

Abstract ID: 203

Non-clinical

POSTER

Genome Comparison of *Actinomyces Naeslundii* with known Probiotics

Noor Afifah Hanin Mohamad¹, Mohd Hafiz Arzmi², Noratikah Othman²

¹*Department of Basic Medical Sciences, Kulliyah of Nursing Internasional Islamic University Malaysia, Kuantan, Pahang, Malaysia*

²*Department of Fundamental Dental and Medical Sciences, Kulliyah of Dentistry, Internasional Islamic University Malaysia, Kuantan, Pahang, Malaysia*

Introduction: *Actinomyces naeslundii* is an oral microbiome that has been suggested to involve in actinomycosis particularly in immunocompromised patients. However, studies have also shown that the bacterium can inhibit the colonisation of *Candida albicans* and cariogenic bacterium, *Streptococcus mutans*. Even though various studies have been conducted to characterise *A. naeslundii*, however, the role of the bacterium in the oral cavity either to induce pathogenicity or to improve oral health remain unclear. The objective of this study is to determine the role of *A. naeslundii* in the oral cavity using bioinformatic tools with the hypothesis that *A. naeslundii* possesses genome similarity to oral probiotics. **Materials and method:** The study was conducted by data mining of the genomic sequences of *A. naeslundii* NCTC10301 from GenBank. Following that, genomic comparison was performed with 25 species of well-known probiotics. MAUVE version 2.3.1 was used to find similarities between *A. naeslundii* with the known probiotics through identification of potential relevance probiotic properties in *A. naeslundii*. Phylogenetic tree was constructed using PHYLIP package to identify evolutionary relationship of *A. naeslundii* with the known probiotics. The 16s rRNA sequences of *A. naeslundii* and known probiotics were harvested from GenBank using BLAST. Finally, the functions of all *A. naeslundii* genes that shared similarity with known probiotics were identified using INTERPRO. **Result:** Genome comparison analysis of the present study showed that *A. naeslundii* genome exhibited high similarity to *Bifidobacterium* species such as *B. animalis* subsp. *lactis*, *B. bifidum*, *B. longum* and *B. breve*. In addition, phylogenetic tree analysis showed that *Bacillus* species, *B. subtilis* and *B. cereus*, appeared to clade together with *A. naeslundii*, with bootstrap value of 98%. **Conclusion:** *A. naeslundii* had high similarity with probiotic *Bifidobacterium* species thus supported the hypothesis of the present study that *A. naeslundii* possesses genome similarity to oral probiotic.