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MOLECULAR CHARACTERIZATION OF A NEW *BACILLUS THURINGIENSIS* STRAIN FROM ARGENTINA TOXIC AGAINST LEPIDOPTERA AND COLEOPTERA BASE ON ITS WHOLE-GENOME ANALYSIS

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The insecticidal proteins of *Bacillus thuringiensis* are used as formulations of spore-crystal complexes and their genes have been incorporated into several crops, which has provided a model for genetic engineering in agriculture. Despite the variability of the Cry proteins described so far, it is still necessary to look for toxins with a broad spectrum of action, since a significant number of pests are not controlled with the available Cry proteins. It is also important to provide alternatives to address the problem of insect resistance, which has already appeared with the use of formulations and in transgenic plants that express cry genes that code for insecticidal proteins. We report the characterization of a novel *B. thuringiensis* isolate native to Argentina (FCC7) toxic against lepidoptera and coleoptera insects. The strain shows a rounded crystal harboring mainly a protein of about 130 kDa. Through the whole-genome sequencing by Illumina Miseq 1500 platform we detected two crystal protein genes with cry8-like genes homology, three vegetative insecticidal proteins (Vips) genes and multiple virulence factors such as phospholipases, proteases, enhancins, chitinases, among others. The two cry8-like genes, homologues of Cry8Ac1 and Cry8Qa1 sequences with 73,4 % and 88,9 % of identity respectively, were cloned and expressed into the 4Q7/pSTAB system and the larvicidal activity were assayed against *Spodoptera frugiperda* and *Tenebrio molitor*. Two of the Vips genes were identified as Vip1-like with 74,9% and 70,3% identity respectively while the third Vip gene was 82% identical to Vip2 sequences.

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Poster Distinguido