

A Hitchhiker's Guide to...

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A Hitchhiker's Guide to...

HUMAN MIGRATION

Last month two Australians, pathologist Robin Warren and physician Barry Marshall, won the Nobel Prize in Physiology or Medicine for discovering the infectious agent responsible for ulcers, *Helicobacter pylori*. Typically contracted in childhood and carried for life, *H. pylori* is spread primarily within families and is chronically present in half the human population worldwide, though most people carrying the bacterium are asymptomatic. Improved hygiene and antibiotic usage have begun to reduce its prevalence in industrialized countries, while in developing countries most adults still carry the bacterium.

Humans have been living with *H. pylori* for so long, passing it vertically from generation to generation instead of horizontally like epidemic bacteria, that the pathogen can be used as a marker to track the migrations of human populations. In a review published in the October issue of *Molecular Ecology*, molecular biologists Thierry Wirth, Axel Meyer, and Mark Achtman describe the qualities that make *H. pylori* an ideal candidate for tracing human groups.

For the most part, *H. pylori* behaves like a commensal microorganism colonizing the human gut, and during its long occupancy it has coevolved with its host. And because it evolves more rapidly—its sequence diversity is 50 times greater than that of humans—its population genetic structure offers information about human populations that is unavailable from human genetics alone.

The modern populations of *H. pylori* can be traced to five ancestral populations originating in East Asia, Africa, and Europe. The geographic distribution of the seven subpopulations that have been identified corresponds to the major movements of people through history. Phylogenetic analyses of *H. pylori* isolated from North Americans, for example, confirm that Amerindians are of East Asian origin, whereas people who settled in cities are primarily of European

origin. Other examples: the distribution of the two main European subpopulations of *H. pylori* show a north-to-south introgression gradient, and a high proportion of *H. pylori* of African origin is found in Spain, reflecting the historical interactions of Spaniards and North Africans.

The use of *H. pylori* sequences as markers of human populations may prove to be a powerful tool, in the same way mitochondrial DNA sequences are used, as more populations are sampled. A study of Buddhist and Muslim communities in India showed that *H. pylori* gene sequences were even better than host mtDNA sequences at resolving the ancestry of the two ethnic groups.

RIGHT WHALE EVOLUTION

Also in the October issue of *Molecular Ecology*, an international group of scientists led by University of Utah's Jon Seger, Vicky Rowntree, and then-undergraduate Zofia Kaliszewska (now a graduate student at Harvard University) reports another case in which host-parasite coevolution is used to understand populations with weak genetic structure.

Right whales, hunted to near extinction by the late 1800s, have experienced an extreme bottleneck. Cyamids are crustacean ectoparasites, known as whale lice, that cling to whales. Because cyamids don't have a swimming form, they are confined to the whales they live on (or come into contact with) and are transmitted from mother to offspring. Their shared histories allow scientists to trace whale populations back to their isolation from one another millions of years ago.

North Atlantic right whales (*Eubalaena glacialis*) have not recovered in the 70 years since hunting was banned. The population essentially got even smaller when it was determined recently—through DNA sequence analysis of baleen from specimens preserved in museum collections—that North Pacific right

whales are a separate species (dubbed *Eubalaena japonica*). Only a few hundred individuals of each northern species remain. Southern right whales (*Eubalaena australis*) are faring better, with a growing population of about 7500 whales.

There are three *Cyamus* species living in different niches on each whale: one on the head callosities (*Cyamus ovalis*), one between the callosities (*Cyamus gracilis*), and one in the genital and mammary slits (*Cyamus erraticus*). Each species has a different average population size—roughly 5000, 1000, and 2000 per whale, respectively. Because the cyamids are vastly more abundant than their hosts and have higher mutation rates, they provide population genetic information that can't be gleaned from the whales themselves.

Seger and colleagues obtained cyamids from beached whales around the world and looked at the sequence diversity of a mitochondrial gene. The patterns of genetic variation they found within species show that cyamids frequently move between right whales within the same ocean system. Evidence from the largest cyamid, *C. ovalis*, shows there may have been an exchange between the southern and North Pacific whale populations a million years ago, possibly from just one whale swimming north.

However, the isolation of right whales in separate oceans has led to speciation of their cyamids (in addition to themselves), so that there appear to be nine (not three) *Cyamus* species associated with right whales. Divergence times among the oceanic lineages of each cyamid "species" were consistent with each other and also fell within the estimated range for the divergence of right whales, indicating that right whales and their cyamid passengers all diverged around 5 million to 6 million years ago.

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