Plasmids of Curtobacterium: a Nexus of Carbohydrate Utilization Genes

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The decomposition of plant-litter, aided by the metabolic activity of plant-litter microbial communities, is a vital process in nutrient cycling. Taxa such as Curtobacterium are involved in litter decomposition via the utilization of carbohydrate active enzymes (CAZymes), which depolymerize the recalcitrant polysaccharides of plant cell walls and tissues. The genes encoding CAZymes have been well characterized in the Curtobacterium chromosome. Here, we explore the potential for variation in carbon utilization traits on plasmids, a mobile genetic element capable of sharing traits within microbial communities. We ask the following: what are the proportion and types of carbohydrate utilization genes present on Curtobacterium plasmids from plant litter and second, how do these genes vary among Curtobacterium plasmids from different isolation sources? To address our questions, we analyzed 19 complete Curtobacterium plasmids for their CAZyme profiles using dbCAN2 and identified 10 distinct families of CAZymes. We found that glycoside hydrolases were the predominant CAZyme functional group identified on the plasmids, in addition to polysaccharide lyases and carbohydrate-binding molecules. Additionally, there exist differences between the types of CAZymes harbored on Curtobacterium plasmids from grassland environments and plasmids from agricultural environments. To the best of our knowledge, this is the first paper describing the compositional differences in the CAZyme profiles of Curtobacterium plasmids from diverse environments.

Awards Won:
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