biology and life sciences forum

MDPI

Proceeding Paper

Analyzing Botanical Origin of Honey Content via Metabarcoding †

Pelin Taş [1,2] and Emre Keskin [2,*]

[1] Biotechnology Institute, Ankara University; pelintas1989@gmail.com
[2] Evolutionary Genetics Laboratory (eGL), Department of Fisheries and Aquaculture, Agricultural Faculty, Ankara University,
* Correspondence: amfibiksubstans@gmail.com
† Presented at the 3rd International Electronic Conference on Foods: Food, Microbiome, and Health—A Celebration of the 10th Anniversary of Foods' Impact on Our Wellbeing; Available online: https://foods2022.sciforum.net.

Keywords: metabarcoding; environmental DNA (eDNA); honey; botanical origin; high throughput sequencing

Currently, honey fraud and adulteration have become a global issue. Due to the ongoing finding of new ways to circumvent old analyses, new analysis techniques are being evolved. One of the molecular-based techniques, DNA metabarcoding, allows for the rapid and accurate identification of short genetic markers in the DNA of various species by matching them with reference sequences. Using this identification, it is frequently able to go beyond the species and determine the regional variants and geographic origin of the product. In addition to high throughput sequencing, metabarcoding is presented as an impartial method for determining the taxonomic composition of complicated materials. This study evaluated the applicability of the "DNA from honey" based approach by developing metabarcoding procedure.

A total of twenty varieties of honey were acquired from local markets. Following pretreatment, DNA was extracted from 20 samples using the optimized process, and PCR amplifications were conducted with primers targeting the P6-loop region of the trnL gene for the plant. Twenty honey samples were evaluated in a single tube, in addition to the analysis of a single flower honey. PCR yields were indexed using an adaptor ligation procedure for a 2 × 150 bp pair-ended 300 K read per sample and examined by high throughput sequencing. The terminal of the Linux/Unix-based operating system was used to analyze the sequencing data using several pipelines.

Each of the targeted taxa had a ≥97% match to a species in NCBI GenBank. Our results confirmed the vast majority of the species listed on the product label. Twenty percent of the raw data permitted identification of the species listed on the label. Additionally, the percentage of matches at the genus level exceeds 80%. In mixed honey, 90% of the honey was found to be flower honey. Some species were not identified and necessitate additional research for verification.

Citation: Taş, T.; Keskin, E. Analyzing Botanical Origin of Honey Content via Metabarcoding. *Biol. Life Sci. Forum* **2022**, *2*, x. https://doi.org/10.3390/xxxxx

Academic Editor: Firstname Lastname

Published: 1 October 2022

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