THE VALIDATION AND UTILIZATION OF SNPs FOR HUMAN PARENTAGE ANALYSIS

Cynthia Barceleau, Esperanza Anguiano, Christine Filidoro, Robert C. Giles, Ph.D.,
and Jeanine M. Baisch, Ph.D.
Orchid BioSciences, Dallas, Texas USA

* * *

Orchid BioSciences has developed a panel of SNP markers that can be used to evaluate human parentage. This parentage marker panel consists of 48 SNPs that were selected for approximately 50-50 allele frequency across each of three races (African Americans, Asian Americans, and Caucasians), similar Tm for amplifications primers, and the same extension biochemistry (T/C, for this panel). Validation studies conducted for these SNP markers include sensitivity and reproducibility studies, analysis of extended CEPH families, and comparison to STR results on over 200 paternity trios for each of three races (African Americans, Caucausians, and Hispanics). There was 100% concordance between the STR and SNP data on all cases tested. The average PI for each SNP is 1.3, and the average number of exclusions per trio is 10. Experiments performed by Orchid to validate the usefulness and reliability of this panel of markers has resulted in approval by the AABB for its use as a stand-alone parentage test in accredited laboratories. Much of the validation data will be presented, as well as the usefulness of this technology on a variety of testing platforms.