ANALYSIS OF COMPLEX DNA MIXTURES USING MASSIVELY PARALLEL SEQUENCING OF SNPs WITH LOW MINOR ALLELE FREQUENCIES

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DNA mixtures from 3 or more contributors have proven difficult to analyze using the current state-of-the-art method of short-tandem repeat (STR) amplification followed by capillary electrophoresis (CE).   Here we analyze samples from both laboratory-defined mixtures and complex multi-contributor touch samples using a single nucleotide polymorphism (SNP) panel comprised of 2311 low-minor-allele-frequency loci, combined with massively parallel sequencing (MPS) which can provide sequence information with very low amounts of template. This approach demonstrates that as many as 10 people can be identified from touch samples recovered from a variety of different materials.

KEYWORDS Forensic science, complex DNA mixtures, massively parallel sequencing, single nucleotide polymorphism, touch samples, low template