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PP-407 [Bee Biology]

A rapid cost-effective genotyping method for Africanized *Apis mellifera* bees with high honey production potential

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INTRODUCTION

Beekeeping has increasingly incorporated technological advancements, particularly in genetic improvement and colony selection for high honey productivity, aiming to enhance profitability. However, most beekeepers still rely on capturing migratory swarms, dividing colonies, and purchasing colonies from other producers, without implementing any structured breeding program. These practices may reduce efficiency and competitiveness, highlighting the need for precise and accessible genetic selection techniques.

OBJECTIVES

This study aimed to develop a rapid and cost-effective genotyping kit for high honey-producing colonies using the G-quadruplex PCR technique. A total of 220 colonies from 10 beekeepers in the Pólo Cuesta region, São Paulo, Brazil, were evaluated.

MATERIALS AND METHODS

Honey production was individually assessed during the orange blossom (2021), wildflower (2021), and eucalyptus (2022) honey flows. The two highest- and lowest-producing colonies from each beekeeper were selected, forming the High Honey Production (HHP) and Low Honey Production (LHP) groups (20 colonies each) (Figure 1). The HHP and LHP groups produced an average of 89±23.9 kg and 25±9.3 kg of honey per colony over the three seasons, respectively. A total of 120 worker bee pupae larvae were collected from each selected colony, and genomic DNA was extracted and genotyped for two pre-selected SNPs (FAPESP Project 2013/01588-1) using allele-specific primers for G-Quadruplex-based genotyping and Taqman probes.

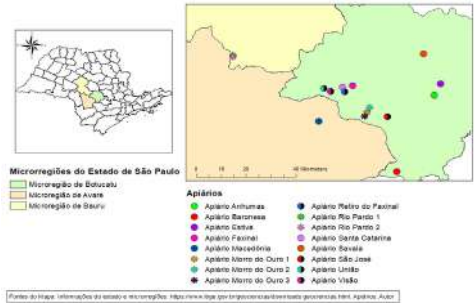

Figure 1. Locations of apiaries in São Paulo State

RESULTS

The comparison between TaqMan probes and the G-quadruplex technique for SNP 1 and SNP 3 genotyping results is shown in Figure 2. Samples that turned blue after the G-quadruplex reaction were considered positive for the SNP tests.

The genotyping results were analyzed using a chi-square test (χ^2) to assess the correlation between SNPs 1 and 3 and honey production, revealing a significant association ($P<0.05$). Thus, the G-Quadruplex genotyping method effectively validated SNPs 1 and 3 as markers for honey production.

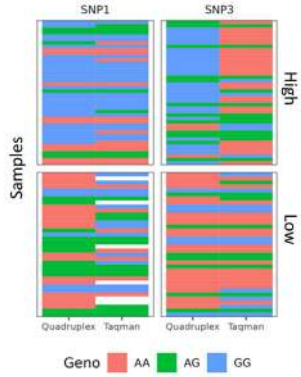

Figure 2. Genotyping results of SNP 1 and SNP 3 using TaqMan probes and the G-quadruplex technique.

CONCLUSION

This technique offers a precise, cost-effective alternative to TaqMan® probe-based genotyping, providing rapid and easily interpretable results for honeybee breeding programs.

ACKNOWLEDGMENTS

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