SEMI-AUTOMATION OF mtDNA ARRAYS: RESULTS FROM 666 POPULATION SAMPLES \ AND COMPARISONS

Margaret C. Kline, Janette W. Redman, Peter M. Vallone, and John M. Butler
National Institute of Standards and Technology, Gaithersburg, MD

➢◇◁

At the National Institute of Standards and Technology (NIST) we have used the Linear Arrays for mtDNA HVI/HVII region-sequence typing (Roche Molecular Systems, Alameda CA) to evaluate our population collection of self declared Hispanic (128), African American (252), and Caucasian (286) samples. The samples were previously evaluated with Short Tandem Repeat Loci (STRs) to assure no sample duplicates exist in the collection. The amplified products were quantified and sized using an Agilent 2100 Bioanalyzer (Agilent Technologies, Wilmington DE).

Arrays were processed both manually (120 samples) and using a Tecan Profiblot instrument that applied all the regents and was "walk away" after the amplified samples were loaded until reading the arrays. Frequencies of the mitotypes within and between populations have been calculated and will be presented along with sequencing results and single nucleotide polymorphism (SNP) typing results from Caucasian samples exhibiting the most common mitotype.