

**DEVELOPMENT OF A Y CHROMOSOME SNP MULTIPLEX FOR THE SEQUENOM
MASSARRAY® SYSTEM**

Elizabeth Serbi¹, Ryan S. Sprissler¹ and Matthew E. Kaplan²

¹ *Genomic Analysis and Technology Core, Arizona Research Laboratories, University of Arizona, Tucson, AZ*

² *Human Origins Genotyping Laboratory, Arizona Research Laboratories, University of Arizona, Tucson, AZ*

The human Y chromosome continues to have useful applications in many fields including evolutionary biology, forensics, medical genetics, and genealogical reconstruction. The introduction of mass spectrometry into the genomics laboratory has streamlined high-resolution sizing of DNA fragments. This technology has great power to assist in the studies of both DNA methylation and SNP variation. We are developing a SNP multiplex for the non-recombining region of the Y chromosome on the Sequenom MassARRAY® system. We have designed this multiplex to simultaneously genotype over 40 SNPs that define the major Y chromosome haplogroups. The Sequenom platform allows for flexible assay construction and high-throughput genotyping. This system may be of special interest to the forensics community for use on degraded DNA samples because it targets amplicons of only 100 bp. Y chromosome haplogroups are a useful addition to the investigator's tool kit because of their correlation with the geographic location of an individual's ancestry.