

Detection of *Tannerella forsythia* from saliva samples in different ethnic majority groups in Sarawak

Elexson Nillian^{a*}, Grace Bebey^a, Fatin Nabilah Ngu^a, Nur Diyana^a, Amirah Zakirah^a, Eddy Boli^a,
Melvin Chung Hsien Liang^b

^aFaculty of Resource Science and Technology, University Malaysia Sarawak, 94300, Kota Samarahan, Sarawak, Malaysia

^bFaculty of Medicine and Health Sciences, University Malaysia Sarawak, 94300, Kota Samarahan, Sarawak, Malaysia

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Abstract. Nowadays racial and ethnic differences in health care has become a growing concern. It is one of the critical determinant in influencing the genotype of the host in which may results in some diseases such as periodontal disease. *Tannerella forsythia* can be found in oral cavity and have the strongest relation in resulting on the destruction of connective tissue in periodontal disease. This research is aim to investigate the prevalence of periodontal pathogens, particularly *T. forsythia* in four major ethnic groups in Sarawak which may result in periodontal disease in Sarawak. This disease may due to the results from the infection of the tissue supporting the teeth. A total of (n = 40) saliva samples consist of 10 samples for each ethnic groups such as Iban, Malay, Chinese and Bidayuh were collected in Kuching and Kota Samarahan using culture-independent method. The DNA was extracted from saliva based on Phenol Chloroform Isoamyl Alcohol method. After that, 16S rRNA gene was then amplified via PCR for bacterial detection using 27 F and 1492 R primers, followed by PG-F and PG-R primers set in identifying *T. forsythia*. The PCR product was observed on 1.5% gel electrophoresis. As a result, the presence of bacteria *T. forsythia* was found more frequently from saliva samples of ethnic in Iban (70%), followed by Malay (60%), Bidayuh (60%) and lastly Chinese (50%). The differences of demographic, certain cultural beliefs and practices might affect the oral health status. This finding show that it may help to identify the risk groups and has contributed an additional evidence for the association between ethnicity and periodontal disease.

Keywords: *T. forsythia*, Sarawak Ethnic group, periodontal disease

INTRODUCTION

Approximately more than 1000 of bacteria species are present in the human body, in which some of it may promote health while the others may lead to certain disease (Li *et al.*, 2014). The oral cavity consists of a wide variety of oral microbiome which consist of over 700 different bacterial species. The component of these microbial populations in the community plays a crucial aspect in ecological balance (Aas *et al.*, 2005). Bacterial DNA in saliva is important in the

microbiological studies which can also act as an indicator in monitoring health and for disease diagnosis (Yoshizawa *et al.*, 2013). However, increase in the number of the oral bacteria may also lead to human oral disease such as caries disease and periodontal disease (Paster *et al.*, 2001; Dewhirst *et al.*, 2010).

Periodontal disease has been recognized as the most common human infections (Camelo-Castillo *et al.*, 2015). Nasruddin *et al.* (2014) stated that the

*Author for correspondence: Elexson Nillian, Faculty of Resource Science and Technology, Universiti Malaysia Sarawak, 94300 Kota Samarahan, Sarawak, Malaysia. Email – nelexson@unimas.my