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### **INEXHAUSTIBLE TRACE EVIDENCE? – APPLYING WHOLE GENOME AMPLIFICATION TO FORENSIC DNA CASEWORK**

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Forensic trace evidence is hampered, literally, by the amount of material to conduct analysis from. Often there is just enough material to do a “single shot” PCR, let alone conducting repeat tests, third party confirmation, or archiving. At the same time the set of available options to gain additional sequence based information from case evidence increases: besides STR based identity and sex markers, biometric information such as color of hair, skin coloration and ethnic relationships may complement DNA investigational work. Whole Genome Amplification (WGA) provides a promising concept to overcome trace evidence constraints by expanding the amount of starting material through an extremely accurate replication mechanism. WGA is based on an isothermal DNA replication technology called Multiple Displacement Amplification (MDA) and provides a comprehensive genome representation with very low error rate ( $10^{-7}$ ) and large fragment sizes (>20 kb). The amplified DNA has been validated successfully for various downstream genetic applications such as SNP and STR analyses, genotyping using arrays and other methods, sequencing and haplotyping. It has also been applied in various other applications like WGA from unculturable bacteria, single-cell analysis (sperm, blastomeres and bacteria) and pre-implantation genetic diagnosis. Tailored concepts such as WGA for degraded DNA and mito-specific WGA for mtDNA analysis are discussed. With its ability to limitlessly expand source DNA, WGA fosters a vision of “single cell forensics” from an “inexhaustible trace”.