

CHARACTERIZATION OF 67 Y-STR LOCI FROM A DATABASE OF OVER 100,000 MALES

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The University of Arizona's Human Origins Genotyping Laboratory (HOGL) provides Y-chromosome STR testing for two large public genotyping projects – Family Tree DNA (www.familytreeDNA.com) and National Geographic's and IBM's Genographic Project (www.nationalgeographic.com/genographic). The HOGL currently performs Y-STR testing for 67 loci. Here, we present summary statistics from a database containing more than 100,000 individuals. Using the tandem approach described in Schleck *et al.* 2008, we assigned samples to Y-chromosome haplogroups, then compared allelic ranges and frequencies among and within haplogroups. When developing STR multiplexes, it is useful to know allelic ranges and variability of each locus for ease and accuracy of data interpretation, especially when highly variable loci are desired.

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