

Scanning genomes for recent human evolution

Continuing the unveiling of our top ten papers selected from the papers published in PLOS Biology over the last decade, the latest choice morsel comes from 2006.

The authors compared SNP data from three populations – Yorubans from sub-Saharan Africa, a combination of Japanese and Chinese individuals from Asia, and a cohort from Europe. They specifically looked across the genome for long blocks of co-inherited DNA (haplotypes) that indicate that a particular SNP (or a nearby feature in the genome) confers some positive advantage on the individual that carries it, and that it is increasing in prevalence in that population. Their new method was a breath of fresh air, and has been widely adopted since then, and they found lots of intriguing biologically and medically relevant results.

Read the full, original story here: [Scanning for Recent Human Evolution](#)