

1 **Draft genome sequence of root-associated sugarcane growth promoting**

2 ***Microbispora* sp. GKU 823**

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20 **Abstract**

21 The endophytic plant growth promoting *Microbispora* sp. GKU 823 was isolated from
22 the roots of sugarcane cultivated in Thailand. It has an estimated 9.4 Mbp genome and a G+C
23 content of 71.3%. The genome sequence reveals several genes associated with plant growth-
24 promoting traits and extensive secondary metabolite biosyntheses.

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26 Endophytic actinomycetes are free-living filamentous bacteria that mutually colonize
27 inside plants and facilitate plant growth through direct and indirect mechanisms employing
28 plant growth-promoting (PGP) traits (1). Endophytic *Microbispora* sp. GKU 823 was isolated
29 from roots of sugarcane cultivated in Thailand and has been shown to enhance sugarcane
30 growth (2). This strain exhibits PGP traits including production of indole-3-acetic acid (IAA)
31 and siderophores, solubilization of phosphate, and suppression of *Aspergillus niger* ATCC
32 6275 (2). Based on 16S rRNA gene sequence analysis, *Microbispora* sp. GKU 823 closely
33 related to *Microbispora hainanensis* 211020^T (99.09% similarity, GenBank accession no.
34 KR560040). The whole genome sequence of *Microbispora* sp. GKU 823 was obtained in which
35 displays genes associated with plant growth promotion and secondary metabolite biosynthesis.

36 Total genomic DNA of *Microbispora* sp. GKU 823 was extracted using ISOLATE II
37 genomic DNA extraction kit (BIOLINE, UK) according to manufacturer's instruction. The
38 genome was sequenced using the platform Ion PGM system generating 1,230,781 reads (with
39 approximately 30× coverage) with an average read length of 225 bp. The genome was
40 assembled using SPAdes version 3.9 (3) and evaluated by QUAST version 3.2 (4), the reads
41 were assembled into 262 contigs (coverage ≥ 10 and length ≥ 1000 bp) with an N_{50} of 69,483.
42 The largest contig obtained is 321,219 bp in length. The draft genome is estimated to be
43 9,430,099 bp with a G+C content of 71.3%.

44 Functional gene annotation of the assembled genome was carried out by the Rapid
45 Annotations using Subsystems Technology (RAST) server (5). rRNA and tRNA genes were
46 determined by RNAmmer (6) and tRNAscan-SE (7), respectively. The annotation predicted a
47 total 9,248 coding sequences, 58 tRNA and 3 rRNA genes. The average nucleotide identity
48 values of the genome were calculated using BlastN (ANiB) in JSpeciesWS (8). The genome
49 comparison revealed that *Microbispora* sp. GKU 823 had an ANiB value of 92.47% similar to
50 *Microbispora rosea* NRRLB-2630, 90.70% to *M. rosea* NRRL B-2631 and 81.20%
51 *Microbispora* sp. ATCC PTA-5024.

52 Genes related to PGP traits including phosphate solubilization (alkaline phosphatase,
53 and isocitrate dehydrogenase; 9, 10); IAA production (tryptophan 2-monooxygenase; 11) and
54 genes involved in fungal cell wall degradation (family 18 chitinase; 12) were detected in the
55 genome of *Microbispora* sp. GKU 823. Moreover, genes involved in stress tolerance (betaine
56 aldehyde dehydrogenase, proline dehydrogenase, superoxide dismutase and trehalose synthase;
57 13) were also present. These genes sustain the capability of *Microbispora* sp. GKU 823 to
58 promote growth of sugarcane (2). AntiSMASH version 3.0 (14) predicted 23 secondary
59 metabolite gene clusters in the genome of *Microbispora* sp. GKU 823 including seven gene
60 clusters of nonribosomal peptide synthetase (NRPS), four gene clusters of Type I polyketide
61 synthase (T1PKS) and terpene, three gene clusters of bacteriocin, two gene clusters of
62 siderophore (including desferrioxamine E), and a single gene cluster encoding a lanthipeptide.
63 These secondary metabolite gene clusters indicate that endophytic *Microbispora* species are
64 potential sources of novel specialized metabolites.

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66 **Nucleotide sequence accession numbers**

67 The draft genome sequence of *Microbispora* sp. GKU 823 has been deposited in the
68 DDBJ/ENA/GenBank databases under the accession number MWJN00000000.

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