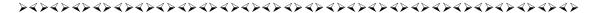# Loci D16S539, D7S820, D13S317 (SilverSTR™ III):
Comparison of Different Populations of Argentina

Andrea Sala, Gustavo Penacino, Nancy Iannucci and Daniel Corach.
Servicio de Huellas Digitales Genéticas y Cátedra de Genética y Biologia Molecular, Facultad de Farmacia y Bioquímica, Universidad de Buenos Aires, Junin 956, Buenos Aires, Argentina. Fax: (541) 964-8282 Email: shdg@huemul.ffyb.uba.ar

➢◁

Sample economy, highly standardized technical platforms and cost/time efficiency characterize the PCR based STR typing approach. Nevertheless, these markers, if considered independently, provided a reduced number of alleles, some of which may present a high frequency in the population. Multiplexing such markers in a combined PCR reaction allows obtaining "multilocus" genotypes. Increasing the number of multiplex systems may speed up typing procedures even for forensic case work or paternity testing. The most popular optimized STRs have been used all over the world, chiefly in the silver detection format, were CTT and FFV, which provided suitable matching probabilities for forensic casework and allowed an efficient rapid screening for exclusion in paternity testing or complementing VNTR/RFLP typing. Availability of an additional optimized triplex including loci D16S539, D7S820, D13S317 included in the SilverSTR™ III Promega, strongly reinforced the trend towards STRs preference for human identification. The aim of this work was to evaluate the genetic attributes (e.g. allele and genotype frequencies, Power of Exclusion, Discriminative Power and Matching Probability) depicted by three aboriginal communities belonging to the Mapuche, Lehuelche and Wichi tribes and the European Population of Argentina. Interpopulation comparison was carried out using FST calculation. Comparisons also involved other populations whose database was available.