

The social dimension of microbial niches

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▶ To cite this version:

Emilie Muller. The social dimension of microbial niches. Nature Ecology & Evolution, 2023, 10.1038/s41559-023-02020-0. hal-04064424

HAL Id: hal-04064424

https://hal.science/hal-04064424

Submitted on 27 Oct 2023

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1 Microbial ecology: The social dimension of microbial niches 2 3 **Author** 4 Emilie E.L. MULLER 5 Equipe Adaptations et Interactions Microbiennes dans l'Environnement, Université de Strasbourg, 6 UMR 7156 UNISTRA-CNRS, Génétique Moléculaire, Génomique, Microbiologie, Strasbourg, France 7 8 Corresponding author: Emilie E.L. MULLER: emilie.muller@unistra.fr 9 10 Standfirst: For long, the ecological niche concept was less popular for microbes than for other 11 organisms. A new proxy of a microorganisms's ecological niche breadth, based on the variability of 12 the communities it associates with, allows interrogation of the correlates of being a social generalist 13 or social specialist. 14 15 16 Main text: 17 18 Species vary in the range of abiotic and biotic conditions that they can cope with; generalist species 19 can thrive in a variety of habitats or situations, while specialists are restricted to a smaller set of 20 conditions. Microbes vary on this continuum as well, with generalists (e.g. most of our heavily 21 studied cultivable model bacteria) having a wider ecological niche and specialists like strict 22 endosymbiotic bacteria, having a narrower on 1. Defining an organism's niche requires a solid 23 understanding of the conditions in which it persists. This is hard enough for larger and better-studied 24 organisms, and feels nearly impossible for the microbial world, for which micrometre scale conditions 25 and interactions matter. Fortunately, the era of DNA sequencing derived from environmental samples 26 has changed the game – so what can we learn about microbial niches from the thousands of available 27 datasets? Writing in Nature Ecology & Evolution, Von Meijenfeldt et al ² define one aspect of the 28 microbial niche, the "social niche", reflecting how much is constrained the community of other 29 microbes the species is observed with in environmental samples. 30 Some microbial species occur in a variety of compositionally dissimilar communities, while some 31 other always share their surroundings with a consistent suite of other microorganisms. The authors 32 classified over 20'700 microbial taxa from all ranks along a gradient based on their Social Niche 33 Breadth (SNB) and examined genomic correlates of being a social specialist versus a social generalist 34 species. The SNB is defined as the mean of the pairwise compositional dissimilarity between the 35 samples in which a taxon is found (Fig. 1). The rationale for using the SNB score as a proxy of 36 ecological niche breadth is that the broader are the environmental conditions a species can cope 37 with, the more likely it is to share its habitat with a wide array of other species. This thinking has already been used for plants and animals ^{3,4}. 38 Von Meijenfeldt et al ² computed SNB scores for every known prokaryote taxon from over 22 39 40

thousand published environmental samples. Importantly, the SNB score can be calculated at any

41 taxonomical rank level, from phylum to species; this taxonomic distinction allows them to show that

42 higher taxonomic levels that are social generalists can contain subtaxa that include either social

generalists or specialists. For example, the family *Flavobacteriaceae* is a social generalist, but the

44 clade contains daughter taxa that are mostly social specialist genera. On the other hand, the social

45 generalist Lactobacillaceae contains many social generalist genera. This suggests numerous and

independent social specialization or niche range expansion throughout evolution.

The study also explores the various ecological properties of being a microbial social generalist or a social specialist. Notably, social specialists have a relatively even abundance across samples in which they appear, whereas social generalists tend to locally dominate the communities but with a more variable relative abundance across samples. This result supports the hypothesis that social specialists have a low but constant abundance near carrying capacity (K-selected), and some social generalists

are opportunistic taxa that reach high relative abundance when circumstances permit (r-selected)^{5,6}.

Secondly, the SNB score was correlated with genomic properties, such as genome size and additional related features (i.e., the number of nucleotides, of genes, or of unique functions, as well as genome size variation within the genus, pan-genome size and openness). Indeed, a number of recent studies support the theoretical association between genome size and niche breadth, with ecological generalists having larger genome to adapt to diverse conditions and specialists having reduced genome due the loss of unnecessary genes⁷. Here, the authors found no direct correlation between genome size and SNB score, but the genomes of social generalists were found to be more variable in size than the genomes of social specialists that encode for a smaller and more closed pan-genome. These properties point to an increased genomic fluidity of social generalists, as confirmed by their enrichment in invasive mobile elements (plasmids, phages), highlighting a possible mechanism by which social generalists keep open pan-genomes.

In addition, social specialists are overall enriched in fewer gene categories than social generalists. This is because the functional genes kept during specialization depend on the conditions encounter by the taxon. The analysis also demonstrates different properties of social specialists typically found in communities of low or high biodiversity, with high-diversity specialists having more enriched functions. Overall, the authors suggest that social specialization comes in many forms in the microbial world.

Future work will need to test how SNB scores compare to other niche breadth metrics (e.g. based on genomics⁸). How much will the metric be adopted. and contributory to the scientific community – being either "specialists" research groups focused on specific taxa or habitats, or "generalists" driven by general questions in microbial ecology? Most importantly, one can look forward to seeing how the SNB score will improve ecosystem fate predictions ⁹ by understanding ecological properties (e.g. invasion and colonization capacity, ecological relationships such as competition or mutualism, resistance and resilience to perturbations, etc) of studied taxa or communities in order to promote our overall understanding of microbial ecology.

Competing Interests

The author declares no competing interests.

References

- 1. Bell, T. H. & Bell, T. Many roads to bacterial generalism. FEMS Microbiology Ecology 97, fiaa240
- 85 (2021).

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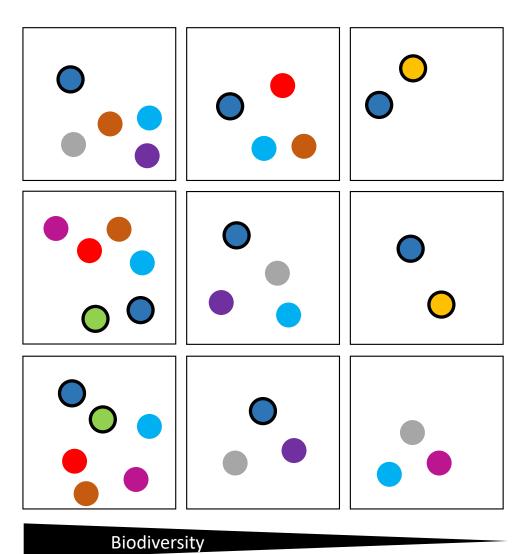
- 2. Bastiaan von Meijenfeldt, Hogeweg, P. & Dutilh, B. E. On specialists and generalists: niche range
- 87 strategies across throughout the tree of life.
- 88 3. Ducatez, S., Tingley, R. & Shine, R. Using species co-occurrence patterns to quantify relative
- habitat breadth in terrestrial vertebrates. *Ecosphere* **5**, art152 (2014).
- 90 4. Fridley, J. D., Vandermast, D. B., Kuppinger, D. M., Manthey, M. & Peet, R. Ksp. Journal of Ecology
- 91 **95**, 707–722 (2007).
- 92 5. Andrews, J. H. & Harris, R. F. r- and K-Selection and Microbial Ecology. in Advances in Microbial
- 93 Ecology (ed. Marshall, K. C.) 99–147 (Springer US, 1986). doi:10.1007/978-1-4757-0611-6_3.
- 94 6. Pianka, E. R. On r- and K-Selection. The American Naturalist 104, 592–597 (1970).
- 95 7. Beier, S., Werner, J., Bouvier, T., Mouquet, N. & Violle, C. Trait-trait relationships and tradeoffs
- vary with genome size in prokaryotes. Frontiers in Microbiology 13, (2022).
- 97 8. Herold, M. et al. Integration of time-series meta-omics data reveals how microbial ecosystems
- 98 respond to disturbance. Nat Commun 11, 5281 (2020).
- 99 9. Muller, E. E. L. Determining Microbial Niche Breadth in the Environment for Better Ecosystem Fate
- 100 Predictions. *mSystems* **4**, e00080-19 (2019).

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- 104 Figure 1. Community composition similarity as a quantitative ecological feature of the microbial
- w social niche ». The graphic is a simplified depiction of how von Meijenfeldt et al² determined
- 106 microbes' Social Niche Breadth (SNB). The squares represent independent environmental samples
- 107 (from published datasets), comprised of several microbial taxa depicted as colored circles. The dark
- 108 blue microbe occurs in compositionally very dissimilar communities across the different samples; its
- 109 SNB score would be high and thus considered a social generalist. The yellow microbe always occurs
- 110 with the same dark blue taxon; its SNB score would be low and it should be considered a social
- specialist. Social specialists can be found in either low-diversity samples, like the yellow microbe, or in
- 112 high-diversity samples, like the green microbe, which is always found in samples with the same
- 113 composition.



- Environmental sample
- A microbial taxon
- A low-diversity social specialist
- A high-diversity social specialist
- A social generalist