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PP-448 [Bee Biology]

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IDENTIFICATION OF INFORMATIVE DNA MARKERS FOR HONEYBEE RESISTANCE TO VARROOSIS

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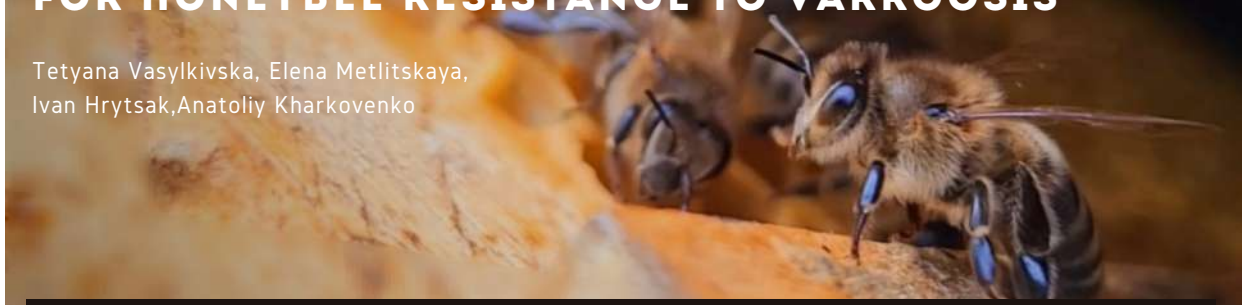


Understanding the genetic mechanisms underlying honey bee resistance to Varroa destructor is crucial for identifying DNA markers associated with this trait. This may enable marker-assisted selection to improve the genetic structure of bee populations. Key resistance-related behaviors, such as hygienic behavior and grooming, contribute to mite control in colonies. Hygienic behavior, which involves the removal of dead or infested brood, is controlled by multiple genetic loci (Spötter et al., 2012). Grooming behavior, including self-grooming and mutual grooming among worker bees, remains less studied in terms of inheritance mechanisms (Traynor, Mondet 2020).

AIM

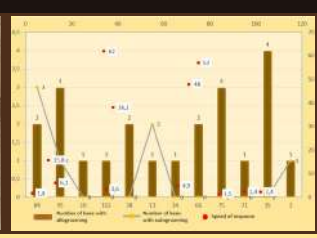
The aim of this study was to evaluate the informativeness of three ISSR primers for the detection of genetic polymorphisms associated with honey bee resistance traits, in particular grooming behaviour.

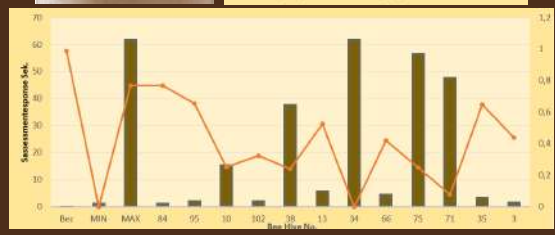
METODS

The research was conducted at an apiary in Donets village, Kharkiv region, Ukraine, where 57 colonies were assessed morphometrically. The colony composition included A.m. carnica (78%), A.m. macedonica (A.m. sossimai) (20%), and A.m. buckfast (2%). Only A.m. carnica (var. ukrainica carpatica) colonies were selected for further analysis. Based on ethological assessments, two groups of seven hives were formed, representing high and low grooming activity. Worker bees were collected, preserved in ethanol, and stored at -20°C before DNA extraction using the NeoPrep100 DNA Magnen Plant kit. PCR amplification was performed using primers S1, S6, and S8 under previously established conditions (Metlytska, 2012), with amplicon separation in 2% agarose gel.

RESULTS

The analysis of ISSR-PCR electrophoregrams revealed a significant level of polymorphism only with the ISSR-S1 primer: (AGC).C. The other primers used were not informative for detecting genetic differences between the studied honeybee groups. The use of ISSR-S1 identified amplicons of 500, 550, and 600 bp in bees from resistant lineages, whereas these fragments were absent in bees with low grooming behavior. The presence of ISSR-S1 marker loci in colonies exhibiting high grooming activity suggests potential genetic determinants of varroosis resistance. However, due to the anonymous nature of ISSR markers, further sequencing of identified amplicons is required to determine their chromosomal localization and genomic function. Additionally, subspecies variations in bee grooming behaviour and mechanisms of its inheritance require further study.





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Identification of Informative DNA Markers for Honeybee Resistance to Varroosis

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