

Louse genetics offer clues on human migrations

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A new genetic analysis of human lice from across the world sheds light on the global spread of these parasites, their potential for disease transmission and insecticide resistance. The results are published February 27 in the open access journal *PLOS ONE* by Marina S. Ascunce and colleagues from the Florida Museum of Natural History, University of Florida.

Lice have been constant travel companions for humans ever since they left Africa and began colonizing other parts of the world. Since they have evolved along with humans, the geographic distribution of lice can reveal patterns of human migrations.

In the present research, the authors used available genomic data from human lice to identify genetic markers that can be used to determine which louse populations bred with one another. Their results improve our understanding of how lice have evolved resistance to insecticides, and can help improve methods of controlling these pests. These genetic markers can also be used to understand the differences between head and clothing lice, since the latter are capable of transmitting deadly bacterial diseases.

The authors suggest that these genetic markers may also reveal the tracks of human migrations across the globe, and can be used to test ideas about human evolution.

More information: Ascunce MS, Toups MA, Kassu G, Fane J, Scholl

K, et al. (2013) Nuclear Genetic Diversity in Human Lice (*Pediculus humanus*) Reveals Continental Differences and High Inbreeding among Worldwide Populations. PLoS ONE 8(2): e57619.

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