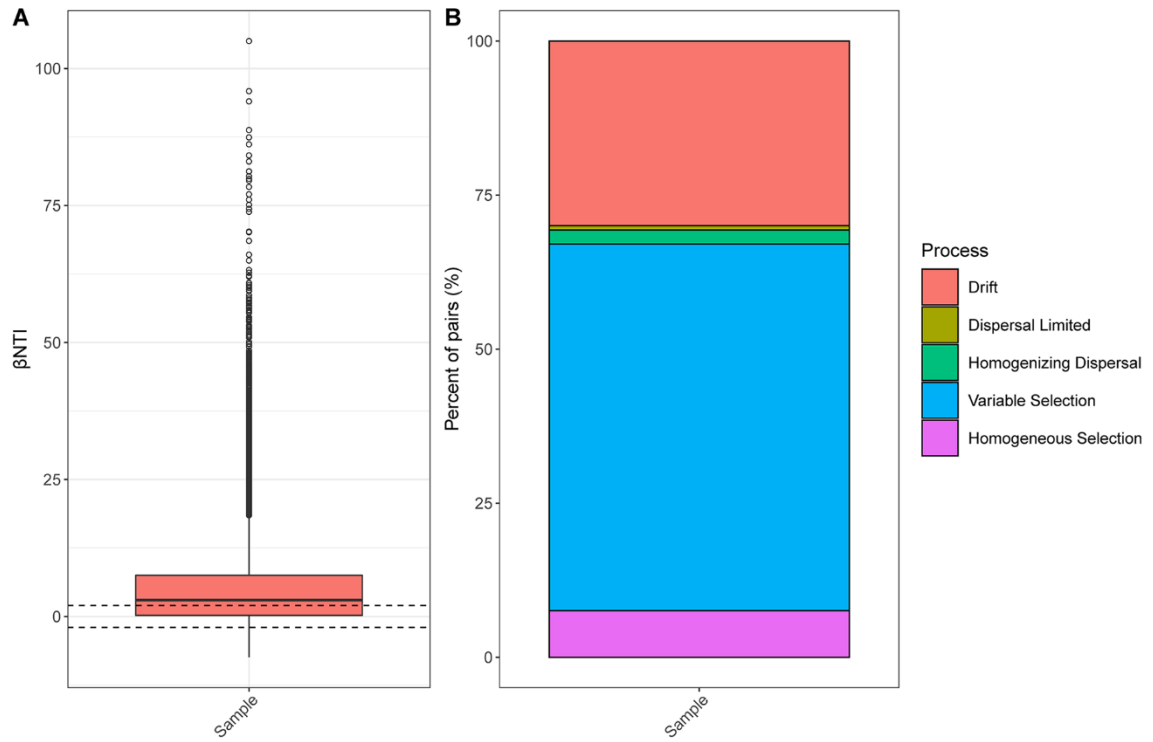


FIG S7 Ecological processes driving the assembly of bacterial communities in all samples. (A) Effects of deterministic (β NTI ≥ 2 or β NTI ≤ -2) and stochastic processes ($-2 < \beta$ NTI < 2) in shaping bacterial community in all samples. (B) The quantified major ecological processes in governing the microbial community.

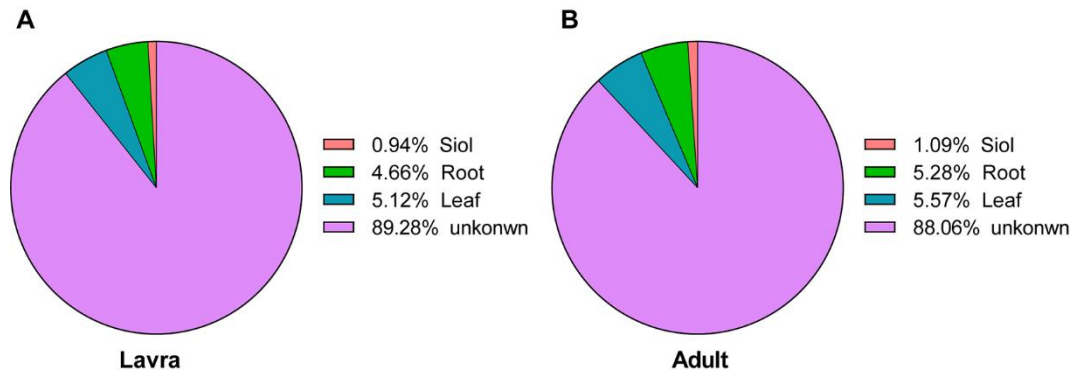


FIG S8 Source-tracking analysis of larva (A) and adult (B) of leaf miner microbes derived from leaf, root and soil.