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Systemic Infection and Aggressiveness of *Curtobacterium flaccumfaciens* pv. *flaccumfaciens* Analysed by Scanning Electron Microscopy in Different Genotypes of *Phaseolus vulgaris*

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Abstract

Bacterial wilt due to *Curtobacterium flaccumfaciens* pv. *flaccumfaciens* (*Cff*) ranks first in order of economic importance. It reduces grain yield by colonizing xylem vessels impeding the translocation of water and nutrients to the superior plant parts. Genetic resistance is the most efficient and cheapest way to control this disease in common bean. To obtain resistant cultivars, a genetic improvement programme must consider pathogenic variability, genetic control over pathogen resistance, and methods of evaluating resistant genotypes. This study aimed to analyze, using the scanning electron microscopy, the xylem vessels colonized by the *C. flaccumfaciens* pv. *flaccumfaciens* in resistant, moderately resistant and susceptible genotypes of the common bean plant and identify different levels of aggressiveness of *Cff* isolates, and the horizontal /vertical resistance of common bean genotypes. The isolates were classified into four aggressiveness groups and the most aggressive isolates were BRM 14939, BRM 14942, that cause further reduction in height, differing from the control (non-inoculated plants). Plants inoculated with these isolates showed all symptoms evaluated and higher intensity of disease. It was observed variation in plant height according to the isolates used. In contrast, the less aggressive ones were BRM 14941 and BRM 14946, and the plants showed lower intensity of disease, and symptoms of wilt and flaccidity were more frequent. The genotypes IPA 9, Ouro Branco and Michelite were selected as more resistant among the test isolates. The genotypes Coquinho, BRS Cometa, CNFP 10104, BRS Requite, and A211 exhibited horizontal resistance and the genotypes IPA 9, Ouro Branco, Michelite, BRS Requite, and TU genotypes exhibited specific resistance to the major isolates of the pathogen that causes bacterial wilt. In contrast, the TO, Cornell 49242, IAC Carioca Pyatã, Uirapuru, IPA 7419, PI 207 262, Widusa, IPA 6, Pérola, BAT 477, BRS Esplendor, CNFC 10408, BRS Estilo, Vermelho, BRS Campeiro, IAC Carioca Aruã, AND 277, IAC Carioca Akytã, and IPA 1 genotypes did not contain horizontal resistance to the inoculated isolates. The BRS Cometa, A 211, Coquinho, CNFP 10104, CNFRS 11997, and Frijólica 0-3-1 are highly susceptible to bacterial wilt.

Keywords: Bacteria, common bean, disease, genetic control, resistance structures