



## Prenatal diagnosis of Chinese families with phenylketonuria

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**ABSTRACT.** The aim of this study is to investigate the ability to prenatally diagnose phenylketonuria (PKU) by using phenylalanine hydroxylase (PAH) gene mutation analysis combined with short tandem repeat (STR) linkage analysis in 118 fetuses from 112 Chinese families. Genomic DNA was extracted from the peripheral blood from members of 112 families and the exons and exon-intron boundaries of the *PAH* gene were amplified by PCR. PCR products were analyzed by bi-directional Sanger sequencing and multiplex ligation-dependent probe amplification (MLPA). The three variable number of tandem repeat (VNTR) markers PAH-1, PAH-26, PAH-32 were used in the prenatal diagnosis for the PKU families. We identified a spectrum of 63 different mutations, including 61 point mutations and indels, two large exon deletion mutations, and five novel mutations. A substantial proportion of mutant alleles were accounted for by p.R243Q (15.62%), EX6-96AG (9.82%), p.V399V (7.59%), p.Y356X (6.70%), and p.R413P

(5.36%). The same mutations were identified in 31 prenatally genotyped fetuses. We identified 58 fetuses that carried only one mutant allele and 29 fetuses that carried no mutations of PAH and were presumed normal. *PAH* gene mutation analysis combined with STR linkage analysis can provide rapid and accurate prenatal diagnosis for PKU families.

**Key words:** Phenylketonuria; Phenylalanine hydroxylase gene; Mutation; Prenatal diagnosis