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Evidence for a Link Between Pathogenicity and the Role of Imp Bacterial Transport Effector Proteins in Soybean Infection by *Xanthomonas axonopodis* pv. *glycines*

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***Xanthomonas axonopodis* pv. *glycines* (Xag) is the causal agent at bacterial pustule disease of soybeans. A non-pathogenic mutant of Xag (M715) was constructed employing transposon mutagenesis which showed similar epiphytic survival *in planta* to its wild type strain (YR32). The objective of this work was to identify and to analyze genes involved in pathogenicity in Xag YR32. Inverse Polymerase Chain Reaction (IPCR) was used to isolate the DNA flanking transposon insertion. A 1.3 kb flanking DNA fragment was sequenced and analyzed employing BLAST program to study homology, the position of transposon insertion and to predict the structure and function of the gene. One of the Open Reading Frames (ORFs) shared homology with *inner membrane proteins (imps)* of *Xanthomonas axonopodis* pv. *citri* (GenBank accession No. NC 003919). Northern blot analysis revealed that an imps gene was monocistronic and the size of *imps* mRNA in YR32 was slightly longer than in M715. Reverse Transcriptase-PCR analysis demonstrated that the *imps* transcript in M715 was much less abundant than In the wild type YR32. Transposon (mini-Tn5-Km'-Tp') was determined to be inserted close to the end of C-terminal region of *Imps* gene and might be sufficient to destabilize the *imps* transcript In M715 and so influence effectors transportation from Xag to plant cell.**

Key words : ***Xanthomonas axonopodis*, transposon insertion, non-pathogenic mutant, *imps***