



Julie Birgel, Kamila Canale Tabet, Thibault Leroy

GenPhySE, Université de Toulouse, INRAE, ENVT, Castanet Tolosan 31326, France

The degradation of honey quality, along with the lack of traceability, are main concerns in the apiary industry. The globalization of trade markets has indeed led to large-scale exchanges of bee products, often with limited knowledge of their geographic origin. These long commercial channels make them furthermore particularly vulnerable to fraud. As a matter of fact, honey is considered to be the third most fraudulent food production worldwide. Due to the unfair competition with imported low-cost products, it represents a serious challenge for the beekeeping sector and its sustainability in many countries. The current state-of-the-art chemical and mellisopallinological methods aiming at detecting adulteration (e.g., mixing syrup with honey) or misdeclared geographical origin are still not sensitive enough to systematically highlight those frauds. To overcome these limitations, we propose to develop an alternative and more resolutive approach using a molecular technique called metagenomics. This method allows the analysis of shotgun sequencing data generated from the overall DNA content of an environmental sample (eDNA). Applied to honeys, it offers the possibility to access a large range of eukaryotic and prokaryotic species related to bees, including plants, fungi, and microorganisms. To be exhaustive, we analyzed sequencing data from 450 honey samples coming from a great diversity of geographical origins, combining data generated in our laboratory and those available in public databases. One of our first objectives was to evaluate the presence of bee DNA, which can be informative on the geographical origin of honeys. Our results highlight that we successfully were able to identify a fraction of DNA corresponding to honey bees in all the samples (mean = 12.76%). It should be noted that this proportion can vary widely from one honey sample to another (from 0.1% to 80% of all the reads sequenced). The next step of our analyses will be to continue this characterization, in order to identify the different plant species that could serve as biotracers to enhance honey traceability. The overall aim of our research is to determine whether genomic and metagenomic approaches will represent a promising strategy to address the current challenges facing the beekeeping industry mentioned previously.