The first ITS1 profiling of honey samples from the Southeast Asian region Lombok, Bali and Banggi Island

ABSTRACT

Southern Asian fowers ofer honeybees a diversity of nectar. Based on its geographical origin, honey quality varies. Traditional methods are less authentic than DNA-based identifcation. The origin of honey is determined by pollen, polyphenolic, and macro-microorganisms. In this study, amplicon sequencing targets macro-microorganisms in eDNA using the ITS1 region to explore honey's geographical location and authentication. The variety of honey samples was investigated using ITS1 with Illumina sequencing. For all four honey samples, raw sequence reads showed 979,380 raw ITS1 amplicon reads and 375 ASVs up to the phylum level. The highest total number of 202 ASVs up to phylum level identifed Bali honey with 211,189 reads, followed by Banggi honey with 309,207 a total number of 111 ASVs, and Lombok represents only 63 ASVs up to phylum level with several read 458,984. Based on Shannon and Chao1, honey samples from Bali (B2) and (B3) exhibited higher diversity than honey from Lombok (B1) and green honey from Sabah (B4), while the Simpson index showed that Banggi honey (B4) had higher diversity. Honey samples had signifcant variance in mycobiome taxonomic composition and abundance. Zygosaccharomyces and Aspergillus were the main genera found in Lombok honey, with percentages of 68.81% and 29.76% respectively. Bali honey samples (B2 and B3) were identifed as having a signifcant amount of the genus Aureobasidium, accounting for 40.81% and 25% of the readings, respectively. The microbiome composition of Banggi honey (B4) showed a high presence of Zygosaccharomyces 45.17% and Aureobasidium 35.24%. The ITS1 analysis efectively distinguishes between honey samples of diferent origins and its potential as a discriminatory tool for honey origin and authentication purposes.