

MOLECULAR ANALYSIS OF MICROBIAL COMMUNITY DYNAMICS DURING *IN VITRO* FERMENTATION OF FIBRES DERIVED FROM THREE INDONESIAN LOCAL TUBERS BY A HUMAN FECAL INOCULUM

Z. H. Hassan, E. G. Zoetendal, H. A. Schols, H. Smidt

Each type of fibre, depending on its physicochemical properties, is differently fermented by colonic microbiota, which subsequently leads to different alterations in the microbial community composition.



Aim:

to examine the alteration on the microbial composition during *in vitro* fermentation of three different fibres derived from Indonesian local tubers : taro (*Colocasia esculenta*), cassava (*Manihot utilisima*) and sweet potato (*Ipomoea batatas*), by human fecal microbiota

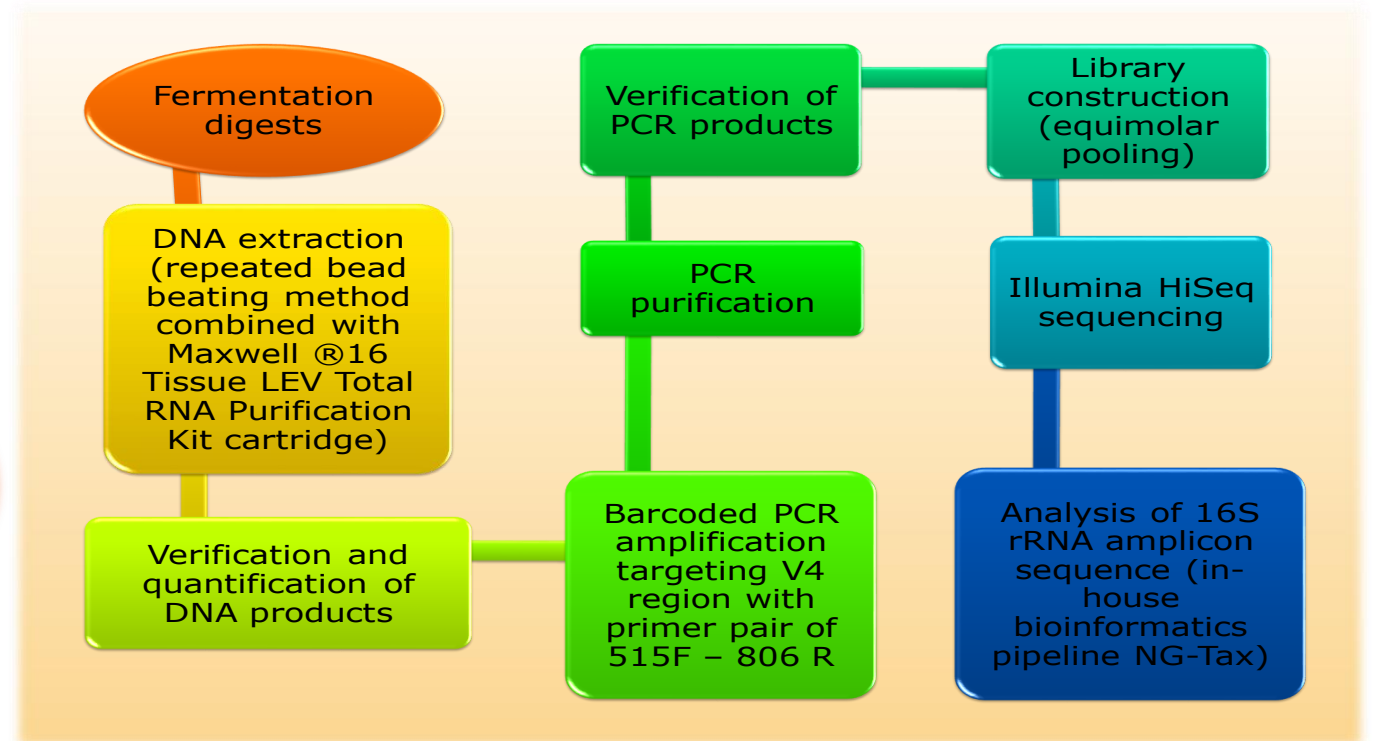


Fig 1. The scheme of work research method used in this study.

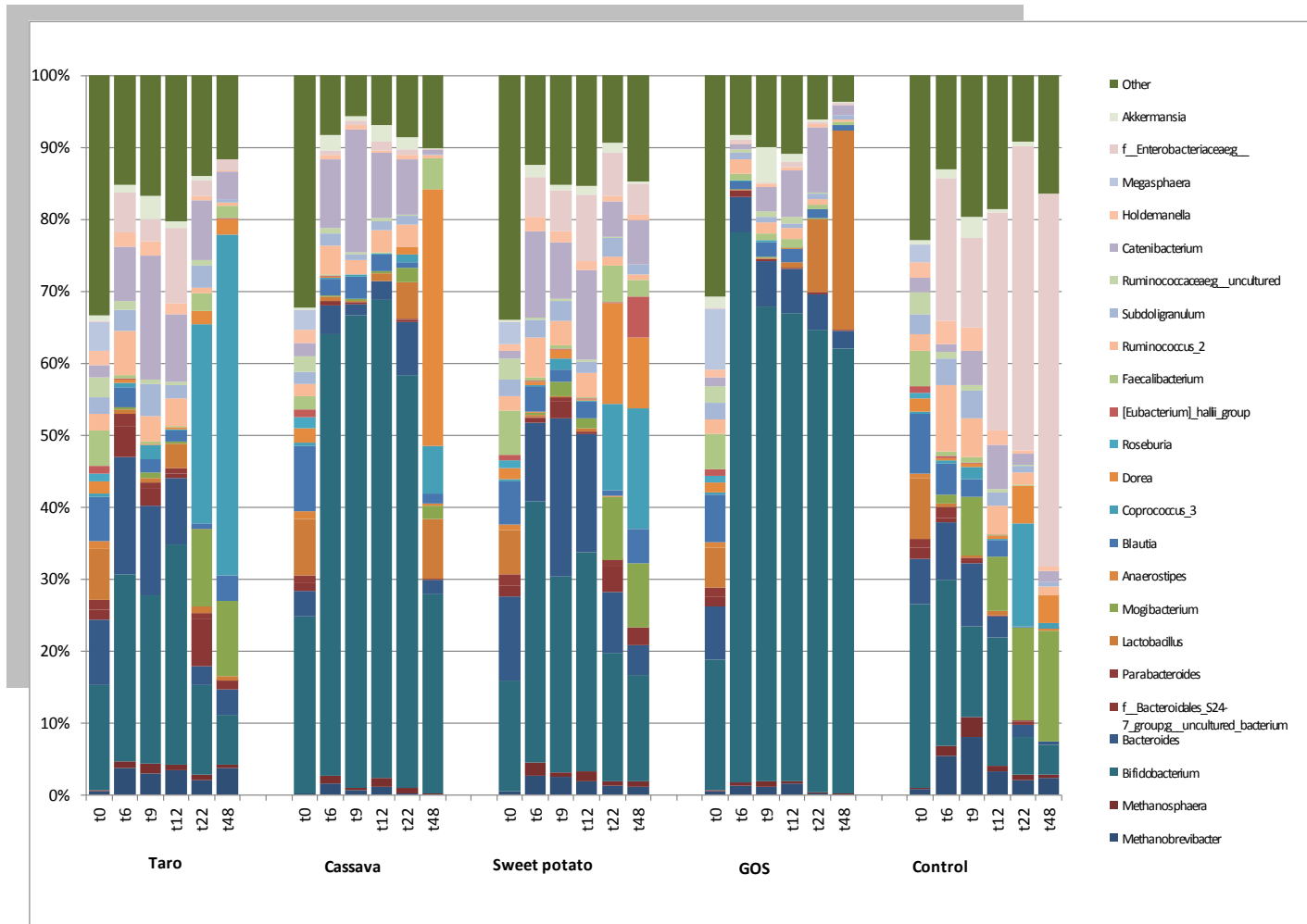


Fig 2. Genus level abundance in the fermentation digests of taro, cassava, and sweet potato fibres through time.

Conclusion

The alterations in the microbial community composition were distinctive for each fibre as a result of their unique properties.

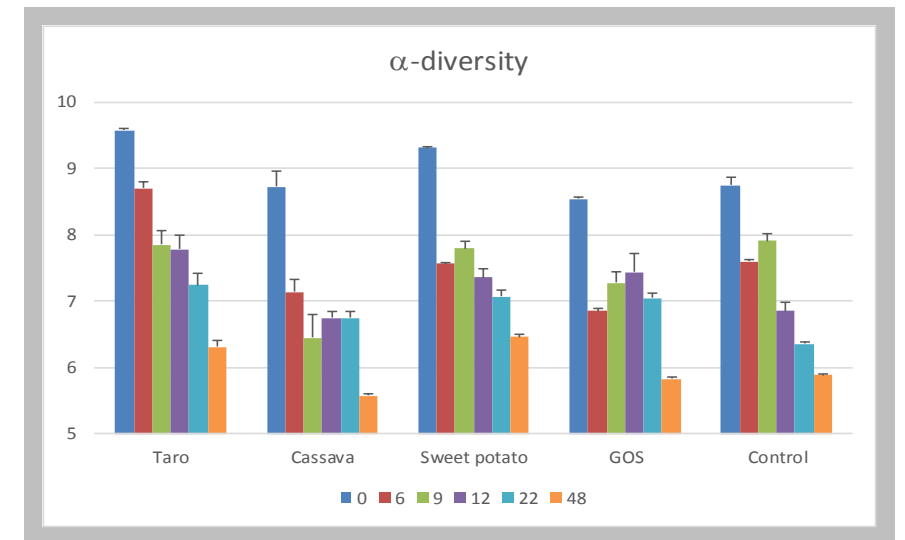


Fig 3. Alpha diversity metrics of phylogenetic diversity of the fermentation digests of taro, cassava, and sweet potato fibres through time.