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Evaluation of molds and yeasts in Melipona bicolor honey

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INTRODUCTION & AIM

The honey of Stingless Bees creates an unfavorable environment for pathogenic microorganisms due to its low pH and high acidity, making it safe for human consumption. However, it is to the prone development of molds, yeasts, and lactic acid bacteria at a pH below 4.5 [1-3]. Therefore, in this study, the objective was to quantify molds and yeasts in stingless bee honey and identify the detected microorganisms.

RESULTS & DISCUSSION

- •Growth: No molds were observed in the samples, with the exclusive growth of yeasts with similar characteristics observed macroscopic all in samples.
- •Counts: Ranged from 3.28 to 7.30 log CFU.mL⁻¹ in raw honey.
- •Identification: identified The yeast was as belonging to the genus Starmerella.

METHOD

• **Samples**: Raw honey from *Melipona bicolor*.

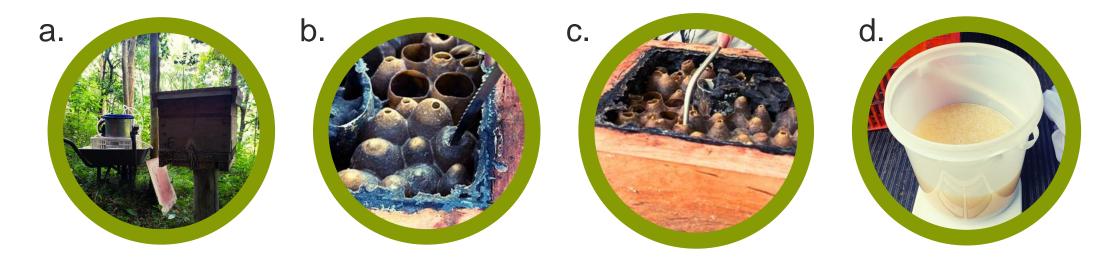


Figure 1. Sample collection: a. Hive location; b. Opening of the pots; c. Honey collection by suction; d. honey after collection

• Culture medium: Acidified potato agar to quantify yeasts [4].

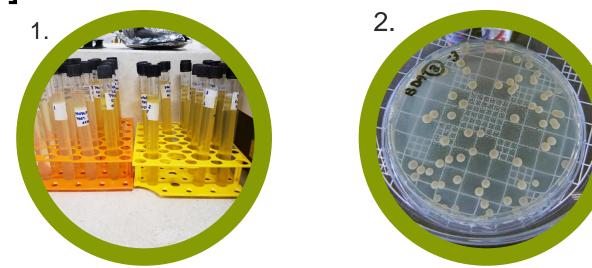


Figure 2. 1. Aliquots of samples. 2. Microbiological analysis.

• Food Safety: Despite the high yeast count, these microorganisms pose no risk to human health.

CONCLUSION

Although a high quantity of yeasts was observed in the analyzed honey, molecular analysis indicated that non-pathogenic microorganisms they were for humans and associated with stingless bees, highlighting a relevant symbiotic relationship between these insects and the microorganisms present in the honey.

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• Molecular identification: Genomic DNA extraction, ITS region amplification by PCR using V9G and ITS4 primers.

• PCR cycles:

Initial denaturation: 94°C, 5 min;

∘35 cycles: 94°C, 30 sec; Annealing: 48°C, 30 sec; Extension: 72°C, 1 min;

• Final extension: 72°C, 10 min;

- Sequencing: BigDye kit, ABI3500 sequencer, V9G and ITS4 primers.
- Preliminary identification: NCBI BLAST tool.

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