



Genetic identification of populations of *Bactrocera dorsalis* (Diptera Tephritidae) in the Niayes and Lower Casamance areas in Senegal

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ABSTRACT

Objectives: the study examines the effect of the host plant and of the agro-ecological area on the genetic structure of populations of *Bactrocera dorsalis* in order to apprehend an appropriate period to fight this pest.

Methodology and results: this study was conducted in two large areas mango productions Senegal (area Niayes and the forest area South) on 41 individuals of *Bactrocera dorsalis* with mitochondrial gene sequencing (cytochrome B). Several haplotypes (28) of which 27 individual have been identified with a high level of genetic diversity (Hd 0.972 and Pi 0.1563). The genetic demo tests suggested a population in equilibrium, a moderate expansion and a grouping according to the areas thus revealing a genetic structure linked to the localities. In addition, the haplotype network showed a majority haplotype comprising all areas, 24 individual haplotypes and a typical haplotype to Notto.

Conclusion and application of findings : this exploratory study was in addition to having provided information on the genetic characterization of the species *Bactrocera dorsalis*, describes its structure and its genetic differentiation based on two areas - ecological where mango is practically cultivated in Senegal. It helped to understand the genetic identity card of the species *Bactrocera dorsalis*, whose purpose will be to know its weakest link and food preferences to provide alternative struggles.

Keywords: *Bactrocera dorsalis*, Niayes, lower Casamance, mangoes, citrus, PCR, sequencing, cytochrome B