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POPULATION GENETICS

Mobile elements across human populations

Various types of mobile elements are pervasive throughout the human genome, and the polymorphic nature of their insertion sites among populations is beginning to be appreciated. A new study applies a multiplexed method to identify rare and common mobile element insertion sites across 169 humans of diverse ethnicity.

Witherspoon *et al.* used their previously devised mobile element scanning (ME-Scan) method for locating mobile element insertion sites. Briefly, genomic DNA is sheared, and sample-specific adaptors are ligated to allow subsequent multiplexed analyses across multiple samples. A PCR-based strategy carried out on the pooled DNA amplifies mobile elements of a particular type (here, *Alu* elements of the Yb8 and Yb9 family, which account for approximately one-third of the recent *Alu* retrotransposition events in humans). Finally, high-throughput sequencing of the flanking genomic DNA is used to locate the insertion sites.

Across the 169 individuals analysed in the current study, 5,799 high-confidence *Alu* insertions were identified, including 2,524 novel insertion sites. Previously known insertion sites were retrieved with a sensitivity of >90%. The authors found great variability in the population prevalence of the insertion sites, from highly conserved to present in only a single individual. The insertions also gave insights into population history: insertion site distributions could be used to cluster the individuals into geographic regions, and African populations had greater inter-individual diversity in insertion sites than non-African populations; this is consistent with a population bottleneck during the migration of humans out of Africa.

Analysis of the genomic context of insertion sites found only one confirmed insertion in a protein-coding sequence (in the *FAM187B* gene in one individual). Additionally, insertions in exonic (but untranslated) regions had a lower prevalence in the population relative to those in intronic regions. Both observations are suggestive of ongoing negative selection of putative deleterious variants in exons, although the consequences of these particular insertions on fitness are yet to be functionally characterized.

For analyses of selected families of mobile elements across large populations of a species of interest, this method represents an efficient and economical alternative to whole-genome sequencing. Furthermore, the ability to identify rare insertion events may provide a snapshot into the evolutionary mechanisms that are currently active in populations.

Darren J. Burgess

ORIGINAL RESEARCH PAPER Witherspoon, D. J. *et al.* Mobile element scanning (ME-Scan) identifies thousands of novel *Alu* insertions in diverse human populations. *Genome Res.* 18 Apr 2013 (doi:10.1101/gr.148973.112)