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Metagenomic analysis of an African beer ecosystem using FoodMicrobiomeTransfert application

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Tchapalo is a traditional beer produced in Ivory Coast. Its production results from a two-step fermentation of sorghum: first a spontaneous lactic fermentation yielding a sour wourt, and then, an alcoholic fermentation leading to Tchapalo. This cloudy beer has a low alcohol-content, a short shelf life (about 3 days) and its quality varies from a production to another. The precise composition of Tchapalo ecosystem is unknown, and a metagenomic approach could help to better characterize this flora and identify precisely the strains involved in Tchapalo manufacturing.

To analyze this ecosystem, we used FoodMicrobiomeTransfert, a tool we developed for metagenomic analysis of food ecosystems (<http://migale.jouy.inra.fr/foodMicrobiome/>). This tool, based on a mapping of the metagenomic reads on a reference genome database, identifies, for each reference genome, which genes are present in the ecosystem and gives the percentage of differences with the reference genome. It allows the user to analyze metagenomic samples via a user-friendly web interface. The user can upload metagenomes and reference genomes, choose reference genomes used for the analyze, analyze results, and share data with colleagues. Computations are performed transparently for the user on Migale platform's calculation cluster via the Bioblend API and a Galaxy portal. The web interface was developed using the Python Django framework and JavaScript for web interfaces. All the data are stored in a PostgreSQL relational database.

To illustrate the power of this tool, we will present a detailed analysis of Tchapalo ecosystem composition combining cultural, metabarcoding and metagenomic approach. In particular we performed 23 metabarcoding analysis on samples collected in different traditional producers in Abidjan, and that were further analyzed by metagenomics using ~10 million 150bp HiSeq reads. Our analysis showed that Tchapalo lactic fermentation is carried out mainly by 2 *Lactobacillus* species, with 5-8 other species of lactic acid bacteria present at low level. Interestingly, one of the major species appears to be poorly cultivable and its genomes reduced compared to other strains of this species. Analysis at the nucleotide level revealed that several strains of this species are present in each sample.