

## Poster C-14

### A new approach for using genome scans to detect recent positive selection in the human genome



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**Short Abstract:** We present a new approach for using genome scans to detect recent positive selection in the human genome. We applied this method on both the Perlegen and the HapMap SNP data. A set of candidate genomic regions with strong signals of selection were identified across the genome.

#### Long Abstract:

Detecting recent positive selection (i.e., selection localized to specific populations) promotes understanding of recent human adaptation and may aid in the identification of genes involved in common diseases. Here we present a new approach for detecting the signature of recent positive selection based on genome scans consisting of high-density SNP data. This approach detects an unusually high level of extending haplotype homozygosity in the target population, compared to a reference population. A new procedure was developed to contrast the empirical data against the expected outcome of neutral evolution, as generated by coalescent simulation; results of such comparisons revealed a clear departure of certain portions of the genome from neutrality. We applied this approach to both the Perlegen and HapMap genome-wide SNP diversity datasets, and defined candidate regions that may have been subject to recent positive selection. A Long range haplotype (LRH) test further confirmed that a high proportion (~40%) of the identified candidate regions showed strong evidence of selection. This new approach provides an efficient way for scanning the genome for signs of recent positive selection, utilizing high-density SNP diversity data.