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 louse-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.