COMPARISON OF DETECTION RATE BETWEEN SNP AND STR FOR TYPING OF DEGRADED DNA

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Currently, the main technique for human identification in forensic casework analysis is short tandem repeat (STR) typing, however some kinds of single nucleotide polymorphism (SNP) typing for forensic applications have been reported. Typing of SNP has advantages in forensic DNA identification because SNP are abundant in genomic DNA and easily detected using an automated high-throughput system. And the primary benefit of SNP typing is that more successful typing for degraded samples compared with STR typing. Actually, based on the principle that the smaller the target for PCR, the more likely the sequence will be intact and detectable, much focus has been placed on designing reduced length amplicon (mini-STR, SNP). In this study, we investigated the comparative genotyping success of artificially degraded samples using STR, mini-STR and SNP typing system based on the Invader assay.

An artificial degradation series was prepared by digesting human blood genomic DNA with DNase I for progressive lengths of time (1, 3, 5, 7, 10, 15, 20 and 30 min), by treating human blood genomic DNA with Methylene blue in the presence of visible light for progressive lengths of time (0, 2, 10, 20, 60, 120 and 240 min) and by irradiating human blood genomic DNA in UV crosslinker for progressive amounts of energy (0, 0.05, 0.1, 0.2, 0.4, 0.6, 0.8 and 1 J/cm^2).

Significant improvement was observed in the typing success of degraded DNA using SNP analysis or mini-STR over STR typing (75% vs 56% vs 22%, respectively). Mini-STR and SNP typing system were more successful in typing degraded samples and yielded significantly more complete profiles and lower match probabilities than STR typing system. Moreover, STR and mini-STR typing systems showed off-scale alleles and pull-up artifacts with large amounts of degraded DNA due to the underestimate of the quantity of amplifiable DNA. On the other hands, SNP typing system showed tolerance to wide range of input DNA amounts and DNA degradation. Taken together, these results indicate that our SNP typing system would probably provide a better alternative to STR and mini-STR typing for degraded DNA.