

**Title :** Genetic Diversity Analysis of STR Locus DXS6809 in the Thai Male Population for Forensic Applications

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## ABSTRACT

Short Tandem Repeats (STRs) or microsatellites on the X chromosome are valuable genetic markers in forensic analysis, particularly in relationship testing and human identification. However, genetic information on X-STR variation in the Thai population remains limited. DXS6809 locus is a highly polymorphic X-linked tetranucleotide repeat marker with high power of discrimination (PD) and exclusion rendered, making it a useful locus for human identification investigating complex kinship or deficiency cases. This study aimed to analyze the STR locus DXS6809 in Thai male population to evaluate its genetic variation and parental identification. Thirty-six unrelated Thai male samples were collected from buccal swabs and DNAs were extracted using the NucleoSpin® Tissue Kit. DNA quantity and quality were examined by agarose gel electrophoresis and a Biodrop Spectrophotometer. The extracted DNAs were amplified by Polymerase Chain Reaction (PCR), purified using the PrimeWay Gel Extraction/PCR Purification Kit, and DNA sequencing were performed using the Big Dye terminator method. Sequencing data were analyzed with BioEdit version 7.7. The PCR products were approximately 300–400 bp in length. Here, only male samples were analyzed, as males carry a single X chromosome that facilitates straightforward interpretation of allelic variation. The STR repeats of DXS6809 was identified as (CTAT)<sub>n</sub>-(ATCT)<sub>n</sub>-N<sub>9</sub>-(TATC)<sub>n</sub>-(ATCT)<sub>n</sub>-N<sub>10</sub>-(ATCT)<sub>n</sub>, with eight observed allelic patterns. Among these, (CTAT)<sub>9</sub>-(ATCT)<sub>3</sub>-N<sub>9</sub>-(TATC)<sub>3</sub>-(ATCT)<sub>5</sub>-N<sub>10</sub>-(ATCT)<sub>13</sub> showed the highest allele frequency. Allele frequencies ranged from 0.03 to 0.22, with a Power of Discrimination (PD) of 0.861 and a Polymorphic Information Content (PIC) of 0.847, indicating that DXS6809 is informative for forensic identification. However, as this study analyzed only one X-STR locus in male samples, additional loci, larger sample sizes, and female participants should be included to enhance population representativeness for future work.

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