

Horizontal gene transfer to a defensive symbiont with a reduced genome in a multipartite beetle microbiome.

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Abstract

Symbiotic mutualisms of bacteria and animals are ubiquitous in nature, running a continuum from facultative to obligate from the perspectives of both partners. The loss of functions required for living independently but not within a host gives rise to reduced genomes in many symbionts. Although the phenomenon of genome reduction can be explained by existing evolutionary models, the initiation of the process is not well understood. Here, we describe the microbiome associated with the eggs of the beetle *Lagria villosa*, consisting of multiple bacterial symbionts related to *Burkholderia gladioli*, including a reduced-genome symbiont thought to be the exclusive producer of the defensive compound lagriamide. We show that the putative lagriamide-producing symbiont is the only member of the microbiome undergoing genome reduction and that it has already lost the majority of its primary metabolism and DNA repair pathways. The key step preceding genome

reduction in the symbiont was likely the horizontal acquisition of the putative lagriamide lga biosynthetic gene cluster. Unexpectedly, we uncovered evidence of additional horizontal transfers to the symbiont's genome while genome reduction was occurring and despite a current lack of genes needed for homologous recombination. These gene gains may have given the genome-reduced symbiont a selective advantage in the microbiome, especially given the maintenance of the large lga gene cluster despite ongoing genome reduction. **IMPORTANCE** Associations between microorganisms and an animal, plant, or fungal host can result in increased dependence over time. This process is due partly to the bacterium not needing to produce nutrients that the host provides, leading to loss of genes that it would need to live independently and to a consequent reduction in genome size. It is often thought that genome reduction is aided by genetic isolation-bacteria that live in monocultures in special host organs, or inside host cells, have less access to other bacterial species from which they can obtain genes. Here, we describe exposure of a genome-reduced beetle symbiont to a community of related bacteria with nonreduced genomes. We show that the symbiont has acquired genes from other bacteria despite going through genome reduction, suggesting that isolation has not yet played a major role in this case of genome reduction, with horizontal gene gains still offering a potential route for adaptation.

Beteiligte Forschungseinheiten

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