

## Characterization of volatile profiles in Montes del Quequay honeys by HR-GC-MS and their correlation with botanical origin

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The most considered parameter for honey botanical identification is pollen composition, that is, the proportion of dominant pollen. However, it is important to note that certain plants are underrepresented in terms of pollen content, such as citrus, acacia, and lavender. Moreover, the pollen composition of honey depends on the botanical origin, the foraging distance of the bees, and the sampling method used. Consequently, the results of pollen analysis are influenced by many factors beyond botanical origin alone. In this context, the metabolomic study of volatile organic compounds in honey offers a valuable tool for deepening the understanding of its chemical composition, quality, and functional properties. Through HS-GC-MS analysis, it is possible to identify and quantify a wide range of volatile compounds that serve as markers of botanical and geographical origin, while also contributing to the bioactive properties of honey. This approach enables the evaluation of variations associated with floral environment, climatic conditions, and beekeeping practices, providing robust scientific evidence to differentiate products, protect designations of origin, and enhance their commercial value (1). Additionally, the metabolomic approach offers essential insights into the potential of honey and its role as a natural source of bioactive compounds (2). The aim of this study was to evaluate the volatile composition of honey produced across different harvests in the protected area with managed resources Montes del Quequay (Uruguay, 32°09'00"S 57°29'00"O) using HS-GC-MS, and to explore the possible relationship between polyphenol patterns and botanical origin. Honey samples (2.0g) were extracted by SPME using the Shimadzu AOC-6000 Multifunctional Autosampler equipped with a DVB/CAR/PDMS fiber. After extraction, the volatiles were directly desorbed at the injection port of a GC-MS system Shimadzu GC-2010/QP2020 using an Agilent GC capillary column (30 m × 0.25 mm × 0.25 µm), with H<sub>2</sub> as carrier. MS was programmed in electron ionization (70eV) scanning m/z from 50 to 350 amu. The volatiles were identified by comparison with commercial mass spectral libraries (Wiley, FFNSC, NIST) and by calculation of LRIs, injecting in the same conditions a n-alkane solution (C<sub>9</sub>-C<sub>26</sub>) (3). Volatile abundances were obtained directly by area normalization, without the use of correction factors. The results obtained included the identification of marker compounds, data analysis (data mining/extraction, statistical analysis), and the assessment of the potential relations between melissopalynology and metabolomics analyses.

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