Brief Communication

Genetic analysis: future diagnostic tool in clinical Orthodontics

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Orthodontic diagnosis and treatment planning, genetic basis of a skeletal anomaly should think through. The collaboration of various genes has been shown to be the primary cause of an unbalanced mal-shaped craniofacial structure[1].

Facial profile and structure seems to have a familial trend. From population studies proof gained, that families and twin have shown a genetic factor is responsible for the etiology of malocclusions. A predicted value of more than 25,000 human genes adds contribution to the development of craniofacial structure[2].

With recent technological advances that allow the simultaneous characterization of entire genomes via high throughput genotyping of Single-nucleotide polymorphisms (SNPs)or sequencing of the genome to evaluate human genetic variation, future gene and gene-environment studies of malocclusion can be performed on precisely defined phenotypes. This will provide valuable insights into the etio-pathogenesis underlying malocclusion[3].

Tung Yuen et al.,[4] surveyed class I occlusion with crowding in the Hong Kong Chinese population using MassArray technique for the first time and conclude that there is link of EDA and XEDAR genes in dental crowding in Chinese population (Table 1).

Both genetic and environmental influences play a role in the development of Class II malocclusion. Studies of Class II division 1 patients have shown that this condition is heritable and is consistent with a polygenic mode of inheritance. A polygenic model implies that a number of genes with small additive effects provide genetic predisposition to the phenotypic expression observed in the class II division 2 malocclusion. Gutierrez et al.,[5]analyzed four Colombian families with Class II malocclusion and found the be homozygous for the rare allele in SNP on the Nog gene (Table 1).

Evidence from previous studies also established that class III malocclusion is strongly influenced by the genetic factors. May be class III malocclusion had developed by polygenic or monogenic mode of inheritance. But the environmental factors also responsible for this trait.

Few works has been done to evaluate the quantitative role of heredity in the etiology of this condition. Various studies discussed various susceptible loci and genes for the class III malocclusion. DUSP6, EPB41, IGF1, HOXC, COL2A, TGFB3, LTBP2 (Table 1)are the mostly founded genes for class III malocclusion[6-9].

Genetic analysis is an important tool in clinical Orthodontics. The etiological diversity is the main complicating factor for treatment and diagnosis in various types of malocclusions. But it still need time to be better accepted by dentists and explore the advantages.

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Table 1. Type of malocclusions and related genes in mutation.

Class I malocclusion	Class II malocclusion	Class III malocclusion
EDA	NOG	IGF1, EPB41, TGFB3, COL2A1
XEDAR		LTBP2, HOXC

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