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ullah, S.[a] , Huda, N.[b] , Wahab, R.A.[c] , Hamid, A.A.A.[d] , Nasir, M.H.M.[d] , Mohamad, M.A.N.[d] , Ahmad, H.F.[e] , Oyewusi, H.A.[a] [f] , Huyop, F.[a]

Baseline amplicon sequencing data for the ITS2 region in the green honey of Banggi Island, Sabah
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[a] Department of Biosciences, Faculty of Science, Universiti Teknologi Malaysia, Johor Bahru, 81310, Malaysia
[b] Faculty of Sustainable Agriculture, Universiti Malaysia Sabah, Sabah, Sandakan, 90509, Malaysia
[c] Department of Chemistry, Faculty of Science, Universiti Teknologi Malaysia, Johor Bahru, 81310, Malaysia
[d] Research Unit for Bioinformatics and Computational Biology (RUBIC), Kulliyyah of Science, International Islamic University Malaysia, Bandar Indera Mahkota, Pahang, Kuantan, 25200, Malaysia
[e] Faculty of Industrial Sciences and Technology, Universiti Malaysia Pahang Al Sultan Abdullah, Pahang, Gambang, 26300, Malaysia
[f] Department of Biochemistry, School of Science and Computer Studies, Federal Polytechnic Ado Ekiti, Ekiti State, Ado Ekiti PMB, 5351, Nigeria

Abstract
Green honey, was discovered on Banggi Island, Sabah, showing high in essential amino acids and chlorophyll derivatives. Despite its lucrative market potential owing to its distinctive color, uncertainties persist regarding its nature. This study leverages amplicon sequencing by targeting micro- and macro-organisms present in honey environmental DNA (eDNA) using Internal Transcribed Spacer 2 (ITS2) region, enabling the identification of floral and microorganism sources that represent the honey's composition. The investigation into green honey from Banggi Island concerns the prevalence of honey adulteration and authenticity for economic gain. Adulteration methods, such as the addition of sugar syrups, compromise honey purity. Using a sequencing approach would help in determining the geographic origin and verifying the authenticity of the honey. The study aims to identify plant species or microorganisms in honey's eDNA. To authenticate honey, we utilized ITS2 with Illumina sequencing, exploring the diversity of green honey samples. Raw sequence reads obtained for the green honey sample revealed 1,438,627 raw reads, with a GC average of 49.22 %. A total of 44 amplicon sequence variances (ASVs) were identified, including three genera: Zygosaccharomyces with two species, Fraxinus with three species, and the genus Ficaria with only one species. Their respective relative abundances were 98.55%, 0.94%, and 0.51%. Zygosaccharomyces rouxii and Zygosaccharomyces mellis were identified as the pre-dominant yeast species in honey, while the Fraxinus and Ficaria genus represent common plant species in Sabah, particularly in Banggi Island. The dominance of Zygosaccharomyces species aligns with their known prevalence in honey, affirming the reliability of our findings. The presence of Fraxinus and Ficaria in the honey sample correlates with its abundance in the local environment. This amplicon sequencing approach not only contributes to our understanding of green honey composition but also serves as a valuable resource for authenticating honey origin in Malaysia, particularly for green honey from Banggi Island, Sabah. Our study pioneers the application of ITS2 amplicon sequencing for green honey amplicon sequencing, providing valuable insights into its composition and origin. This methodology, with a focus on eDNA, contributes to the authentication and quality determination of honey in Malaysia, addressing the pressing concerns of adulteration and variability in production practices. © 2024 The Author(s)

Author Keywords
ASVs; Banggi Island; eDNA; Green honey; Illumina sequencing; Internal Transcribe Spacer 2

Index Keywords
Authentication, Food products, Gene encoding; Amplicon sequence variance, Amplicon sequences, Amplicons, Banggi island, Environmental DNA, Green honey, Illumen sequencing, Illumina, Internal transcribe spacer 2, Internal transcribed spacers; Microorganisms

References
- Huda, N.
  The first ITS2 sequence data set of eDNA from honey of Malaysian giant honeybees (Apis dorsata) and stingless bees (Heterotrigona itama) reveals plant species diversity
  (2023) *BMC Res. Notes*, 16, p. 211.

- Bovo, S.
  Shotgun metagenomics of honey DNA: evaluation of a methodological approach to describe a multi-kingdom honey bee derived environmental DNA signature
  (2018) *PLoS ONE*, 13.

- Wirta, H.
  DNA traces the origin of honey by identifying plants, bacteria and fungi
  (2021) *Sci. Rep.*, 11, pp. 1-14.

- Vit, P.
  A novel integrative methodology for research on pot-honey variations during post-harvest
  (2022) *Sociobiology*, 69, p. e8251.

- Wei, S.S.
  Gut microbiome and metabolome of sea cucumber (Stichopus ocellatus) as putative markers for monitoring the marine sediment pollution in Pahang, Malaysia
  (2022) *Mar. Pollut. Bull.*, 182.

- Rustiati, E.
  Comparative study on DNA extraction's qualitative analysis of captive sumatran elephant in elephant training center, Way Kambas National Park
  (2019) *J. Phys.*,
  IOP Publishing

- Cheng, T.
  Barcoding the kingdom Plantae: new PCR primers for ITS regions of plants with improved universality and specificity
  (2016) *Mol. Ecol. Resour.*, 16, pp. 138-149.

- Glenn, T.C.
  Adapterama II: universal amplicon sequencing on Illumina platforms (TaggiMatrix)
  (2019) *PeerJ*, 7, p. e7786.

- Martin, M.
  Cutadapt removes adapter sequences from high-throughput sequencing reads
  (2011) *EMBnet. J.*, 17, pp. 10-12.

- Chen, S., Zhou, Y., Chen, Y., Gu, J.
  fastp: an ultra-fast all-in-one FASTQ preprocessor
  (2018) *Bioinformatics*, 34, pp. i884-i890.

- Bolyen, E.
  Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2
  (2019) *Nat. Biotechnol.*, 37, pp. 852-857.

- Callahan, B.J.
  DADA2: high-resolution sample inference from Illumina amplicon data
  (2016) *Nat. Methods*, 13, pp. 581-583.

- Bokulich, N.A., Mills, D.A.
  Improved selection of internal transcribed spacer-specific primers enables quantitative, ultra-high-throughput profiling of fungal communities
  (2013) *Appl. Environ. Microbiol.*, 79, pp. 2519-2526.

- Tedersoo, L.
  The Global Soil Mycobiome consortium dataset for boosting fungal diversity research
  (2021) *Fungal Divers.*, 111, pp. 573-588.

• Chong, J., Liu, P., Zhou, G., Xia, J.
  Using MicrobiomeAnalyst for comprehensive statistical, functional, and meta-analysis of microbiome data
  (2020) *Nat. Protoc.*, 15, pp. 799-821.

• Friedman, J., Alm, E.J.
  Inferring correlation networks from genomic survey data
  (2012) *PLoS Comput. Biol.*, 8.

• Segata, N.
  Metagenomic biomarker discovery and explanation
  (2011) *Genome Biol.*, 12, pp. 1-18.

• Ondov, B.D., Bergman, N.H., Phillippy, A.M.
  Interactive metagenomic visualization in a Web browser
  (2011) *BMC Bioinformatics*, 12, pp. 1-10.
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Correspondence Address
Huyop F.; Department of Biosciences, Malaysia; email: fahrul@utm.my