

Getting rid of unwanted visitors

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Baka pygmies show a low incidence of *Helicobacter* infection. Credit: Hermes Images/TIPS/picturedesk.com

Gut-dwelling bacteria are attracting increasing attention, particularly those associated with human diseases. *Helicobacter pylori* is found in the stomach of humans, where it may cause chronic gastritis and gastric ulcers, although the majority of infections are asymptomatic. The bacterium has been associated with man since over 100,000 years ago, when it first infected San hunter-gatherers. An international consortium coordinated by Yoshan Moodley at the University of Veterinary Medicine, Vienna (Vetmeduni) has discovered that the Baka pygmies of Cameroon, another community of hunter-gatherers, have a surprisingly

low rate of *Helicobacter* infection. The findings are reported in the online journal *PLOS Genetics* and cause us to question how the bacteria are maintained in human populations.

The digestive systems of all animals contain a large number of different bacteria. Humans are no exception and our intestines provide warmth, shelter and food to a vast range of [unicellular organisms](#), many of which are either beneficial to their hosts or at least cause no ill effects other than consuming some of the food we ingest. However, several species have been associated with disease. Among them is *Helicobacter pylori*, which may play a part in causing chronic gastritis and [gastric ulcers](#).

An ancient colonizer recently discovered

Helicobacter pylori was only discovered about thirty years ago. Subsequent investigations have shown that it originated in Africa and has been associated with humans for at least 100,000 years. The first humans to be infected with the [bacterium](#) were San hunter-gatherers in southern Africa and the infection spread to Europe and Asia when humans left Africa and migrated north and east. Eventually, colonization of Australia and the Americas brought *Helicobacter pylori* into these continents. The bacterium is now found in about 50% of humans worldwide, making it the most widespread and prevalent infection in our species.

In view of the ancient nature of the association between *Helicobacter pylori* and man, it seems likely that the stomachs of other hunter-gatherer communities might also contain longstanding and distinct populations of the bacterium. This assumption has now been tested – and shown to be incorrect – by an international consortium coordinated by Yoshan Moodley of the Vetmeduni's Department of Integrative Biology.

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infection

Gastric biopsies were taken from Baka [pygmies](#) and neighbouring agricultural communities in south-eastern Cameroon and sent to the Hannover Medical School in Germany for sequencing. The researchers found the expected high prevalence (over 80%) of *Helicobacter pylori* in the guts of non-Baka individuals, although only about 20% of the hunter-gatherer Baka pygmies were infected with the bacterium. Furthermore, the scientists were unable to detect any strains of *Helicobacter pylori* specific to the pygmies: the bacteria instead appeared to come from groups associated with Nilo-Saharan populations or with a new subpopulation that seemed to relate to the expansion of Bantu-speaking tribes.

Bacteria are lost from small populations

Valeria Montano in Moodley's lab in Vienna used a population demographic model to estimate the age of association between Baka and non-Baka *Helicobacter* populations, which she found to be as recent as two to four thousand years. Further simulations suggested that the pygmies could easily "lose" the bacterium from their guts because of the small population size of the Baka tribe, possibly combined with the relatively low life expectancy of individual tribe members. The *Helicobacter* now infecting Baka pygmies are thus not the descendants of an ancient bacterial population but instead come from repeated re-infections from the pygmies' non-Baka neighbours over the last few thousand years.

Moodley is naturally excited by the findings. "We had expected to find an ancient lineage of bacteria in the pygmies but instead showed that certain demographic factors such as small population size and unusually low life expectancy could lead to the natural eradication of the bacteria

from [human populations](#)."

More information: Nell, S. et al. Recent acquisition of *Helicobacter pylori*, *PLOS Genetics*. www.plosgenetics.org/article/info%3Adoi%2F10.1371%2Fjournal.pgen.1003775

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