ABSTRACT ID: 49
Oral

Analysis Of *MYO1H* Single Nucleotide Polymorphism In Class III Malocclusion With Mandibular Prognathism: A Preliminary Study

Siti Nazirah Yahya[a] | Nurul Syafiqah Abdul Razak[a] | Noraini Abu Bakar[b] | Khairani Idah Mokhtar[c] | Azrul Fazwan Kharuddin[d]

[a]Kulliyyah Of Dentistry, IIUM | *[b]Unit Of Orthodontics, Kulliyyah Of Dentistry, IIUM* | *[c]Unit Of Oral Biology, Kulliyyah Of Dentistry, IIUM* | *[d]Kulliyyah Of Science, IIUM*

Introduction: Evidence suggests that several genes; including *MYO1H*, play an important role in the etiology of Class III malocclusion. Single nucleotide polymorphism (SNP) in marker rs10850110 (locus 12q24.11) within *MYO1H* gene has been associated with the incidence of mandibular prognathism (MP). MYO is a class 1 myosin that is responsible for the synthesis of Matrilin-1; an important protein involved in the formation of cartilage's extracellular matrix, hence is implicated in the formation of mandibular condyle cartilage. This study aimed to detect the presence of *MYO1H* (rs10850110) SNP and to determine its genotype and allele distribution in MP patient in the local population. **Materials and Methods:** The sample comprises of 31 patients; 14 patients from class I malocclusion (control samples) and 17 patients from class III malocclusion (MP). Cephalometric measurements were performed prior to saliva samples collection. The DNA was amplified using the specific primers for the marker rs10850110 and the genotyping was done by sequencing. Chi-square test was used to determine the over-representation of marker allele ($p<0.05$). **Results:** Presence of *MYO1H* SNP (rs10850110) was detected in local population analysed and the distribution of its genotype and allele could be observed. There were significant differences between allele ($p=0.000$) and genotype ($p=0.000$) frequency within control (Class I) and Class III malocclusion. **Conclusion(s):** Our findings are in agreement with previous studies suggesting positive influence of *MYO1H* (rs10850110) SNP in the incidence of MP. Further studies should be developed in order to understand the exact role and mechanism of *MYO1H* in different classes of malocclusions.

KEYWORDS: malocclusion, mandibular prognathism, gene polymorphism, *Myo1H*