

A new symbiotic lineage related to *Neisseria* and *Snodgrassella* arises from the dynamic and diverse microbiomes in sucking lice

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August 4, 2020

Abstract

Phylogenetic diversity of symbiotic bacteria in sucking lice suggests that lice have experienced a complex history of symbiont acquisition, loss, and replacement during their evolution. By combining metagenomics and amplicon screening across several populations of two louse genera (*Polyplax* and *Hoplopleura*) we describe a novel louse symbiont lineage related to *Neisseria* and *Snodgrassella*, and show its independent origin within dynamic lice microbiomes. While the genomes of these symbionts are highly similar in both lice genera, their respective distributions and status within lice microbiomes indicate that they have different functions and history. In *Hoplopleura acanthopus*, the *Neisseria*-related bacterium is a dominant obligate symbiont universally present across several host's populations, and seems to be replacing a presumably older and more degenerated obligate symbiont. In contrast, the *Polyplax* microbiomes are dominated by the obligate symbiont *Legionella polyplacis*, with the *Neisseria*-related bacterium co-occurring only in some samples and with much lower abundance.

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1 **A new symbiotic lineage related to *Neisseria* and *Snodgrassella* arises from**
2 **the dynamic and diverse microbiomes in sucking lice**

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4 **Running title:** *Neisseriaceae*-related symbionts in lice

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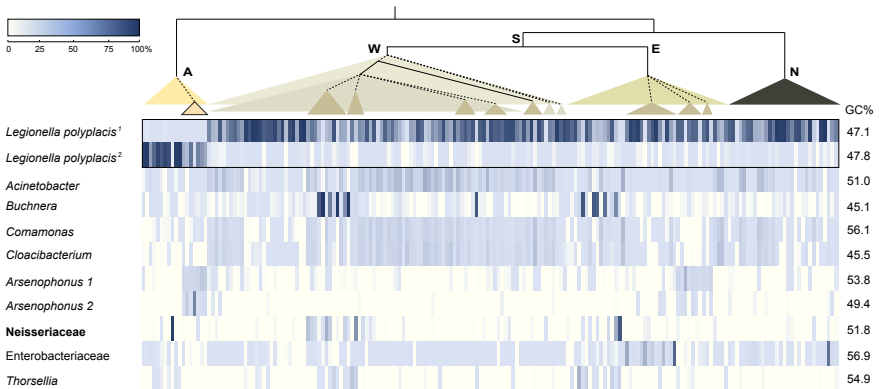
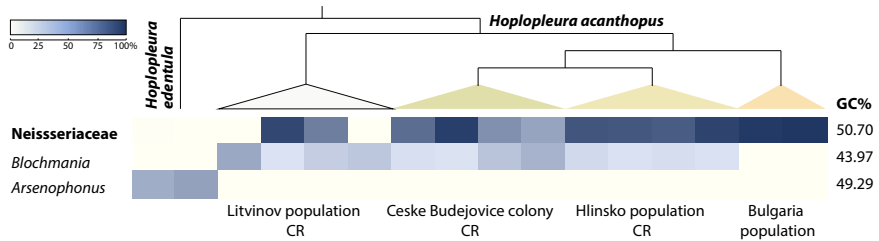
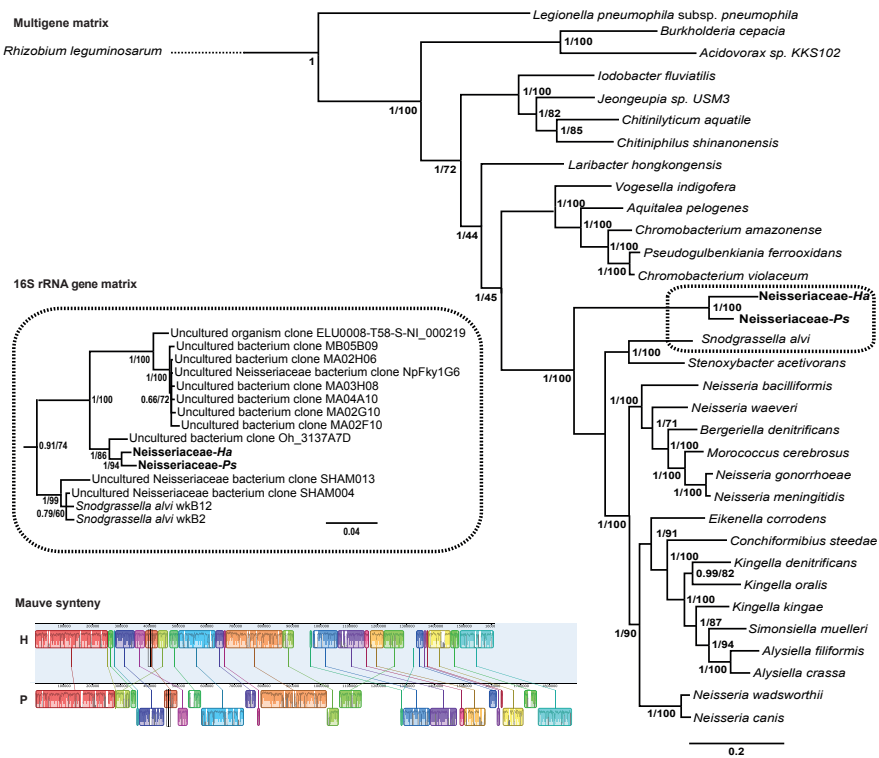
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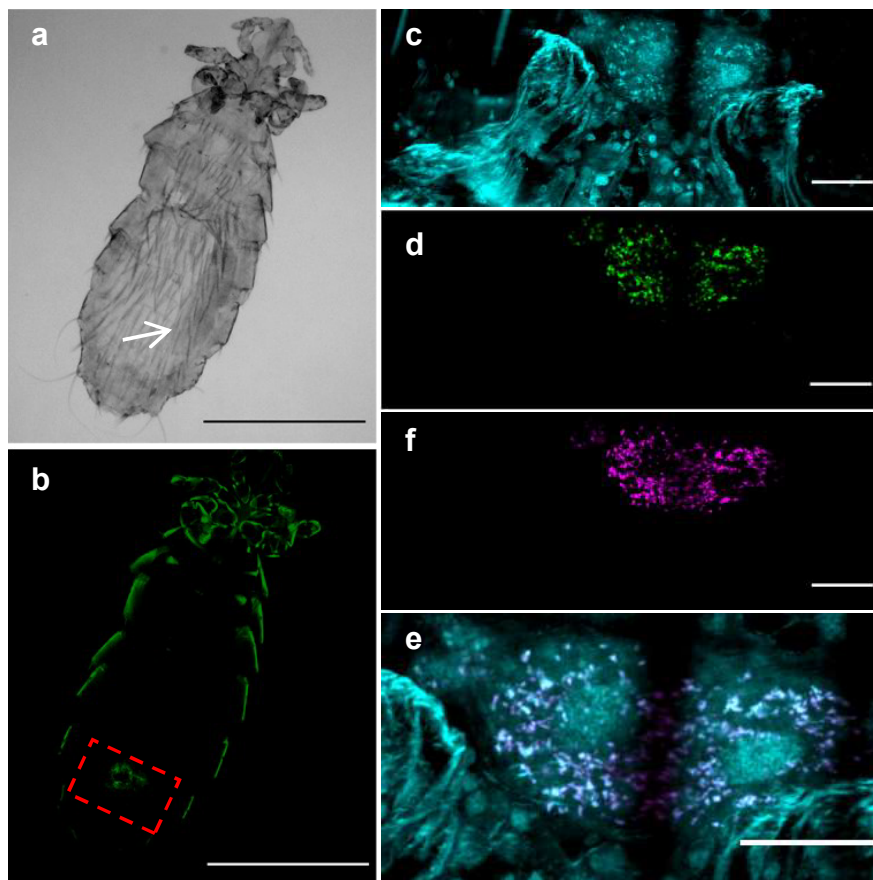


Table 1. Comparison of main genomic characteristics. Louse symbionts highlighted by grey background.

Bacterium	Genome size (Mb)	GC%	No. of protein coding genes	Source
Neisseriaceae - <i>Hoplopleura acanthopus</i>	1.6	33.4	1421	this study
Neisseriaceae - <i>Polyplax serrata</i>	1.8	34	1789	this study
<i>Legionella polyplacis</i> - <i>Polyplax serrata</i>	0.5	23	473	CP021497.1
<i>Riesia</i> spp.	0.5-0.6	25-28.5	476-557	Boyd et al., 2017
<i>Puchtella pedicinophila</i>	0.6	24.2	564	Boyd et al., 2017
<i>Sodalis (Proechinophthirus fluctus)</i>	2.2	50	1287†	Boyd et al., 2016
<i>Snodgrassella alvi</i>	2.5	41.3	2125	CP007446.1
<i>Neisseria meningitidis</i>	2.2	51.7	2118	NC_003112.2

† number of genes annotated in the shotgun library available in the GenBank under the accession numbers LECR01000001-92