

# Individual dietary specialization in a generalist bee varies across populations but has no effect on the richness of associated microbial communities

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## Overview

We examine the occurrence of individual specialization in a solitary bee species, *Ceratina australensis* in three different wild populations from Australia. We use data previously published by McFrederick and Rehan (2019) on metabarcoding of the pollen contents of *Ceratina* nests to characterize the plant, bacteria, and fungi present in each individual nest. We show that bee individuals have marked dietary specialization and that the level of specialization varies across populations. In the most specialized population, we also show that individuals' diet breadth was positively related to the richness of fungi, but not bacteria. Overall, individual specialization appeared to have a weak or negligible effect on the microbial richness of nests, suggesting that different mechanisms beyond environmental transmission may be at play regarding microbial acquisition in wild bees.

The analyses and data are in Zenodo and the github repo *ceratinaIndDiet*, and previously published sequence data are publicly available under NCBI/EMBL/DDBJ accession numbers SAMN08911168-SAMN08911424.

## Session Info

```
sessionInfo()
```

```
## R version 4.1.1 (2021-08-10)
## Platform: x86_64-pc-linux-gnu (64-bit)
## Running under: Ubuntu 20.04.3 LTS
##
## Matrix products: default
## BLAS: /usr/lib/x86_64-linux-gnu/blas/libblas.so.3.9.0
## LAPACK: /usr/lib/x86_64-linux-gnu/lapack/liblapack.so.3.9.0
##
## locale:
##  [1] LC_CTYPE=en_US.UTF-8      LC_NUMERIC=C
##  [3] LC_TIME=en_US.UTF-8      LC_COLLATE=en_US.UTF-8
##  [5] LC_MONETARY=en_US.UTF-8  LC_MESSAGES=en_US.UTF-8
##  [7] LC_PAPER=en_US.UTF-8     LC_NAME=C
##  [9] LC_ADDRESS=C             LC_TELEPHONE=C
## [11] LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C
##
## attached base packages:
## [1] stats      graphics  grDevices  utils      datasets  methods   base
```

```
##
## loaded via a namespace (and not attached):
## [1] compiler_4.1.1      magrittr_2.0.1      tools_4.1.1         htmltools_0.5.1.1
## [5] yaml_2.2.1          stringi_1.7.5       rmarkdown_2.10      knitr_1.33
## [9] stringr_1.4.0       xfun_0.25           digest_0.6.27       rlang_0.4.11
## [13] evaluate_0.14
```

## Data

Each line in the file `data.csv` relates to one individual nest (`inds`) from each of the three different populations (`pop`). The column `degree` refers to the total number of plant genera present in the nest (richness), `weighted.closeness` to the centrality of that individual in their network (as a measure of resource overlap among individuals), `psis` is the individual specialization (Schoener 1968; Roughgarden 1979; Zaccarelli, Bolnick, and Mancinelli 2013). We used the R packages `bipartite` (Dormann, Gruber, and Fründ 2008) to calculate centrality and `RInSp` (Zaccarelli, Bolnick, and Mancinelli 2013) to calculate specialization. The next six columns refer to the richness of bacteria and fungi associated to the pollen, in three different rarefaction depths (see Methods and Online Supplement for details).

```
## # A tibble: 38 x 11
##   inds pop degree weighted.closeness psis bact.rich bact.rich.2
##   <chr> <chr> <dbl> <dbl> <dbl> <dbl> <dbl>
## 1 Q116 Q      14      0.0954 0.530    35.0    30.0
## 2 Q119 Q      12      0.113 0.647    NA      NA
## 3 Q31 Q       13      0.0968 0.577    42.2    34.4
## 4 Q36 Q       8       0.121 0.817    15.8    14.3
## 5 Q55 Q       6       0.136 0.391    21.3    19.4
## 6 Q74 Q       5       0.121 0.640    40.5    33.3
## 7 Q77 Q       9       0.128 0.602    NA      NA
## 8 Q89 Q       5       0.126 0.369    35.8    31.3
## 9 Q94 Q       7       0.131 0.742    48.5    37.6
## 10 S104 S       7       0.0593 0.493    21.7    19.1
## # ... with 28 more rows, and 4 more variables: bact.rich.notrare <dbl>,
## #   fungi.rich <dbl>, fungi.rich.2 <dbl>, fungi.rich.notrare <dbl>
```

## Code

The script `analysis.R` loads the data file above and details the statistical analysis and recreates the plots from the main text.

## References

- Dormann, C., B. Gruber, and J. Fründ. 2008. “Introducing the Bipartite Package: Analysing Ecological Networks.” *R News* 8: 8.
- McFrederick, Quinn S, and Sandra M Rehan. 2019. “Wild Bee Pollen Usage and Microbial Communities Co-Vary Across Landscapes.” *Microbial Ecology* 77 (2): 513–22.
- Roughgarden, Joan. 1979. *Theory of Population Genetics and Evolutionary Ecology: An Introduction*.
- Schoener, Thomas W. 1968. “The Anolis Lizards of Bimini: Resource Partitioning in a Complex Fauna.” *Ecology* 49 (4): 704–26.
- Zaccarelli, Nicola, Daniel I Bolnick, and Giorgio Mancinelli. 2013. “RI n s p: An r Package for the Analysis of Individual Specialization in Resource Use.” *Methods in Ecology and Evolution* 4 (11): 1018–23.