

Baseline amplicon sequencing data for the ITS2 region in the green honey of Banggi Island, Sabah

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 microand 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