

# Prevalence of parental consanguinity in children with precocious puberty and kisspeptin gene polymorphisms

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## OBJECTIVES

Puberty is considered as a complex network of coordinated biological process with multiple level of neuroendocrine and genetic regulations. Timing of puberty could influence by different environmental and genetic factors. Precocious puberty (PP) is one of its variations which defines as appearance of physical signs of sexual development in a child prior to the earliest accepted age of sexual maturation, 7 years in girls and 9 years in boy. The exact mechanisms and genetic background of PP are not well understood. It is suggested that the kisspeptin neuropeptide, encoded by the KISS1 gene, could have role in this regard. Considering the higher rate of parental consanguinity among Iranian population and its possible role in the occurrence of PP, the aim of current study was to determine the mutation of kisspeptin gene (KISS1) among a group of patients with PP and role of parental consanguinity in this regard.

## METHODS

In this case control study, a group of children with diagnosed PP and a group of healthy children were selected. Bone age of patients with PP was evaluated and MRI and pelvic ultrasonography was performed. Stage of puberty was determined using Tanner staging method. Selected patients had advanced bone age (Greulich and Pyle method), and normal central nervous system (CNS) MRI. Genomic DNA was extracted from peripheral blood of selected population by salting out method. Occurrence of any mutation or polymorphism in KISS1 gene was investigated using PCR method. The rate of parental consanguinity was determined in patients with and without KISS1 gene polymorphism/mutation.

**Table1:** Characteristics of patients with precocious puberty and control group

	Patients with precocious puberty n=33	Control group n=30	P value
Age(years)	10.42 +/- 3.6	10.8 +/- 4.1	0.72
Sex(female/male)	15/18	16/14	0.69
Age of puberty	6.88 +/- 1.51	9.76 +/- 1.8	0.02

**Table2:** Allelic variants identification in the KISS1 gene of patients with precocious puberty

Location	nucleotide	Amino acid change	number
5'URT	c.-148 T>A	-	NOT REPORTED
5'URT	c.-145 del T	-	rs5780218 del
5URT	c.-89G>A	-	rs3924587
EXON2	c.58 G>A	E20k	rs12998

## RESULTS

In these study 33 patients with idiopathic PP and 30 control age and sex matched children were studied (Table1). Genetic analysis indicated that there was not any polymorphism or mutation in studied participants of control group. Among patients with PP, 4 SNPs within the promoter and coding regions of KISS1 gene were determined in 9 patients (5 boys and 4 girls) (Table2). Among them the c.-148 T>A was novel variant. Pathogenicity of these variants is predicted by inSilico prediction softwares e.g. polyphen2, phyloP and mutationtaster. As only 3 exons of these genes were sequenced, presence of mutations outside these regions, not included in our study. There was not any case of familiar PP as well as any case with parental consanguinity among patients with detected polymorphism.

## CONCLUSIONS

The findings of current study identified one novel polymorphism and three reported polymorphism in KISS1 gene among patients with PP in Iran. Considering that parental consanguinity was not associated with reported polymorphism of KISS1 gene, it is suggested that it could not have important role in the occurrence of PP in Iranian population. Studying other related genes as well as further epigenetic studies is recommended. Moreover, designing studies for evaluating the interaction of different environmental and nutritional factors with detected polymorphisms in the is necessary for better understanding of the disease pathogenesis.

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