

SUMMARY OF THE STUDY: Hernandez-Gomez et al. test if habitat type (dominant tree species) is associated with changes in either soil or salamander bacterial communities. They sampled bacterial communities from the salamander *Batrachoseps attenuates* and soil from two habitat types: native oak-dominated compared with invasive eucalyptus-dominated sites. Soil bacterial community composition differed between habitat types (although there is some confusion here, see below), but alpha diversity and dispersion of community composition did not differ. In contrast the salamander skin microbiome differed in alpha diversity and dispersion but community composition was similar between habitat types. The proportion of ASVs from salamanders that were also found in both salamander and soil did not differ between habitat types. Salamander microbiome composition covaried with geographic distance (Mantel test). Salamander body condition (mass-length residual) was lower in eucalyptus-dominated sites. Overall, the results show that native- and invasive-dominated habitats correspond to differences in environmental and salamander-associated microbial communities as well as salamander body condition.

GENERAL ASSESSMENT: Many studies have surveyed amphibian skin bacteria, but the comparison between habitats dominated by native versus invasive plants is novel. The finding that salamander and soil bacterial communities showed nearly opposite patterns with respect to habitat type was interesting because it suggests that the effect of habitat type on the microbiome was mediated by factors other than simply the environmental bacterial pool. This paper is exceptionally well written, thorough, clear, and concise. The methods section is detailed and transparent. The discussion is thoughtful and consistent with the results. The study itself was well designed and rigorous. I much appreciate the authors' attention to the quality of their manuscript because it made my job as a reviewer simpler and will no doubt be appreciated by readers as well. I recommend that this paper be accepted with minor revisions. Below are a few specific questions/comments.

The results show a significant effect of habitat type on soil bacterial community composition (PERMANOVA $p < 0.05$ for effect of habitat type for all three beta diversity metrics, L278), but the rest of the paper (abstract, discussion, and title of results section L. 274) claim there was no effect. Please clarify.

Based on the finding that the proportion of salamander ASV's that were also found in soil was similar between oak and eucalyptus habitats, the authors conclude that host-filtering of environmental bacteria does not differ between sites. I wasn't quite convinced of this interpretation of the data. The host-environment filter could differ in which taxa are selected, even if the total proportion of taxa that overlap between host and environment is the same. Also, a proportion (count) of taxa doesn't account for differences in abundances. The authors might consider calculating the Unifrac (and/or Bray Curtis) distance between each soil sample and its corresponding amphibian sample(s), and testing if that distance differs by habitat type. Alternatively, they could simply qualify their conclusion about host-environment filtering. ((L. 329-332, 353. "We observed no differences in the soil microbial communities between *Eucalyptus* and *Quercus* dominated sites and a similar proportion of salamander skin microbes shared with their environment. Thus, the filter acting on microbial richness is likely operating at the host level, rather than the passive uptake of different soil microbial communities.")

The analyses of whole-community metrics (e.g. composition, alpha diversity) are excellent and thorough. However, there are no analyses to determine which ASVs differ between salamander and soil or between habitat types. Sometimes individual taxa show interesting patterns even in the absence of whole-community differences. If there are compelling reasons not to identify ASVs that differ among treatments, please state. Otherwise, I suggest including basic analysis - it need not be a central focus of the paper, and can be as simple as one additional sentence in the methods and results sections, and a supplemental table. These types of tests are admittedly exploratory due to the compositional nature of relative abundance data, but the information is still valuable to future research, either as context or as a jumping-off point for deeper investigations.

Minor comments:

How did you decide on 70% as the criterion to define core ASV's?

L. 106 – what is meant by ‘discrete but intersperse’? From the map, it looks like Eucalyptus sites cluster away from Native sites.

L. 138 – Do you mean that the manufacturer provides different protocols for swab and soil samples?

L. 212 – It looks like site is random in the models of alpha diversity but fixed for PERMANOVA. Why is that?

L. 275 – write out “likelihood ratio test” the first time you use the abbreviation.

L. 317 – how do you define “rare”?

L. 417 I didn't see analyses correlating body condition with skin microbiome. As far as Bd infection goes, I don't think one could conduct a valid analysis here since there was only one Bd-positive swab in the entire study.