

Two distinct subspecies of plague associated with differences in geographical elevation

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Researchers from the Centers for Disease Control and Prevention in America have carried out a genetic study of plague caused by the bacteria *Yersinia pestis* in Uganda. Although Uganda has one of the highest incidences of plague in the modern world there is very limited research on the bacterial lineage specific to the region. This study uses three different genetic typing methods to examine 61 isolates from culture-confirmed plague cases and identifies two genetically distinct subspecies within the West Nile region of Uganda.

Between 2004 and 2012 there were 1092 suspected human plague cases recorded in Uganda's West Nile region. 61 of these cases were confirmed to be caused by the *Yersinia pestis* bacteria by culturing blood samples. Clinical and demographic data for each case were also collected as part of ongoing surveillance and diagnosis of plague in the region. The researchers isolated DNA samples from each of these 61 cases and used three different genetic typing methods to identify any genetically distinct subpopulations.

All 61 isolates belonged to the 1.ANT plague lineage. This has previously been identified as geographically restricted to East and Central Africa, however there is very little research on the genetics or epidemiology of the strain. The three genetic typing methods ([single nucleotide polymorphisms](#), pulsed field gel electrophoresis, and multiple variable tandem repeat analysis) identified two distinct subgroups with 100% correlation despite these methods recognizing different mutation types. The two subgroups persist through the 9 year period of the study.

Epidemiologically there was no difference between the age, sex, mortality or clinical presentation of the two plague subspecies, however they were geographically distributed differently. Group 1 was found at lower elevations and group 2 at higher elevations with some overlap between elevation levels. The researchers hypothesize that this may be due to two different communities of the flea vector and the small mammal hosts of the bacteria. This is supported by previous research showing different species of the *Xenopsylla* flea host found at different geographical elevations.

Identification and characterization of *Yersinia pestis* subgroups that cause human plague in the West Nile region is an important part of understanding the disease and identifying ecological and environmental factors associated with an increased risk of [plague](#). As well as isolating two distinct subtypes and their associations with geographical elevation, the researchers show a correlation between three different methods of genotyping that can be used for studying *Yersinia pestis* lineages in future research.

The study is published in *PLOS Neglected Tropical Diseases*.

More information: *PLOS Neglected Tropical Diseases*, [dx.plos.org/10.1371/journal.pntd.0004360](https://doi.org/10.1371/journal.pntd.0004360)

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