

**El Salvador (Central America) Population Data With the New *GenePrint*<sup>®</sup>  
SilverSTR<sup>™</sup> III Multiplex (D16S539, D7S820 & D13S317)**

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Genetic typing of short tandem repeat (STR) loci in DNA derived from biological evidence is of great interest in forensic science. The STR loci are composed of tandemly repeated sequences of 2-7 base pairs in length, and because the allele size of STRs is generally less than 350 base pairs, they are amenable to amplification by the polymerase chain reaction (PCR).

PCR amplification and silver staining of polyacrylamide gels is an easy, reliable, and non-expensive approach for a large number of forensic laboratories around the world.

We have analyzed a total of 223 individuals from El Salvador, Central America, with Promega's new *GenePrint*<sup>®</sup> SilverSTR<sup>™</sup> III Multiplex, which includes the following loci: D16S539, D7S820, D13S317. Bloodstains were extracted with Phenol:chloroform:IAA, quantified by slot-blot and submitted to amplification according to the manufacturer's instructions. Alleles were separated using a 32 cm-long denaturing vertical polyacrylamide gel, and visualized by silver staining. Results are summarized in the following table:

Locus	Observed Homozygosity	P.D.*	P.E.**	Most common allele	Least common allele
D13S317	12.6%	0.941	0.655	#9 (0.23)	#8 (0.054)
D7S820	22.9%	0.898	0.533	#11 (0.32)	#14 (0.002)
D16S539	26.0%	0.909	0.557	#11 (0.32)	#15 (0.002)

\*Total PD: 0.9995- \*\*Total PE: 0.929

According to our results, the El Salvador population sample analyzed met Hardy-Weinberg expectations and therefore can be used to estimate the frequency of a multiple STR loci DNA in El Salvador.