

Human lice, *Pediculus humanus*, are obligate blood-sucking parasites. Phylogenetically, they belong to several

mitochondrial clades exhibiting some geographic differences. Currently, the body louse is the only recognized

disease vector, with the head louse being proposed as an additional vector. In this article, we study the genetic

diversity of head and body lice collected from Bobigny, a town located close to Paris (France), and look for

lice-borne pathogens. By amplifying and sequencing the *cytb* gene, we confirmed the presence of clades A and

B in France. Besides, by amplifying and sequencing both *cytb* and *cox1* gene, we reported, for the first time, the

presence of clade E, which has thus far only been found in lice from West Africa. DNA from *Bartonella*

*quintana* was detected in 16.7% of body lice from homeless individuals, but in none of the head lice collected

from 47 families. *Acinetobacter* DNA was detected in 11.5% of head lice belonging to all three clades and

29.1% of body lice. Six species of *Acinetobacter* were identified, including two potential new ones. *Acinetobacter*

*baumannii* was the most prevalent, followed by *Candidatus Acinetobacter Bobigny-1*, *Acinetobacter*

*calcoaceticus*, *Acinetobacter nosocomialis*, *Acinetobacter junii*, and *Candidatus Acinetobacter Bobigny-2*.

Body lice were found to be infected only with *A. baumannii*. These findings show for the first time, the presence

of clade E head lice in France. This study is also the first to report the presence of DNAs of several species of

*Acinetobacter* in human head lice in France