INVESTIGATION OF A RAPE CASE BY USING NGS BASED MiSeq FGx FORENSIC GENOMICS SYSTEM – A CASE OF DELETED AMELOGENIN MALE

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Two girls were raped by two boys in the metro city of Haryana, India. MiSeq FGx Forensic Genomics System was used to generate DNA profiles by using Forenseq™ DNA Signature Prep kit in crime exhibits. The results of 231 markers i.e. Autosomal, Y, and X-STRs; Identity, Ancestry, and Phenotype SNPs amplified, sequenced and analyzed simultaneously from semen detected on the trousers of one girl matched with that of the one accused. Autosomal STR called this boy XX Amelogenin but because Y-STRs were concurrently run, the sample was determined to be XY indicating a case of amelogenin deletion. Further a single STR profile was generated from the semen stains ruling out the possibility of DNA mixture. D2S441 loci indicated two alleles with repeat 10 but showed different DNA sequence in that Adenine nucleotide was replaced with Guanine in the ninth repeat sequence. Further D13S317 loci locus showed two alleles with repeat 12 but with different sequences. Hair color results showed 0.19 brown, 0.80 black color character. Eye color showed 100 percent brown characters. Hence first accused has black hair and brown eyes. In contrast DNA pattern obtained from the trousers of another girl matched with that of another boy. The DNA profile of this man was also determined to be amelogenin deleted male. Hair color results of this person showed 0.32 brown and 0.66 black and 0.03 blond character. Eye color showed 100 percent brown characters. Thus he has brownish black hair and brown eyes. The Y-STR profile was observed to be the same whereas the X-STR profile was different in both boys. Thus both have the same patrilineal lineage but different maternal lineage. Kinship relations were not revealed by the boys at the time of crime reporting. Ancestry results showed the DNA pattern of both accused to be matching with Ad Mixed American. Markedly the software at the time of analysis contained data of only Ad Mixed American, African, East Asian, European, and Centroids only indicating the requirement of the Indian ancestry database. NGS, based on massive parallel sequencing, provided vast information at hand as compared Capillary Electrophoresis which although is a gold standard but only a set of few genetic loci can be analyzed at a time with no information of phenotype and genealogy. NGS has the potential to resolve DNA mixtures of more than one individual, complex paternity studies having mutations in STR sequence, monozygotic twin differentiation, etc. Hence NGS technology will soon offer rapid genome analysis helping to solve many cold crime cases.