UNIVERSITI TEKNOLOGI MARA

PROTEIN EXPRESSION PROFILES POST ORTHODONTIC TREATMENT BY SALIVARY PROTEIN ANALYSIS

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ABSTRACT

The biological reactions involved in post-orthodontic treatment relapse have been the topic of research interest for many years but the knowledge in this field is rather limited. It has been postulated that biological mechanism in relapse is similar to active orthodontic tooth movement with various involvement of interactions at molecular level. Proteomic analysis of known orthodontic biological mediators and bone biomarkers could also provide novel and relevant information about the progression of orthodontic treatment. It may allow for some degree of prediction of a given patient's response to orthodontic force application. The research aim was to detect the protein expression in the saliva of post-treatment orthodontic patients. This research was based on the data obtained from the saliva samples of post-orthodontic patients at debond (T1), 6 months post-debond (T2) and also from non-orthodontic patients as control. A total of 5 ml of unstimulated whole saliva were collected through passive drooling and immediately centrifuged at 10,000 rpm, 4^{o}C for 10 minutes. The supernatant were collected and aliquoted into centrifuge tubes and stored at -80^{o}C. The pellets were discarded. Samples were then subjected to Liquid Chromatography Mass Spectrometry (LC-MS). The data was analysed to identify the differences of protein expressed between groups. Venn diagram was used to detect the co-expressed proteins between groups whilst PANTHER software was used for further identification of related biological process involved. Clinical result showed no relapse more than 3mm were found thus, no relapse group could be formed. Hence, the comparison of expressed protein between relapse and non-relapse group could not be made. 146 proteins were expressed in control group, whilst 128 protein and 135 proteins were expressed in debond and 6 months post-debond group respectively. Two types of proteins namely Laminin subunit gamma-3 and Putative WASP homolog associated protein were identified to be co-expressed in all groups while a total of six, eight and fifteen proteins were identified to be co-expressed between control and debond group, debond and 6 months post-debond group and control and 6 months post-debond group respectively. These proteins could be involved in various biological processes. The processes were similar for all groups. The proteins involved in locomotion and innate immune system were only detected in the debond and 6 months post-debond group. From T1 to T2, even though no relapse was observed, changes were detected in the number and biological processes of protein expressed that could be used to monitor the stability of orthodontic treatment. As a conclusion, differences in protein expression were detected between non-orthodontic and orthodontic groups. The main biological difference between these two groups is the presence of response to stimulus, locomotion and immune system process. The proteins of immune system related with inflammatory mediators were identified and their roles have been recognized. Thus, it can be suggested that, the proteins involved in immune response, response to stimulus and locomotion process could be used as biomarkers in monitoring outcomes and stability of completed orthodontic treatment.

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CHAPTER ONE
INTRODUCTION

1.1 Research Background

The main objective of orthodontic intervention outcomes is to produce a normal or so-called ideal occlusion that is morphologically stable, aesthetically and functionally well adjusted. Unfortunately, long-term stability after orthodontic treatment is unpredictable and vary among individuals (Bondemark et al., 2007; Francisconi et al., 2014; Gardner & Chaconas, 1976; Little et al., 1981). The tendency of relapse to occur is considered when there is a presence of contact point displacement after the correction of malocclusion with active orthodontic treatment (Horowitz & Hixon, 1969).

Most orthodontic stability studies were carried out for long term duration up to 20 years (Artun et al., 1996; De la Cruz et al., 1995; Francisconi et al., 2014; Little & Riedel, 1989; Little et al., 1981; Renkema et al., 2008) and majority of the relapse findings were collected from the case records of patients such as dental casts. According to Little (1999), the degree of anterior crowding that develops after retention is unpredictable and highly variable. The length of retention, age at the start of treatment, angle classification, sex, or any dental cast or cephalometric measured variables were proven to be unable to serve as reliable predictors for future success or long-term stability. This is also supported by Birgit Thilander (2000), who suggested that no parameter can be systematically used to predict the potential relapse tendency even with; 1) long-term follow-up of orthodontic patient post-retention, 2) differences in gender and type of treatment (i.e. extraction or non-extraction) 3) dental parameters and 4) cephalometric parameters. A study by Myser et al. (2013), evaluated the long-term post-treatment changes of orthodontically corrected mandibular anterior malalignment. They found that only 26% of the patients experienced crowding and irregularity (> 3.5 mm) post-retention. Additionally, Myser et al. (2013) highlighted that growth variables and interarch variables (incisor-mandibular plane angle, interincisal angle, overbite, and overjet) were not significantly related to malalignment.