

**TITLE:** GENOME SEQUENCING OF *Pantoea agglomerans* 33.1, A PLANT GROWTH-PROMOTING BACTERIA, PROVIDES INSIGHTS ABOUT ITS PROTEIN SECRETION SYSTEMS

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**ABSTRACT:**

Many bacteria use the Protein secretion systems (Pss) to ensure their survival, transport proteins and interact with the environment, other bacteria and even eukaryotes. Although the Pss are well related to bacterial pathogenicity, some reports have shown that the Pss can also be used in a beneficial plant interaction. The genus *Pantoea* comprises Gram-negative ubiquitous bacteria that can be found in several environments and hosts, and have been described as pathogens, commensals or symbionts. Besides the biotechnological potential, some *Pantoea* strains are also described as plant growth-promoting bacteria. Among these bacteria, *Pantoea agglomerans* 33.1, isolated from Eucalyptus, stands out for their potential to promote the growth of crops of agricultural interest, such as sugarcane, and to establish beneficial interaction with the plant host. This study aimed at sequencing the whole genome of strain 33.1 to better understand its characteristics, especially regarding the presence of Pss and their impact on plant growth promotion. The genome sequencing was conducted with Illumina NextSeq 550 and PacBio CLR platforms. Genome assembly was performed with SMRTLink v. 9.0 using the Microbial Assembly Pipeline, followed by polishing with Pilon v. 1.23, and the annotation was performed with Prokka v. 1.14.6, RAST v. 2.0, BlastKOALA v. 2.2 and TXSScan (Galaxy v. 1.0.5). Genomic analysis revealed that *P. agglomerans* 33.1 harbors a genome of 4,087,626 bp and four plasmids of 527,897; 207,704; 16,637 and 4,460 bp, respectively. BUSCO v. 4.1.3 reported 99% of genome completeness considering the class Enterobacterales. Three different types of Pss were identified: types 1, 5 (subgroups 5a- autotransporter and 5b- two-partner secretion) and 6. Our preliminary results indicate that types 1 and 5 are complete, but type 6 does not present all the necessary components for their operation. Another interesting insight is that, according to the literature, type 3 Pss is encoded by the *hrc/hrp* gene cluster, which is related to hypersensitive response and pathogenicity in susceptible plants, and the absence of this system in *Pantoea agglomerans* 33.1 can be an indicative of its safety. The results obtained here will contribute to future molecular studies in the understanding of the function of Pss in the interaction between 33.1 and plants.

**Keywords:** *Pantoea agglomerans*; protein secretion systems; plant growth-promoting bacteria; whole genome sequencing.

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