

Multi-stress responses depend on the microbiome in the planktonic crustacean *Daphnia*

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The critical role that gut microbiota play in many aspects of an animal's life, including pathogen resistance, detoxification, digestion, and nutritional physiology, is becoming more and more apparent (Engel and Moran 2013; Lindsay et al., 2020). Gut microbiota recruitment and maintenance can be largely affected by the surrounding environment (Chandler et al., 2011; Callens et al., 2020). The environment may thus dictate gut microbiota composition and diversity, which in turn can affect organismal responses to stress. Only few studies have, however, taken the gut microbiota into account to estimate life histories in response to multiple stressors in aquatic systems (Macke et al., 2016).

Houwenhuysse et al., investigate how the microbiome affects life histories in response to ecologically relevant single and multiple biotic stressors (an oomycete-like parasite, and a toxic cyanobacterium) in *Daphnia magna* (Houwenhuysse et al., 2023). *Daphnia* is an excellent model, because this aquatic system lends itself extremely well for gut microbiota transplantation and manipulation. This is due to the possibility to sterilize eggs (making them free of bacteria), horizontal transmission of bacteria from the environment, and the relative ease of culturing genetically similar *Daphnia* clones in large numbers.

The authors use an elegant experimental design to show that the *Daphnia* gut microbial community differs when derived from a laboratory versus natural inoculum, the latter being more diverse. The authors subsequently show that key life history traits (survival, fecundity, and body size) depend on the stressors (and combination thereof), the microbiota (structure and diversity), and *Daphnia* genotype. A key finding is that *Daphnia* exposed to both biotic stressors show an antagonistic interaction effect on survival (being higher), but only in individuals containing laboratory gut microbiota. The exact mechanism remains to be determined, but the authors propose several interesting hypotheses as to why *Daphnia* with more diverse gut microbiota do less well. This could be due, for example, to increased inter-microbe competition or an increased chance of contracting opportunistic, parasitic bacteria. For *Daphnia* with less diverse laboratory gut microbiota, a monopolizing species may be particularly beneficial for stress tolerance. Alongside these interesting findings, the paper also provides extensive information about the gut microbiota composition (available in the supplementary files), which is a very useful resource for other researchers.

Overall, this study reveals that multiple, interacting factors affect the performance of *Daphnia* under stressful conditions. Of importance is that laboratory studies may be based on simpler microbiota systems, meaning that stress responses measured in the laboratory may not accurately reflect what is happening in nature.

References

- Callens M, De Meester L, Muylaert K, Mukherjee S, Decaestecker E. The bacterioplankton community composition and a host genotype dependent occurrence of taxa shape the *Daphnia magna* gut bacterial community. *FEMS Microbiology Ecology*. 2020;96(8):fiae128. <https://doi.org/10.1093/femsec/fiae128>
- Chandler JA, Lang JM, Bhatnagar S, Eisen JA, Kopp A. Bacterial communities of diverse *Drosophila* species: ecological context of a host-microbe model system. *PLOS Genetics*. 2011;7(9):e1002272. <https://doi.org/10.1371/journal.pgen.1002272>
- Engel P, Moran NA. The gut microbiota of insects - diversity in structure and function. *FEMS Microbiology Reviews*. 2013;37(5):699-735. <https://doi.org/10.1111/1574-6976.12025>
- Houwenhuyse S, Bulteel L, Vanoverberghe I, Krzynowek A, Goel N et al. Microbiome mediated tolerance to biotic stressors: a case study of the interaction between a toxic cyanobacterium and an oomycete-like infection in *Daphnia magna*. 2023. *Peer Community in Zoology*. <https://doi.org/10.31219/osf.io/9n4mg>
- Lindsay EC, Metcalfe NB, Llewellyn MS. The potential role of the gut microbiota in shaping host energetics and metabolic rate. *Journal of Animal Ecology*. 2020;89(11):2415-2426. <https://doi.org/10.1111/1365-2656.13327>
- Macke E, Tasiemski A, Massol F, Callens M, Decaestecker E. Life history and eco-evolutionary dynamics in light of the gut microbiota. *Oikos*. 2017;126(4):508-531. <https://doi.org/10.1111/oik.03900>