

## RECENT ADAPTIVE EVOLUTION OF HUMAN GENES RELATED TO HEARING

JOHN HAWKS

*University Department of Anthropology, University of Wisconsin–Madison, 1180  
Observatory Drive,  
Madison, WI 53706, USA  
jhawks@wisc.edu*

Language requires not only a detailed anatomical and neurological system of language production, but also a highly adapted system of reception. Listening entails hearing. Yet theories of language origins have made very little reference to the sense of hearing. For example, a review of 8 recent books about language origins finds none that even have “hearing” listed in the index. This apparent blind spot is defensible in terms of comparative biology: other primates also have sophisticated patterns of vocal communication that would require highly adapted hearing faculties. Moreover, the brain organs that enable language production and perception would seem to have followed a more unique evolutionary pathway in humans than the primary auditory apparatus.

But compared the complex developmental processes of the brain, the auditory pathway is more analytically tractable. Network analyses and gene expression profiles of developing cochlear tissue provide ways to analyze the genetic basis of human hearing. In short: a selected substitution in a brain development gene might have any one (or several) of hundreds of phenotypic targets, while a selected substitution in a gene underlying auditory development probably (although not certainly) corresponds to a change in hearing.

Still, it remains to demonstrate that human language has unique auditory requirements compared to the vocal communication systems of other primates. Four observations make this hypothesis plausible: (1) Humans live much longer than other primates, exacting persistent requirements from the auditory system over 70 or more years. (2) Human children must begin to distinguish phonemes from a very early age in order to allow further development of language processing. (3) Humans engage in age-dependent, sex-dependent, and social group-dependent speech patterns that are distinguished by fine auditory cues. (4) Significant speech over long distances, in large groups (crowds), or at low amplitudes (whispering) make significant demands on the auditory system, with a greater range than other primates.

This study tests the hypothesis of significant selection on the human auditory system, by genomic comparisons of humans and other primates and genome-wide selection scans in living people. Consistent with earlier work (Clark et al., 2003), a set of hearing-related human genes shows clear signs of recurrent selected substitutions in humans compared to chimpanzees and macaques. These recurrent substitutions may have occurred at any time during human evolutionary history, but they were repeated with several selected variants for each gene. A smaller set of genes shows signs of significant population differentiation in living humans, due to recent strong selection (Williamson et al., 2007). In these cases, a selected allele is at or near fixation in one human HapMap sample, and rare in other samples, showing very strong selection within the last 50,000 years. Most interesting, a relatively large set ( $\sim 10$ – $15$ ) of hearing-related genes have variants currently at low frequency under recent strong selection in one or more human populations (Wang et al., 2006; Voight et al., 2006; Hawks et al., in press). These genes have been undergoing selection in historic times, with maximum increases in frequency during the last 2000–3000 years.

These selection scans may yield a chronology of language evolution that has been challenging to obtain from fossil or archaeological sources. It is clear that humans have continued to adapt their hearing systems within the Holocene. A reasonable hypothesis is that human communication systems emerged gradually during the Pleistocene, but that the full attainment of language was evolutionarily recent. In strong contrast to the view that evolution stopped at the origin of modern humans, it appears that hearing-related adaptations have continued to emerge in the context of recent population growth.

## References

- Clark AG, Glanowski S, Nielsen R, Thomas PD, Kejariwal A, Todd MA, Tanenbaum DM, Civello D, Lu F, Murphy B, Ferriera S, Wang G, Zheng X, White TJ, Sninsky JJ, Adams MD, Cargill M. 2003. Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios. *Science* 302:1960–1963.
- Hawks J, Wang ET, Cochran G, Harpending HC, Moyzis RK. in press. Recent acceleration of human adaptive evolution. *Proc Natl Acad Sci U S A*.
- Voight BF, Kudaravalli S, Wen X, Pritchard JK. 2006. A map of recent positive selection in the human genome. *PLoS Biol* 4:e72.
- Wang ET, Kodama G, Baldi P, Moyzis RK. 2006. Global landscape of recent inferred Darwinian selection for *Homo sapiens*. *Proc Natl Acad Sci U S A* 103:135–140.
- Williamson S, Hubisz MJ, Clark AG, Payseur BA, Bustamante CD, Nielsen R. 2007. Localizing recent adaptive evolution in the human genome. *PLoS Genet* 3:e90.