

Evolutionary Fast Forward

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Evolutionary Fast Forward

WHITE-EYE SPECIATION

Nothing says “origin of species” like an island archipelago. The radiation of finches in the Galápagos is a prime example. Cichlid fish, known for their extraordinarily rapid species diversification, inhabit rift lakes, a restricted geography that for fish is rather like an archipelago. Species-rich groups that lend themselves to biogeographic study tend to have these scattered insular landscapes in common.

A spectacular avian example, dubbed a “great speciator” lineage, comes from the Solomon Islands, a large archipelago east of Papua New Guinea that is famous for its avifaunal diversity. It was here that Ernst Mayr and Jared Diamond, conducting surveys 40 years apart, identified a great speciator commonly known as white-eyes (*Zosteropidae*). White-eyes not only epitomize a rapidly evolving group, but they also present a paradox: unlike other rapidly diversifying groups, which are characterized by reduced dispersal ability, these are highly vagile species.

A new phylogenetic study of white-eyes by Robert Moyle, Christopher Filaridi, Catherine Smith, and Diamond confirms what Diamond and Mayr first documented in 1976: white-eyes diversified at a rapid rate (approaching that of cichlids) while paradoxically dispersing to distant islands and even new continents. The study appears in the 10 February issue of the *Proceedings of the National Academy of Sciences*.

Using nuclear and mitochondrial DNA analyses of white-eyes and their closest relatives, the researchers discovered that white-eye species emerged recently and surprisingly rapidly. They calculated a conservative diversification rate of 2.24 species per million years for *Zosteropidae*. (The most rapid avian diversification rate documented to date is 0.5 species per million years for *Dendroica* warblers.)

In addition, white-eye diversification spanned the Eastern Hemisphere, far outdistancing the lineage from which it arose.

Not all Solomon Island bird species underwent such explosive diversification during the Pleistocene. Why did white-eyes? The vast geographic range and speed of the white-eye radiation argue against environmental variables and for intrinsic qualities as likely drivers. White-eyes are highly social, have a short generation time, and can almost be said to physically morph—populations have been known to diverge morphologically from their source populations within a span of 200 years. They are also such good foraging generalists that some populations exhibit specialization among individuals.

The most significant trait distinguishing white-eyes from other, less-diversified species may be the rapid changes in vagility, or ability to disperse. White-eye evolution appears to have accelerated by shifts in vagility toward both extremes: dramatic increases that dispersed populations farther and wider than other species, and decreases that served to isolate populations and minimize gene flow. No single explanation fits white-eye diversification, which only underlines the fact that they are indeed “great speciators.”

BIASED GENE CONVERSION AND ACCELERATED HUMAN EVOLUTION

With the sequencing of the chimpanzee genome in 2005, scientists can now look for genomic clues to what makes humans unique. Sequence comparisons between human and chimpanzee genomes have revealed regions of accelerated change, called human-accelerated regions, in both coding and conserved noncoding sequences, permitting new insights into human evolution.

In a recent study, Uppsala University scientists Jonas Berglund and Matthew Webster, working with Katherine Pol-

lard, of the University of California–San Francisco, compared more than 10,000 human genes (nearly 85,000 exons) with their chimpanzee and macaque orthologs. The researchers identified 83 exons (from 82 human genes) showing accelerated change, and these accelerated exons exhibit a pattern of biased nucleotide substitutions, which indicates that a nonselective process has been at work, speeding the fixation of mutations. The work appears in the January issue of *PLoS Biology*.

The biased substitutions, which favor AT (“weak”) to GC (“strong”) conversions, are significantly more frequent in both the exons and their flanking noncoding sequences, compared with the rest of the exons in the data set. The more highly diverged the sequence, in fact, the stronger the AT-to-GC bias. Accelerated exons are commonly located near regions with the highest recombination rates, close to telomeres.

The researchers also looked at the pattern of amino acid substitutions in their exon dataset, generating sets of genes with different levels of nonsynonymous base substitutions. These nonsynonymous base solutions also showed a bias toward AT-to-GC substitutions.

The findings suggest that a process associated with recombination, called biased gene conversion, is speeding up the evolution of certain genes without the benefit of selection. During recombination, when heteroduplexes of DNA form, mismatches are repaired in a way that favors AT-to-GC substitutions. Whether this is the cause or the effect of rapid evolution remains to be seen, but the rapid fixation of these mutations obscures the traces of natural selection.

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