

Abstract

Analysis of microsatellite markers is the most common method used in human genetic identification. This study is an assessment of the usefulness of flanking region DNA sequence of these markers in forensic genetics. We analyzed 27 STRs (ang. *Short Tandem Repeats*) in 308 unrelated individuals from Polish population. The results were obtained with NGS (ang. *Next Generation Sequencing*) technology - Illumina ForenSeq DNA Signature Prep Kit and MiSeq FGx sequencing platform. The impact of the flanking regions polymorphism on common biostatistical parameters was studied. The obtained data were also used to assess frequency of the detected polymorphisms in Polish population and compared with available data on the polymorphisms frequencies in other populations.