

Dekkera/Brettanomyces yeasts for ethanol production from renewable sources under oxygen-limited and low-pH conditions

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Abstract Industrial fermentation of lignocellulosic hydrolysates to ethanol requires microorganisms able to utilise a broad range of carbon sources and generate ethanol at high yield and productivity. *D. bruxellensis* has recently been reported to contaminate commercial ethanol processes, where it competes with *Saccharomyces cerevisiae* [4, 26]. In this work *Brettanomyces/Dekkera* yeasts were studied to explore their potential to produce ethanol from renewable sources under conditions suitable for industrial processes, such as oxygen-limited and low-pH conditions. Over 50 strains were analysed for their ability to utilise a variety of carbon sources, and some strains grew on cellobiose and pentoses. Two strains of *D. bruxellensis* were able to produce ethanol at high yield (0.44 g g^{-1} glucose), comparable to those reported for *S. cerevisiae*. *B. naardenensis* was shown to be able to produce ethanol from xylose. To obtain ethanol from synthetic lignocellulosic hydrolysates we developed a two-step fermentation strategy: the first step under aerobic conditions for fast production of biomass from mixtures of hexoses and pentoses, followed by a second step under oxygen limitation to promote ethanol production. Under these conditions we

obtained biomass and ethanol production on synthetic lignocellulosic hydrolysates, with ethanol yields ranging from 0.2 to 0.3 g g^{-1} sugar. Hexoses, xylose and arabinose were consumed at the end of the process, resulting in 13 g l^{-1} of ethanol, even in the presence of furfural. Our studies showed that *Brettanomyces/Dekkera* yeasts have clear potential for further development for industrial processes aimed at production of ethanol from renewable sources.

Keywords Ethanol · *Dekkera* · *Brettanomyces* · Pentoses · Renewable sources

Introduction

Agricultural wastes and forest biomass represent attractive substrates for production of fuel ethanol. Hydrolysis of cellulose and hemicellulose produces a mixture of hexoses, as glucose, galactose and mannose, and pentoses, as xylose and arabinose. Fermentation of this mixture of sugars has been a challenge for strain development, because complete substrate utilisation is one of the prerequisites for economic feasibility of such processes in industrial applications. During the steps of pre-treatment and hydrolysis, low-molecular-weight organic acids, furans and aromatics are released, and these compounds are potent inhibitors of microbial metabolism [23, 24]. Industrial fermentation of lignocellulosic hydrolysates to ethanol therefore requires microorganisms which can utilise a broad range of carbon sources, producing ethanol at high yield and productivity, but also which are able to tolerate high ethanol concentrations and inhibitors.

Wild-type strains of *Saccharomyces cerevisiae* are well established for industrial ethanol production from sugar cane and starch-based plants, but they cannot utilise pentoses. Due

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to the large knowhow and availability of molecular tools, during recent years *S. cerevisiae* has been the preferred species for metabolic engineering aimed at introducing the ability to ferment pentose sugars [8, 32]. Recombinant xylose-fermenting strains of *S. cerevisiae* have recently been described to approach economically feasible ethanol production from undetoxified hydrolysates [21, 22]. These strains over-produce *Pichia stipitis* xylose reductase (XR) and xylitol dehydrogenase (XDH), and the non-oxidative pentose phosphate pathway (PPP) genes are over-expressed. Beside metabolic engineering strategies, also evolutionary engineering has been used to obtain *S. cerevisiae* strains possessing suitable characteristics for industrial employment [18]. Industrial recombinant arabinose-fermenting *S. cerevisiae* strains have been reported, too [14].

So far, only a few other yeasts have been characterised for their fermentative metabolism on pentose sugars, such as *P. stipitis*, *Candida shehatae* and *Pachysolen tannophilus* [1, 5, 7, 27, 30]. *Pichia stipitis* exhibits great ability to produce ethanol from xylose [11, 12], but it is aerobic and sensitive to organic acids as well as to other inhibitors. Adaptation strategies have been employed to increase its tolerance [11].

The *Brettanomyces/Dekkera* complex is composed of five species: *Dekkera bruxellensis*, *D. anomala*, *Brettanomyces naardenensis*, *B. nanus* and *B. custersianus*. A couple of *Brettanomyces/Dekkera* strains have been reported to be able to utilise xylose [25, 34]. *D. bruxellensis* is a frequent and increasing problem in the wine industry, causing economic losses in the wine sector [6]. Interestingly, *D. bruxellensis* has recently been reported even to contaminate distilleries, specially in continuous fermentation systems, where this yeast can compete with *S. cerevisiae*, due to its ability to grow under anaerobic conditions and at high ethanol concentrations [4, 26]. However, in general this group of yeasts has been only poorly studied so far [2, 31].

In this work a large screening of *Dekkera/Brettanomyces* strains was carried out for their ability to grow on a variety of sugars as carbon sources. Here we report on physiological and biochemical characterisation of *D. bruxellensis* and *B. naardenensis* strains under different growth conditions suitable for industrial fermentation processes, such as oxygen-limited and low-pH conditions. Finally, we describe a two-step batch process to produce biomass and ethanol from synthetic lignocellulosic hydrolysates.

Materials and methods

Yeast strains

The strains used throughout this work belong to the *Dekkera/Brettanomyces* group, isolated from beer, wine and

soft drinks in various part of the world. Twenty-eight strains of *Dekkera bruxellensis* (CBS 72, CBS 73, CBS 74, CBS 75, CBS 78, CBS 96, CBS 98, CBS 1940, CBS 1941, CBS 1942, CBS 1943, CBS 2336, CBS 2499, CBS 2547, CBS 2796, CBS 2797, CBS 3025, CBS 4459, CBS 4602, CBS 6055, CBS 4481, CBS 8027, CBS 4482, CBS 4601, CBS 4914, CBS 5206, CBS 5512, CBS 5513), 15 strains of *Dekkera anomala* (CBS 76, CBS 77, CBS 1938, CBS 3026, CBS 4210, CBS 4211, CBS 4212, CBS 4460, CBS 4608, CBS 7250, CBS 4711, CBS 4712, CBS 7654, CBS 8138, CBS 8139), 4 strains of *Brettanomyces naardenensis* (CBS 6040, CBS 6108, CBS 6115, CBS 7540), 2 strains of *Brettanomyces nanus* (CBS 1945, CBS 1947) and 5 strains of *Brettanomyces custersianus* (CBS 4805, CBS 4806, CBS 5207, CBS 5208, CBS 8347), all obtained from the Centraalbureau Voor Schimmel Culture Collection, were tested. The strains were stored at -80°C in 15% v/v glycerol and inoculated on YPD agar plates (yeast extract 10 g l $^{-1}$, Bacto-peptone 20 g l $^{-1}$, glucose 20 g l $^{-1}$, agar 20 g l $^{-1}$).

Carbon source utilisation on silica plates

Since we found that some strains can utilise agar or agarose as a carbon source, silica plates were made, composed of silica 83 g l $^{-1}$, potassium hydroxide 58 g l $^{-1}$, phosphoric acid 33 g l $^{-1}$, Yeast Nitrogen Base w/o amino acids 5.8 g l $^{-1}$ and the carbon source added to final concentration of 17 g l $^{-1}$. The carbon sources tested were pentoses (D-xylose, xylitol, L-arabinose), hexoses (D-glucose, D-galactose, D-mannose), disaccharides (sucrose, maltose, cellobiose) and polysaccharide (starch). Strains were grown overnight in rich YPD medium (glucose, 20 g l $^{-1}$, peptone 20 g l $^{-1}$, yeast extract, 10 g l $^{-1}$) and washed twice before being spotted (about 200 cells) onto silica plates with various carbon sources and a negative control without any carbon source. They were grown at 25°C up to 6 weeks. Each experiment was repeated twice. Growth was checked twice a week. To confirm species designation under the experiments, the cells were checked under microscope, and any “suspicious” cells were analysed for the ribosomal DNA sequence D1/D2 domain of 26S RNA [17].

Batch cultivations

Batch cultivations were performed in shake flasks and in a Biostat-Q system bioreactor (B-Braun) with working volume of 0.8 l. The temperature was set at 30°C and the stirring speed at 500 rpm. The medium used was a defined synthetic medium [33] with some modifications in the final concentrations, being as follows: ammonium sulphate, 5.0 g l $^{-1}$; potassium dihydrogen phosphate, 3.0 g l $^{-1}$; magnesium sulphate heptahydrate, 0.5 g l $^{-1}$; ethylenediamine tetraacetic acid (EDTA), 22.5 mg l $^{-1}$; zinc sulphate

heptahydrate, 6.75 mg l^{-1} ; manganese chloride tetrahydrate, 1.5 mg l^{-1} ; cobalt(II) chloride hexahydrate, 0.45 mg l^{-1} ; copper(II) sulphate pentahydrate, 0.45 mg l^{-1} ; disodium molybdate dihydrate, 0.60 mg l^{-1} ; calcium chloride dihydrate, 6.75 mg l^{-1} ; iron sulphate heptahydrate, 4.5 mg l^{-1} ; boric acid, 1.5 mg l^{-1} ; potassium iodide, 0.15 mg l^{-1} ; D-(−)-biotin, 0.08 mg l^{-1} ; calcium D-(+)-panthotenate, 1.5 mg l^{-1} ; nicotinic acid, 1.5 mg l^{-1} ; myo-inositol, 37.5 mg l^{-1} ; thiamine hydrochloride, 1.5 mg l^{-1} ; pyridoxol hydrochloride, 1.5 mg l^{-1} ; *p*-aminobenzoic acid, 0.3 mg l^{-1} . For cultivation under oxygen-limited conditions the medium was supplemented with ergosterol, 10 mg l^{-1} ; Tween-80, 420 mg l^{-1} ; uracil 50 mg l^{-1} . Different carbon sources were used: D-glucose, 20 g l^{-1} ; D-xylose, 20 g l^{-1} .

Biomass obtained from an overnight culture (pre-inoculum) on YPD medium was washed twice and used to inoculate the fermenter at biomass concentration of around $0.05 \text{ g dry cell weight (DCW) l}^{-1}$. Neither air nor nitrogen was supplied during the experiments under oxygen-limited conditions, and the stirring speed was set at 400 rpm. At the time of inoculum, the dissolved oxygen concentration was 100% of the air saturation, but it dropped to 0%, due to cell respiration during growth. During cultivation of *Dekkera bruxellensis* strains CBS 2499 and CBS 2796, the pH decreased from the initial value of 5 to a final value of about 2.5, whereas during fermentation of *Brettanomyces naardenensis* CBS 7540, pH was maintained at 5 by automatic addition of 2 M KOH.

Two-step cultivations

In the two-step batch cultivations the first step (to obtain the biomass) was performed under controlled aerobic conditions and started with 400 ml initial volume. In the experiments with mixtures of glucose and xylose the medium was the defined synthetic one described above but containing D-glucose 10 g l^{-1} and D-xylose, 40 g l^{-1} (1:4 ratio). In the experiments performed with synthetic soft-wood hydrolysate, the concentration of carbon sources was: D-glucose 16 g l^{-1} , D-mannose 10 g l^{-1} , D-xylose 7 g l^{-1} , galactose 4 g l^{-1} , L-arabinose 3 g l^{-1} and acetic acid 2.5 g l^{-1} (as reported in [15]), with or without addition of furfural (Sigma) 1.4 g l^{-1} [20]. To obtain aerobic conditions in the first step, the stirring speed was kept at 800 rpm and the air flow at 1 l min^{-1} (2.5 vvm) until complete exhaustion of the initial carbon sources [dissolved oxygen tension (DOT) over 20% of the saturation value]. At the end of this step (biomass approximately 10 g DCW l^{-1}), to induce fermentative metabolism, the air flow and the stirring speed were lowered (to 400 rpm), obtaining different dissolved oxygen concentrations. In particular, air flows of 0.007, 0.016 and 0.032 vvm generated oxygen

transfer rates (OTR) of 0.08, 0.12 and $0.21 \text{ mg}_{\text{oxygen}} \text{l}^{-1} \text{ min}^{-1}$, respectively. In this second step, to restore the initial concentration of nutrients, 400 ml of two times concentrated fresh medium was added to the fermentor. In the two-step processes performed with the feeding, after the first step under aerobic conditions, 400 ml fresh medium was introduced by a Masterflex L/S 751920 pump (Cole Parmer) to achieve feeding flows of $0.04 \text{ g}_{\text{xylose}} \text{ g}_{\text{cells}}^{-1} \text{ h}^{-1}$ and $0.01 \text{ g}_{\text{glucose}} \text{ g}_{\text{cells}}^{-1} \text{ h}^{-1}$ at the lower flow rate, and $0.16 \text{ g}_{\text{xylose}} \text{ g}_{\text{cells}}^{-1} \text{ h}^{-1}$ and $0.04 \text{ g}_{\text{glucose}} \text{ g}_{\text{cells}}^{-1} \text{ h}^{-1}$, at the higher flow rate. During the processes, pH was maintained at the value of 5 by addition of 2 M KOH. All fermentations were performed in triplicate.

Biomass and metabolites quantification

Samples were withdrawn from the fermenter at appropriate intervals and used to monitor cell growth by measuring optical density at 660 nm using a spectrophotometer, after appropriate dilution. For dry weight determination, washed culture samples were filtered on a $0.45\text{-}\mu\text{m}$ glass microfiber GF/A filter (Whatman) and dried at 80°C for 24 h. The concentration of extracellular metabolites, such as glucose, ethanol, glycerol, acetate, galactose and arabinose, in the supernatants were determined by commercial enzymatic kits (Roche). Xylose and xylitol were quantified by high-performance liquid chromatography (HPLC). Two different columns were used: a Polyspher OA-HY (Merck), followed by an Aminex Hpx-87P (Bio-Rad). The system was operated at 80°C using water as the mobile phase at flow rate of 0.5 ml min^{-1} and pressure of 60 bar. All assays were performed in triplicate, and standard deviations varied between 1 and 5%.

Specific consumption rates of glucose and specific production rates of ethanol, glycerol and acetic acid were calculated during the exponential phase of growth under oxygen-limited condition. In the experiments performed with xylose or with sugar mixtures, specific consumption rates of glucose and xylose as well as specific production rates of ethanol were calculated during the fermentation phase as the amount of sugar utilised or ethanol produced by the average biomass present during the time interval considered. The yields of ethanol and other metabolites relative to the consumed carbon sources were calculated as the total amount of produced metabolites divided by the total amount of sugars utilised.

Enzyme activity assays

Cell extracts were prepared by extraction with acid-washed glass beads (Sigma), and the total amount of extracted proteins was quantified using the Biorad Protein Assay kit (Bio-Rad). Alcohol dehydrogenase (ADH), pyruvate

decarboxylase (PDC), acetaldehyde dehydrogenase (AcDH), acetyl coenzyme A (CoA) synthetase (ACS) and glucose 6-phosphate dehydrogenase (G6PDH) were assayed according to Ref. [28]. Cell extracts for glycerol 3-phosphate dehydrogenase (GPDH) were desalted [3] prior to the assay, which was performed in TrED buffer (triethanolamine 10 mmol l⁻¹, EDTA 1 mmol l⁻¹, dithiothreitol 1 mmol l⁻¹, pH 7.5), MgCl₂ 1 mmol l⁻¹ and nicotinamide adenine dinucleotide (NADH) 0.1 mmol l⁻¹. The reaction was started by addition of dihydroxyacetonephosphate at 0.67 mmol l⁻¹. Xylose reductase (XR) and xylitol dehydrogenase (XDH) were assayed as described in Ref. [13], with the exception that the XR activity was assayed in the presence of 0.4 mmol NADH.

One unit (U) of enzyme activity was defined as 1 μmol substrate transformed per minute using an extinction coefficient for NADH of 6.22 l mmol⁻¹ cm⁻¹. Enzyme assays were performed in triplicate, and the obtained standard deviations varied between 3 and 12%.

Results and discussion

Screening for ability to grow on different sugars as carbon source

The ability to use a wide range of carbon sources represents a very interesting feature to develop suitable fermentative strategies for ethanol production from renewable sources. Fifty-four *Dekkera/Brettanomyces* strains were screened on solid media for their ability to grow on different sugars as carbon source: saccharose, cellobiose, maltose, lactose, starch, xylose, galactose and arabinose (Table 1). Surprisingly, we observed that several *D. anomala* strains, one strain of *B. custersianus* and one strain of *B. nanus* were even able to use agar as sole carbon source. To avoid any “contamination” for testing alternative carbon sources we then developed a plate assay by using silica support. In this way we could observe that all species grew on plates containing hexoses, disaccharides and starch, although with some individual variation due to strain specificity. Only *B. naardenensis* was able to utilise pentoses, such as D-xylose and D-arabinose. In conclusion, *Dekkera/Brettanomyces* yeasts can be cultivated on a wide variety of sugars.

D. bruxellensis ethanol production under oxygen-limited and low-pH conditions

Our analysis of *D. bruxellensis* was mainly focused on ethanol production when oxygen is present in very limited amount and at low pH, which are conditions characteristic for ethanol production at industrial level and under which *D. bruxellensis* has been shown to be able to contaminate

industrial fermentations [4, 26]. Presence of *D. bruxellensis* in this kind of environment, as well as in wine [6], suggests that this yeast is also tolerant to higher ethanol concentration. Two strains of *D. bruxellensis* were chosen: CBS 2499, because its genome has already been partially sequenced [10, 37], and CBS 2796, because it has a higher number of chromosomes (5 and 7, respectively). The two strains were cultivated under uncontrolled pH. In this way the pH decreased from a value of 4.5 at the beginning of the cultivation to 2.5 at the end of the process (Fig. 1a, b). The growth kinetics were very similar, and both strains converted glucose mainly to ethanol, leading to high ethanol yields (Table 2). Noteworthily, under these conditions *D. bruxellensis* produced glycerol and a very low amount of acetic acid (Table 2). Specific glucose consumption rates and ethanol production rates were determined during the exponential growth phase. Both strains displayed very similar fermentative metabolism in terms of ethanol yield, but differed in terms of specific glucose consumption rate and ethanol production rate, with higher values observed in CBS 2796 (Table 2).

B. naardenensis ethanol production under oxygen-limited conditions

To date, neither cultivation under oxygen-limited conditions nor ethanol production by *B. naardenensis* have been reported in literature. To study the fermentative growth of *B. naardenensis*, four strains that have previously been tested on plates were cultivated in liquid on glucose and on xylose under aerobic conditions, to determine their specific growth rates. Strain CBS 7540 exhibited the fastest rates (0.3 h⁻¹ on glucose and 0.23 h⁻¹ on xylose) and for this reason was selected to be studied in more detail for its ability to produce ethanol.

Under conditions of oxygen limitation, *B. naardenensis* was able to grow on synthetic medium containing glucose as carbon source (Fig. 1c, Table 2), but at a lower growth rate than *D. bruxellensis*, even though their glucose consumption rates were similar. *B. naardenensis* produced ethanol at a specific production rate similar to that determined in *D. bruxellensis* cultures, but with lower yield (Table 2). In addition, *B. naardenensis* showed higher production of glycerol and acetic acid than *D. bruxellensis* (Table 2).

B. naardenensis failed to grow on xylose under oxygen-limited conditions (data not shown).

Ethanol production from xylose by a two-step batch process

The observation that *B. naardenensis* CBS 7540 was unable to grow on xylose when cultured under oxygen-limited conditions prompted us to explore the possibility of

Table 1 Carbon utilisation, as tested on silica plates, of strains of *Dekkera/Brettanomyces*

CBS strains	Xylose	Xylitol	Ara	Glu	Gal	Man	Sucr	Mal	Cellob	Starch	Agar
<i>B. custersianus</i>											
4805	—	—	—	+	+	+	+	+	+	—	+
4806	—	—	—	+	+	+	+	—	+	+	—
5207, 8347	—	—	—	+	+	+	+	+	+	—	—
5208	—	—	—	+	+	+	+	—	+	—	—
<i>B. naardenensis</i>											
6040	+	+	+	+	+	+	+	+	+	+	—
6108	—	—	—	+	—	+	+	+	+	+	—
6115	+	+	—	+	+	+	+	+	+	+	—
7540	+	+	—	+	+	—	+	—	+	+	—
<i>B. nanus</i>											
1945	—	—	—	+	+	+	+	+	+	+	—
1947	—	—	—	+	+	+	+	+	+	+	+
<i>D. anomala</i>											
76, 3026	—	—	—	+	+	+	+	+	+	+	—
77, 4460, 7250	—	—	—	+	+	+	+	+	+	—	—
1938, 4211, 4212, 7654, 8138	—	—	—	+	+	+	+	+	+	+	+
4210, 8139	—	—	—	+	+	+	+	+	+	—	+
4608	—	—	—	+	+	+	+	—	+	—	—
4711	—	—	—	+	+	—	+	+	+	—	—
4712	—	—	—	+	+	+	+	—	+	+	+
<i>D. bruxellensis</i>											
72, 73, 75, 96, 98, 1940, 1941, 1942, 1943, 2499, 2547, 2796, 3025, 4482, 5206, 5512, 5513	—	—	—	+	+	+	+	+	+	+	—
74, 78	—	—	—	+	+	+	+	+	—	—	—
2336, 2797, 4459, 6055, 4481, 8027	—	—	—	+	+	+	+	+	+	—	—
4602	—	—	—	+	—	+	+	—	—	+	—
4601	—	—	—	+	+	+	+	—	—	—	—
4914	—	—	—	+	+	+	+	—	+	+	—

ara arabinose, glu glucose, gal galactose, man mannose, sucr sucrose, mal maltose, cellob cellobiose. Approximately 200 cells were spotted onto the plate: “+” means growth, and “—” means no growth after 6 weeks of incubation

running a batch process in two steps, to separate the phase of biomass production from the phase of ethanol production. In this process the first step was performed under aerobic conditions to produce biomass from xylose rapidly and efficiently. This step was then followed by a second step under oxygen-limited conditions, obtained by reducing the air supply and stirring (see “Materials and methods” section for details), to induce ethanol production. As expected, during this second step no new biomass was formed (data not shown). Ethanol production was analysed at different dissolved oxygen concentrations (OTR) (Fig. 2). We observed that *B. naardenensis* CBS 7540 was able to produce ethanol from xylose only in a strict range of dissolved oxygen concentrations. In fact, when the dissolved oxygen concentration was close to 0, the ethanol production rate and the ethanol yield were extremely low

(Fig. 2). The increased availability of oxygen at higher OTR stimulated fermentation, allowing an increase in both ethanol yield and productivity. Nevertheless, at OTR higher than $0.21 \text{ mg}_{\text{oxygen}} \text{l}^{-1} \text{ min}^{-1}$, the cells started to exhibit respiratory metabolism, arresting ethanol production and starting new biomass formation (data not shown).

Analysis of enzymatic activities involved in glucose and xylose fermentation

The main enzymatic activities involved in sugar metabolism and in the fermentative pathway were analysed in *D. bruxellensis* and in *B. naardenensis* under different growth conditions. We found that biochemical and physiological observations supported each other (Table 3). *D. bruxellensis* has been reported to produce ethanol under

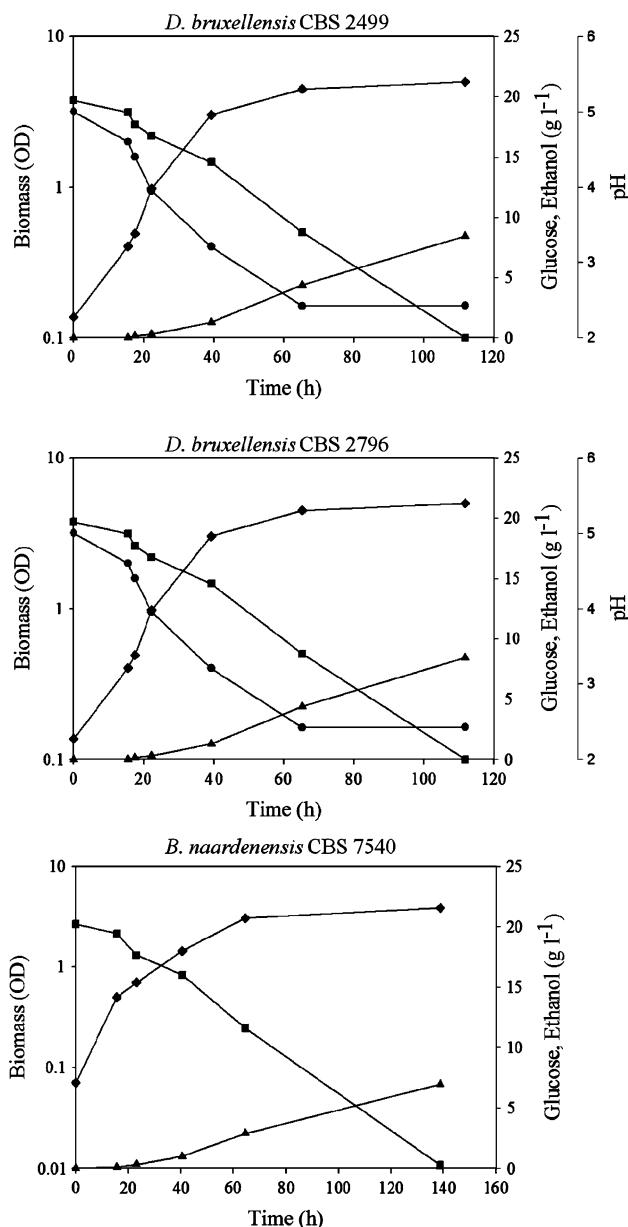


Fig. 1 Kinetics of growth, glucose consumption and ethanol production of *D. bruxellensis* CBS 2499 (a), *D. bruxellensis* CBS 2796 (b) and *B. naardenensis* CBS 7540 (c) during batch fermentation under oxygen-limited conditions. Filled diamonds biomass, filled squares glucose, filled triangles ethanol, filled circles pH. Representative experiments are shown

aerobic conditions, thus behaving like a Crabtree-positive yeast [31]. We could detect activities of the main fermentative enzymes, pyruvate decarboxylase (PDC) and alcohol dehydrogenase (ADH), under aerobic conditions as well as under conditions of oxygen limitation, and they were found to be unaffected by the dissolved oxygen concentration, as expected for a Crabtree-positive yeast (Table 3). Acetaldehyde dehydrogenase (ACDH), involved in the production of acetic acid, was detected at a lower

level under oxygen-limited conditions, in agreement with the concomitant low production of acetic acid. Undetectable activities of acetyl CoA synthetase (ACS) were found in both aerobic and oxygen-limited conditions. Glycerol 3-phosphate dehydrogenase activity (GPDH), involved in the production of glycerol, was detected only during the growth under oxygen-limited conditions, accordingly to the production of this metabolite.

In *B. naardenensis*, on the contrary, PDC and ADH were strongly induced at reduced oxygen supply (Table 3), as reported for Crabtree-negative yeasts [35]. Very low activity of ACDH was detected under aerobic conditions on glucose, but higher levels were observed on xylose. This could affect the redox balance during xylose fermentation (see paragraph below), due to the presence of NAD-dependent acetaldehyde dehydrogenase activity [13, 29]. GPDH was undetectable even under conditions of oxygen limitation. Interestingly, the detected activity of glucose 6-phosphate dehydrogenase (G6PDH) in *B. naardenensis* was higher than in *D. bruxellensis*, as well as the activity of ACS.

Xylose utilisation in *B. naardenensis* was found to be dependent on the activity of a specific nicotinamide adenine dinucleotide phosphate (NADPH)-dependent xylose reductase (XR) activity and on the activity of a NAD-dependent xylitol dehydrogenase (XDH) (Table 3). We observed an 8–10-fold lower level of XR and a twofold lower level of XDH in comparison with those reported for *P. stipitis* [36]. Furthermore, XR was found to be specific only for NADPH (Table 3), thereby not participating in re-oxidation of NADH produced by XDH. This could cause a cofactor imbalance during xylose fermentation, resulting in xylitol accumulation.

Fermentation of synthetic lignocellulosic hydrolysates

The composition of the sugar fraction in lignocellulosic hydrolysates is dependent on the raw material [9]. We first carried out a fermentation process by using a mixture of glucose and xylose with the typical 1:4 ratio obtained in hardwood hydrolysates. Also in this case we used the two-step process described above, with the first phase for fast biomass production in batch mode and under controlled aerobic conditions on the glucose/xylose mixture. When the final biomass was reached and both sugars consumed, the conditions of oxygen limitation were applied ($OTR\ 0.12\ mg_{oxygen}\ l^{-1}\ min^{-1}$) to induce ethanol production. In this process we tested also the possibility of feeding the biomass during the ethanol production phase by using the same mixture containing glucose and xylose at 1:4 ratio employed for the biomass production phase (for details see “Materials and methods” section). Also in this case no further increase of biomass was observed in the second

Table 2 Growth parameters of *D. bruxellensis* CBS 2499, *D. bruxellensis* CBS 2796 and *B. naardenensis* CBS 7540 strains in batch culture under conditions of oxygen limitation

	<i>D. bruxellensis</i>		<i>B. naardenensis</i>
	CBS 2499	CBS 2796	CBS 7540
Specific growth rate (h^{-1})	0.083 ± 0.006	0.11 ± 0.01	0.042 ± 0.005
Yields ($\text{mg g}_{\text{glucose}}^{-1}$)			
Biomass	73 ± 4	80 ± 3	89 ± 7
Ethanol	440 ± 30	430 ± 25	360 ± 30
Glycerol	7.8 ± 0.7	5.2 ± 0.6	36 ± 3
Acetic acid	1.3 ± 0.2	1.4 ± 0.2	4.3 ± 0.2
Production rates ($\text{mmol g}_{\text{cells}}^{-1} \text{h}^{-1}$)			
Ethanol	2.83 ± 0.03	5.3 ± 0.3	3.07 ± 0.15
Glycerol	0.022 ± 0.002	0.01 ± 0.006	0.25 ± 0.02
Acetic acid	0.025 ± 0.002	0.021 ± 0.001	0.047 ± 0.005
Glucose consumption rate ($\text{mmol g}_{\text{cells}}^{-1} \text{h}^{-1}$)	2.50 ± 0.18	3.99 ± 0.32	2.99 ± 0.24

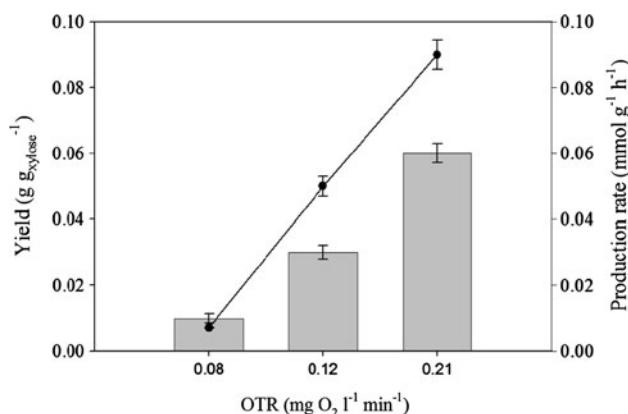


Fig. 2 Ethanol production rates and yields in batch fermentations of *B. naardenensis* CBS 7540 on xylose (20 g l^{-1}) and at different levels of oxygenation (OTR). Grey bars yield, filled circles ethanol production rate

phase under oxygen-limited conditions, as expected. We analysed processes at different feeding rates (Table 4). Due to the presence of glucose in the feed, a higher ethanol yield than that observed in the process on xylose only (see paragraph above and Fig. 2 for comparison) was obtained. In addition, by increasing the feeding rate, higher ethanol yield and productivity were obtained (Table 4), but this resulted in xylitol accumulation (data not shown). This fact could indicate that xylose fermentation under oxygen-limited conditions causes a redox imbalance, probably due to the different cofactor utilisation by the two enzymes (XR and XDH) involved in the first steps of xylose metabolism (Table 3). Recombinant pentose-fermenting *S. cerevisiae* strains often experience such a redox imbalance, leading to undesired xylitol accumulation [16, 36]. Several strategies to reduce xylitol formation have been explored, and one of the most successful has been the expression of xylose isomerase from *Piromyces* sp., which converts xylose to xylulose without any cofactor involvement [19].

Softwood hydrolysates yield a high proportion of hexose sugars, mainly mannose and glucose. To approach the real conditions occurring when this kind of hydrolysate is utilised, the fermentation process was performed by using a mixture containing hexoses and pentoses at the same concentrations as in undetoxified spruce hydrolysate [15]. Again, we ran the process in batch mode in two steps: the first step, for fast biomass production, on the sugars mixture under controlled aerobic conditions; and the second step, for ethanol production, under oxygen-limited conditions ($\text{OTR } 0.12 \text{ mg}_{\text{oxygen}} \text{l}^{-1} \text{ min}^{-1}$). In this experiment no feeding was applied during the second step. Table 5 summarises the calculated fermentation parameters. All hexoses and xylose, and half of the initial amount of arabinose, were consumed at the end of the process, leading to production of 13 g l^{-1} of ethanol, which represented the highest yield and productivity obtained. Also in this case production of glycerol, acetic acid and xylitol occurred. Undetoxified hydrolysates are known to contain inhibitory compounds such as furfural. We therefore investigated the resistance of *B. naardenensis* to this compound. We observed that, in the presence of furfural (0.8 g l^{-1}), the growth rate of *B. naardenensis* strain CBS 7540 showed a 40% reduction (data not shown). Addition of furfural to the synthetic lignocellulosic hydrolysate affected also the fermentation process by decreasing the specific rate of ethanol production, but the final ethanol yield remained almost the same (Table 5).

Conclusions

In this work we demonstrated that *Dekkera/Brettanomyces* yeasts are able to use a wide range of carbon sources, even pentoses. Under conditions suitable for industrial processes, such as under oxygen limitation and low-pH conditions, *D. bruxellensis* produced ethanol with yields

Table 3 Activity of *D. bruxellensis* CBS 2499 and *B. naardenensis* CBS 7540 enzymes involved in glucose and xylose fermentation

Enzyme	<i>D. bruxellensis</i> CBS 2499		<i>B. naardenensis</i> CBS 7540			
	Glucose		Glucose		Xylose	
	+O ₂	O ₂ lim	+O ₂	O ₂ lim	+O ₂	O ₂ lim
HXK	0.58 ± 0.01	0.79 ± 0.05	0.37 ± 0.03	1.71 ± 0.04	–	–
G6PDH	0.21 ± 0.09	0.32 ± 0.04	0.65 ± 0.01	1.35 ± 0.005	0.60 ± 0.04	0.45 ± 0.04
PDC	0.26 ± 0.01	0.22 ± 0.06	0.02 ± 0.005	1.19 ± 0.02	0.10 ± 0.0025	0.29 ± 0.01
ADH	4.19 ± 0.11	4.40 ± 0.52	0.05 ± 0.007	1.72 ± 0.03	0.31 ± 0.01	1.45 ± 0.04
ACDH	0.31 ± 0.02	0.06 ± 0.003	0.003 ± 0.001	ND	0.05 ± 0.002	0.04 ± 0.004
ACS	ND	ND	0.133 ± 0.04	0.031 ± 0.004	–	–
GPD	ND	0.034 ± 0.004	ND	ND	ND	ND
XR-NADH	–	–	ND	ND	ND	ND
XR-NADPH	–	–	0.018 ± 0.004	0.011 ± 0.006	0.07 ± 0.003	0.113 ± 0.003
XDH	–	–	ND	ND	0.23 ± 0.01	0.26 ± 0.03

Cell extracts were taken during the exponential phase of growth under aerobic (+O₂) and under oxygen-limited (O₂ lim) conditions

ADH alcohol dehydrogenase, ACDH acetaldehyde dehydrogenase, ACS acetyl CoA synthetase, G6PDH glucose 6-phosphate dehydrogenase, GPD glycerol 3-phosphate dehydrogenase, HXK hexokinase, PDC pyruvate decarboxylase, XR-NADH xylose reductase NADH-dependent, XR-NADPH xylose reductase NADPH-dependent, XDH xylitol dehydrogenase, ND not detectable, “–” not measured

Table 4 Ethanol yield and productivity of *B. naardenensis* CBS 7540 in batch

fermentations fed by mixtures of glucose and xylose (1:4) at different feeding flow rates

Feeding flow			Ethanol yield	Ethanol production rate
	Xylose g xylose g _{cells} ⁻¹ h ⁻¹	Glucose g glucose g _{cells} ⁻¹ h ⁻¹		
0.04		0.01	0.20 ± 0.01	0.13 ± 0.01
0.16		0.04	0.25 ± 0.02	0.38 ± 0.02

Table 5 Ethanol yield and productivity during *B. naardenensis* CBS 7540 fermentation of a synthetic softwood hydrolysate-like medium (with or without addition of furfural, 1.4 g l⁻¹)

Strain and medium	Ethanol		Yield			
	Specific productivity (mmol g _{cells} ⁻¹ h ⁻¹)	Volumetric productivity (g l ⁻¹ h ⁻¹)	Ethanol (g g _{sugars} ⁻¹)	Acetate (g g _{sugars} ⁻¹)	Glycerol (g g _{sugars} ⁻¹)	Xylitol (g g _{pentoses} ⁻¹)
<i>B. naardenensis</i> CBS 7540						
Softwood hydrolysate	0.73 ± 0.09	0.135 ± 0.016	0.31 ± 0.02	0.063 ± 0.004	0.034 ± 0.002	0.42 ± 0.03
Softwood hydrolysate with furfural	0.42 ± 0.04	0.10 ± 0.015	0.28 ± 0.02	0.086 ± 0.006	0.033 ± 0.003	0.43 ± 0.02
<i>S. cerevisiae</i> TMB 3400 ^a						
Softwood hydrolysate with furfural	0.43 ± 0.26	–	0.41 ± 0.02	–	0.035 ± 0.006	0

S. cerevisiae data are from literature [15]

ND not detectable, “–” not measured

comparable to those of *S. cerevisiae* (0.44 g g⁻¹ glucose). If we compare the ethanol productivities, it is clear that *D. bruxellensis* cannot compete with *S. cerevisiae* in batch processes, but it can in continuous fermentation systems. Notably, *D. bruxellensis* has been found as a major contaminant in industrial continuous fermentation processes. In addition, for the first time we show that *B. naardenensis*

is able to produce ethanol from glucose and xylose under oxygen-limited conditions. A batch process in two steps was exploited to obtain ethanol from synthetic lignocellulosic hydrolysates. Comparison between *B. naardenensis* and a metabolically engineered *S. cerevisiae* strain (Table 5) shows that *B. naardenensis* exhibits lower ethanol yield but similar ethanol specific productivity.

Therefore, our studies demonstrate that *Brettanomyces/Dekkera* yeasts have clear potential for further development for industrial production of ethanol from renewable sources.

Use of optimised fermentation strategies as well as understanding of the metabolic control and development of genetically modified strains could further improve the basic abilities of *Dekkera/Brettanomyces* yeasts and subsequently promote their utilisation as new industrial species. A partial genome sequence of *Dekkera bruxellensis* is now available [10, 37], opening the possibility for genetic manipulation of this yeast. Also some other approaches, such as evolutionary engineering, could be used to increase the ethanol yield.

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References

- Agbogbo F, Coward-Kelly G, Torry-Smith M, Wenger K, Jeffries TW (2007) The effect of initial cell concentration on xylose fermentation by *Pichia stipitis*. *Appl Biochem Biotechnol* 137:653–662
- Aguillar Uscanga MG, Delia M-L, Strehaino P (2003) *Brettanomyces bruxellensis*: effect of oxygen on growth and acetic acid production. *Appl Microbiol Biotechnol* 61:157–162
- André L, Hemming A, Adler L (1991) Studies on the osmotic induction of glycerol production and glycerol 3-phosphate dehydrogenase (NAD⁺). *FEBS* 286:13–17
- de Souza Liberal AT, Basilio ACM, do Monte Resende A, Brasileiro BTV, da Silva-Filho EA, de Moraes JOF, Simões DA, de Moraes MA Jr (2007) Identification of *Dekkera bruxellensis* as a major contaminant yeast in continuous fuel ethanol fermentation. *J Appl Microbiol* 102:538–547
- du Preez JC, Prior BA, Monteiro AMT (1984) The effect of aeration on xylose fermentation by *Candida shehatae* and *Pachysolen tannophilus*. *Appl Microbiol Biotechnol* 19:261–266
- Fuglsang KC (1996) Wine microbiology. Chapman & Hall, New York
- Hahn-Hägerdal B, Jeppsson H, Olsson L, Mohagheghi A (1994) An interlaboratory comparison of the performance of ethanol-producing micro-organisms in a xylose-rich acid hydrolysate. *Appl Microbiol Biotechnol* 41:62–72
- Hahn-Hägerdal B, Karhumaa K, Fonseca C, Spencer-Martins I, Gorwa-Grauslund MF (2007) Towards industrial pentose-fermenting yeast strains. *Appl Microbiol Biotechnol* 74:937–953
- Hayn M, Steiner W, Klinger R, Steinmuller H, Sinner M, Esterbauer H (1993) Basic research and pilot studies on the enzymatic conversion of lignocellulosics. In: Saddler JN (ed) Bioconversion of forest and agricultural plant residues. CAB International, Wallingford, UK, pp 33–72
- Hellborg L, Piskur J (2009) Complex nature of the genome in a wine spoilage yeast, *Dekkera bruxellensis*. *Eukaryot Cell* 8:1739–1749
- Huang C-F, Lin T-H, Guo G-L, Hwang W-S (2009) Enhanced ethanol production by fermentation of rice straw hydrolysate without detoxification using a newly adapted strain of *Pichia stipitis*. *Bioresour Technol* 100:3914–3920
- Jeffries TW, Grigoriev IV, Grimwood J, Laplaza JM, Aerts A, Salamov A, Schmutz J, Lindquist E, Dehal P, Shapiro H, Jin Y-S, Passoth V, Richardson PM (2007) Genome sequence of the lignocellulosic-bioconverting and xylose-fermenting yeast *Pichia stipitis*. *Nature Biotechnol* 25:319–326
- Jin YS, Jeffries TW (2004) Stoichiometric network constraints on xylose metabolism by recombinant *Saccharomyces cerevisiae*. *Metab Eng* 6:229–238
- Karhumaa K, Wiedemann B, Boles E, Hahn-Hägerdal B, Gorwa-Grauslund MF (2006) Co-utilization of L-arabinose and D-xylose by laboratory and industrial *Saccharomyces cerevisiae* strains. *Microp Cell Fact* 5:18–24
- Karhumaa K, Sanchez RG, Hahn-Hägerdal B, Gorwa-Grauslund MF (2007) Comparison of the xylose reductase-xylitol dehydrogenase and the xylose isomerase pathways for xylose fermentation by recombinant *Saccharomyces cerevisiae*. *Microp Cell Fact* 6:5
- Kotter P, Ciriacy M (1993) Xylose fermentation by *Saccharomyces cerevisiae*. *Appl Microbiol Biotechnol* 38:776–783
- Kurtzman CP, Robnett CJ (1998) Identification and phylogeny of ascomycetous yeasts from analysis of nuclear large subunit (26S) ribosomal DNA partial sequences. *Antonie Van Leeuwenhoek* 73:331–371
- Kuyper M, Toirkens MJ, Diderich JA, Winkler AA, van Dijken JP, Pronk JT (2005) Evolutionary engineering of mixed-sugar utilization by a xylose-fermenting *Saccharomyces cerevisiae* strain. *FEMS Yeast Res* 5:925–934
- Kuyper M, Hartog MM, Toirkens MJ, Almering MJ, Winkler AA, van Dijken JP, Pronk JT (2005) Metabolic engineering of a xylose-isomerase-expressing *Saccharomyces cerevisiae* strain for rapid anaerobic xylose fermentation. *FEMS Yeast Res* 5:399–409
- Larsson S, Cassland P, Jönsson LJ (2001) Development of a *Saccharomyces cerevisiae* strain with enhanced resistance to phenolic fermentation inhibitors in lignocellulose hydrolysates by heterologous expression of laccase. *Appl Environ Microbiol* 63:1163–1170
- Öhgren K, Bengtsson O, Gorwa-Grauslund MF, Galbe M, Hahn-Hägerdal B, Zacchi G (2006) Simultaneous saccharification and co-fermentation of glucose and xylose in steam-pretreated corn stover at high fiber content with *Saccharomyces cerevisiae* TMB3400. *J Biotechnol* 126:448–498
- Olsson L, Soerensen HR, Dam PB, Christensen H, Krogh KM, Meyer AS (2006) Separate and simultaneous enzymatic hydrolysis and fermentation of wheat hemicellulose with recombinant xylose utilizing *Saccharomyces cerevisiae*. *Appl Biochem Biotechnol* 133:117–129
- Palmqvist E, Hahn-Hägerdal B (2000) Fermentation of lignocellulosic hydrolysates I: inhibition and detoxification. *Bioresour Technol* 74:17–24
- Palmqvist E, Hahn-Hägerdal B (2000) Fermentation of lignocellulosic hydrolysates II: inhibitors and mechanisms of inhibition. *Bioresour Technol* 74:25–33
- Parekh SR, Parekh RS, Wayman M (1988) Fermentation of xylose and cellobiose by *Pichia stipitis* and *Brettanomyces clausenii*. *Appl Biochem Biotechnol* 18:325
- Passoth V, Blomqvist J, Schnürer J (2007) *Dekkera bruxellensis* and *Lactobacillus vini* from a stable ethanol-producing consortium in a commercial alcohol process. *Appl Environ Microbiol* 73:4354–4356
- Perego P, Converti A, Palazzi E, Del Borghi M, Ferraiolo G (1990) Fermentation of hardwood hemicellulose hydrolysate by *Pachysolen tannophilus*, *Candida shehatae* and *Pichia stipitis*. *J Ind Microbiol* 6:157–164
- Postma E, Verduyn C, Scheffers WA, van Dijken JP (1989) Enzymatic analysis of the Crabtree effect in glucose-limited

- chemostat cultures of *Saccharomyces cerevisiae*. *Appl Env Microbiol* 55:468–477
29. Sonderegger M, Jeppsson M, Hahn-Hägerdal B, Sauer U (2004) Molecular basis for anaerobic growth of *Saccharomyces cerevisiae* on xylose, investigated by global gene expression and metabolic flux analysis. *Appl Env Microbiol* 70:2307–2317
 30. Skoog K, Hahn-Hägerdal B (1990) Effect of oxygenation on xylose fermentation by *Pichia stipitis*. *Appl Environ Microbiol* 56:3389–3394
 31. Van Dijken JP, Scheffers WA (1986) Redox balances in the metabolism of sugars by yeasts. *FEMS Microbiol Rev* 32:199–224
 32. Van Vleet JH, Jeffries TW (2009) Yeast metabolic engineering for hemicellulosic ethanol production. *Curr Opin Biotechnol* 20:300–306
 33. Verduyn C, Postma E, Scheffers WA, van Dijken JP (1992) Effect of benzoic acid on metabolic fluxes in yeast: a continuous-culture study on the regulation of respiration and alcoholic fermentation. *Yeast* 8:501–517
 34. Toivola A, Yarrow D, van den Bosch BE, van Dijken JP, Scheffers WA (1984) Alcoholic fermentation of D-xylose by yeasts. *Appl Env Microbiol* 47:1221–1223
 35. Zeeman A-M, Kuyper M, Pronk JT, van Dijken JP, Steensma HY (2000) Regulation of pyruvate metabolism in chemostat cultures of *Kluyveromyces lactis* CBS 2359. *Yeast* 16:611–620
 36. Wahlbom CF, van Zyl WH, Jönsson LJ, Hahn-Hägerdal B, Cordero Otero RR (2003) Generation of the improved recombinant xylose-utilizing *Saccharomyces cerevisiae* TMB 3400 by random mutagenesis and physiological comparison with *Pichia stipitis* CBS 6054. *FEMS Yeast Res* 3:319–326
 37. Woolfit M, Rozpedowska E, Piskur J, Wolfe KH (2007) Genome survey sequencing of the wine spoilage yeast *Dekkera (Brettanomyces) bruxellensis*. *Eukaryot Cell* 6(4):721–733