

# Genome Sequence of the *Trichosporon asahii* Environmental Strain CBS 8904

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**This is the first report of the genome sequence of *Trichosporon asahii* environmental strain CBS 8904, which was isolated from maize cobs. Comparison of the genome sequence with that of clinical strain CBS 2479 revealed that they have >99% chromosomal and mitochondrial sequence identity, yet CBS 8904 has 368 specific genes. Analysis of clusters of orthologous groups predicted that 3,307 genes belong to 23 functional categories and 703 genes were predicted to have a general function.**

*Trichosporon asahii* is an important yeast fungus that exists widely under natural conditions (2) and forms colonies in some human tissues and organs (3, 11). *T. asahii* can invade the human body and cause disease (7, 12, 15). It is widely used in food fermentation (4, 6, 8, 10, 13) and other industrial production (9, 14, 16) processes. CBS 8904 is an environmental strain of *T. asahii* that was isolated in 1998 from maize cobs (<http://www.cbs.knaw.nl/collections/BioloMICS.aspx?Table=CBS%20strain%20database&Name=CBS%208904&Fields=All&ExactMatch=T>). To date, the genome sequence of this *T. asahii* environmental strain has not been published.

Whole-genome sequencing of *T. asahii* CBS 8904 was performed with a combined strategy of 454 sequencing (5) and Solexa sequencing technology (1). A genomic library containing 8-kb inserts was constructed, and 935,617 paired-end reads were generated by using the GS FLX system, giving 21.1-fold coverage of the genome. Overall, 83.26% of the reads were assembled into 194 scaffolds totaling 1.9 Mbp by using Newbler version 2.3 (454 Life Sciences, Branford, CT). A total of 51,221,338 reads were generated to reach a depth of 204-fold coverage with an Illumina Solexa Genome Analyzer Iix and mapped to the scaffolds by using the Burrows-Wheeler alignment tool.

The genome of *T. asahii* strain CBS 8904 contains 25,015,122 bp of nuclear chromosomal DNA and 32,568 bp of mitochondrial DNA. The average GC content is 59% in the chromosomal DNA and 29% in the mitochondrial DNA. Overall, the chromosomal DNA contains 8,507 protein-encoding genes and 530 tRNA-encoding genes. The mitochondrial DNA has 22 protein-encoding genes and 25 tRNA-encoding genes.

Comparison with the previously published genome of *T. asahii* CBS 2479 (NCBI GenBank accession number [ALBS000000000](http://www.ncbi.nlm.nih.gov/GenBank/ALBS000000000)) revealed that the chromosomes of CBS 8904 and CBS 2479 have 99.59% identity and the mitochondria of these two strains have 99.99% identity. CBS 8904 has 8,161 orthologous coding sequences in common with CBS 2479, and CBS 8904 has 368 specific genes compared with CBS 2479, most of which are of unknown function. Analysis of clusters of orthologous groups of *T. asahii* CBS 8904 predicted that 3,307 of the protein-encoding genes belong to 23 functional categories, i.e., cell motility ( $n = 4$ ); extracellular structures ( $n = 5$ ); nuclear structure ( $n = 26$ ); defense mechanisms ( $n = 29$ ); cell wall/membrane/envelope biogenesis ( $n = 38$ ); nucleotide transport and metabolism ( $n = 58$ ); coenzyme transport and metabolism ( $n = 68$ ); chromatin structure

and dynamics ( $n = 76$ ); cytoskeleton ( $n = 84$ ); inorganic ion transport and metabolism ( $n = 103$ ); secondary metabolite biosynthesis, transport, and catabolism ( $n = 112$ ); cell cycle control, cell division, and chromosome partitioning ( $n = 139$ ); replication, recombination, and repair ( $n = 153$ ); RNA processing and modification ( $n = 178$ ); amino acid transport and metabolism ( $n = 202$ ); energy production and conversion ( $n = 230$ ); carbohydrate transport and metabolism ( $n = 230$ ); lipid transport and metabolism ( $n = 214$ ); intracellular trafficking, secretion, and vesicular transport ( $n = 238$ ); transcription ( $n = 248$ ); translation, ribosomal structure, and biogenesis ( $n = 263$ ); signal transduction mechanisms ( $n = 249$ ); and posttranslational modification, protein turnover, and chaperones ( $n = 360$ ). A total of 703 genes were predicted to have only a general function, and the functions of 709 genes were unknown.

**Nucleotide sequence accession numbers.** This whole-genome shotgun sequencing project has been deposited in DDBJ/EMBL/GenBank under accession no. [AMBO000000000](http://www.ncbi.nlm.nih.gov/GenBank/AMBO000000000). The version described in this paper is the first one ([AMBO010000000](http://www.ncbi.nlm.nih.gov/GenBank/AMBO010000000)).

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