

Comparing the Melissopalynological and Next Generation Sequencing (NGS) Methods for the Determining of Botanical Origin of Honey

The aim of this study is to compare the melissopalynological method with Next-Generation Sequencing (NGS) for determining the botanical origin of honey. Forty honey samples were selected by considering the total number of pollen, honeydew elements, and dominance pollen status to facilitate NGS analysis. The quality of the isolated DNAs was determined by spectrophotometric and electrophoretic methods. Presence of possible amplification inhibition factors in isolated DNA was determined by amplification of 18S rRNA region..