

OR226*Nesting and genetic diversity of Melipona subnitida in Brazil***Marcela Barbosa**, Rafael Pinto, Márcia Rêgo, Vanessa Bonatti, Tiago Franco

The species *Melipona subnitida*, Ducke, 1910, is considered endemic from the Brazilian northeast backwoods and was uncovered lately in 2006 in the sandbank of National Park of Lençóis Maranhenses and has been adjusted to other places. Even though the important role played by these bees to ecosystems maintenance, they are threatened by extinction due the high rates of deforestation into the region. Thus, the goal of this study is to understand patterns of distribution and nesting of *M. subnitida* into the sandbank region and the genetic diversity between other populations from Maranhão seaside. The search for nests in Lençóis Maranhenses was established through a systematic methodology from a meliponary well known and from it transects were surveyed in different distances totaling 18 hectares. Therefore, three different groups of *M. subnitida* were genetically compared: individuals collected in the wild nests in Park of Lençóis Maranhenses; individuals identified through informations from communities in the Parnaíba Delta and a group previously studied from Barreirinhas to determine genetic diversity among them. The majority of nest sites were represented by *Humiria balsamifera* Mart harboring 88% of the nests of *M. subnitida*. However, uncommon results were observed, as *M. subnitida* nesting in mangrove forest, in *Avicennia germinans* L. Density on nests per hectare was 1.02 and distribution index Variance/Average was equal 2 into the National Park of Lençóis Maranhenses and the species showed an aggregated spreading pattern which, possibly, is related to vegetation composition besides dependence behavior between daughter and mother colonies. Molecular results demonstrated absence of genetic variability among the groups of *M. subnitida* involving common ancestral origin; nonetheless it was observed haplotypes formation in each one of the communities. The absence of genetic variability might be explained for being a young species with low rate of fecundity and restricted spreading.