A NEW APPROACH TOWARDS THE RAPID DETECTION OF SNP

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We developed a method called OPA (Orphan Peak Analysis) to detect point mutations efficiently by using DNA sequencer. We applied this method for rapid SNPs (Single Nucleotide Polymorphism) detection in multiple samples.

Genomic DNA was extracted from blood samples. Equal amounts of DNA from 4 to 8 individuals were mixed and subjected to PCR amplification followed sequence reaction.

We could detect the variation of 1 sample among 8 samples by the OPA analysis. We searched SNPs targeting 149 people which existed in the exon domain of Human Period gene. We could search several SNPs in exon domain as this result.

We confirmed that OPA was effective in as a form that SNP was searched. We will make an automation system of the sample preparation and the speed-up of electrophoresis further, and will establish a rapid and cheap technique.

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