

ABSTRACT

Priestia is a genus of biotechnologically important bacteria adapted to thrive in a wide range of environmental conditions including the marine sediments. Here, we screened and isolated a strain from the Bagamoyo marine mangrove inhabited sediments and then employed whole genome sequencing to recover and define its full genome. De novo-assembly with Unicycler (v. 0.4.8) and annotation with Prokaryotic Genome Annotation Pipeline (PGAP) revealed that that its genome contains one chromosome (5,549,131 bp), with a GC content of 37.62%. Further analysis showed that the genome contains 5,687 coding sequences (CDS), 4 rRNAs, 84 tRNAs, 12 ncRNAs, and at least 2 plasmids (1,142 bp and 6,490 bp). On the other hand, antiSMASH-based secondary metabolite analysis revealed that the novel strain (MARUCO02) contains gene clusters for biosynthesis of MEP-DOXP-dependent versatile isoprenoids (eg. carotenoids), siderophores (synechobactin and schizokinen) and polyhydroxyalkanoates (PHA). The genome dataset also informs about the presence genes encoding enzymes required for generation of hopanoids, compounds that confer adaption to harsh environmental conditions including industrial cultivation recipes. Our data from this novel Priestia megaterium strain MARUCO02 can be used for reference and in genome-guided selection of strains for production of isoprenoids as well as industrially useful siderophores and polymers, amenable for biosynthetic manipulations in a biotechnological process.