Draft Genome Sequence of the Yeast *Vanrija humicola* (Formerly *Cryptococcus humicola*) Strain UJ1, a Producer of D-Aspartate Oxidase

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ABSTRACT   *Vanrija humicola* (*Cryptococcus humicola*) strain UJ1 is a basidiomycetous yeast that produces D-aspartate oxidase, which is highly specific to D-aspartate. Here, we report the 22.6-Mb draft genome sequence of *V. humicola* strain UJ1, which comprises 22.6 Mb in 46 scaffolds, with an overall G+C content of 62.82%, comprising 46 scaffolds with an N_{50} of 1.34 Mb.

*V*anrija humicola* strain UJ1 (=JCM 9575), formerly known as *Cryptococcus humicola* strain UJ1, is a basidiomycetous yeast that utilizes D-aspartate as a sole source of carbon, nitrogen, or both, which is caused by a flavin enzyme, D-aspartate oxidase (DDO) (1, 2). DDO of *V. humicola* UJ1 is produced only in the presence of D-aspartate in culture media and has higher catalytic activity and specificity toward D-aspartate than DDOs from other origins (1, 3), which makes it useful for D-aspartate identification and quantification. The yeast draft genome sequence provides information on the D-aspartate-specific induction mechanism and the physiological significance of DDO in the yeast.

The genome sequence of *V. humicola* strain UJ1 was generated using an Illumina HiSeq 2500 platform. The sequencing generated 44,746,782 paired ends that were used for *de novo* assembly with Velvet version 1.2.10 (4) and Platanus version 1.2.4 (5) software. This assembly represents a total of 46 scaffolds with total and average lengths of 22,628,423 and 491,922 bp, respectively. The maximum and minimum scaffold lengths were 3,532,612 and 151 bp, respectively. The scaffold N_{50} and N_{90} values were 1,340,400 and 602,907 bp, respectively. The overall G+C content was determined to be 62.82%. Gene prediction using AUGUSTUS (6) trained with the parameters of the species *Cryptococcus neoformans* resulted in 8,919 genes and 37,033 exons. Additionally, 320 tRNAs were predicted using tRNAscan-SE (7). An automatic annotation of predicted open reading frames was carried out using Blast2GO Basic (8).

Accession number(s). This whole-genome shotgun sequencing project has been deposited in DDBJ/EMBL/GenBank under the accession numbers BFAH01000001 to BFAH01000046 (scaffolds 1 to 19 and 21 to 47, respectively). This paper describes the first version of the genome.

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