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Gut up and go

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Helicobacter pylori, a Gram-negative bacterium resident in the human gut that can cause ulcers, occurs in several forms that differ genetically and geographically. In the 7 March Science, Mark Achtman and colleagues at the Max Planck Institute for Infectious Biology, Berlin, Germany, show that sequence differences among extant *H. pylori* populations correlate with large-scale human migrations - both ancient and recent - and may help resolve questions about human movements through time (*Science* 2003, **299:**1582-1585).

Achtman *et al.* sequenced eight genes from 370 strains of *H. pylori*, isolated from 27 geographical, ethnic, or linguistic groups throughout the world, and using a computer program, derived the most likely ancestral tree. Their model identified seven modern populations and subpopulations: three in East Asia, one in Europe, and three in Africa. A West African strain was also found at high frequency among blacks in Louisiana and Tennessee, consistent with migration to the US through the slave trade. Further analysis of these seven groups identified five ancestral *H. pylori* populations, including two ancient European populations, one of which derived from an even older Asian group, the other from North Africa and the Near East, reflecting the migration of Neolithic farmers into Europe from these regions.

"*H. pylori* has probably accompanied modern humans since their origins," they conclude, making them useful for resolving ambiguities of human migration in conjunction with linguistic, archeological, and human DNA studies. Medical treatment of *H. pylori* infection "needs to account for global diversity and will be aided by the availability of representative isolates."

References

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