

UC Merced

UC Merced Previously Published Works

Title

A complex interplay of evolutionary forces continues to shape ancient co-occurring symbiont genomes

Permalink

<https://escholarship.org/uc/item/5562c5vk>

Journal

iScience, 26(1)

ISSN

2589-0042

Authors

Vasquez, Yumary M

Bennett, Gordon M

Publication Date

2023

DOI

10.1016/j.isci.2022.105810

Copyright Information

This work is made available under the terms of a Creative Commons Attribution-NonCommercial-NoDerivatives License, available at

<https://creativecommons.org/licenses/by-nc-nd/4.0/>

Peer reviewed

Correction

A complex interplay of evolutionary forces continues to shape ancient co-occurring symbiont genomes

Yumary M. Vasquez* and Gordon M. Bennett*

(iScience 25, 104786; August 19, 2022)

In the original version of this article, genes annotated as being lost in the genomes of the *Nesophrosyne* Hawaiian leafhopper symbionts "*Candidatus* *Sulcia muelleri*" and "*Ca. Nasuia deltocephalinicola*" are actually present. Several of these genes, particularly in *Nasuia*, were not recognized by initial annotation efforts and software packages. The authors revised their annotation approach and manually inspected each identified loss for further annotation inference errors. Following reannotation of these gene regions, the authors updated their gene loss and retention counts and revised Figures 1 and 2 to reflect these new data and results. The discussion section of the original text related to the inferred loss of the following genes no longer applies: *Sulcia* (*rpsO*, *pheT*, *rbfA*, *infC*) and *Nasuia* (*rsmD*, *rpmJ*, *rpmG*, *rpsQ*, *rpsS*, *SCO2*, *hisD*). The authors confirm that this does not impact the scientific message of the paper, as convergent and unique gene loss still occurs in closely related species. The authors apologize for any inconvenience caused to the readers. The authors cordially invite others to continue to check and reproduce scientific work. The authors thank Dr. Alejandro Manzano Marín for pointing out these errors to us, as well as pointing out the methodological errors that can result in these kinds of mis-annotations. The methodological problems leading to these kinds of mis-annotations may be common in other such comparative genomic work for tiny A+T nucleotide rich symbiont genomes.

*Correspondence:

yvasquez8@ucmerced.edu

(Y.M.V.),

gbennett2@ucmerced.edu

(G.M.B.)

<https://doi.org/10.1016/j.isci.2022.105810>

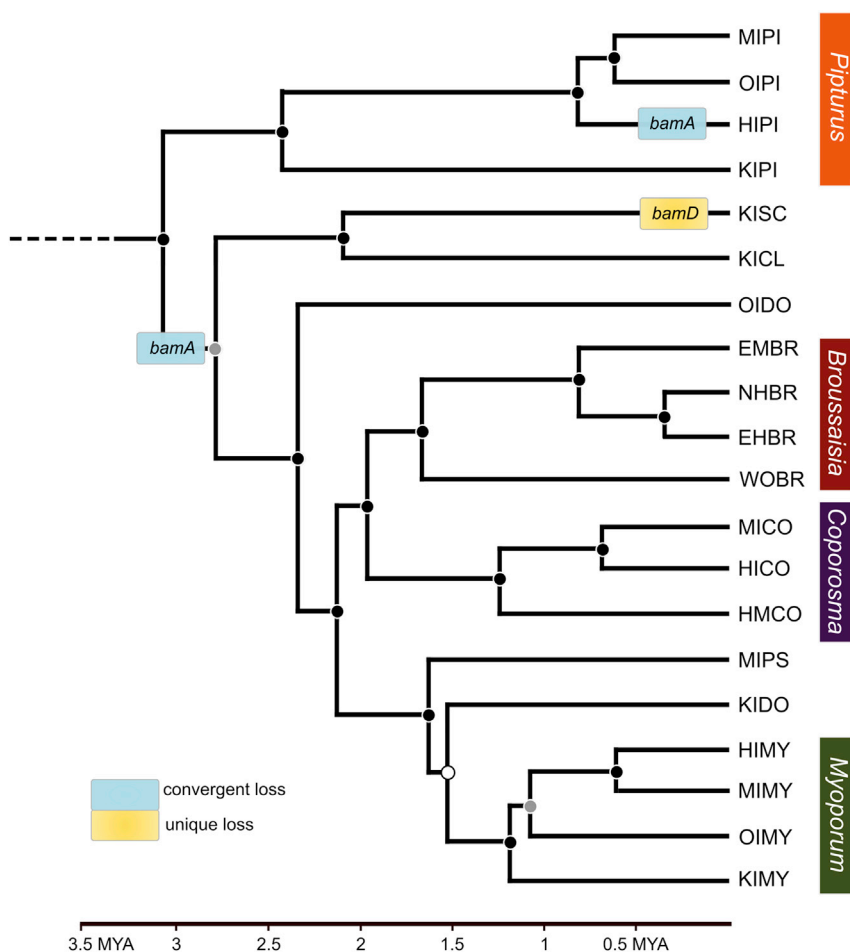


Figure 1. Convergent and unique gene loss among *Sulcia* genomes from endemic Hawaiian leafhoppers (*Nesophrosyne*) (corrected)

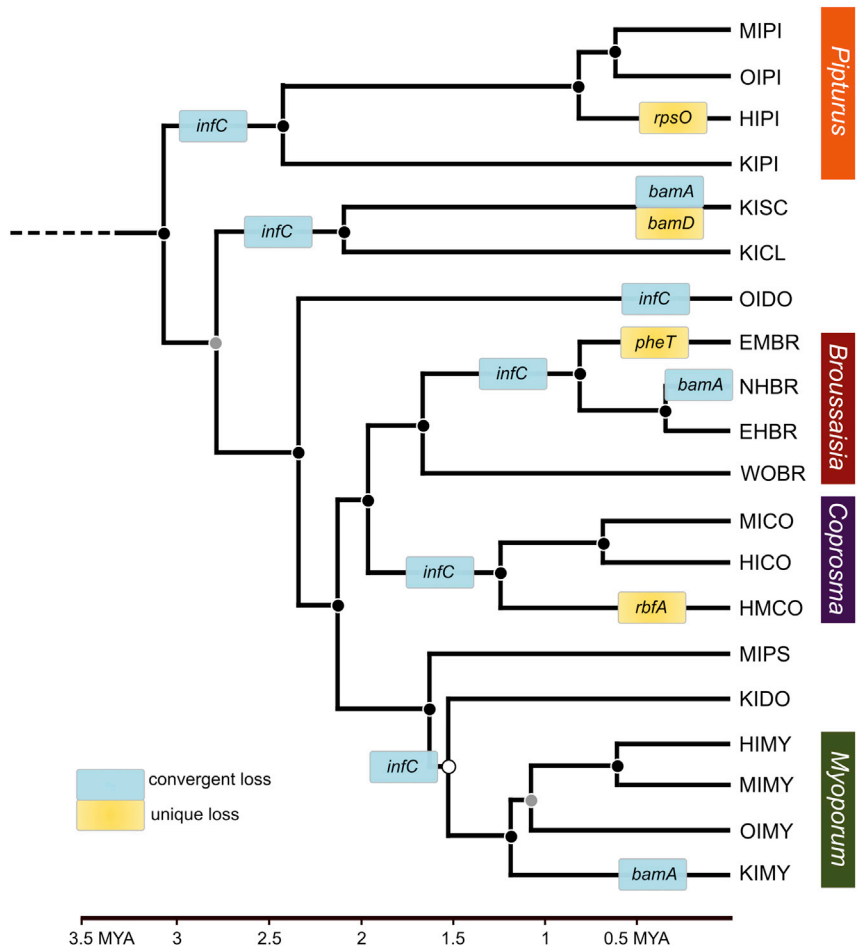


Figure 1. Convergent and unique gene loss among *Sulcia* genomes from endemic Hawaiian leafhoppers (*Nesophrosyne*) (original)

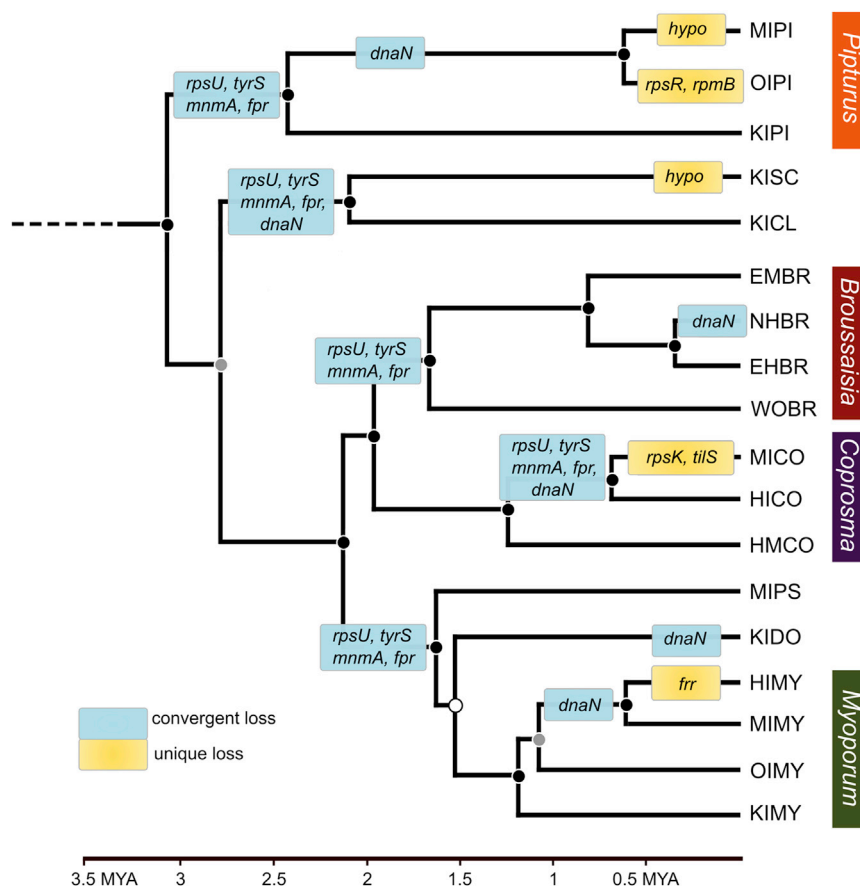


Figure 2. Convergent and unique gene loss among *Nasuia* genomes from endemic Hawaiian leafhoppers (*Nesophrosyne*) (corrected)

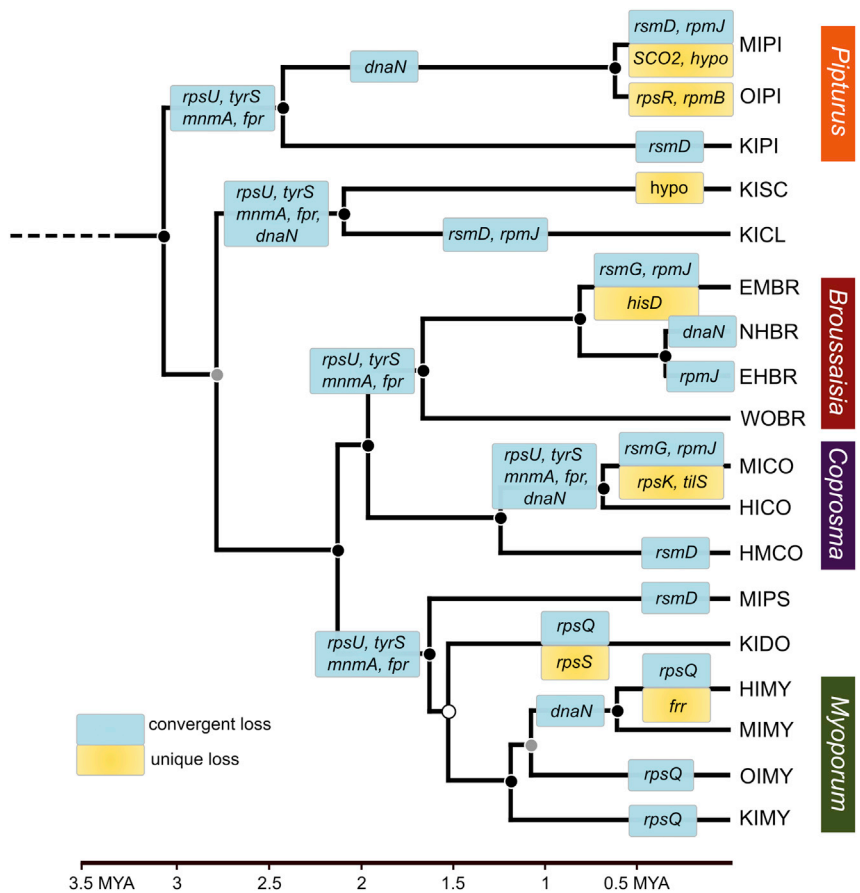


Figure 2. Convergent and unique gene loss among *Nasuia* genomes from endemic Hawaiian leafhoppers (*Nesophrosyne*) (original)