



Genome Sequence of the Nonconventional Wine Yeast *Hanseniaspora guilliermondii* UTAD222

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ABSTRACT In this work, we disclose the genome sequence and a corresponding manually curated annotation of the non-*Saccharomyces* yeast *Hanseniaspora guilliermondii* UTAD222, a strain shown to have interesting oenological traits for the production of wines with improved aromatic properties.

Non-*Saccharomyces* yeasts have several interesting metabolic and enzymatic properties that are absent in *Saccharomyces cerevisiae* and that contribute to the improvement of wine sensory profiles (1–4). Species of the *Hanseniaspora* genus are among those found to be more interesting for the production of wines with stylistic properties in coculture with *S. cerevisiae*. In this work, we have sequenced the genome of *Hanseniaspora guilliermondii* UTAD222, a strain that was isolated from a wine must and that was found to have multiple interesting oenological traits, including high tolerance to ethanol, low production of H₂S, and high proteolytic and β -glycosidase activities (1, 5). Coculture of *H. guilliermondii* UTAD222 with *S. cerevisiae* also significantly enhanced the floral and the fruity character of wines (6), and led to a significant remodeling of *S. cerevisiae* genomic expression along alcoholic fermentation (7). Other genomic sequences of *Hanseniaspora* wine strains were released including *H. opuntiae*, *H. uvarum*, *H. vineae*, and *H. osmophila* (BioProjects PRJNA325557, PRJNA238564, and PRJNA178141) (8), but this is the first description of a whole-genome of an *H. guilliermondii* strain.

The genome of *H. guilliermondii* UTAD222 was obtained using two rounds of paired-end sequencing using Illumina MiSeq platform (inserts with approximately 300 bp). Around 53,913,308 reads were obtained, which were assembled (using a CLC *de novo* assembler) into 208 contigs (N_{50} length, 91,417 bp), yielding a total of 9,037,850 assembled bases and a coverage of 819-fold. The predicted *H. guilliermondii* UTAD222 genome size and corresponding G+C content (approximately 31%) are in line with the genome sizes reported for other wine strains belonging to the *Hanseniaspora* genus.

Automatic annotation of the genome sequence of *H. guilliermondii* UTAD222 (undertaken using *ab initio* gene detection) was manually curated to validate and refine the results obtained. The predicted ORFeome of *H. guilliermondii* UTAD222 is estimated to include 4,070 protein-encoding genes. BLASTP analysis revealed that the majority of *H. guilliermondii* proteins share a high degree of similarity with proteins from *H. opuntiae* AWRI3578 ($n = 4,026$) and from *H. uvarum* AWRI3580 ($n = 3,918$), reflecting the reported close phylogenetic distance between *H. guilliermondii* and these two species (9). Despite this generalized similarity, *H. guilliermondii* UTAD222 and *H. uvarum* AWRI3580 strains were found to share three proteins that were absent in *H. opuntiae*

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AWRI3578. On the other hand, four genes were shared by *H. guilliermondii* UTAD222 and *H. opuntiae* AWRI3578 but were absent in *H. uvarum*. The disclosure of the *H. guilliermondii* genome sequence is expected to boost research focused on this species and on others belonging to the *Hanseniaspora* genus, helping to further understand their role in wine fermentation when cocultured with *S. cerevisiae*.

Accession number(s). The genome sequence of the *H. guilliermondii* UTAD222 sequence has been deposited in ENA (accession numbers [FQNF01000001](https://ENA/01000001) to [FQNF01000208](https://ENA/01000208)).

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