

Geography and history shape genetic differences in humans

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New research indicates that natural selection may shape the human genome much more slowly than previously thought. Other factors -- the movements of humans within and among continents, the expansions and contractions of populations, and the vagaries of genetic chance - have heavily influenced the distribution of genetic variations in populations around the world. The study, conducted by a team from the Howard Hughes Medical Institute, the University of Chicago, the University of California and Stanford University, is published June 5 in the open-access journal *PLoS Genetics*.

In recent years, geneticists have identified a handful of genes that have helped human populations adapt to new environments within just a few thousand years—a strikingly short timescale in evolutionary terms.

However, the team found that for most genes, it can take at least 50,000-100,000 years for natural selection to spread favorable traits through a human population. According to their analysis, gene variants tend to be distributed throughout the world in patterns that reflect ancient population movements and other aspects of [population](#) history.

"We don't think that selection has been strong enough to completely fine-tune the adaptation of individual human populations to their local environments," says co-author Jonathan Pritchard. "In addition to selection, demographic history -- how populations have moved around -- has exerted a strong effect on the distribution of variants."

To determine whether the frequency of a particular variant resulted from natural selection, Pritchard and his colleagues compared the distribution

of variants in parts of the genome that affect the structure and regulation of proteins to the distribution of variants in parts of the genome that do not affect proteins. Since these neutral parts of the genome are less likely to be affected by natural selection, they reasoned that studying variants in these regions should reflect the demographic history of populations.

The researchers found that many previously identified genetic signals of selection may have been created by historical and demographic factors rather than by selection. When the team compared closely related populations they found few large genetic differences. If the individual populations' environments were exerting strong selective pressure, such differences should have been apparent.

Selection may still be occurring in many regions of the genome, says Pritchard. But if so, it is exerting a moderate effect on many genes that together influence a biological characteristic. "We don't know enough yet about the genetics of most human traits to be able to pick out all of the relevant variation," says Pritchard. "As functional studies go forward, people will start figuring out the phenotypes that are associated with selective signals," says lead author Graham Coop. "That will be very important, because then we can figure out what selection pressures underlie these episodes of [natural selection](#)."

But even with further research, much will remain unknown about the processes that have resulted in human traits. In particular, Pritchard and Coop urge great caution in trying to link selection with complex characteristics like intelligence. "We're in the infancy of trying to understand what signals of selection are telling us," says Coop, "so it's a very long jump to attribute cultural features and group characteristics to selection."

More information: Coop G, Pickrell JK, Novembre J, Kudaravalli S, Li

J, et al. (2009) The Role of Geography in [Human](#) Adaptation. *PLoS Genet* 5(6): e1000500. doi:10.1371/journal.pgen.1000500, [www.plosgenetics.org/article/i ... journal.pgen.1000500](http://www.plosgenetics.org/article/i...journal.pgen.1000500)

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