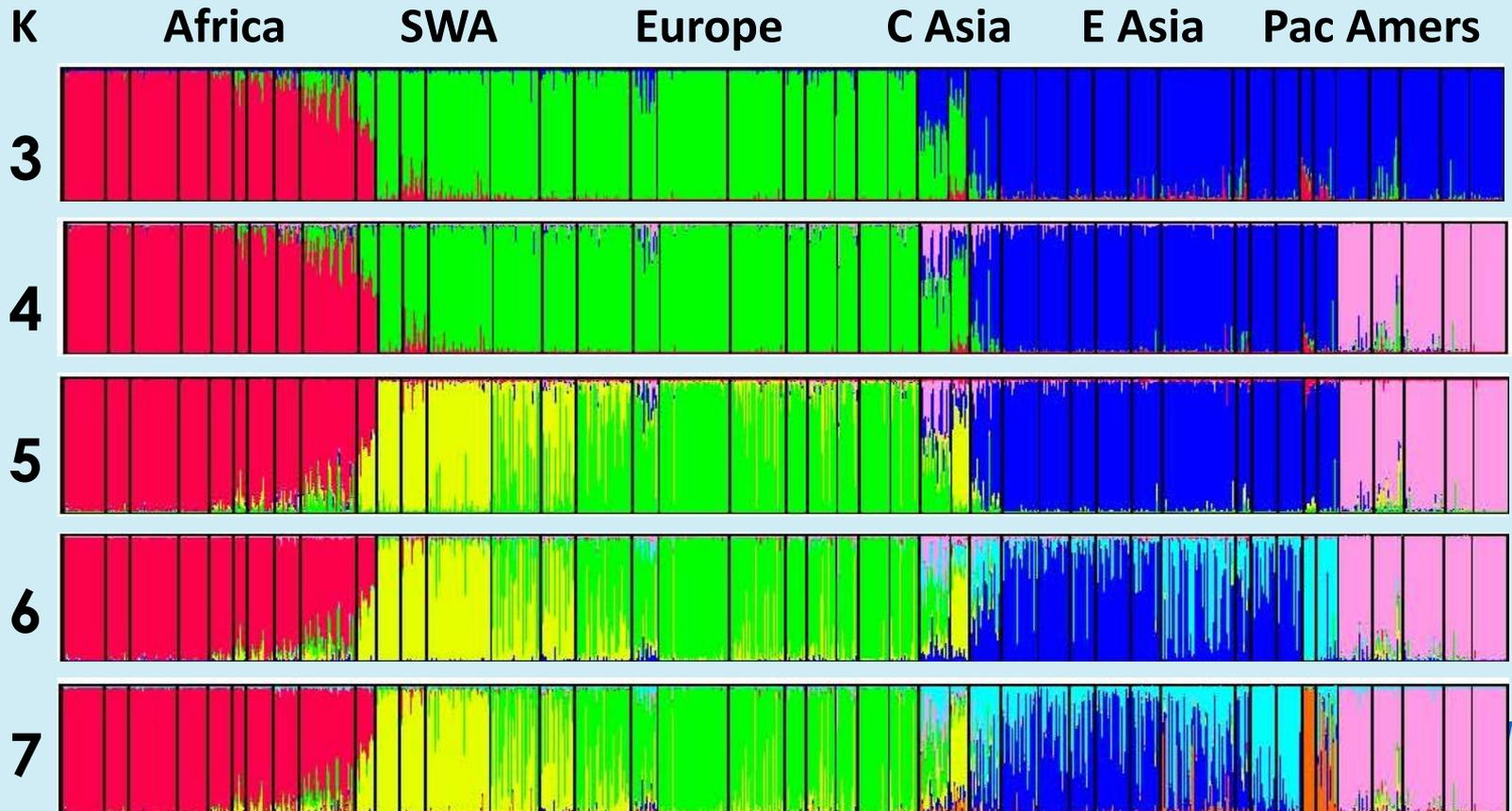


STRUCTURE Analyses of 2278 Individuals from 43 Populations Using 39 Provisional AISNPs

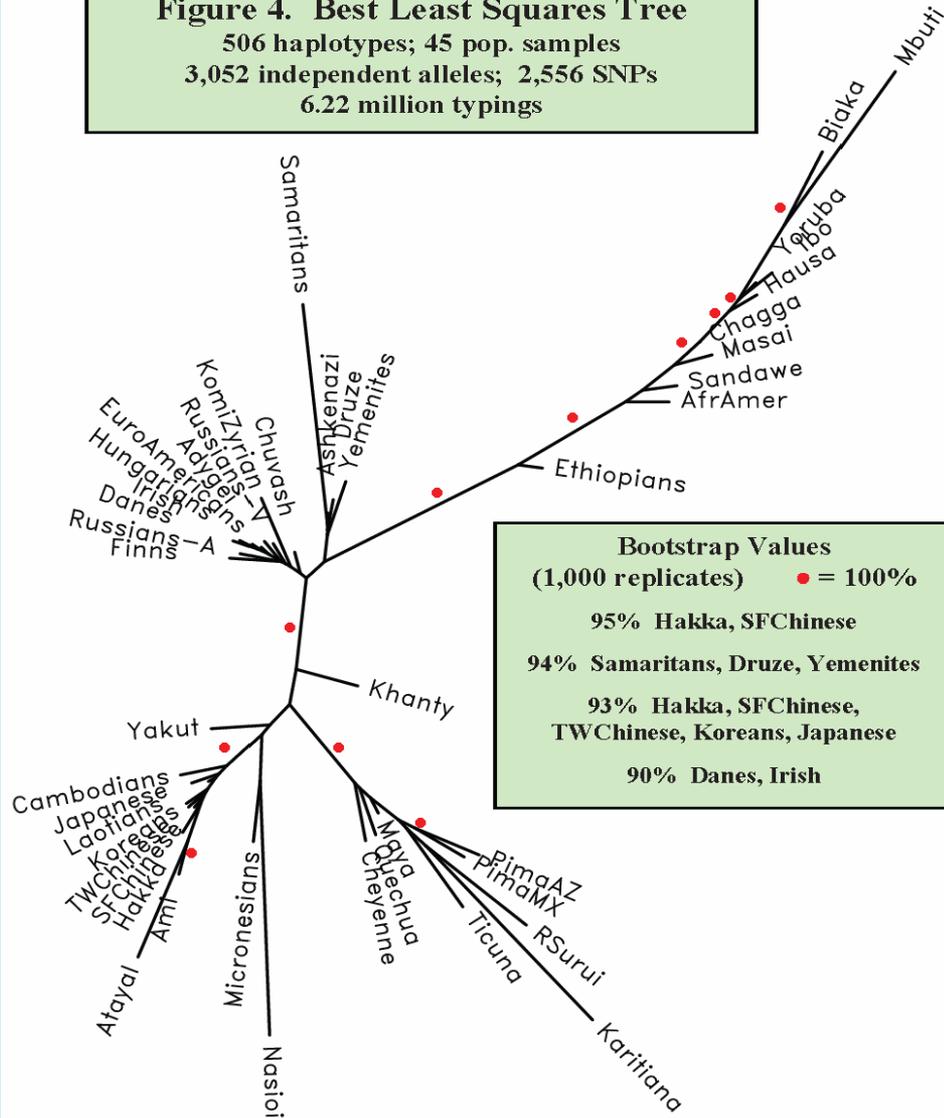


Interpreting STRUCTURE Analyses

STRUCTURE estimates by a search varying the parameters (allele frequencies) the allele frequencies of the K assumed populations that have the best “fit” to the genotypes of all individuals by placing them in one or another of the K populations. STRUCTURE does not consider prior knowledge of the origins of the individuals, but their placement into the K populations can be colored and origin displayed by grouping by known origin.

The optimal number of underlying populations (K) and pattern of assignment are determined by likelihood. The results are a function of the numbers and similarities of the individuals in the dataset analyzed.

Figure 4. Best Least Squares Tree
 506 haplotypes; 45 pop. samples
 3,052 independent alleles; 2,556 SNPs
 6.22 million typings



A Haplotype-based Tree with High Bootstrap Support

A redrawn version of this tree is being published in Kidd et al., *Amer. J. Phys. Anthro.* 2011, in press.

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SNP Database Resource

- **SNP allele frequencies are essential for forensic applications of SNP panels**
- **ALFRED is making those data accessible for for the scientific and forensic communities**

ALFRED: the ALlele FREquency Database
<http://alfred.med.yale.edu>

Forensic **R**esource **O**n **G**enetics

knowledge base

A pilot version of our new web site/database is online. To date it has only a pilot (pre-beta) version of a function to calculate probabilities of genotypes by population for certain IISNP and AISNP panels.

<http://frog.med.yale.edu>

Technology
Transition Workshop 

Other SNP Resources

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- NIST STRBase Forensic SNP Information webpage at <http://www.cstl.nist.gov/strbase/SNP.htm> (accessed Aug 2, 2011)