**ABSTRACT**

**Background:** The genetic impact directly or indirectly predefines maxillofacial dimensions, potentially leading to an inappropriate relationship of the jaws and subsequently skeletal malocclusion. The effect of genetic factors have been reported to be associated with mandibular and maxillary prominence or deficiency, naso-labial angle, nasal shape, anterior face height, width of the face and in craniofacial phenotypes. An understanding of the genetic factors underlying malocclusion will improve an orthodontist’s diagnostic and treatments modalities. Therefore this study set out to investigate any association between skeletal Class II Div.1 malocclusion and genes polymorphism and study the association of gene polymorphisms with the maxillary and mandibular bone dimentions.

**Material and methods:** Pre-treatment lateral cephalometric radiographs were utilized for phenotyping assessment of all subjects. The lateral cephalograms were imported into Dolphin Imaging software for digitization and further investigation. Accordingly, sixty patients were classified into two groups Skeletal Class I (n=30) and Class II division 1 (n=30). Saliva sample was collected and DNA was extracted and sent for Sanger sequencing. Using the software eight anatomical hard tissue points (point A, point B, Nasion (N), Sella (S) , Gnathion (Gn), Menton (Me), Gonion (Go) and Condylion (Co), three angular measurements (SNA,SNB.ANB) and four linear measurements (Sella-Gonion (S-Go), Nasion-Menton (N-Me), Condylion-Gnathion (Co-Gn) and Condylion-A point (Co-A) were measured and analysed. Pilot study was performed on ten samples (five from each group) as a result two genes were identified and selected (*BMP2* and *MYO1H*) for further investigation. Lateral cephalometric radiographs measured the maxillary and mandibular length, anterior and posterior facial high and anterior–posterior relationship of maxillary and mandibular bone. Hardy-Weinberg equilibrium analysis of genotype frequencies was performed using Chi-square test to compare genotype distribution among groups and multiple logistic regression analysis was performed.

**Results:** The rs235768 polymorphism in *BMP2* was associated with hypodivergent face, increased maxillary length and decreased mandibular length. Meanwhile, the rs11066446 polymorphism in *MYO1H* was associated with decreased mandibular length. New polymorphism was identified in *MYO1H* (rs10850090) in association with decreased mandibular length.

**Conclusion:** A potential association between polymorpisms in *BMP2* rs235768, *MOY1H* rs11066446, rs10850090 and Class II division 1 malocclusion. New polymorphisms (three) were identified in *MYO1H* gene one of them (rs10850090)was significantly associated with decreased mandibular anterio-posterior length in Cl.II div.1 malocclusion

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جامعة بغداد

كلیة طب الأسنان

رسالة مقدمة الى
مجلس كلية طب الأسنان/جامعة بغداد
كجزء من متطلبات نيل درجة الماجستير في تقويم الاسنان

من قبل

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