The family Flavobacteriaceae was established for grouping a diverse array of bacteria showing Gram-negative, aerobic, nonmotile pigmented bacteria that show yellow to orange colored colonies (1) and includes more than 114 genera (http://www.bacterio.net). One of the genera, Jejuia, was proposed in 2009 for nonmotile, yellow, nondiffusible pigment producers in seawater and consists of a single species J. pallidilutea (2, 3). More recently, Takatani et al. (4) have identified a strain 11shimoA1 isolated from the surface of seaweed that produces not only zeaxanthin but also a new monocyclic carotenoid, 2′-isopentenylsaproxanthin. The amount of 2′-isopentenylsaproxanthin production increased under alkaline conditions (4). However, carotenoid synthetic pathways of the 2′-isopentenylsaproxanthin have not been resolved yet.

The genome sequences of J. pallidilutea 11shimoA1 (JCM 19538) and the pigment mutation mutants induced by ethyl methanesulfonate were sequenced with the Illumina HiSeq (Illumina) and Ion PGM systems (Life Technologies, Carlsbad, CA), respectively. The genome sequence of 11shimoA1 was de novo assembled using Velvet version 1.2.08. Those mutants were de novo assembled using Newbler version 2.8. The annotation and genome analysis were performed by RAST (Rapid Annotation Subsystem Technology) (5). The sizes of the draft genome of J. pallidilutea 11shimoA1, the pigment-deficient mutant A1W, and the red-pigmented mutant AIR were 3,805,351 bp, 3,773,436 bp, and 3,195,388 bp, respectively. The genome data have been deposited in DDBJ/EMBL/GenBank under the accession numbers BBNY01000001 to BBNY01000098, BBRN01000001 to BBRN01000075, and BBSN01000001 to BBSN01000087 for Jejuia pallidilutea strains 11shimoA1, A1W, and A1R, respectively.

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