



P131

THE COMPLETE GENOME ANALYSIS OF *BACILLUS AMYLOLIQUEFACIENS* UMAF6614 AND UMAF6639 REVEALS GENETIC FEATURES INVOLVED IN BIOCONTROL ACTIVITY AND BACTERIAL FITNESS

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The *Bacillus amyloliquefaciens* strains UMAF6614 and UMAF6639 were originally isolated from healthy leaf areas of melon plants naturally infected with the cucurbit powdery mildew fungus *Podosphaera fusca*. In previous works, we have demonstrated the multifaceted biocontrol activity of these strains based on: i) direct antagonism against fungal and bacterial pathogens of cucurbits, and ii) induction of plant defense mechanisms (ISR) and promotion of plant growth when applied to roots. With the idea to look for bacterial features responsible for the outstanding biocontrol activity of these strains we decided to sequence and analyze their genomes. Some of the most relevant findings obtained from initial genome analyses are: First, though initially identified as *B. subtilis*, a more robust phylogenetic analysis has confirmed the identification of both strains as *B. amyloliquefaciens*. Second, detection of bacterial features involved in diverse mechanisms of action and engaged in the biocontrol activity of these strains: the synthesis of secondary metabolites, production of phytohormones, or multicellular behavior as biofilm formation. Third, the development of new bioinformatics tools in combination with open access softwares have permitted to identify unique regions in either of our strains and non-conserved within the *Bacillus* genus. Ongoing studies are focused on elucidating the putative implication of these uncharacterized regions in the biocontrol activity of these strains.

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