

Research Insight

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Comparative Genomics of Bt and Related *Bacillus* Species

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Abstract *Bacillus thuringiensis* (Bt) and related *Bacillus* species hold significant importance in the fields of biocontrol and biotechnology. This study employs comparative genomics to systematically analyze the genomic features of Bt and related *Bacillus* species, exploring gene expression, the structure and evolution of toxin gene clusters, and the roles of plasmids and mobile genetic elements. The research also includes a comparison with other *Bacillus* species, revealing their phylogenetic relationships, conserved and unique genomic regions, and mechanisms of horizontal gene transfer. Additionally, functional genomics studies investigate the expression profiles of specific genes, proteomics and metabolomics characteristics, and their roles in environmental adaptation and co-evolution with hosts. This study aims to provide scientific evidence for the agricultural, medical, and industrial applications of Bt, and addresses regulatory and safety considerations. Through this research, new directions for Bt genomics research are anticipated, and practical applications are suggested.

Keywords *Bacillus thuringiensis*; Comparative genomics; Toxin genes; Functional genomics; Biocontrol

1 Introduction

Bacillus thuringiensis (Bt) is a Gram-positive, spore-forming bacterium renowned for its insecticidal properties due to the production of crystal (Cry) proteins. These proteins are highly specific to various insect orders, including Lepidoptera, Diptera, and Coleoptera, making Bt a valuable tool in integrated pest management (IPM) and agricultural biotechnology (Hằng et al., 2021). The insecticidal activity of Bt results from the formation of pores in the midgut epithelial cells of susceptible insects, leading to cell lysis and death. Bt has been extensively utilized in the development of biopesticides and genetically modified crops, such as Bt cotton and Bt corn, which express Cry proteins to protect against insect pests (Hằng et al., 2021; Lazarte et al., 2021).

Comparative genomics, which involves the analysis and comparison of genetic material from different organisms, helps to understand their evolutionary relationships, functional genomics, and genetic diversity. In the study of Bt and related *Bacillus* species, comparative genomics is crucial for several reasons. It aids in identifying new insecticidal genes and understanding their mechanisms of action, thereby developing more effective biopesticides (Hằng et al., 2021). It provides insights into the genetic basis of insect resistance to Bt toxins, enabling the design of strategies to mitigate resistance development (Lazarte et al., 2021; Chen et al., 2021). Furthermore, comparative genomics can reveal the evolutionary adaptations and ecological niches of different *Bacillus* strains, contributing to a broader understanding of their roles in natural and agricultural ecosystems (Reyaz et al., 2019; Crickmore et al., 2020).

This study provides a comprehensive analysis of the comparative genomics of Bt and related *Bacillus* species, summarizing current knowledge on the genetic diversity and evolutionary relationships among Bt strains and related *Bacillus* species. It identifies and characterizes new insecticidal genes and their potential applications in pest management, discusses the mechanisms of insect resistance to Bt toxins and potential strategies to overcome resistance, and explores the ecological and functional roles of Bt and related *Bacillus* species in various environments. By synthesizing findings from multiple research studies, this study aims to advance our understanding of Bt genomics and its applications in sustainable agriculture and pest management.