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Physiological and biochemical characteristics of the ethyl tiglate production pathway in the yeast Saprochaete suaveolens

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Abstract

A yeast identified as Saprochaete suaveolens was investigated for its capacity to produce a large panel of flavouring molecules. With a production of 32 compounds including 28 esters, S. suaveolens seems to be a good producer of fruity flavours and fragrances and especially of unsaturated esters, such as ethyl tiglate. Physiological and biochemical analyses were performed in this study in an attempt to comprehend the metabolic route to the formation of this compound. We show that the accumulation of ethyl tiglate by S. suaveolens is specifically induced by isoleucine. However, and contrary to S. cerevisiae, which harbours a classical Ehrlich pathway leading to the production of 2-methylbutanol from isoleucine, our results provide phenotypic and enzymological evidence of ethyl tiglate biosynthesis in S. suaveolens through the catabolism of this amino acid by the β-oxidation pathway, which generates tiglyl-CoA as a probable intermediate. A kinetic analysis of this flavour molecule during growth of S. suaveolens on glucose and isoleucine showed a phase of production of ethyl tiglate that culminated concurrently with isoleucine exhaustion, followed by a disappearance of this compound, likely due to reassimilation by the yeast.

Keywords: Ehrlich pathway; flavours and fragrances; esters; β-oxidation; Saprochaete suaveolens; ascomycetes

Introduction

With renewed interest for natural products during the last decade, there is an increasing need to produce natural molecules using microbial systems for many applications. Flavours and fragrances are important compounds in the food, cosmetic, pharmaceutical and chemical industries (Pinotti et al., 2006; Schrader, 2007). In 2013, the worldwide market of the flavour industry was estimated as 24 billion US$ (http://www.leffingwell.com, accessed in June 2014). Disadvantages of the conventional processes of production, such as extraction of plant material and chemical synthesis, has recently motivated both academic laboratories and several industrial companies to identify microbial sources that may naturally produce these molecules and develop biotechnological processes to optimize the production and productivity of them, or to engineer microbial systems to produce new added-value chemicals (Keasling, 2012).
The microbial production of flavouring molecules has been extensively studied during recent decades and many reviews in this field have been published (Krigs and Berger, 1998; Abbas, 2006; Berger, 2009; Buzzini and Vaughan-Martini, 2006; Feron et al., 1996; Schrader, 2007; Mdaini et al., 2006; Dastager, 2009; Pires et al., 2014; Styger et al., 2011; Löser et al., 2014; Kim et al., 2014; Cheon et al., 2014). Biotechnological production of flavour compounds is nowadays considered to be a mature discipline in the industry, with an estimated 100 molecules in the market produced by enzymatic or microbial processes (Schrader, 2007). Among them, molecules such as vanillin, γ-decalactone, 2-phenylethanol and raspberry ketone are considered to be high added-value products (Serra et al., 2005; Schrader, 2007; Hua and Xu, 2011; Prieffert et al., 2001).

Ethyl tiglate, also known as ethyl (E)-2-methylbut-2-enoate, is a branched-chain alkyl ester naturally found in some organisms, such as Mangifera indica L. (mango) (Pino et al., 2005), Malus domestica Borkh. (red apple) (Matich and Rowan, 2007), Cydonia vulgaris (quince) (Schreyen et al., 1979), Pyrus serotina (Asian pear) (Takeoka et al., 1992) and Pelargonium graveolens (geranium rosal) (http://www.perfumerflavorist.com, accessed in May 2014). This FEMA-GRAS (Flavor and Extract Manufacturers Association; generally recognised as safe) compound is characterized by a fruity odour and is mainly used in perfumery to add unusual top notes, particularly for the non-floral fragrance types (Arctander, 1969). This compound is also used in the food industry for the production of alcoholic beverages, such as rum, and for tobacco flavouring (http://www.perfumerflavorist.com, accessed February 2014). Ethyl tiglate is also described by entomologists as an aggregation pheromone in some Drosophila species (Bartelt et al., 1985, 1988; Moats et al., 1987); mature males of D. borealis and D. littoralis produce these pheromones that attract both males and females. Data regarding the production of ethyl tiglate by microorganisms is rather scarce. Pinotti et al. (2006) reported the production of ethyl tiglate by the yeast Geotrichum candidum under some specific growth conditions. An extensive analysis carried out by another group did not identify ethyl tiglate among the volatile compounds produced by Saprochaete suaveolens when cultivated on cassava waste water (Takeoka et al., 1992; Damasceno et al., 2003).

Finally, two European patents refer to the production of ethyl tiglate by some microbial strains, including Geotrichum klebahnii (Geotrichum penicillatum, CBS 62774) and Saprochaete suaveolens (Geotrichum suaveolens, CBS 38236 and Geotrichum fragrans ATCC 11247) (Farbood et al., 1987, 1992).

The metabolism of ethyl tiglate has never been described in yeast and has only been described in red apple (Matich and Rowan, 2007); the results of the latter study suggested that the synthesis of ethyl tiglate in fruit occurred from isoleucine metabolism via a modified Ehrlich pathway. This pathway is well known for the production of higher alcohols and related flavour compounds, such as 2-methylbutanol, 2-methylbutanoic acid, ethyl 2-methylbutanoate, 2-methylbutyl ethanoate or 2-phenylethanol (Hazelwood et al., 2008).

In the present study we focused on the production of ethyl tiglate by the yeast Saprochaete suaveolens, a yeast also known as Geotrichum fragrans, which belongs to the Saccharomycetes class of microorganisms (De Hoog and Smith, 2004, 2011) and which we isolated from Pitaya fruit (Hylocereus polyrhizus) in Reunion Island as part of a screening programme of yeasts capable of producing volatile aromatic molecules of particular interest for industry. We show here that the main precursor of ethyl tiglate is isoleucine, and provide evidence that the metabolic pathway leading to this compound is distinct from the Ehrlich pathway, which converts this amino acid into 2-methylbutanol (amyl alcohol) in other yeasts, such as Saccharomyces cerevisiae.

Materials and methods

Yeast strains

The strain GEC0 of Saprochaete suaveolens (Geotrichum fragrans) (De Hoog and Smith, 2004, 2011) used in this study was isolated from Pitaya fruits (Hylocereus polyrhizus) in the area of Saint Paul in Reunion Island (France). The microorganism was first identified using an API 20C AUX strips (bioMérieux) and further confirmed by 26S rDNA D1/D2 sequencing, identified according to Kurtzman and Robnett (1997). This study was performed by the Centre International de Ressources Microbiennes (CIRM, INRA, Paris.
Wild-type strain used for qualitative analysis was grown in an Erlenmeyer flask containing 20 g/l glucose (α-D-glucose, anhydrous, Sigma-Aldrich), 20 g/l peptone (Becton-Dickinson), and 10 g/l yeast extract (Biokar Diagnostics) and 15 g/l agar (agar-agar for microbiology; Merck). The cells were refreshed at 28 °C for 24 h prior to their utilization.

For qualitative study of flavour compounds produced by the yeast strains, a loop of fresh cells was spread on inclined YPD slants incubated at 28 °C for 48 h. The tubes were sealed after 24 h of incubation.

For quantitative experiments and enzymatic assays, experiments were performed in 250 ml Erlenmeyer flasks containing 50 ml YNB–glucose medium (0.67% w/v Yeast Nitrogen Base without Amino Acids, 2% w/v glucose, Sigma-Aldrich). Liquid cultures were inoculated at an initial optical density measured at 600 nm of 0.1 U with cells precultivated in YNB–glucose and incubated at 28 °C and 110 rpm for 24 h. Growth cultures were incubated under the same conditions for 120 h. When appropriate, 1 g/l L-isoleucine (Sigma-Aldrich) was added to the medium, as indicated in the legends to figures. Cell growth was measured at regular intervals, using a Jenway Spectrophotometer 6450 set to 600 nm (OD600 = optical density at 600 nm). Quantitative and qualitative experiments were performed in independent triplicates.

Qualitative analysis of volatile metabolites

Isolation and characterization of volatile metabolites was performed using solid-phase micro-extraction (SPME), followed by gas chromatography–mass spectrometry (GC–MS) analysis. Prior to analysis, 25 µl octanol (1 g/l in ethanol) was added into the sealed vials containing the yeast culture, as an internal standard. The headspace of the inclined cultures on YPD was subjected to SPME analysis, using a 2 cm-long fibre coated with 50/30 µm divinylbenzene/Carboxen™ on polydimethylsiloxane, bonded to a flexible fused silica core (Supelco) (Buzzini et al., 2005). The fibre was exposed to the headspace for 15 min at 30 °C and inserted into the injection port of the GC–MS (Agilent Technologies 6890 N Network GC system) for thermal desorption at 270 °C for 15 min. Metabolites were separated by gas chromatography (GC) on a SPB5 column ((Supelco, 60 m x ...) 60 m ×0.32 mm, 0.25 µm film thickness), coupled to a mass spectrometer (Agilent Technologies 5973 Network mass-selective detector). The carrier gas (He) was set at a flow rate of 0.8 ml/min. The column temperature was maintained at 45 °C for 2 min, raised to 230 °C at 4 °C/min and finally kept at this temperature for 12 min. Volatile compounds were identified by comparing their mass spectra with the NIST and Wiley mass spectral databases and their Kovats retention indexes with those from the NIST retention index library (http://webbook.nist.gov/chemistry, accessed May 2014).

Quantitative assay of ethyl tiglate

The metabolites in the culture medium were extracted by liquid–liquid extraction. Samples containing 475 µl fermentative medium were supplemented with 25 µl octanol (1 g/l in ethanol). The mixture was then extracted using 500 µl dichloromethane and the aqueous phase separated by centrifugation at 14 000×g for 5 min. Quantitative determination of ethyl tiglate was carried out by GC (Varian 430), using a CP-WAX 52 CB (25 m ×0.25 mm, 0.2 µm film thickness) column, coupled to a flame ionization detector (FID). Injector and detector were set at 230 °C and 250 °C, respectively; 0.2 µl organic phase of each sample was injected for analysis. The carrier gas (He) was set at a flow rate of 0.8 ml/min. The column temperature was maintained at 45 °C for 2 min, raised to 230 °C at 4 °C/min and finally kept at this temperature for 12 min. Ethyl tiglate and 2-methylbutanol used for the response factor curve and as a standard were purchased from Sigma-Aldrich.

HPLC analysis of sugars and amino acids

The concentration of glucose and isoleucine was measured using an Ultimate 3000 HPLC system ( Dionex) coupled to a Varian 380 LC evaporative light-scattering detector (Raessler, 2011; Noga et al., 2013) (evaporation temperature 50 °C,
nebulization temperature 50°C, N₂ flow 1.6 slm Standard liter per minute). For glucose analysis, separation was performed using a Hi-Plex Ca column (Agilent, 7.7×300 mm, 8 μm film thickness) under isothermal conditions (85°C). The injection volume of filtered samples (through 0.45 μm Sartorius filters) was 10 μl and MilliQ water was used as mobile phase, at a flow rate of 0.6 ml/min. Isoelectric was analysed using an Atlantis Silica HILIC column (100 Å, 3 μm, 2.1 mm×100 mm) under isothermal conditions (30°C). 2 μl filtered samples (through 0.20 μm Sartorius filters) were injected into the chromatographic system and methanol:water (80:20 v/v) was used as the mobile phase, at a flow rate of 0.8 ml/min.

Preparation of crude extracts and assays of enzymatic activities

Cells were collected by centrifugation at 1000×g at 4°C, washed twice in demineralized water and stored at −20°C until use. Cell-free extracts from early stationary phase culture samples were prepared using a Qiagen Retsch TissueLyser II (3 min, 30 Hz). The buffer was 50 mM potassium phosphate buffer, pH7.4, containing 2 mM EDTA, 100 mM KCl and 1 mM DTT. The extract was centrifuged at 4°C for 5 min at 1000×g in an Eppendorf tabletop centrifuge and the supernatant was used for determination of enzyme activities and protein concentration. Pyruvate and 2-oxo-acid decarboxylase (DC) activity on α-keto acids, pyruvate and 2-oxo-3 methylpentanoic acid was determined according to Ullrich (1970), with some modifications. The medium contained 50 mM citrate buffer, pH6.2, 100 mM KCl, 0.2 mM DTT, 0.5 mM TPP, 5 mM MgSO₄, 0.1 mM NADH and 5 U/ml yeast alcohol dehydrogenase (Sigma-Aldrich). The reaction was started by the addition of 50 mM pyruvate or 0.2 mM 2-oxo-3-methylpentanoic acid (determined at saturated concentrations of substrate), and oxidation of NADH was followed spectrophotometrically at 340 nm. Alcohol dehydrogenase (ADH) was assayed in a mixture containing 50 mM citrate buffer, pH6.2, 100 mM KCl, 0.2 mM DTT, 0.5 mM TPP, 5 mM MgSO₄ and 0.1 mM NADH, according to Hansen and Hensgens (1994). The reaction was measured spectrophotometrically following the oxidation of NADH at 340 nm after addition of 2 mM 2-methylbutanal. ADH was also assayed in a mixture containing 20 mM HEPES buffer, pH 7.6, 2 mM DTT and 1.5 mM NAD; the reaction was started by the addition of 40 mM ethanol. The reduction of NAD to NADH was followed at 340 nm. Aldehyde dehydrogenase (AIDH) was assayed in a mixture containing 50 mM citrate buffer, pH6.2, 100 mM KCl, 0.2 mM DTT, 0.5 mM TPP, 5 mM MgSO₄ and 1.5 mM NAD, as described by Tamaki et al. (1982); the reaction was started by the addition of 2 mM 2-methylbutanal. The reduction of NAD to NADH was followed at 340 nm. The branched-chain α-keto acid dehydrogenase (BCKAD) assay was performed following the reduction of NAD to NADH at 340 nm (Patston et al., 1988) in 50 mM potassium phosphate buffer, pH7.4, containing 2 mM EDTA, 0.2 mM DTT, 0.5 mM TPP, 5 mM MgSO₄, 1.5 mM NAD and 0.5 mM CoA-SH; the reaction was started by the addition of 0.2 mM 2-oxo-3-methylpentanoic acid. The acyl-CoA dehydrogenase (ACyD) activity was determined spectrophotometrically following the reduction of DCIP (2,6-dichlorophenolindophenol) into DCIPH₂ at 655 nm (Ikeda and Tanaka, 1988). The reaction was performed in 50 mM potassium phosphate buffer, pH7.4, containing 2 mM EDTA, 100 mM KCl, 0.1 mM FAD and 0.5 mM DCIP; the reaction was started by the addition of 0.2 mM 3-methylbutanoyl-CoA. For the assay of alcohol acyltransferase activity, p-nitrophenol production (Schermers et al., 1976) was followed at 415 nm in a medium containing 50 mM potassium phosphate buffer, pH7.4, 2 mM EDTA and 100 mM KCl; the reaction was started by the addition of 2 mM p-nitrophenylbutyrate. A blank without addition of the corresponding substrate was run in parallel for each sample in all the enzymatic assays. Protein concentration was determined at 550 nm by a modified Bradford (1976) method, with bovine serum albumin (BSA; Sigma-Aldrich) as the standard. All assays were performed on three biological replicates.

Results and discussion

Volatile organic compounds production by S. suaveolens and S. cerevisiae on YPD

The volatile organic compounds produced by the yeast S. suaveolens (GEC0) and S. cerevisiae strain CENPK122-2N after 48h of growth on YPD medium were determined by headspace GC–MS (Table 1). This chemical analysis allowed
The most abundant esters produced by S. suaveolens were ethyl 3-methylbutanoate (ethyl isovalerate), ethyl (E)-2-methylbut-2-enoate (ethyl tiglate), 2-methylpropyl 3-methylbutanoate (2-methylpropyl isovalerate) and 3-methylbutyl 3-methylbutanoate (isoamyl isovalerate), whose identification of 32 molecules produced by S. suaveolens and 21 molecules by S. cerevisiae. These molecules could be classified into two main groups, esters and alcohols. S. suaveolens mostly produced esters (28 of 32 molecules), with 15 found only in cultures of this yeast species and not of S. cerevisiae.
values were in the range 258–1065 μg/l in the headspace of cultures. These esters were also detected in *G. candidum* (Mdaini et al., 2006) and were classified by Verstrepen et al. (2003) as having strong fruity notes with low odour thresholds. In addition, some of these esters, such as ethyl tiglate, could have potential applications as flavouring agents (Christoph and Bauer-Christoph, 2007). On the other hand, alcohols (1-butanol, 2-methylpropanol, 2-methylbutanol, 3-methylbutanol and 2-phenylethanol) were more abundantly produced by the yeast *S. cerevisiae*. Both yeast species also produced ethanol, but it was not quantified here because it co-eluted with the dilution solvent of the internal standard (data not shown). Altogether, these results indicate that *S. suaveolens* has a greater ability to produce ester-type flavour compounds, and hence suggested more efficient alcohol acyltransferase activities in this yeast than in *S. cerevisiae*.

### Influence of metabolic precursors and kinetic production of ethyl tiglate in *S. suaveolens*

The metabolic pathway by which ethyl tiglate is produced by microbial cells has not yet been elucidated. However, as depicted in Figure 1, Matich and Rowan (2007) proposed that this volatile compound is produced from isoleucine through mitochondrial β-oxidation. According to this hypothesis, we investigated the effects on the production of ethyl tiglate

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**Figure 1.** Proposed metabolic routes for the metabolism of isoleucine to some esters in the yeast *Saprochaete suaveolens* (adapted from Matich and Rowan, 2007): TA, transaminase; DC, decarboxylase; BCKAD, branched-chain α-keto acid dehydrogenase; ACyH, acyl-CoA hydrolase; AAT, alcohol acyltransferase; ACyD, acyl-CoA dehydrogenase; AlDH, aldehyde dehydrogenase; ADH, alcohol dehydrogenase; EH, enoyl Co-A hydratase; BHACyDH, β-acyl-CoA dehydrogenase; BKT, β-keto acyl Co-A thiolase.
of various amino acids added at 1 g/l to the culture medium. In agreement with this hypothesis, it is shown in Figure 2 that ethyl tiglate increased from <1 mg/l in the control experiment to >60 mg/l in YNB-glucose supplemented with 1 g/l isoleucine, whereas there was no production of ethyl tiglate upon addition of alanine, valine, leucine, methionine or phenylalanine. When \(\alpha\)-keto-glutarate was added together with isoleucine in the YNB-glucose medium, the concentration of ethyl tiglate increased further to 113 mg/l. A production of 2-methylbutanol at about half that of ethyl tiglate was also observed upon addition of isoleucine to the medium. These results, taken as a whole, clearly indicate that the Ehrlich pathway in \textit{S. suaveolens} is fully functional and that ethyl tiglate production may likely occur through the \(\beta\)-oxidation of isoleucine, as has been suggested for the production of this flavour compound in apple (Matich and Rowan, 2007).

The kinetics of production of ethyl tiglate during fermentation in YNB glucose medium supplemented with 1 g/l isoleucine is reported in Figure 3. It can be seen that accumulation of ethyl tiglate began at the end of growth on glucose and reached its maximum at 24 h, concomitantly with the complete exhaustion of isoleucine. This result confirmed that the production of ethyl tiglate was fully dependent on the presence of isoleucine in the growth medium. Under these conditions, a productivity of 6.5 nmol/min/mg protein was estimated. This result indicated that the production of ethyl tiglate, as well as that of 10 mg/l 2-methylbutanol, arose as a metabolic consequence of the degradation of excess isoleucine. However, upon complete exhaustion of glucose and isoleucine, ethyl tiglate disappeared, which suggested the action of an esterase that converted ethyl tiglate into tiglic acid (or 2-methylbut-2-enoic acid). This latter compound could then be assimilated by the cells as a carbon source through the \(\beta\)-oxidation pathway (Figure 1).

**Figure 3.** Ethyl tiglate production by \textit{Saprochaete suaveolens} during growth on YNB-glucose medium; LOG biomass (– – –), glucose (Glc; - - X - -), isoleucine (Ile; – O –) and ethyl tiglate (– - - - -) concentrations in the medium. The cultures were performed in 50 ml YNB-glucose (20 g/l) supplemented with Ile (1 g/l), pH\text{\textsubscript{initial}} = 5.5 at \(T = 27^\circ\text{C}\) under agitation at 110 rpm. For convenience, the concentrations of glucose and isoleucine were multiplied by 3 and 50, respectively.

**Figure 2.** Ethyl tiglate (black bars) and 2-methylbutanol (grey bars) production by \textit{Saprochaete suaveolens}, as influenced by supplementation of the medium with isoleucine (Ile) alone or associated with the amino acceptor \(\alpha\)-ketoglutarate (\(\alpha\)-KG). Samples were harvested during stationary phase after glucose and isoleucine depletion. The cultures were performed in 50 ml of YNB-glucose (20 g/l) supplemented with Ile or Leu or Val or Met or Phe or Ile + \(\alpha\)-KG (1 g/l each), pH\text{\textsubscript{initial}} = 5.5 at \(T = 27^\circ\text{C}\) under agitation at 110 rpm. Tween 80 (surfactant, 1 g/l) was added to the medium in order to stabilize ethyl tiglate concentration in the medium.

**Phenotypic and enzymatic evidence that ethyl tiglate production required \(\beta\)-oxidation in \textit{S. suaveolens}**

To provide evidence that the production of ethyl-tiglate in \textit{S. suaveolens} implicates the \(\beta\)-oxidation pathway, we carried out two complementary
experiments. The first experiment was to show that this yeast species can grow on branched-chain amino acids, such as leucine, isoleucine or valine, because the β-oxidation of these amino acids leads to acetyl-CoA (plus propionyl-CoA in the case of isoleucine), which are then incorporated into the TCA cycle. As depicted in Figure 1, this pathway requires an oxidative decarboxylation of the keto-acids by a branched-chain α-keto-acid dehydrogenase into the corresponding acyl-CoA. In the yeast *S. cerevisiae*, this β-oxidation of branched-chain amino acids does not take place (Dickinson *et al.*, 1997, 1998), which explains why this yeast species cannot grow on these branched-chain amino acids but converts them into fusel alcohols through the Ehrlich pathway (Hazelwood *et al.*, 2008). In agreement with this hypothesis, we show in Figure 4 that *S. suaveolens* can grow very well on leucine but less efficiently on valine and isoleucine as sole carbon source present in the synthetic minimal medium, whereas *S. cerevisiae* was totally unable to grow on these media. The reason why growth of *S. suaveolens* on leucine was more efficient than on isoleucine and valine could be due to differences in β-oxidation metabolism. Indeed, while the first three reaction steps employed the same enzymes for the three amino acids (see Figure 1), the fourth step is catalysed by an enoyl-CoA hydratase in valine and isoleucine metabolism, whereas it is a 3-methylcrotonyl carboxylase that is required in the β-oxidation of leucine. Thus, one can hypothesize that enoyl-CoA hydratase is poorly active as compared to the carboxylase. This hypothesis would further explain the production of ethyl tiglate, which results from accumulation of tiglyl-CoA.

The second experimental evidence was to determine the activity of key enzymes in the Ehrlich and β-oxidation pathways and compared these activities between the two yeast species (Table 2). Under the conditions tested, the decarboxylase activity (DC) was 20 times more active in *S. cerevisiae* (2760 nM/min/mg protein) than in *S. suaveolens* (137 nM/min/mg protein) using pyruvate as substrate, and three-fold more active with 2-oxo-3-methylpentanoic acid. In addition, alcohol dehydrogenase acting on ethanol was much more active in *S. cerevisiae* than in *S. suaveolens*, but similar activity was found in both yeasts using 2-methylbutanal as substrate. Finally, the absence of activity of aldehyde dehydrogenase in both strains indicated a preference to use the reductive

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**Figure 4.** Growth of *Saccharomyces cerevisiae* (A) and *Saprochaete suaveolens* (B) strains on branched-chain amino acids as sole carbon source (YNB medium without amino acids). The cells were pregrown on YNB medium supplemented with 2% glucose and resuspended in MilliQ water at OD600 = 3; 5 μl of each cell suspension and two serial 1:10 dilutions were spotted on YNB plates supplemented with 2 g/l glucose or 1 g/l leucine, isoleucine or valine as sole carbon source. The plates were incubated at 28 °C for 2 days.

**Table 2.** Activities of some enzymes involved in the Ehrlich and β-oxidation pathways in *Saprochaete suaveolens* and *Saccharomyces cerevisiae*

<table>
<thead>
<tr>
<th>Enzyme activities (nM/min/mg protein)</th>
<th>DC</th>
<th>ADH</th>
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<tbody>
<tr>
<td><strong>On pyruvate</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td><em>S. suaveolens</em></td>
<td>137±37</td>
<td>56±6</td>
</tr>
<tr>
<td><em>S. cerevisiae</em></td>
<td>2760±374</td>
<td>149±18</td>
</tr>
</tbody>
</table>

*Yeast cells were grown on YNB–glucose (20 g/l) supplemented with isoleucine (1 g/l). Crude extracts were prepared as described in Materials and methods. Bd, below detection level; DC, decarboxylase; ADH, alcohol dehydrogenase; AIDH, aldehyde dehydrogenase; BCKAD, branched-chain α-keto-acid dehydrogenase; ACyD, acyl-CoA dehydrogenase; AAT, alcohol acyltransferase.*

*Data are presented as an average of three independent biological assays ± SD.*
pathway (aldehyde reduced into alcohol) instead of the acid transformation. Altogether, these data are in agreement with an Ehrlich pathway that is apparently more effective in S. cerevisiae than in S. suaveolens, and accounted for the production of 2-methylbutanol, 3-methylbutanol and 2-phenylethanol in S. cerevisiae (see Table 1).

In contrast, an acyl-CoA dehydrogenase (ACyD) activity was measured in the crude extract from S. suaveolens, while the activity of this enzyme was below detection levels in the S. cerevisiae extract. These data are therefore in agreement with the existence of a β-oxidation of isoleucine in S. suaveolens, and the failure to detect any ACyD activity in S. cerevisiae confirmed that this β-oxidation pathway is absent in this yeast species. However, we were unable to detect a branched-chain α-keto-acid dehydrogenase (BCKAD) activity in S. suaveolens extract under our experimental conditions. We hypothesized that this enzyme is present in the cells but likely very unstable, since all attempts to detect any activity of this enzyme using different buffer conditions have failed.

Taken together, our phenotypic and enzymatic data clearly showed that this yeast species can catabolize branched-chain amino acids through classical Ehrlich pathway, as in S. cerevisiae, and through β-oxidation. This β-oxidation leads to accumulation of tiglyl-CoA, probably because of the weak activity of enoyl-CoA hydratase. This intermediate is then taken over by an alcohol acyl transferase (AAT), whose activity in S. suaveolens was found to be at least two-fold higher than in S. cerevisiae. This higher AAT could also explain that S. suaveolens has a stronger capacity to produce different esters as compared to S. cerevisiae (28 esters were detected in S. suaveolens vs 16 in S. cerevisiae). Definitive proof for the existence of a mitochondrial β-oxidation pathway in S. suaveolens will require additional work, such as using 13C-labelling to trace the metabolic fate of branched-chain amino acids, or cloning of the genes encoding this pathway, as done for some filamentous fungi (Maggio-Hall and Keller, 2004; Maggio-Hall et al., 2008). These studies will likely help us to design process fermentation and genetic strategies to optimize the production of this biotechnologically relevant product, in order to favour the flux of isoleucine into β-oxidation and increase the availability of tiglyl-CoA for the AAT, instead of being diverted to the TCA.

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