USING DNA METABARCODING IN POLLEN SAMPLES FOR THE IDENTIFICATION OF FLORAL SPECIES

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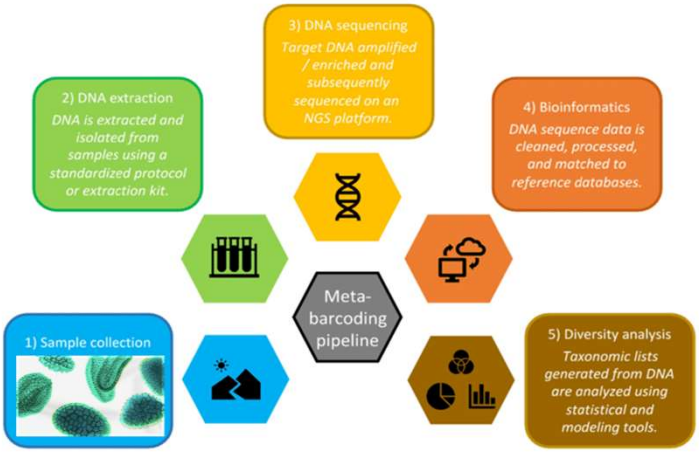
Introduction

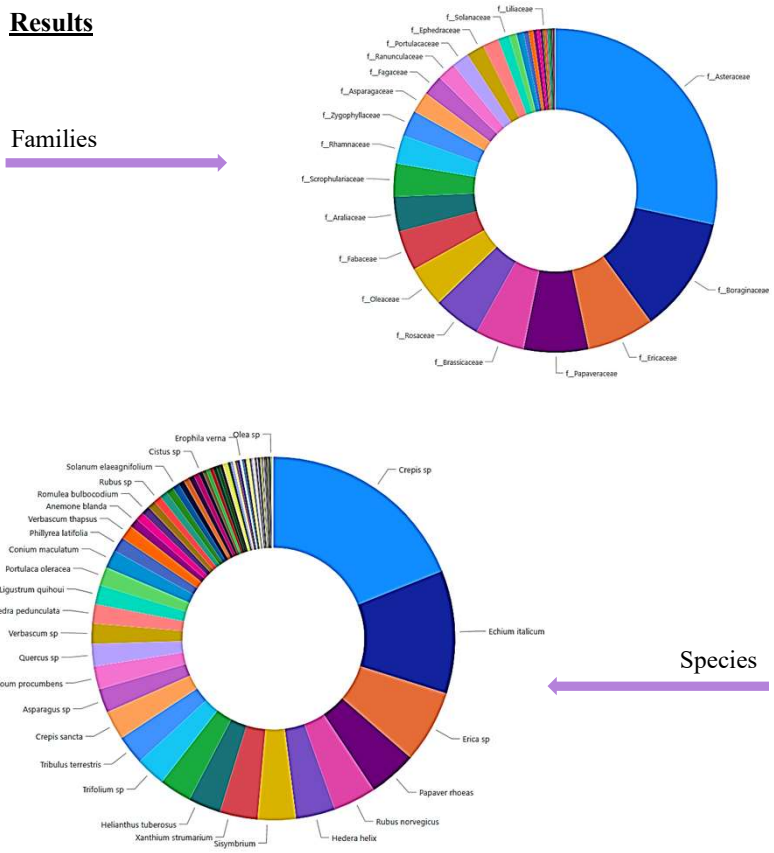
During the last decade numerous studies have highlighted the importance of DNA metabarcoding in pollen samples collected from pollen traps and honey, to identify floral visitation across honeybees. In the presented study, 40 pollen samples collected from pollen traps that were attached in selected beehives around Peristera (Thessaloniki region).

Materials & Methods

Pollen samples were preserved at -20ºC, until DNA extraction was performed according to the protocol from NucleoSpin™ Plant II kit (Macherey-Nagel, Germany). PCR amplification of extracted DNA was performed using primers that target the ITS2 region. Multiplexing and library preparation was performed according to Illumina's 16S Metagenomics Protocol with modifications using the Nextera® XT Index Kit. The libraries' pool was loaded on the Illumina Miseq (2 x 300 bp) using a MiSeq® Reagent Kitv3. Raw sequence data was processed using the DADA2 ITS Pipeline within Galaxy.



Results



Conclusions

- Ten most abundant plant families detected were: Asteraceae, Boraginaceae, Ericaceae, Papaveraceae, Brassicaceae, Rosaceae, Oleaceae, Fabaceae, Araliaceae and Scrophulariaceae.
- Ten most abundant plant species were: *Crepis sp*, *Echium italicum*, *Erica sp*, *Rubus norvegicus*, *Papaver rhoeas*, *Hedera helix*, *Sisymbrium sp*, *Xanthium strumarium*, *Helianthus tuberosus* and *Trifolium sp*.
- DNA metabarcoding provide researchers a powerful tool for a large-scale identification of known and unknown taxa within a mixed pollen sample using specific DNA barcode markers and high-throughput sequencing.

References

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European Union
European Regional Development Fund

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«Co-financed by the European Regional Development Fund of the European Union and Greek national funds through the Operational Program Competitiveness, Entrepreneurship and Innovation, under the call RESEARCH-CREATE - INNOVATE (project code: T1EDK-04396)