Data from: Bee movement across heterogeneous tropical forests: multi-paternal genetic analyses reveal the importance of neighborhood composition for pollen-mediated gene flow

O'Connell, Megan C., The University of Texas at Austin

Castilla, Antonio R., University of Lisbon**,** The University of Texas at Austin

Lee, Leticia X., Boston University**,** The University of Texas at Austin

Jha, Shalene, The University of Texas at Austin

Citation

O'Connell, Megan C.; Castilla, Antonio R.; Lee, Leticia X.; Jha, Shalene (2018), Data from: Bee movement across heterogeneous tropical forests: multi-paternal genetic analyses reveal the importance of neighborhood composition for pollen-mediated gene flow, Dataset, https://doi.org/10.5061/dryad.j1344c7

Abstract

Animal pollination is critical for maintaining the reproduction and genetic diversity of many plant species, especially those in tropical ecosystems. Despite the threat to pollination posed by tropical deforestation, it remains an understudied process. In particular, little is known about these dynamics in multi-paternal, successional plant species whose fruits can contain substantial genetic diversity. Given the importance of successional plants in reforestation, quantifying the factors that impact their reproduction is essential for understanding plant gene flow in the context of global change. In this study, we investigated pollen-mediated gene flow

at the multi-paternal fruit level to quantify how tropical pollinators navigate and mediate gene flow in altered forests. Utilizing microsatellite genotyping and paternity analyses, we revealed that distinct plant neighborhood and individual factors drive pollen dispersal at the intra-fruit scale. Variance in pollen dispersal distances was greater for neighborhoods with higher conspecific density, indicating that density-dependent reproductive patterns play a role at this scale. Additionally, both the diversity of sires mediated by a single pollinator was affected by the size of the mother tree, i.e. larger mothers received pollen from a less diverse, less even pool of sires per fruit. Pollinator body size was not found to be a significant driver of pollen dispersal, indicating that both small and large-bodied pollinators were equally important pollen dispersers at this scale. By exploring patterns of variation at the intra-fruit level, we show that conspecific density and tree size significantly impact multi-paternal pollen-mediated gene flow, reinforcing the importance of investigating intraspecific, intra-individual variance in plant reproduction.

Usage Notes

PollenDispersal_SeedLevel

File lists identities of sires (as per Cervus paternity analyses) of several Miconia affinis seeds within individual fruits and the dispersal distance traveled by specific pollinator species between the sires and the mother trees where they deposited pollen.

PollenDispersal_MotherLevel

File includes data on study system independent variables per mother tree (1 fruit per mother tree), our calculations of the standard deviation, mean and maximum pollen dispersal distances, as well as our calculations of sire diversity and evenness per multi-paternal fruit.

Funding

References

This dataset is supplement to https://doi.org/10.1111/btp.12603

Location

🌐 Panama

Keywords

tropical deforestation, Trigona buyssoni, ecological variance, Trigona muzoensis, Melipona fuliginosa, Centris dichootricha, Density-dependence, pollinator body size, Miconia affinis, 2013, Trigona fulviventris, Trigona fuscipennis, Xylocopa fimbriata, Melipona panamica, Paratetrapedia lineata, Pollen-mediated gene flow, Pseudochloropsis schrottky, Tetragonisca angustula

Files

2 files for this dataset

PollenDispersal_MotherLevel.csv	5.32 kB	text/csv
PollenDispersal_SeedLevel.csv	24.38 kB	text/csv

License