Short Report

Report of VNTR with 13 Repeats Linked to Phenylalanine Hydroxylase Locus in Unaffected Members of Two PKU Families

Maryam Kamkar¹, Mostafa Saadat*¹, Iraj Saadat¹ and Golbahar Haghighi²

¹Dept. of Biology, College of Science, Shiraz University, Shiraz 71454; ²Dept. of Biochemistry, School of Medicine, Shiraz University of Medical Sciences, Shiraz, Iran.

ABSTRACT

Phenylketonuria (PKU) is one of the most common metabolic inborn diseases caused by mutations in the phenylalanine hydroxylase (PAH) gene. This gene is linked to a variable number of tandem repeats (VNTR) region which is a polymorphic marker that facilitates the implementation of prenatal diagnosis and carrier screening. In this study, VNTR with 13 repeats that has not been reported previously was observed in 2 PKU families from Fars province, south of Iran. This allele showed 4% frequency in normal individuals. Iran. Biomed. J. 7 (2): 89-90, 2003

Keywords: Phenylketonuria (PKU), Phenylalanine hydroxylase (PAH), Variable number of tandem repeats (VNTR)

INTRODUCTION

Phenylketonuria (PKU) with autosomal recessive inheritance is one of the most common inborn metabolic diseases caused by a large number of mutations in a gene encoding a liver-specific enzymes phenylalanine hydroxylase (PAH). The PAH gene is linked to a variable number of tandem repeats (VNTR) region which is located on the 3′-end of the gene. Since the VNTR is a highly polymorphic genetic marker and is inherited in a Mendelain fashion, it is used to give a risk estimation of linked defective allele. These alleles contain 3, 6-9 and 12 copies of VNTR [1-9]. So far the VNTR with more than 12 repeats has not been reported. Here, we report alleles with 13 copies of VNTR in two PKU families and so normal individuals from Fars province, south of Iran.

RESULTS AND DISCUSSION

As shown in Figure 1, DNA fragments of 625 bp corresponding to the 13 copies of the VNTR units were observed in the mothers and unaffected children of the both families. Therefore, the newly reported VNTR 13 was associated with normal alleles in both families.

A unit less than 3 or more than 12 repeats has not been observed in other studied populations of United State of America, Brazil, Italy, Russia, Poland, Sweden, England, Turkey, Ireland, Spain, Switzerland, and Denmark [1-9]. At present, the molecular mechanism for formation of VNTR 13 is unclear, however, it is suggested that the alleles of VNTR are produced by the gain or loss of a single VNTR unit, possibly by slippage during DNA replication [1, 9]. Finding of this new VNTR encouraged us to perform further study on a control
group. Analysis of VNTR alleles in 50 normal individuals (100 alleles) from the general population was performed. The result showed that the frequencies of VNTR alleles, containing 3, 6, 7, 8, 9, and 13 repeats were 44, 4, 13, 26, 9, and 4 percent, respectively. Notably, the VNTR 13 was present only in four heterozygous individuals.

The observed heterozygosity of this VNTR system was 66 percent in the studied population, which is equal to that of European Caucasians and is higher than that of Chinese population [4]. This finding is of interest, because, based on population genetic studies, Iran has one of the most heterogeneous populations in the world [10, 11]. In this regard, frequencies of the VNTR alleles in other Iranian populations and DNA sequences of VNTR with 13 repeats are under investigation.

ACKNOWLEDGEMENTS

We are deeply indebted to the families and individuals who willingly participated in this study. This study was supported by Shiraz University.

REFERENCES