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Genetic variability of captive breeding populations of Tetragonisca angustula*.*

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Animal breeding has been a common practice since centuries ago. Honeybees, bumblebees and stingless bees are amongst the most managed bee species, especially by their role as pollinators. Studies have shown that animals breeding leads to a decrease in their genetic diversity. Indeed, managed captive populations of bees have shown low genetic variability. Here we analyzed feral and captive breeding populations of *Tetragonisca angustula*, a highly eusocial stingless bee. We aimed at detecting genetic variability differences by microsatellites genotyping and mitochondrial DNA (mtDNA) sequencing. Ours results showed that nuclear genetic variability was similar between feral and captive breeding populations. Nonetheless genetic variability differences at mtDNA were remarkable between them. Higher differentiation was verified inter-populations but not intra-population. Gene flow by males, artificial transportation and colony split are the most probable explanations for the genetic scenario observed. It is worth noting that meliponaries with different degrees of management showed different results. We concluded that increasing population density by colony split does not affect negatively the nuclear genetic variability. This later seems to be maintained high through male dispersal. Keywords: Management, genetic variability, *Tetragonisca angustula*, meliponaries.