

## MODELLING WITH BAYESIAN INFERENCE OF SPODOPTERA FRUGIPERDA BALLOONING AND WALKING DISPERSAL ON BT AND NON-BT COTTON AGROECOSYSTEMS

II Congresso Internacional de Ecologia Online, 1ª edição, de 18/01/2021 a 20/01/2021  
ISBN dos Anais: 978-65-86861-52-5

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### RESUMO

Active and passive larval movement of pests can impact the resistance evolution to genetically modified crop traits expressing *Bacillus thuringiensis* (Bt crops) (Berliner) toxin genes. We hypothesized in our research that neighborhoods with Bt and non-Bt cotton plants on small scales could influence the ballooning dispersal of *Spodoptera frugiperda* (J. E. Smith) (Lepidoptera: Noctuidae). We also simulated with a genetic population model with Bayesian inference how ballooning dispersal combined with walking movement could impact resistance evolution in different scenarios of plant mixtures involving non-Bt and Bt cotton plants with high and non-high doses. The ballooning frequency on Cry1F-resistant larvae found on a treatment with non-Bt cotton as natal plant and Bt cotton in adjacent sites was twice as low as when Bt cotton was the natal plant and non-Bt cotton was in the adjacent sites. In terms of resistance evolution, we observed that the higher the rate of walking movement associated with ballooning promoted faster resistance evolution in non-high-dose events. The higher the rate of walking movement associated with ballooning promoted faster resistance evolution in non-high-dose events. Contamination of Bt cotton fields with non-Bt cotton plants in a high-dose event showed the longest time to resistance. With our results, it is possible to emphasize the necessity of implementing resistance management strategies, such as replacement with emergency of single-trait Bt with Bt events at high doses that produce multiple proteins targeting *S. frugiperda*.

**PALAVRAS-CHAVE:** dispersal, fall armyworm, resistance, contamination, Bt fields.

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