Histidine Degradation via an Aminotransferase Increases the Nutritional Flexibility of Candida glabrata

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The ability to acquire nutrients during infections is an important attribute in microbial pathogenesis. Amino acids are a valuable source of nitrogen if they can be degraded by the infecting organism. In this work, we analyzed histidine utilization in the fungal pathogen of humans Candida glabrata. Hemiascomycete fungi, like C. glabrata or Saccharomyces cerevisiae, possess no gene coding for a histidine ammonia-lyase, which catalyzes the first step of a major histidine degradation pathway in most other organisms. We show that C. glabrata instead initializes histidine degradation via the aromatic amino acid aminotransferase Aro8. Although ARO8 is also present in S. cerevisiae and is induced by extracellular histidine, the yeast cannot use histidine as its sole nitrogen source, possibly due to growth inhibition by a downstream degradation product. Furthermore, C. glabrata relies on Aro8 for phenylalanine and tryptophan utilization, since ARO8, but not its homologue ARO9, was transcriptionally activated in the presence of these amino acids. Accordingly, an ARO9 deletion had no effect on growth with aromatic amino acids. In contrast, in S. cerevisiae, ARO9 is strongly induced by tryptophan and is known to support growth on aromatic amino acids. Differences in the genomic structure of the ARO9 gene between C. glabrata and S. cerevisiae indicate a possible disruption in the regulatory upstream region. Thus, we show that, in contrast to S. cerevisiae, C. glabrata has adapted to use histidine as a sole source of nitrogen and that the aromatic amino acid aminotransferase Aro8, but not Aro9, is the enzyme required for this process.

As an opportunistic fungal pathogen, Candida glabrata is one of the leading causes of candidiasis (1, 2) and is responsible for several thousand systemic infections and deaths worldwide each year (3), yet C. glabrata is much more closely related to the nonpathogenic yeast Saccharomyces cerevisiae than to other pathogenic fungi, like Candida albicans. Identifying differences in the genetic, phenotypic, and metabolic setups of S. cerevisiae and C. glabrata is therefore highly relevant for understanding the basis of C. glabrata virulence (4, 5).

C. glabrata can cause several types of infections, ranging from superficial to systemic. During the course of these infections, C. glabrata cells face many different and rapidly changing host environments and have to adapt to each of these microniches. The ability to use as many nutrient sources as possible is vital for this kind of flexibility. Thus, a detailed knowledge of the fungal metabolic pathways involved can help in understanding, and consequently in fighting, fungal infections (6). Examples of the relevance of nutrient uptake in the host are trace elements, like iron or zinc (7–10), but also carbon and nitrogen compounds (11, 12). For their utilization, fungi like S. cerevisiae and C. glabrata possess large families of different small and broad-spectrum permeases (17). In C. albicans and some of its pathogenic close relatives, these permease families are significantly expanded compared to other related, nonpathogenic species (18), indicating a role for flexibility of nitrogen utilization in pathogenicity. This flexibility includes the ability to use proteins, peptides, amino acids, and other low-molecular-weight nitrogen sources.

For humans, histidine is an essential amino acid. In the body, it can be converted to histamine by a histidine decarboxylase or to uracil and ammonia by a histidine ammonia-lyase (HAL), also known as histidinase (19). In this work, we investigate the initiation of histidine degradation in C. glabrata and show that it uses an aromatic aminotransferase instead of a histidinase for histidine utilization.

MATERIALS AND METHODS

Strains and growth conditions. The following strains were used in the experiments: C. glabrata ATCC 2001, S. cerevisiae ATCC 9763, C. albicans SC5314, and Saccharomyces kluveri CBS3082. The fungi were maintained on solid YPD medium (2% glucose, 1% yeast extract, 1% peptone, 2% agar) and grown at 30°C. The aroΔ deletion mutant has been described previously (20).

Growth curve experiments were performed in 1× YNB medium (BD Biosciences, CA, USA) with 2% glucose (Rotth, Germany), 100 mM phosphate buffer (pH 5.8), and 10 mM the respective amino acid (Rotth) or 0.5% NH₄SO₄ (Rotth). For competitive-inhibition experiments, 10 mM (aminoxy)acetate (AOA) (Sigma) was added to these media. In selected experiments, 5 mM histidine was combined with 5 mM other amino acids as indicated. Fungi were inoculated from a YPD overnight culture at an optical density at 600 nm (OD₆₀₀) of 0.2. Growth was measured every 15 min in a 1-ml volume in a 24-well plate (TPP, Switzerland) using a Tecan Infinite M200 microplate reader at 30°C with intermittent shaking.

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**In vitro transaminase assays.** The *C. glabrata* Aro8 (*CgAro8*) protein was expressed heterologously in *Escherichia coli* and purified via a His tag, as described previously (20). The transaminase activity of the protein was measured spectrophotometrically in an assay solution consisting of 100 mM Tris buffer, pH 7.5, 1 μM pyridoxal phosphate (Sigma), 5 μg purified protein, and different amounts of the amino acid to be tested (0.75 to 36 mM) (all from Roth, Germany). To start the reaction, the amino acceptor α-ketoglutarate (10 mM) was added. The formation of indolepyruvate (from tryptophan; molar extinction coefficient $[\epsilon] = 9,300 \text{ M}^{-1} \text{ cm}^{-1}$ at 338 nm), phenylpyruvate (from phenylalanine; $[\epsilon] = 5,900 \text{ M}^{-1} \text{ cm}^{-1}$ at 300 nm), and imidazol-5-yl-pyruvate (from histidine; $[\epsilon] = 11,000 \text{ M}^{-1} \text{ cm}^{-1}$ at 293 nm) was followed in an Amersham Ultraspec 3100pro spectrophotometer (21). As a negative control for intrinsic transaminase activity of the expression system, LacZ protein expressed and purified under the same conditions was used. $K_{\text{m}}$ and $V_{\text{max}}$ values were calculated from the data using GraphPad Prism software version 5.03 (GraphPad Software, San Diego, CA, USA).

**Histidine uptake assay.** Yeast cells were cultivated in 1 X YNB medium supplemented with 100 mM histidine as the sole nitrogen source at 30°C. Samples of cultivation broths were harvested after 1, 2, 4, and 24 h of cultivation and kept at −80°C until further analysis. For histidine quantification, samples were diluted 20-fold in high-performance liquid chromatography (HPLC)-grade water before analysis on a Biochrom 30+ amino acid analyzer (Biochrom) according to the manufacturer’s protocol for standard amino acid determination in physiological fluids. Briefly, the diluted samples were deproteinated with sulfosalicylic acid, and amino acids were HPLC separated, followed by postcolumn derivatization using ninhydrin and photometrical detection at 570 nm.

**Transcription analyses.** Yeast cells were grown in media containing 10 mM the appropriate amino acid, as described previously. Samples were taken at 0 min (YPD preculture) and after 1, 4, and 8 h of growth. RNA was isolated using an RNeasy kit (Qiagen) after glass bead disruption in a Precellys homogenizer (PeqLab). RNA quality was ensured with the Bioanalyzer instrument (Agilent). Expression of the expression system, LacZ protein expressed and purified under the conditions tested. Ammonium sulfate (0.5% NH$_4$SO$_4$) and YPD complex medium served as controls. All data are means ± standard deviations (SD).

**RESULTS**

*C. glabrata* and *C. albicans* can use histidine as the sole nitrogen source. We measured the ability of the hemiascomycetes *C. glabrata*, *C. albicans*, *S. cerevisiae*, and *S. kluveyri* to use different amino acids as their sole nitrogen source (Fig. 1). When grown in minimal medium with glucose as a carbon source and 10 mM single amino acids as a nitrogen source, *C. glabrata* and *S. cerevisiae* were able to use most of the standard proteinogenic amino acids. Only cysteine and lysine cannot support the growth of either yeast. Glycine and histidine enable good growth of *C. glabrata*, but not of *S. cerevisiae*. The yeast *S. kluveyri* is similar to *S. cerevisiae* in its growth profile, with the exception of lysine, which can be used by *S. kluveyri* but not by baker’s yeast. In contrast, *C. albicans* was able to use all 20 classical proteinogenic amino acids as its sole source of nitrogen. As expected, all fungi grew best in YPD complex medium or in minimal medium with ammonium sulfate as the nitrogen source.

Furthermore, the overall growth pattern of *C. glabrata* resembles that of *S. cerevisiae* more than that of *C. albicans*, with the exceptions noted above. Compared to the other species, *C. albicans* grows much more slowly with aromatic amino acids (phenylalanine, tryptophan, tyrosine, and, for both *Candida* species, histidine). Importantly, histidine supports the growth of *C. glabrata*, with a generation time of 3.5 h, but both *S. cerevisiae* and the more basal *S. kluveyri* cannot grow, while the more distantly related *C. albicans* multiplies with a generation time of 8.7 h.

The HAL gene is absent in the hemiascomycetes. Histidine ammonia-lyases (HALs), or histidinases (EC 4.3.1.3), catalyze the conversion of histidine into ammonium and urocanic acid, enabling organisms to use histidine as a nitrogen source. Histidine ammonia-lyases are ubiquitous enzymes and can be found in archaea, bacteria, and eukaryota: a pfam search (23) detected HALs in 573 species from all three kingdoms (data not shown). Among the fungi, HALs can be found in many of the ascomycota and the basidiomycota. However, no conserved HAL sequences can be found in the hemiascomycete branch of the ascomycota, which contains (among other fungi) the fungal species investigated here, *S. cerevisiae, C. albicans, C. glabrata*, and *S. kluveyri*. In contrast, HALs can be found in the Pezizomycotina, as related euascomycete phylum, for example, in *Aspergillus* and *Penicillium* spp. Evidently, the histidine ammonia-lyase gene was lost in the evolution of the Saccharomycotina. A TBLASTN search of fungal DNA sequences with the *Aspergillus clavatus* phenylalanine and histidine ammonia-lyase protein sequences as the
query further supported the pfam results (data not shown). While this absence of a histidine ammonia-lyase would explain the lack of growth of *S. cerevisiae* and *S. kluyveri* with histidine as the sole source of nitrogen, both *C. albicans* and *C. glabrata* must have other means available to obtain the nitrogen from histidine. Thus, we propose that these fungi have evolved alternative metabolic pathways in order to use histidine as a potential nitrogen source.

**Deletion of ARO8 in C. glabrata.** Recently, we created a mutant of *C. glabrata* that lacks the homologue of the yeast *S. cerevisiae* aromatic aminotransferase I gene, *ScARO8* (20). In *S. cerevisiae*, aromatic aminotransferases are known to catalyze the transfer of the amino group from phenylalanine, tyrosine, and tryptophan to amino acceptors like 2-oxoglutarate (24). As anticipated, growth with the three aromatic amino acids was strongly reduced in the *C. glabrata aro8Δ* mutant (20), highlighting the broad substrate spectrum of the aminotransferase CgAro8. Unexpectedly, we found that the mutant was also nearly unable to use histidine as a nitrogen source, a phenotype resembling that of wild-type *S. cerevisiae* (Fig. 2). Therefore, it seems that the CgAro8 aminotransferase contributes significantly to the growth of *C. glabrata* on histidine as the sole nitrogen source.

In contrast, deleting the *C. glabrata* homologue of the yeast aromatic aminotransferase II gene, *ScARO9*, or of the downstream decarboxylase gene *ScARO10*, had only a negligible effect on growth with histidine as the sole nitrogen source (Fig. 2). Growth with the aromatic amino acid tryptophan, phenylalanine, or tyrosine was moderately reduced in the *C. glabrata aro9Δ* and *aro10Δ* mutants. In YPD complex medium, none of the deletion mutants displayed a reduced growth rate, while a minor growth

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**FIG 2** Growth curves of different mutants of *C. glabrata* and the *S. cerevisiae* wild type, used for comparison. Deletion of ARO8 nearly abolished growth of *C. glabrata* with histidine, tryptophan, or tyrosine and strongly reduced growth with phenylalanine as the sole nitrogen source. Deleting the aromatic aminotransferase gene ARO9 or the decarboxylase gene ARO10 had much less effect on growth. All mutant strains grew nearly identically to the *C. glabrata* wild type in YPD complex medium.
AOA is a broad-spectrum inhibitor of pyridoxal phosphate-dependent reactions like transaminations (25) and has been shown to inhibit, among others, fungal transaminases (26). In our hands, it strongly inhibited the growth of C. glabrata on histidine and all other aromatic amino acids at a concentration of 10 mM (Fig. 3). Growth with ammonium sulfate in the presence of the inhibitor was also reduced (as in the aro8Δ deletion mutant). There was no general growth reduction by addition of up to 10 mM AOA to YPD complex medium, showing that the reduced growth is likely not due to a general toxicity of AOA at these concentrations. Stronger growth inhibition was also observed for C. albicans. After a long lag phase, growth mostly resumed for C. glabrata. For C. albicans, which grew significantly more slowly even in the absence of the inhibitor (Fig. 1), no significant growth with any single aromatic amino acid was detected even after 36 h in the presence of AOA (Fig. 3). Overall, these results, in combination with the data from the deletion mutants, demonstrate that, like the utilization of other aromatic amino acids, histidine utilization is dependent on the aminotransferase activity of CgAro8 in C. glabrata.

Finally, uptake of histidine was measured by HPLC analyses of the supernatants from growing yeast cultures (Fig. 4). After 24 h, complete removal (a concentration below the detection limit of 34 μM) of the initial 10 mM histidine was observed from the supernatant of C. glabrata wild-type cultures. In contrast, nearly all of the histidine (9.8 mM) remained in the supernatant of the aro8Δ mutant. The remaining histidine level of the S. cerevisiae supernatant (7.4 mM) showed that the yeast can take up histidine, albeit at significantly lower levels than C. glabrata. However, since growth of S. cerevisiae is not supported by histidine as a sole nitrogen source, the exact fate of histidine in S. cerevisiae remains to be elucidated.

Aro8 and Aro9 regulation in C. glabrata and S. cerevisiae.

Previous microarray analyses indicated differences in regulation of ARO8 and ARO9, the genes for aromatic aminotransferases I and II, respectively, between C. glabrata and S. cerevisiae (20). We investigated this regulation on the transcriptional level in more detail using qRT-PCR on RNA isolated from liquid cultures of S. cerevisiae and C. glabrata exposed to histidine, tryptophan, or ammonium sulfate as the sole nitrogen source (Fig. 5A).

ScARO8 was nearly 10-fold upregulated already at 1 h when histidine or tryptophan was offered as a nitrogen source. An early, lower upregulation was also observed with ammonium sulfate in the medium, but the transcript levels of ARO8 decreased over time again in both C. glabrata and S. cerevisiae. This likely reflects the catabolic and anabolic activities of the enzymes, respectively, in the different media.

As described previously (27), the main aromatic aminotransferase gene, ScARO9, was strongly upregulated in S. cerevisiae when tryptophan was provided as the source of nitrogen but downregulated with ammonium sulfate initially at 1 h compared to the preculture (as opposed to ScARO8). With histidine, an increase of ScARO9 mRNA levels was observed, but to a much lesser extent.

For C. glabrata, the most striking difference from S. cerevisiae was the complete lack of induction of the CgARO9 gene under any of our experimental conditions. Even with tryptophan, the strongest inducer of ScARO9 transcription in S. cerevisiae, there was no detectable difference from the preculture RNA levels in C. glabrata. In contrast, the transcription of CgARO8 was upregulated in histidine- and in tryptophan-containing media, in agreement with our previous data (20). With these data, we confirmed the differences in ARO gene regulation between S. cerevisiae and C. glabrata and found that the CgARO9 gene seems to be largely nonresponsive to external aromatic amino acids or histidine.
Genomic differences between the \textit{ARO8} and \textit{ARO9} loci in \textit{C. glabrata} and \textit{S. cerevisiae}. To find an explanation for the differences in the regulation of these aromatic aminotransferase genes, we examined the structures of their respective genomic loci. Using YGOB, the yeast gene order browser (28), we found that \textit{CgARO8} and the next gene located upstream, CAGL0G01232g (an \textit{ScKEX1} homologue), form a pair with synteny to its counterpart in \textit{S. cerevisiae} and the predicted common ancestor. Downstream of \textit{CgARO8} and upstream of the \textit{KEX1} homologue, the synteny is broken.

For \textit{CgARO9}, there is an inversion upstream of the open reading frame (ORF) compared to the genome of \textit{S. cerevisiae} and all other available genomes of the YGOB. Sequence analysis showed that this inversion encompasses several kilobases and includes the neighboring predicted genes \textit{YCK1}, \textit{WSS1}, and \textit{ECM14} (Fig. 5B). In addition, the inversion may also include one or more transcription factor binding sites of the immediate \textit{CgARO9} upstream region. Such a removal of the binding sites from \textit{CgARO9} gives a possible explanation for its lack of regulation in the presence of aromatic amino acids.

\textbf{In vitro activity of the Aro8 proteins.} For further confirmation of the role of \textit{Aro8} in histidine degradation, we heterologously expressed a histidine-tagged \textit{CgARO8} protein in \textit{E. coli} and affinity purified the enzyme. As we have shown before (20), the \textit{CgARO8} protein converted tryptophan into indole pyruvate. The \(K_m\) of this reaction was 14.9 ± 2.5 mM, and the \(V_{\text{max}}\) was 593.3 ± 48.5 nmol \cdot min\(^{-1}\) \cdot mg\(^{-1}\) under our \textit{in vitro} assay conditions (with \(\alpha\)-ketoglutarate as the amino acceptor). In addition, the protein was also able to convert phenylalanine into phenylpyruvate under the same conditions, with a \(K_m\) of 1.39 ± 0.16 mM and a \(V_{\text{max}}\) of 196.7 ± 3.9 nmol \cdot min\(^{-1}\) \cdot mg\(^{-1}\). This reaction is similar to that of the \textit{S. cerevisiae} Aro8 protein (29). However, most interestingly, a test with \(L\)-histidine as the amino donor revealed that \textit{CgARO8} is also able to transfer the amino group of this amino acid to \(\alpha\)-ketoglutarate, producing imidazol-5-yl-pyruvate (Fig. 6A), with a \(K_m\) of 8.80 ± 1.41 mM and a \(V_{\text{max}}\) of 274.9 ± 19.8 nmol \cdot min\(^{-1}\) \cdot mg\(^{-1}\). Interestingly, a heterologously expressed Aro8 protein from \textit{S. cerevisiae} had a similar ability to catalyze the aminotransferase reaction with \(L\)-histidine as a donor (data not shown), implying a principal ability of \textit{S. cerevisiae} for histidine transamination.

\textbf{Interaction of histidine with other nitrogen sources in \textit{S. cerevisiae}.} The Aro8 proteins of both species were able to catalyze the histidine aminotransferase reaction \textit{in vitro}, and in both species, the \textit{ARO8} gene was upregulated in response to histidine. We therefore investigated the effect of adding histidine to the medium on the growth of \textit{S. cerevisiae}. To this end, we mixed histidine 1:1 (5 mM each) with different nitrogen sources: alanine as an amino acid with an independent degradation pathway, phenylalanine as an aromatic amino acid that induces \textit{ARO8} \textit{Aro8} allele and 10-kbp upstream regions in \textit{S. cerevisiae} (top) and \textit{S. cerevisiae} (bottom). An inversion event was detected encompassing the upstream genes \textit{YCK1}, \textit{WSS1}, and \textit{ECM14}. The genes CAGL0G06182 and \textit{YHR131C} are homologues with identical orientations with respect to the \textit{ARO9} genes. The solid arrows indicate ORFs with the same orientation as \textit{ARO9}, and the open arrows indicate opposite orientations. Alignment was performed with GATA (22). Black lines indicate alignments in the same orientation (+/+), and red lines indicate those in inverse orientation (+/−). Darker shadings indicate better alignment scores.

\begin{figure}[h]
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\caption{(A) Relative expression of \textit{ARO8} and \textit{ARO9} after transfer from complex medium to minimal medium containing ammonium sulfate, histidine, or tryptophan as the sole source of nitrogen. In both \textit{S. cerevisiae} (S.c.) and \textit{C. glabrata} (C.g.), \textit{ARO8} expression was upregulated compared to its expression in the precurculture at all time points when the amino acids were offered. There was no regulation observable for \textit{ARO9} in \textit{C. glabrata}, while \textit{S. cerevisiae} very strongly upregulated \textit{ARO9} when tryptophan was present. The error bars indicate standard deviations. (B) Genomic-locus alignment of the \textit{ARO9} gene and 10-kbp upstream loci in \textit{C. glabrata} (top) and \textit{S. cerevisiae} (bottom). An inversion event was detected encompassing the upstream genes \textit{YCK1}, \textit{WSS1}, and \textit{ECM14}. The genes CAGL0G06182 and \textit{YHR131C} are homologues with identical orientations with respect to the \textit{ARO9} genes. The solid arrows indicate ORFs with the same orientation as \textit{ARO9}, and the open arrows indicate opposite orientations. Alignment was performed with GATA (22). Black lines indicate alignments in the same orientation (+/+), and red lines indicate those in inverse orientation (+/−). Darker shadings indicate better alignment scores.
\end{figure}
the pathogenic potential of these fungi. Between the ability to use a broad range of nitrogen sources and amino acids, it is tempting to speculate that a correlation may exist and use histidine. As the pathogenic yeasts in this study, has independently gained this ability in a lineage that is unable to be initiated, downstream processing of the transaminated product or ScARO9 supply, indicates that at least species can utilize histidine as their sole nitrogen source. Comparing Evidently, this pathogen is even more versatile than C. albicans cerevisiae in its ability to use different nitrogen sources, though not amino acids. In baker's yeast, the only exceptions were cysteine, glycine, histidine, and lysine, in accordance with previous observations (30). The pathogenic yeast C. glabrata, on the other hand, was additionally able to grow with either glycine or histidine as the sole nitrogen source. Evidently, this pathogen is even more versatile than S. cerevisiae in its ability to use different nitrogen sources, though not as flexible as C. albicans, which can utilize all 20 proteinogenic amino acids.

We hypothesized that the inability of S. cerevisiae to use histidine as a nitrogen source was due to the loss of the histidine ammonia-lyase gene. Since this loss is common to all hemiascomycetes, it should also affect C. albicans and C. glabrata, yet these two species can utilize histidine as their sole nitrogen source. Comparison with S. kluveri, which also cannot use histidine for a nitrogen supply, indicates that at least C. glabrata, and probably C. albicans, has independently gained this ability in a lineage that is unable to use histidine. As the pathogenic yeasts in this study, C. albicans and C. glabrata, were most flexible with regard to the utilization of amino acids, it is tempting to speculate that a correlation may exist between the ability to use a broad range of nitrogen sources and the pathogenic potential of these fungi.

Having a broad set of catabolic pathways for the specific nutrient sources in the host is clearly advantageous for pathogenic fungi (6). On the other hand, unused metabolic pathways are quickly lost. One striking example of this is the absence of the kynurenine pathway in C. glabrata (31). In baker’s yeast, the aromatic amino acid tryptophan can be degraded by two distinct pathways, via the kynurenine pathway to NAD or via the Ehrlich pathway to indole-3-ethanol (32). C. glabrata has lost six of the seven BNA genes of the kynurenine pathway (31, 33) and is therefore auxotrophic for niacin, as opposed to S. cerevisiae and C. albicans. Due to these losses, the only remaining pathway for tryptophan degradation in C. glabrata is via the Ehrlich pathway, and therefore via the CgAro8 aromatic amino acid aminotransferase (20).

Here, we show that degradation of histidine in C. glabrata also occurs via the Ehrlich pathway. The aromatic amino acid aminotransferase Aro8 is both sufficient for in vitro aminotransferase activity and required for growth with histidine as the sole nitrogen source. The K_m values of C. glabrata Aro8 for the transamination reactions of phenylalanine and tryptophan seem high for its biological function but are similar to those published for its S. cerevisiae counterpart (1.4 versus 0.3 mM and 14.9 versus 6 mM, respectively [24]). Thus, a similar biological role for CgAro8 in the degradation of external aromatic amino acids seems likely, and the histidine transamination observed in vitro should be sufficient to enable in vivo growth with histidine.

Like the deletion of CgAro8, inhibition of the aromatic aminotransferase with the substance AOA led to a severe growth defect of C. glabrata (and C. albicans) with tryptophan and histidine as the sole nitrogen sources. The growth defect with ammonium sulfate is likely due to the general inhibition of aminotransferase activities that are also required in amino acid anabolic processes. In S. cerevisiae, deletion of both ScARO8 and ScARO9 leads to phenylalanine and tryptophan auxotrophy of the double mutant (34). Thus, with only ammonium sulfate as a nitrogen source in the medium, AOA likely blocked the biosynthesis of aromatic and other amino acids by inhibition of the respective aminotransferases, which could lead to a limitation of building blocks for anabolic purposes. Alternatively, inhibition of aminotransferases could lead to accumulation of α-ketoacids that provoke general

**DISCUSSION**

The comparatively close phylogenetic relationship between the normally nonpathogenic yeast S. cerevisiae and the pathogenic yeast C. glabrata allows the detection of specific factors and traits that are associated with fungal pathogenesis (4). These include, for example, the ability of C. glabrata to grow efficiently at body temperature, but also its ability to use nutrients from particular host niches, which likely differ significantly from S. cerevisiae’s normal habitats.

Both S. cerevisiae and C. glabrata were able to grow with most of the proteinogenic amino acids as sole nitrogen sources. For baker’s yeast, the only exceptions were cysteine, glycine, histidine, and lysine, in accordance with previous observations (30). The pathogenic yeast C. glabrata, on the other hand, was additionally able to grow with either glycine or histidine as the sole nitrogen source. Evidently, this pathogen is even more versatile than S. cerevisiae in its ability to use different nitrogen sources, though not as flexible as C. albicans, which can utilize all 20 proteinogenic amino acids.

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**FIG 6** (A) Proposed aromatic amino acid aminotransferase reaction by Aro8 with α-ketoglutarate and histidine as substrates, producing glutamate and imidazol-5-yl-pyruvate. The pathway from histidine to urconic acid via the HAL does not take place in C. glabrata or S. cerevisiae due to the absence of the HAL gene. The transferred amine group is marked in boldface. (B) Effects of histidine supplementation on S. cerevisiae growth with different nitrogen sources. Addition of 5 mM histidine abolishes growth with the aromatic amino acids phenylalanine and tryptophan and reduces growth with alanine or ammonium sulfate as the nitrogen source. Addition of the aromatic amino acid aminotransferase inhibitor AOA slightly increases the growth rate when alanine is supplemented with histidine.
toxic effects and may thus cause reduced growth rates. However, the normal growth rate in YPD medium in the presence of AOA makes the latter scenario rather unlikely, although the possibility that differences in AOA uptake depending on the applied growth medium result in reduced toxicity cannot be excluded. Nevertheless, the strong growth-inhibitory effect of any of the aromatic amino acids used as a sole nitrogen source further indicates that, despite its low specificity, aromatic aminotransferases of \textit{C. glabrata} were indeed inhibited by AOA treatment.

An aminotransferase reaction for histidine degradation has already been proposed to occur in other organisms. In the rat’s liver, for example, this reaction has been reported to take place, but it is most likely not used for catabolic purposes. Instead, it serves a function during mitochondrial transport (35). No gene has been found so far to code for the enzyme. In \textit{E. coli} and other bacteria, like \textit{Pseudomonas testosteroni} (36), a similar histidine transaminase reaction has been described, but the well-investigated \textit{E. coli} K-12 strain lacks this reaction and is unable to catabolize histidine. Other fungi, like \textit{Aspergillus} spp., possess the standard histidine ammonia-lyase, and the protein has been shown to be active, for example, in \textit{A. nidulans} when histidine is the sole nitrogen source (37). Therefore, to our knowledge, catabolism via an aromatic aminotransferase instead of a histidinase presents a novel route for fungal growth with histidine as a nitrogen source.

Interestingly, \textit{S. cerevisiae} Aro8 also catalyzes the aminotransferase reaction from histidine, although the fungus is unable to grow with histidine as the sole nitrogen source. Our data indicate, however, that histidine degradation may lead to an inhibiting metabolic intermediate in yeast, while histidine did not support growth, it also abolished growth under conditions where the Ehrlich pathway was active (in the presence of phenylalanine or tryptophan as a nitrogen source). Under these conditions, histidine will likely be deaminated by the aromatic amino acid amino-transferase from histidine, although the fungus is unable to catalyze this reaction. For this phenomenon is an inversion event in the phylogenetic lineage of \textit{C. glabrata} likely contributed to the observed differences between \textit{C. glabrata} and \textit{S. cerevisiae}.

The presence of an unusual nitrogen metabolic pathway has precedents in the hemiascomycetes. These yeasts catabolize urea via a urea amidolyase instead of the urease of other higher fungi (39). Deleting the urea amidolyase gene, \textit{DUR1}, in \textit{C. albicans} leads to a reduction in virulence and, importantly, of the fungal burden in organs with high urea content (40). This can, at least in part, be explained by the dependency of fungi on external nitrogen sources during infections (40). Hence, like the \textit{DUR1} pathway in \textit{C. albicans}, the unusual histidine metabolism of \textit{C. glabrata} may be considered a possible target for drugs that could reduce growth of the fungus in the host.

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**REFERENCES**


