

Monitoring the bacterial community of spontaneous fermentation of *Tenebrio molitor* powder by using culture-dependent and culture-independent methods.

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Tenebrio molitor (yellow mealworm) is notable for its nutritional profile, which is characterised by high biological value proteins, unsaturated fatty acids, and microelements. Concurrently, its characteristics provide favourable conditions for microbial survival and growth. This work explored the microbiota that developed during the spontaneous fermentation of a dough made from *T. molitor* powder and the creation of a fermented *T. molitor* ingredient. *T. molitor* doughs were backslopped 10 times, and bacterial communities were evaluated using viable plate counts and the identification of lactic acid bacteria (LAB) through PCR-ARDRA, as well as by targeted metagenomic sequencing of the V3-V4 region of the 16S rRNA gene. LAB concentrations in the doughs began at 10² CFU/g, then rapidly increased to approximately 10⁹ CFU/g, remaining stable until the end. The identification of LAB via the culture-dependent method revealed greater biodiversity in the initial backsloppings, with a gradual decline during the refreshments. Ultimately, only *Lactiplantibacillus plantarum* and *Levilactobacillus brevis* were detected. In contrast, the targeted metagenomic analysis showed an increase in the relative abundance of LAB towards the final backsloppings, where 10 LAB genera were found, including *Lactiplantibacillus* and *Levilactobacillus*. This increase corresponded to a reduction in unclassified bacteria; alpha diversity did not experience significant changes during the successive backsloppings. Notably, there was a significant presence of bacteria belonging to the genus *Kurthia*, known to produce chitinolytic enzymes. 8 LAB strains, isolated from the last back-slopping, were tested for their acidification and growth capacity in *T. molitor* powder for ingredient production. The fermented and dried ingredients exhibited a decrease in the *Enterobacteriaceae* population. This research enhances our understanding of bacterial dynamics in these specific matrices and provides a preliminary assessment of their potential for food applications.