A NOVEL APPROACH OF SELECTIVE DETECTION OF PARENTAL ALLELE IN DIFFERENTIALLY METHYLATED REGION

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Identification of parental allele sometimes gives significant information to forensic casework, especially in pedigree study. Imprinting is an epigenetic phenomenon where a gene expression is exclusively arisen from one parental allele, and a status of CpG islands in/around the gene show differentially methylated parental allele (designated DMPA). Recently, we have developed a method to discriminate parental allele of three STRs in an imprinted gene, H19 (11p15.5), by using methylation-sensitive restriction enzymes (Ref.1). In this study, we will show other imprinted genes applicable to this analysis. SNPs in/around imprinted genes were selected from web databases (Imprinted gene catalogue, NCBI, Ensembl etc.). After amplification of presumable DMPA region, SNP was genotyped by RFLP or SSCP analysis. Possibility of parental discrimination was assessed by comparison between genotype detected from native DNA and that from enzyme-digested DNA (Ref.1). Parental alleles of SNPs in several imprinted genes we tested were selectively detectable: SNP rs2281476 in HYMAI (6q24), rs3778859 and rs3807138 in MEST (7q32), rs220028 in SNURF (15q12), and rs2302376 in PEG3 (19q13.4). These SNPs are commonly located in CpG island around exon 1 of each gene. Sequencing results supported that the amplified regions would be under the DMPA status, which is not inconsistent with published data on each imprinted gene. These findings are noteworthy for discriminating parent-of-origin from autosomal polymorphisms, and would be a useful tool in order to find out a parental source in forensic examination. Ref.1 N. Nakayashiki, J Kanetake, Y Aoki (2004) Int J Legal Med, 118: 158-162.