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Inbreeding constrains adaptive capacity and microbiome diversity

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The consequences of a reduction in population size commonly experienced by threatened species are normally interpreted in terms of loss of genetic variation, increased inbreeding, and associated inbreeding depression and reduced adaptive potential. However, large-scale empirical studies testing consequences of population genetic bottlenecks on genome-wide variation and evolutionary adaptation are surprisingly scarce. Also, it is becoming increasingly clear that microbial symbionts may play a so-far underappreciated role in conservation biology/genetics, as fitness effects of host population bottlenecks might also be mediated through the host microbiome diversity. Here we present results from an evolution experiment with 120 lines of *Drosophila melanogaster* having experienced inbreeding caused by low population size for a variable number of generations. Genetic variation in inbred lines and in outbred control lines was assessed by genotyping-by-sequencing (GBS). All lines were subsequently reared on a novel stressful medium for 10 generations during which egg-to-adult viability, body mass, productivity, and extinctions were scored. We found strong positive correlations between levels of genetic variation and evolutionary response in all investigated traits. We also found that lines with lower genetic diversity were at greater risk of extinction. Secondly, we amplified the bacterial 16S rRNA gene in a subset of the lines and found that host population bottlenecks constrained microbiome richness and diversity, with interacting effects of host genetic variation and microbial diversity on host fitness. Combined, this work presents convincing support for long-standing evolutionary theory, while providing novel insights about how population bottlenecks reduce hologenomic variation (combined host and microbial genetic variation). Thus, while the current biodiversity crisis typically focus on population sizes and genetic variation of eukaryotes, an additional focal point should be the microbial diversity carried by these hosts, which in turn may influence host fitness and adaptability and ultimately the persistence of populations.