Genetic variability of captive breeding populations of *Tetragonisca angustula*

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INTRODUCTION

- Studies have shown that animal breeding led to a decrease in their genetic diversity;
- Managed captive populations of bees have shown low genetic variability;
- Here we analyzed wild and captive populations of *Tetragonisca angustula*, a highly eusocial stingless bee;
- This project aimed to investigate the degree of genetic health by microsatellites genotyping and mitochondrial DNA (mtDNA) sequencing.

MICROSATELLITES

- A total of 430 adult workers from nine meliponaries were sampled as well as 89 wild bees from São Sebastião (SSB) and Parque Nacional do Iguaçu (PNI), Brazil (Fig. 1).
- Nine microsatellites loci were analyzed (Tang03-11-12-17-57-60-65-68-70).

MITOCHONDRIAL DNA

- The mitochondrial genes *cytochrome c oxidase subunit 1* (COI) and *cytochrome b* (Cytb) were partially amplified by the primer pairs mtD06/mtD09 and mtD26/mtD28 (Simon et al. 1994), respectively.
- The two gene sequences were concatenated, totaling 764 bp.

CONCLUSIONS

- As expected according to the literature, we verified low NH and mtDNA diversity for managed populations of *T. angustula* here surveyed, but in contradiction the nuclear variability was high.
- Colony divisions seem to not be harmful to the population genetic health in captive conditions.
- Males thus seem to have a key role in maintaining the high genetic variability, preventing the negative consequences of inbreeding.
- We strongly recommend to not transport nests between SP and PR states, to prevent loss of the local genetic identity.