

GENOMIC AND ULTRASTRUCTURAL CHARACTERIZATION AND CYTOPATHOLOGICAL EFFECTS OF NOVEL *BACILLUS* SPP. FROM RECIFE, BRAZIL: AN ALTERNATIVE FOR THE POPULATION CONTROL OF VECTOR MOSQUITO VECTORS OF PARASITIC DISEASES.

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The control of mosquito populations is a critical strategy in attempts to interrupt the transmission cycle of several vector-borne pathogens, with bacteria of the *Lysinibacillus* and *Bacillus* genera currently being widely used as mosquito control agents. The selection of resistant mosquitoes constitutes a concerning challenge, however, with the search for new entomopathogenic bacteria offering a promising alternative for managing vector resistance. Here, we aimed to evaluate the genomic, ultrastructural, and toxic characteristics of two novel bacterial isolates exhibiting excellent and specific larvicidal activity. To achieve this, we first performed whole genome sequencing and annotation, revealing them to be phylogenetically related to *Lysinibacillus sphaericus* (Ls) and *Bacillus thuringiensis* HD-789. Genes encoding several novel and known Cry toxins were identified in the genomes. Ultrastructural analyses of sporulated inoculums were then performed using transmission electron microscopy (TEM), revealing, respectively, a triple crystal formation and parasporal bodies with toxic crystals, for the two isolates. Larvicide toxicity was also evaluated through bioassays, showing 100% larvicidal activity against *Culex quinquefasciatus* colonies resistant to the reference Ls2362 strain for the first isolate, with 100% larvicidal activity against *Culex* and *Aedes* species observed for the second isolate. Cytopathic effects in mosquito larval intestines were also visualized via TEM, revealing complete destruction of microvilli and mitochondrial damage. These analyses indicate that these isolates possess biotechnological potential to produce novel biolarvicides.

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