



## Genome announcement

# Genome sequence of *Trichosporon cutaneum* ACCC 20271: An oleaginous yeast with excellent lignocellulose derived inhibitor tolerance



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## ABSTRACT

Oleaginous yeast *Trichosporon cutaneum* demonstrated excellent lipid accumulation performance and inhibitor tolerance derived from lignocellulose pretreatment. Here we firstly report a 30.45 Mb assembly genome of *T. cutaneum* ACCC 20271 for understanding the microbial lipid biosynthesis and mechanism of inhibitor tolerance and degradation.

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Microbial lipid produced from lignocellulosic biomass has great potentials as an alternative of vegetable oil for biodiesel synthesis. Lignocellulose contains up to 35–45% cellulose and 20–35% hemicellulose, but the release of fermentable sugars requires a harsh pretreatment and the pretreatment step generates various toxic compounds including furfural, 5-hydroxymethylfurfural, acetic acid, formic acid, levulinic acid, as well as vanillin, syringaldehyde, 4-hydroxybenzaldehyde etc. (Klinke et al., 2004). Therefore, an ideal oleaginous fermenting strain should accumulate high lipid content, and also tolerate or even biologically degrade the toxic inhibitors when lignocellulose is used as feedstock.

Oleaginous yeast *Trichosporon cutaneum* demonstrated excellent performance for cellulosic lipid accumulation: high tolerance to lignocellulose derived inhibitors (Chen et al., 2009), utilization of various sugars such as glucose, xylose, sucrose, cellobiose, and lactose (Hu et al., 2011; Mörtberg and Neujahr, 1986), high lipid content using corn stover hydrolysate (Liu et al., 2012), corncob residues hydrolysate (Gao et al., 2014), corncob acid hydrolysate (Chen et al., 2013). Here, we report the *T. cutaneum* ACCC 20271 genome sequence for the purpose of better understanding of genes involved in microbial lipid accumulation, and the molecular mechanisms of inhibitor tolerance and degradation.

*T. cutaneum* ACCC 20271 was obtained from Agricultural Culture Collection of China (ACCC), Beijing, China (<http://www.acc.org.cn/>) to represent the genus of *T. cutaneum* ACCC 20271 has the same origin to *Trichosporon cutaneum* CGMCC 2.1374 (China General Microorganism Collection Center, Beijing, China, ([www.cgmcc.net](http://www.cgmcc.net))). For genome sequencing, both mate-pair library (8 kb insert size) and paired-end libraries (360 bp, 400 bp and 700 bp insert size, respectively) were constructed and sequenced using Illumina-Miseq system at Shanghai Personalbio Co., Shanghai, China. After filtering low-quality and adapter contamination reads, totally 3,538,581,560 bp clean data with an average coverage of 142× were obtained. These sequences were assembled with the Newbler software v2.8 (version 20110517.1502). Finally, a 30.45 Mb genome of *T. cutaneum* ACCC 20271 with the GC content of 57.64% was generated, containing 22 scaffolds (923 contigs) with N50 of 5.63 Mb (Table 1). A number of 5704 protein-coding gene models were predicted using Maker annotation pipeline (version 2008), covering 36.91% of the genome with an average sequence length of 1970 bp. The genome contains 925 non-coding RNA genes, including 915 tRNA, 2 snoRNA, 1 miRNA, 6 snRNA and 1 antisense RNA (tRNAscan-SE, version 1.3.1; RNAmmer, version 1.2; Rfam database). The repeat sequences of 304,113 bp were identified with homologous annotation and *de novo* annotation (RepeatMasker, version 3.3.0; RepeatModeler), representing about 1.00% of the whole genome.

For oleaginous microorganisms, acetyl-CoA as the substrate for *de novo* fatty acid synthesis, was mainly generated through citrate

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**Table 1**  
General genome features of *T. cutaneum* ACCC 20271.

Features	Value
Genome size (bp)	30,446,464
Largest scaffold length (bp)	6,933,627
Shortest scaffold length (bp)	2356
N50 scaffold length (bp)	5,629,136
Largest contig length (bp)	322,954
Shortest contig length (bp)	534
N50 contig length (bp)	101,228
GC content (%)	57.64
Total protein-coding gene length (bp)	11,236,268
Protein-coding gene number	5704
Average length of gene (bp)	1970
Protein-coding region/genome (%)	36.91
tRNA	915
snoRNA	2
miRNA	1
snRNA	6
Antisense RNA	1
ncRNA/genome (%)	0.28

cleavage by ATP-citrate lyase (ACL), then converted into malonyl-CoA by acetyl-CoA carboxylase (ACC) to finish the first step of fatty acid synthesis (Tai and Stephanopoulos, 2013). In the *T. cutaneum* ACCC 20271 genome, the ACL and ACC genes were all identified. The fatty acid synthase (FAS) catalyzing the biosynthesis of fatty acid was composed by Fas1 (beta-subunit) and Fas2 (alpha subunit) in *T. cutaneum* ACCC 20271. Enzymes supplying NADPH to FAS for lipogenesis were also found, including glucose-6-phosphate dehydrogenase (ZWF1) and phosphogluconate dehydrogenase (GND) in pentose phosphate pathway, malic enzyme (ME) and NADP<sup>+</sup>-dependent isocitrate dehydrogenase (IDP1).

Lignocellulose derived inhibitors such as furan and phenolic derivatives are able to be degraded in various microorganisms by alcohol dehydrogenase (ADH), aldehyde dehydrogenase (ALDH), aldo-keto reductase (AKR) and aldehyde reductase (ARI) (Koopman et al., 2010; Wang et al., 2015; Yi et al., 2015). Totally 40 ADH genes, 39 ALDH genes, 14 AKR genes, 4 ARI genes in *T. cutaneum* ACCC 20271 genome were identified, which may play a very important role in furan and phenolic aldehyde degradation. One formate dehydrogenase gene (FDH) and 3 acetyl-CoA synthetase genes (ACS) responsible for degradation of formic acid and acetic acid respectively were also identified.

The genome sequencing of *T. cutaneum* ACCC 20271 in this work provided a promising resource of both metabolism mechanism of microbial lipid accumulation and lignocellulose derived inhibitor degradation for improving lipid fermentation from lignocellulose feedstock.

### Nucleotide sequence accession numbers

This whole genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession LTAL00000000. The ver-

sion described in this paper is version LTAL01000000. This strain is available at Agricultural Culture Collection of China under the accession number ACCC No. 20271 (<http://www.accc.org.cn/>), or at China General Microbiological Culture Collection Center under the accession number CGMCC No. 2.1374.

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