

BeerDeCoded: exploring the beer metagenome

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BeerDeCoded is a project carried out by members of Hackuarium, a Swiss not-for-profit association that supports unconventional research ideas and promote the public understanding of science by making laboratory tools more accessible. The goal of BeerDeCoded is to extend scientific knowledge about beer, while discussing issues related to personal genomics, food technology, and their role in society with the general public. Two years ago, a crowdfunding campaign provided funding for the first stage of the project. Reaching out through this channel also allowed to collect 120 beer samples from 20 countries.

We have now obtained the metagenomic profiles for 39 of these beers using a targeted approach (ITS). We have demonstrated that it is possible to extract DNA directly from bottled beer using low cost methodologies available to citizen scientists. DNA sequenced from these samples identified a variety of wild yeast species in commercial beers. For example, some brews contain traces of more than 30 different fungal species. Brewing is a complex process and it is unclear if the beer microbiome can directly affect the final beer taste or texture and how it could be controlled to create beers with a specific character.

To answer these questions, we are collecting information about the brewing process to correlate the metagenomic profiles with metadata related to the brewing process. For instance, using a hierarchical clustering approach, we built a proximity tree of the different beers. This analysis revealed that two stouts brewed in the same city have a similar wild yeast content. However, there is currently limited access to information about the recipe of commercial beers. A notable exception is BrewDog, a craft brewery from Scotland that recently released all its brewing recipes. We would like to use this resource and pair it with a new protocol based on a portable DNA sequencer to build the proof of concept for a beer metagenome analysis pipeline that could be used in high schools, citizen science laboratories, craft breweries or industrial plants.

Altogether, we demonstrated that coupling simple laboratory procedures with DNA sequencing and metagenomic analysis can allow the detection of the microbial content in commercial beer and can easily trigger a tripartite conversation between the general public, the scientists and professional brewers. The next step is to set up an open repository where these parties can add the metagenomic profiles of their favourite beers, expanding the database and allowing researchers to test new analyses, brewers to try new recipes and the general public to discover more science and more beers.