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The Human Louse Microbiome Insights Into Insect-Bacterial Coevolution and Consequences for Vector Capacity

Kirthana Srinivasan

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Insights Into Insect-Bacterial Coevolution and Consequences for Vector Capacity

Kirthana Srinivasan, Bret M. Boyd

Center for Biological Data Science, Virginia Commonwealth University, Richmond, VA 23284

Abstract

- Body lice appear to present a significant threat to public health as they are competent vectors of disease causing bacteria, while head lice are poor vectors.
- In our review, we carefully examine microbial associates of human lice, identify evidence of louse-bacterial coevolution and host response to symbiont activity.
- We also evaluate the information in light of a modern synthesis of louse evolution, noting the timing of significant louse-bacterial coevolutionary events relative to the appearance of body lice and suggest potential avenues of investigation.
- We conclude by reframing a historic hypothesis of symbiont impact on vectorial capacity given the information aggregated here.

Public Health Threats

- *Pediculus humanus humanus*, the body louse, is an ectoparasite that only feeds on humans.
- Areas of poor hygiene, crowding, and inability to access water/clothes are at a significant risk for drastic consequences of body lice.
- These populations include: homeless, refugee, post-war, and post-natural disaster people.
- Epidemic typhus, trench fever, and epidemic relapsing fever have been the result of body lice transmission.
- Disease vector capability can vary depending on slight environmental changes, but they certainly do come with lice transmission typically in areas where climate, poverty, and social customs or war and social upheaval prevent regular changes and laundering of clothing.

Host-Symbiont Relationship

Interaction

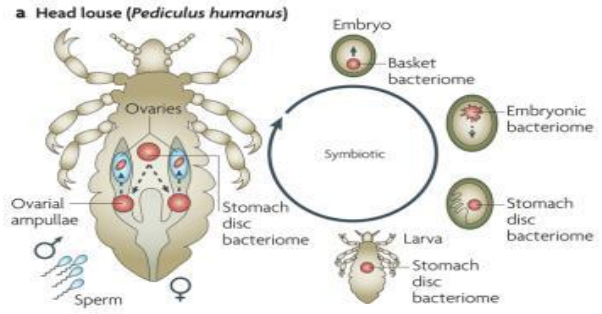

Image is From:
Bright, M., & Bulgheresi, S. (2010). A complex journey: transmission of microbial symbionts. Nature reviews. Microbiology, 8(3), 218–230. https://doi.org/10.1038/nrmicro2262

Coevolution

- Interaction between host and symbiont has been coevolving for over 25 million years.
- Host-symbiont interactions likely influence host-parasite interactions

Table 1. Genes involved in lipid A biosynthesis (Raetz pathway) and candidate homologs in louse symbionts

	Human Head	Human Body	Chimpanzee	Gorilla	Human Pubic+
lpxA^	missing	missing	missing	A0Q88_01230	AOE58_01405*
lpxC	missing	missing	missing	A0Q88_01805*	AOE58_02055*
lpxD	missing	missing	missing	A0Q88_01240	AOE58_01415 & 01420*
lpxH	missing	missing	missing	missing	missing
lpxB	missing	missing	missing	missing	AOE58_01400*
lpxK	missing	missing	missing	missing	missing

^*lpxA* has been demonstrated to be essential for production of lipid A (Anderson et al. 1985; Crowell et al. 1986; Anderson and Raetz 1987; Galloway and Raetz 1990; Moffatt et al. 2020)
*identified as pseudogenes in the current annotation
+genome assembly had many gaps and result may change given better genome assembly

Conclusion

- Here we provide evidence that louse endosymbionts started out as gram-negative bacteria, but subsequently lost the outer coat through the course of coevolution.
- There are two main types of louse endosymbionts, and we find evidence that one is associated with lice that are more efficient vectors of gram-negative pathogens.
- We provide insight on how host-endosymbiont interactions likely drive coevolution and host response to bacterial pathogens.

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