

# Hologenomic insights into the biology of invasive and endangered fishes in Mediterranean wetlands

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## Abstract

Freshwater habitats are under increasing pressure from numerous anthropogenic forces, including the introduction of alien species capable of altering ecosystems and threatening native species. Although alien species themselves are likely to experience loss of genetic diversity when colonising novel environments, some manage to become invasive, suggesting that other factors might facilitate their adaptive capacity. Using a hologenomic approach, we elucidate population genomic trends, the gut microbiota composition and genome-environment-microbiota interaction in the endemic and endangered Spanish toothcarp (*Aphanius iberus*) and the highly invasive Eastern mosquitofish (*Gambusia holbrooki*). We found clear genetic signatures of captive breeding in the populations of *A. iberus*, while *G. holbrooki* are characterised by an overall low level of heterozygosity and likely signs of multiple introductions. Gut microbial communities of the two species differed significantly across locations, but no sign of increased microbial plasticity was detected in *G. holbrooki*. However, we report that the genetic profile of each fish was able to explain a considerable part of the microbiota variation measured across individuals. Using shotgun metagenomics, we observed an overall high functional capacity of the microbiota in both species, but we identified no significant differences in the functional capacity between them. The role of the gut microbiota in invasive species and conservation warrant further research using direct comparisons or controlled mesocosm setups, but based on the results of the current study, the gut microbiota of invasive species

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