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## First insight into oral microbiome diversity in Papua New Guineans reveals a specific regional signature

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# Impact of BETEL nut (*Areca catechu*) on the human oral MICROBIOME in PAPUA NEW GUINEA



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## Context



Fig 1 : Areca nut , the fruit of Areca palm.

Betel nut, also known as areca nut or 'buai', has been highly consumed in Papua New Guinea (PNG), and more widely in South and Southeast Asia for thousands of years (Fig.1). This nut is intensively traded within PNG and is chewed all across the country. However, it is a matter of public health because it can spread various pathogens, through spitting, and is known to have toxic and psychoactive effects (Singh et al, 2020). Betel chewing is also a direct cause, especially oral cancer, by its impact on a major component of human health: the oral microbiome (Hernandez et al 2017). The oral microbiome is composed of at least 700 species of bacteria, acting as regulators of human health (Freire et al, 2021). Our recent work revealed that human oral microbiome in PNG has a diversity specific to this population (Pedro et al. 2022). While the impact of betel nut on the oral microbiome is documented in Southeast Asia (Hernandez et al., 2017; Saleem et al., 2020; Uehara et al., 2021; Zhong et al., 2021), no study has been conducted in Papua New Guinea. The aim of our study is to characterize **qualitatively** and **quantitatively** the impact of betel nut consumption on the oral microbiome of individuals from PNG.

## Methods

- Sampling places : Port Moresby, Mount Wilhelm (Fig.2)
- DNA of 164 saliva samples was sequenced using Whole Genome Sequencing (25 chewers, 139 non chewers)
- Oral microbiome composition + quantitative data on the presence of betel nut in the saliva obtained with Kraken and Bracken software
- Analysis : alpha (within the individual) and beta diversity (between individuals), LEfSe (Linear Discriminant analysis effect size)

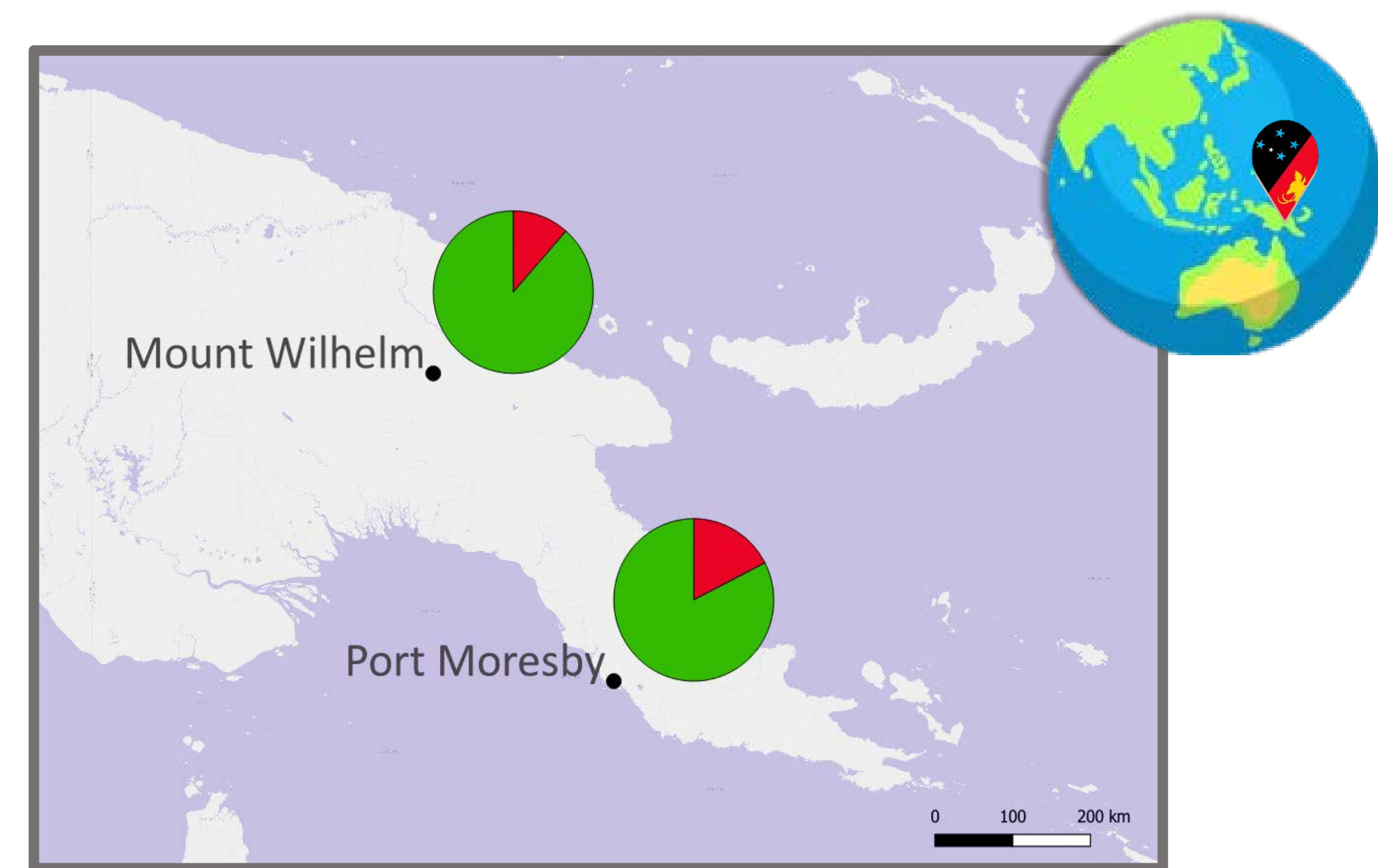


Fig 2 : Map of the distribution of betel nut chewers (in red) and non-chewers (in green) in the different sampling locations in PNG.

## Results

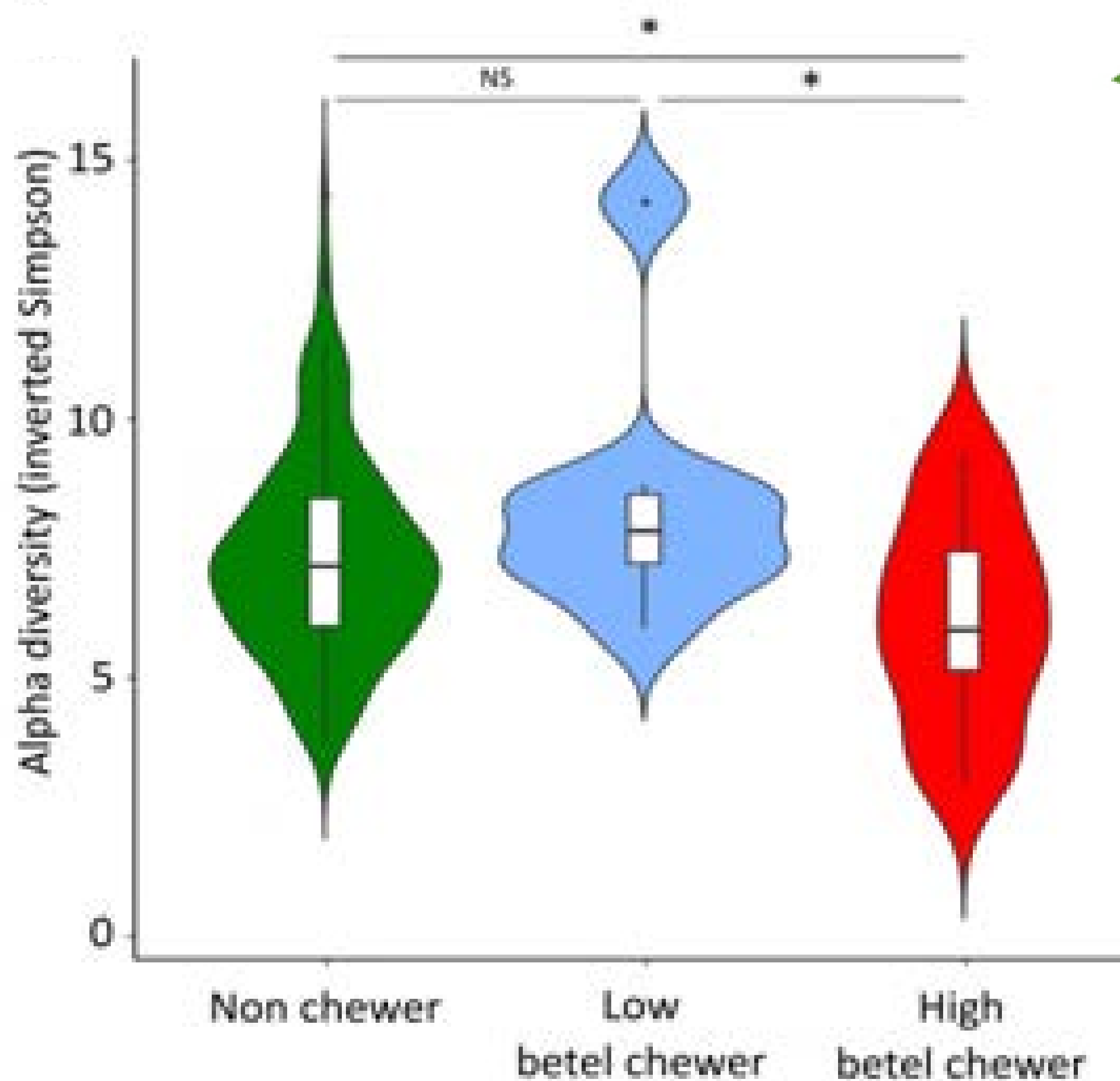


Fig 3 : Boxplot of the alpha diversity for the non chewer (in green), the low betel chewer (in blue) and the high betel chewer (in red) groups (\* :  $p < 0.05$ , NS :  $p > 0.05$ ). To measure the alpha diversity, the 164 individuals were divided into 3 groups : high betel chewers (percentage of reads  $> 10\%$ ), low betel chewers ( $10\% <$  percentage of reads  $< 0\%$ ) and non chewers (percentage of reads =  $0\%$ ).

- High betel chewer
- Non chewer

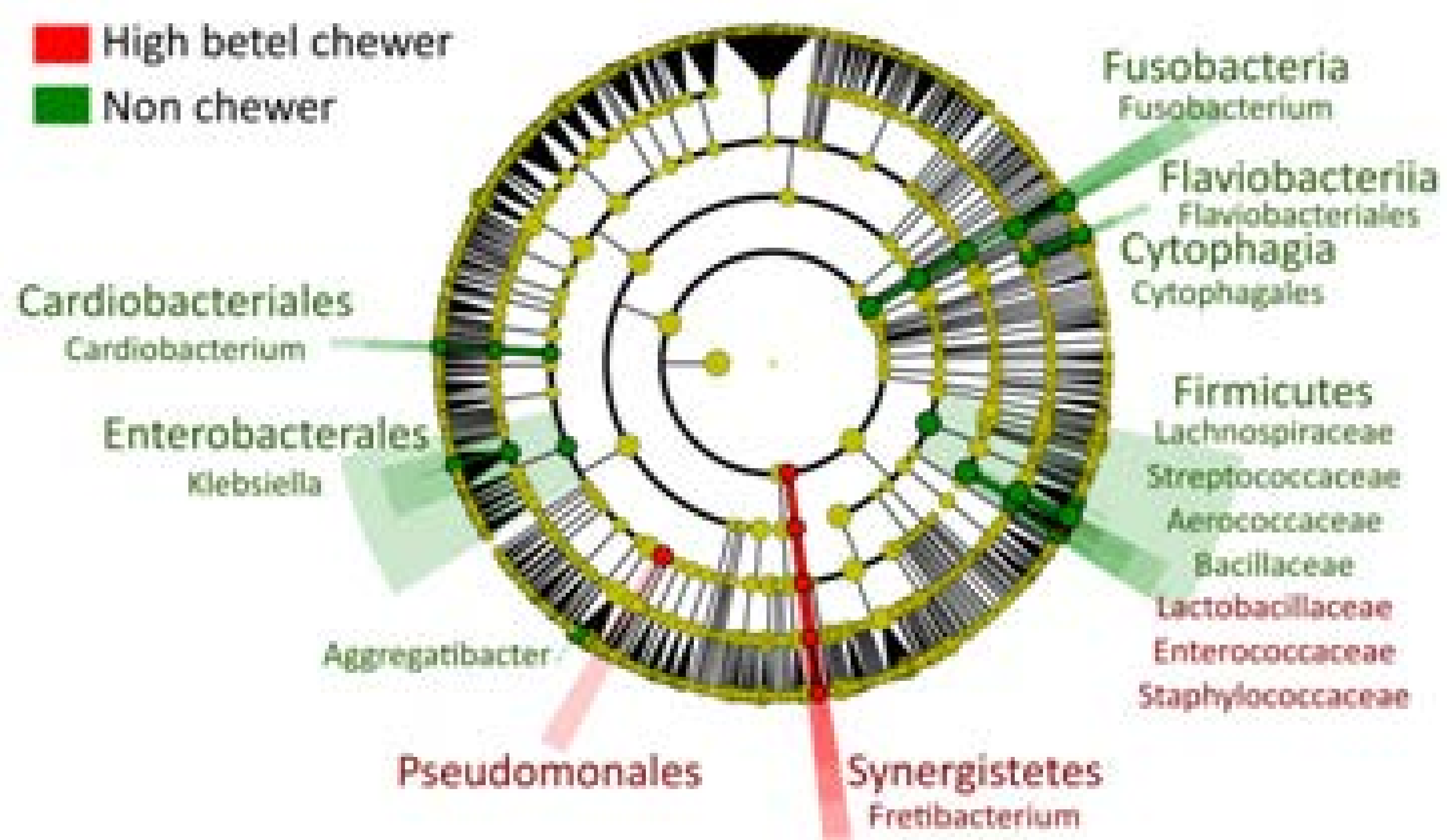


Fig 4 : LEfSe cladogram. Taxa in red are enriched in the high betel chewer group. Taxa in green are enriched in the non-chewer group.

High chewer group has a **less diverse microbiome (alpha diversity, Fig.3)** and **more heterogeneous microbiome (beta diversity)** than the two other groups.

The LEfSe analysis showed enrichment of some specific bacteria in betel chewers, especially those related **periodontal disease**, such as Pseudomonales and Synergistetes (Fig 4).

## Conclusion

The use of betel nut in PNG significantly disrupts the oral microbiome and decreases the abundance of "healthy" bacteria

### References

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