PROTEIN FINGERPRINTING OF MAY WILD HONEY (*Apis dorsata*) FROM MULTIPLE GEOGRAPHIC ORIGINS: A THREE-YEAR PROTEOMIC PROFILING STUDY

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Abstract

This study aimed to classify proteins in May wild honey (Apis dorsata) across five geographical sources using SDS-PAGE combined with LC-MS/MS, with continuous comparative data collected over three years (2024–2026) to enhance the product's economic value. Proteomic analysis revealed common protein bands consistently present across all samples within the 50.2–74.1 kDa molecular weight range, identified as Major Royal Jelly Protein 1 (49.3 kDa), Major Royal Jelly Protein 2 (51.4 kDa), and Alpha-glucosidase (65.7 kDa). In contrast, location-specific bands exhibited dynamic variation across production years. In 2024, the Ban Luang Nuea forest (Doi Saket District) yielded two specific bands corresponding to Uncharacterized protein (134.5 kDa) and Chaoptin isoform X1 (141.8 kDa), while the Ban Hong Ko Muang Song forest (Mueang Lamphun District) showed Dipeptidase PepV (52.4 kDa) and Bee-milk protein (50.2 kDa). In 2025, the same Lamphun site presented Alpha-glucosidase (65.7 kDa) and Uncharacterized protein (134.5 kDa). By 2026, prominent small protein band diversity was detected in the Ban Chom Thong forest (Chom Thong District) and Ban Luang Nuea forest (Doi Saket District), comprising Alpha-glucosidase (65.7 kDa), Alpha-N-terminal protein methyltransferase 1 (27.8 kDa), and two Uncharacterized proteins (40.2 and 42.8 kDa). These geographically and seasonally variable protein fingerprints demonstrate strong potential as biochemical markers for effectively authenticating the geographic provenance of wild honey.

Keyword: Proteomics, Geographical origin, Protein fingerprinting, May wild honey