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P3.16 Assessing risks of GM cotton expressing Cry toxin to non-target herbivores: Evaluation of aphids on cotton

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The expression of Cry toxin by Bt cotton, represents an excellent tool for the control of Lepidopteran pest worms, but presents a potential risk of increased populations of the cotton aphid, *Aphis gossypii*, due to the empty niche left by the worms or due to the pleiotropic effects caused by the transgene. The aim of this work was to develop methodologies following the protocol proposed for non-target herbivores, by the GMO-ERA Project (www.gmo-guidelines.info), to test if aphids reared on Bt cotton can change their bionomics or plant choice for colonization, which results in population dynamics changes and consequently their status as a cotton pest. The bionomics of the aphid was compared in greenhouse with insects reared in individual cages containing Bt cotton plants of the variety DP 404BG (Bollgard) or its not transformed isolate DP 4049. Both seeds were donated by the company Delta & Pine. Cages with Bt and non-Bt cotton were selected as the arena for evaluation of preference by winged adults. In addition, a field experiment with 5 paired blocks of Bt and non-Bt cotton was conducted to confirm the bionomic and colonization behavior patterns of *A. gossypii*, observed in greenhouse. The monitoring of individual females and their daily production of nymphs was an appropriated methodology to evaluate the variables related to the life cycle (survivorship and fecundity) of the cotton aphid in greenhouse and field conditions. Samples of leaves from all experiments were tested by ELISA for Cry 1Ac toxin in the Bt cotton. The comparison between the variables related to the life cycle: pre-reproductive period (immature phase), reproductive period, longevity, survivorship curve and offspring production and intrinsic increase rate of the population were not significantly different. There was also no preference of colonization for any plant by winged adults resulting in equivalent initial populations on Bt and non-Bt plants in the cages. Field monitoring of natural plant colonization by aphids and their population fluctuation followed the same pattern observed in greenhouse, with no differences between the treatments. These results showed that Bt cotton plants, under the tested conditions, did not affect the population dynamics of *A. gossypii*, and consequently do not increase its potential as pest in Bt cotton crop.

P3.17 Base line information and methodologies for assessing risks of Bt cotton to pollinators in Brazil

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The cultivation of Bt cotton raises important environmental risk assessment (ERA) issues in Brazil. Cotton is cultivated in small and large areas and in regions with distinct environmental conditions. A high diversity of arthropods is found associated with the genus *Gossypium* and there are significant variations among different regions. Wild relatives of cotton occur in the country, which raises concerns about gene flow and possible reductions of crop genetic diversity. In this context, flower visitors were considered an important ecological group for ERA because of the possible direct effects of Bt cotton on pollination services in natural and agricultural ecosystems, and the role of flower visitors on pollen transportation and gene flow.

Initially, a survey of flower visitors was conducted in *Gossypium hirsutum latifolium* (cultivated cotton) and *G. barbadense*, a wild cotton species widely distributed in the country. Bees were the main flower visitors on cultivated cotton plants. Taking into account all five studied areas, from 153 insect species collected on flowers, 47.40% (72 species) were from four families of bees and 49.78% (1,630) of the total number of individuals collected (3,274) were bees. Seventy two species of wild bees were collected on cultivated cotton, *G. hirsutum latifolium*, besides *Apis mellifera*, a domesticated species introduced in the country 200 years before for commercial purposes. *Apis mellifera* was the most abundant species on cultivated cotton in all sampling areas, while there was very low abundance on the wild species *G. barbadense* (only three specimens out of 316 total collected individuals). The bee faunas on cultivated cotton were very different among the sampling sites with only two species out of 73 being common to all cotton-producing areas. The large number of flower-visiting species and the difference on local bee fauna makes the selection of priority species on a regional scale necessary before analysis of potential impacts of Bt cotton are proceeded.

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