Biotransformation of hop derived compounds by Brettanomyces yeast strains

Colomer, Marc Serra; Funch, Birgitte; Solodovnikova, Natalia; Hobley, Timothy John; Förster, Jochen

Published in:
Journal of the Institute of Brewing

Link to article, DOI:
10.1002/jib.610

Publication date:
2020

Document Version
Publisher's PDF, also known as Version of record

Link back to DTU Orbit

Citation (APA):
Introduction

The craft brewing boom is driving innovation in the brewing industry, and it places demands on new and alternative practices. Recently, the use of non-conventional yeast species has been explored more rigorously, as the application of the right yeast can strongly influence the flavour profile of a beer. Brettanomyces (anamorph of Dekkera) species have been highlighted for beer flavouring, as their use results in features unachievable with conventional Saccharomyces brewing yeast (1,2). One of these is a positive impact on ester production, leading to fruity flavours. Recently it has been reported that there can be synergistic effects on flavour formation between yeast and hops (3,4). The authors found that monoterpenic alcohols from hops can be metabolised by brewer’s yeast, imparting tropical and citrus flavours, however the exact mechanisms are not fully understood (3,5,6). It is not clear whether similar effects are catalysed by Brettanomyces species and an evaluation of this would aid in understanding the mechanisms behind the positive attributes of brewing with this yeast.

Bioconversion of hop compounds by conventional and non-conventional yeasts has been described previously (4). During fermentation, the hop derived monoterpenic alcohol geraniol - which gives a characteristic rose flavour - is reduced by yeast to β-citronellol (lime flavour), especially in the early stages of fermentation (Fig. 1) (3,7,8). Such a conversion has been correlated with expression of ‘old yellow enzyme’ (Oye) by yeast, which is an oxidoreductase responsible for the transformation step (9,10). The citrusy flavour perceived in beers is caused by the synergistic effect of geraniol and citronellol (11). Therefore, an understanding of the interaction of yeast with hop derived compounds is required. De novo synthesis of monoterpenic alcohols in conventional brewer’s yeast has also been reported, in both natural and genetically engineered strains (6,12).

In addition, beer contains aglycones, sugar molecules bound to monoterpenic alcohols that are not volatile and are odourless (13). When the glycosidic bond is broken the aromatic monoterpenic alcohols are released and can be perceived by the consumer. Beta-glucosidase activity has been linked to this phenomenon (Fig. 1) (5,14). Several studies have focused on screening beta-glucosidase activity in yeasts, and despite the activity being strongly straindependent, Brettanomyces species display remarkably high activity (15–17). In one of these studies, a B. custersianus strain was found with beta-glucosidase activity up to ten fold higher than average (15). It has been reported that Brettanomyces can contain two open reading frames (ORFs), which putatively encode for two beta-glucosidases, however the impact of the presence of these genes during brewing has not been explored (18).

Biotransformation of hop derived compounds by Brettanomyces yeast strains

Marc Serra Colomer,1,2 Birgitte Funch,1 Natalia Solodovnikova,1 Timothy John Hobley2 and Jochen Förster1*

Several hop derived compounds in wort are known to be converted by yeast during fermentation, influencing the overall perception of the beer. A deeper understanding of such metabolic processes during fermentation is needed to achieve better control of the outcome. Here, the interaction between hop derived compounds and the yeast genera Brettanomyces was studied. Several Brettanomyces strains with different genomic backgrounds were selected, focusing on two traits: beta-glucosidase activity and nitrate assimilation. The role of three beta-glucosidases present in Brettanomyces bruxellensis and Brettanomyces anomalus and their impact on the final monoterpenic alcohol profile was analysed. The beta-glucosidase activity was highly strain dependent, with B. anomalus CRL-49 exhibiting the highest conversion. Such activity could not be related to the release of aglycones from hops during fermentation, as a substantial part of such activity was intracellular. Nevertheless, the reduction of geraniol to β-citronellol was remarkably efficient for all Brettanomyces strains during fermentation, and it is suggested that two oxidoreductases BbHy2 and BbHy3 may have an influence. Moreover, the transfer of nitrate from hops to wort and its further assimilation by Brettanomyces species was analysed. The amount of nitrate in wort proved to be linearly proportional to the contact time of the hops with the wort. The level of nitrate assimilation by yeast was shown to be dependent on the nitrate assimilation cluster (YNR, YNI, YNT). Hence, the desired yeast strains may be selected according to the genetic make-up. © 2020 The Authors. Journal of the Institute of Brewing published by John Wiley & Sons Ltd on behalf of The Institute of Brewing & Distilling

Keywords: Brettanomyces bruxellensis; beta-glucosidase; monoterpenic alcohols; nitrate assimilation; beer

* Correspondence: Jochen Förster, Carlsberg Research Laboratory, Group Research, Carlsberg A/S, 1799 Copenhagen V, Denmark. Email: jochen.forster@carlsberg.com

1 Carlsberg Research Laboratory, Group Research, Carlsberg A/S, 1799 Copenhagen V, Denmark

2 National Institute for Food, Technical University Denmark, 2800, Kongens Lyngby, Denmark

This is an open access article under the terms of the Creative Commons Attribution License, which permits use, distribution and reproduction in any medium, provided the original work is properly cited.
Besides the potential for releasing aromatic monoterpene alcohols from hops, *Brettanomyces* can also affect other hop derived compounds. One compound of particular interest is nitrate. There are restrictions on the maximum concentration of nitrate in foods and water. The allowable maximum residual level (MRL) of nitrate in water and beer in the European Union is 50 mg/L. Typically, the concentration of nitrate in beer is much lower with nitrate transferring from hops during boiling and dry hopping (19). Despite assimilating ammonium, conventional brewing yeast cannot assimilate nitrate and the compound has a negative impact on its fermentation performance (20). In a recent publication, nitrate assimilation by a diversity of yeast species was reported, establishing a phylogenetic association with other metabolic traits, such as the biosynthesis of the molybdenum cofactor (21). In certain occasions, *Brettanomyces* yeast species have been reported to assimilate nitrate from several substrates (22–24). This requires a nitrate transporter, nitrate and nitrite reductases, encoded by the genes YNT, YNR and YNI respectively (23–25). Nitrate reduction to ammonia is dependent on NAD(P)H (26) (Fig. 2). Furthermore, the metabolism of *B. bruxellensis* has been reported to be influenced by the presence of nitrate in media, leading to expression of genes in the pentose phosphate pathway and TCA cycle (27,28). Of particular relevance to brewing, is that under anaerobic conditions the fermentative capacity of *B. bruxellensis* is improved when nitrate is assimilated, leading to higher ethanol concentration and growth rates (29).

In this study for the first time, we investigated the role of the two beta-glucosidase genes present in *Brettanomyces* on monoterpene alcohol release, and sought to confirm that this yeast can reduce nitrate levels in beer. A variety of strains were sequenced, the presence or absence of key genes was determined, and relevant strains were then selected. The activity of beta-glucosidase was assayed in selected *Brettanomyces* strains and the impact on the release of hop derived compounds was examined, during both primary fermentation and secondary fermentation after dry hopping. Finally, worts with different nitrate concentrations were produced and fermented with *Brettanomyces* strains with selected genetic backgrounds. This allowed the impact of hop dosage on wort nitrate concentration and nitrate assimilation by *Brettanomyces* strains to be studied.

**Figure 1.** Beta-glucosidase activity on glucosides and bioconversion of monoterpene alcohols by yeast. Flavour descriptors adapted from the literature. Genes responsible for the particular reactions are marked in bold. Enzymes marked with (*) are suggested here but not confirmed. Bb = *Brettanomyces bruxellensis*, Ba = *Brettanomyces anomalus*, Sc = *Saccharomyces cerevisiae*. [Colour figure can be viewed at wileyonlinelibrary.com]

**Figure 2.** Nitrate assimilation pathway by *Brettanomyces* species. The enzymes responsible for transportation and conversion to NH₃ are indicated in white. Cofactors involved in the reaction are indicated in light grey. [Colour figure can be viewed at wileyonlinelibrary.com]
Materials and methods

Microbial strains and media

Strains of Brettanomyces were obtained from the Carlsberg Research Laboratory’s (CRL) collection (CRL-1 to CRL-50 in Table 1). The yeasts were grown on yeast extract (1%, w/v) peptone (2%, w/v) glucose (2%, w/v) (YPD) media, with agar (2%, w/v) added where required. The strains were grown in 100 mL Erlenmeyer flasks containing 50 mL of YPD, under aerobic conditions at 25°C with agitation (100 rpm).

DNA sequencing and bioinformatics

Yeast strains were grown for one week in YPD. Cells were recovered by centrifugation at 4000 g for 5 minutes at 4°C, washed in sterile Milli-Q water and recentrifuged. Samples were sent for DNA extraction and whole-genome sequencing, short insert PE150 library, on Illumina HiSeq4000 (BGI-Tech Solutions, Hong Kong). CLC Genomics Workbench software (www.qiagenbioinformatics.com) was used as a tool for bioinformatics analysis. Genome assembly of strains was performed in CLC software using De novo assembly feature. Genes of interest were found in GenBank, accession number (AKS48905.1, EIF45415.1, AKS48904.1) for BbBGL1, BbBGL2 and BaBGL and (EIF45251.1, EIF45249.1, EIF45250.1) for BbYN1, BbYNR and BbYN, respectively. Nucleotide BLAST tool on CLC software was used to identify the presence or absence of each gene.

Beta-glucosidase assay

To test beta-glucosidase activity in B. bruxellensis and B. anomalus, the yeast strains were grown for one week in yeast extract (1%, w/v) peptone (2%, w/v) cellobiose (2%, w/v) (YPY) media. Extracellular, cell associated and intracellular cell fractions were prepared using the modified method of Daenen et al (15). For the extracellular fraction, 1 mL of culture was transferred to a 1.5 mL Eppendorf tube (ThermoFisher), centrifuged (4,000 g, 10 min) and the supernatant collected as the extracellular fraction. The homogenate was centrifuged (14,000 g, 10 min) and the supernatant was collected as the intracellular fraction. The beta-glucosidase activity of each fraction was determined with the MAK129 β-glucosidase assay kit (Sigma Aldrich). The assay was performed in 96 well plates with p-nitrophenyl-β-D-glucopyranoside (β-NPG) as the substrate. The reaction was measured at 405 nm after a 20 minutes incubation at 37°C. The results are reported in units/L, where one unit is the amount of enzyme that catalyses the hydrolysis of 1.0 μmole of substrate per minute at pH 7 and 37°C.

Table 1. Genomic landscape of Brettanomyces strains used in the study.

<table>
<thead>
<tr>
<th>Strain</th>
<th>Species</th>
<th>Beta-glucosidase ORFs</th>
<th>Nitrate assimilation genes</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>BbBGL1</td>
<td>BbBGL2</td>
</tr>
<tr>
<td>CRL-1</td>
<td>B. bruxellensis</td>
<td>X</td>
<td>-</td>
</tr>
<tr>
<td>CRL-2</td>
<td>B. bruxellensis</td>
<td>-</td>
<td>X</td>
</tr>
<tr>
<td>CRL-19</td>
<td>B. bruxellensis</td>
<td>X</td>
<td>X</td>
</tr>
<tr>
<td>CRL-27</td>
<td>B. bruxellensis</td>
<td>X</td>
<td>-</td>
</tr>
<tr>
<td>CRL-49</td>
<td>B. anomalus</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>CRL-50</td>
<td>B. bruxellensis</td>
<td>-</td>
<td>-</td>
</tr>
</tbody>
</table>

From sequencing of the strains, (X) indicates the gene or ORF present. (−) indicates the gene or ORF is missing. (*) indicates homologous genes in B. anomalus.

Fermentation

To investigate the ability of the Brettanomyces strains to release hop aromas, two experimental approaches were performed: i) An all-malt pale wort, 16ºP was provided by Jacobsen Breweries for primary fermentation; ii) Jacobsen Indian Pale Ale (IPA) dry hopped beer (Jacobsen Breweries) was used for secondary fermentation, with 1.2% (w/v) glucose added to support yeast growth. Fermentations were performed using strains CRL-1, CRL-2, CRL-19, CRL-49 and CRL-50.

To examine the effect of nitrate, standard CRL pilsner wort (Viking malt) with an original gravity of 16ºP was used. Saaz hops were added at 4 g/L. Wort (1.5 L) was transferred to 2 litre glass bottles (Witeg) with the hop pellets contained in a tea bag and the wort was brought to 100°C in a water bath. Three different worts were produced, (i) without an additional boil (W1), (ii) with 30 minutes additional boiling (W2) and (iii) with 1 hour additional boiling (W3). Fermentations were performed using strains CRL-1 and CRL-27.

Strains were propagated in the CRL pilsner wort in 50 mL Erlenmeyer flasks. All fermentations were performed in duplicate in 250 mL Duran bottles containing 200 mL of media. The fermentation was allowed to become anaerobic and the ANKOM RF Gas Production System (ANKOM) used to monitor fermentation performance and CO₂ release. A pitching rate of 1x10⁵ viable cells/mL was used (Cellometer X2, Nexcelom Bioscience). No samples were taken during fermentation so as to ensure anaerobiosis. Fermentation was complete when no further CO₂ release could be measured and the beer was stored at -20°C before analysis.
Quantification of fermentable sugars, ethanol, monoterpenic alcohols and nitrate

Quantitative analyses of carbohydrates in wort was performed by high-performance anion-exchange chromatography (HPAEC) using a Dionex ICS-3000 system (Thermo Scientific) with a Dionex PA200 IC column (Thermo Scientific) with a flowrate of 0.5 mL/min. Eluent gradients were performed with (A) 50mM NaOH and (B) 50mM NaOH/100mM acetate pressurised with Helium. The column temperature was at 30°C. Injection volume was kept at 10 μL full loop. Samples were filtered through a SEP-PAK C18 (Waters Corporation) and diluted 10x before injection. Reference sugar samples were obtained from Sigma Aldrich and calibration curves were prepared for each measurement.

Ethanol content was quantified with Alcolyser BeerME Analyzing System (www.anton-paar.com). Monoterpenic alcohols were quantified using Headspace Gas Chromatography Solid Phase Micro Extraction (HS-GC-SPME) following the method described by (30). Nitrate content in wort was determined with HPLC anion exchange column and detected by conductimetry, based on (31). Beer samples were degassed by agitation, filtered through a 0.45 μm filter and diluted 10 times with pure water before injection.

Results and discussion

Genetic characterisation and selection of strains

Six Brettanomyces strains with different genomic maps were selected to examine the effect of the presence or absence of genes for nitrate assimilation and beta-glucosidase (Table 1). Five of the strains were Brettanomyces bruxellensis and one (CRL-49) Brettanomyces anomalus. For studies of the effect of beta-glucosidase on hop flavour release, CRL-1 and CRL-2 were chosen as they contain just one ORF, BbBGL1 and BbBGL2 respectively. CRL-19 was selected for having both ORFs and CRL-50 for having neither ORF. Furthermore, CRL-1 was chosen as a representative strain possessing all three nitrate assimilation genes, in comparison with strain CRL-27 lacking the nitrate assimilation loci (Table 1).

Genetic background and beta-glucosidase

Five Brettanomyces strains with different arrangements of the beta-glucosidase genes were assayed for enzyme activity. Intracellular, cell related and extracellular activities were measured (Fig. 3). The highest activity in the B. bruxellensis strains (up to 74 units/L) was detected in the intracellular fraction of CRL-19, which contains both beta-glucosidase ORFs. In contrast, little activity was detected in the strains with only one or no beta-glucosidase encoding genes. The results indicate that BbBgl2 is more efficient than BbBgl1 and suggests that there could be an additive effect between the two proteins. Interestingly, Kuo and co-workers purified a heterodimeric structure with beta-glucosidase activity from Dekkera bruxellensis, consisting of two subunits of 50 and 30 kDa (32). Nevertheless, the amino acid sequences of those two subunits do not correlate to the two ORFs found here for the Brettanomyces strains. In contrast to the proteins tested by Kuo (32), our results suggest that such enzymes are primarily located intracellularly, with little secretion (Fig. 3), similar to the findings of Blondin et al (33).

The intracellular fraction of B. anomalus CRL-49 showed the highest activity among all the Brettanomyces strains tested (144 units/L). The potential of B. anomalus beta-glucosidase activity over B. bruxellensis has been reported before (16). Interestingly, beta-glucosidase activity was also detected in the cellular fraction of CRL-49, suggesting that the enzyme could be associated with the cell wall in Brettanomyces anomalus.

Hop aroma conversion by Brettanomyces strains during primary fermentation

Brettanomyces strains producing different beta-glucosidase enzymes were selected to examine whether they could facilitate the release of hop flavour compounds. The effects on primary fermentation (before dry hopping) were examined first, as the Brettanomyces strains would be anticipated to have high viability with little release of the intracellular beta-glucosidase. Fermentations proceeded for 10 days, by which time CO2 release had stopped. The fermentations for all strains were similar, as shown by CO2 production (Fig. 4A) and ethanol formation (7.5 ± 0.2 %; Table 2). However, B. bruxellensis CRL-2 was an exception as it
was not able to metabolise maltose. Ethanol production by CRL-50 was the highest due to its ability to ferment dextrins, as shown by utilisation of maltotetraose (Table 2). At the end of fermentation samples were analysed for monoterpene alcohols and compared to the wort. The results in Fig. 5A show that yeast strains CRL-1 (one ORF) and CRL-50 (no ORFs), which had the lowest beta-glucosidase activities led to the greatest concentrations of β-citronellol, reaching levels up to 31.5 μg/L after fermentation for CRL-50. Furthermore, CRL-2 (lacking one ORF and maltose utilisation) had the lowest conversion of geraniol to β-citronellol. The same pattern was seen in all the strains; the content of geraniol decreased in favour of the production of β-citronellol. Linalool was converted to α-terpineol but at lower rate. Following conventional pathways, myrcene was completely depleted in all cases and isoamyl isobutyrate was slightly increased (34). No correlation between beta-glucosidase activity (Fig. 4) and aroma released from aglycones (Fig. 5) was seen. To our knowledge, such large amounts of β-citronellol are rarely reported without the use of dry-hopping. In Saccharomyces yeast, β-citronellol formation has been strongly correlated with Oye2 activity (9). In the Brettanomyces genome sequences reported here, two proteins were identified as potential homologs of Oye2 and Oye3, showing domains of flavin mononucleotide (FMN) oxidoreductase activity. A BLAST search revealed a 58% similarity with ‘hansenula yellow enzyme’ 2 and 3 of Hansenula polymorpha. Accordingly, the proteins are referred to as BbHye2 and BbHye3 (35). Accordingly, the results reported here suggest that oxidoreductases BbHye2 and BbHye3 cause stronger monoterpenoid alcohol conversion than the conventional brewer’s yeast ScOye2. This could contribute a more stable redox metabolism under anaerobiosis in Brettanomyces by the regeneration of NAD+ (Fig. 1).  

Table 2. Ethanol and fermentable sugars after primary fermentation and secondary fermentation (shaded). Standard deviation is reported (n=2).

<table>
<thead>
<tr>
<th></th>
<th>Ethanol (%, v/v)</th>
<th>Glucose (mg/L)</th>
<th>Maltose (mg/L)</th>
<th>Maltotriose (mg/L)</th>
<th>Maltotetraose (mg/L)</th>
</tr>
</thead>
<tbody>
<tr>
<td>CRL-1</td>
<td>7.49 ± 0.13</td>
<td>4 ± 2</td>
<td>0 ± 0</td>
<td>179 ± 19</td>
<td>3225 ± 150</td>
</tr>
<tr>
<td>CRL-2</td>
<td>1.71 ± 0.02</td>
<td>91 ± 16</td>
<td>60215 ± 3559</td>
<td>16674 ± 839</td>
<td>3325 ± 157</td>
</tr>
<tr>
<td>CRL-19</td>
<td>7.39 ± 0.08</td>
<td>10 ± 14</td>
<td>22 ± 30</td>
<td>67 ± 46</td>
<td>2686 ± 1072</td>
</tr>
<tr>
<td>CRL-49</td>
<td>7.3 ± 0.05</td>
<td>0 ± 0</td>
<td>15 ± 21</td>
<td>3403 ± 388</td>
<td>3064 ± 148</td>
</tr>
<tr>
<td>CRL-50</td>
<td>7.75 ± 0.32</td>
<td>37 ± 4</td>
<td>1570 ± 549</td>
<td>19 ± 7</td>
<td>81 ± 1</td>
</tr>
<tr>
<td>CRL-1</td>
<td>6.97 ± 0.0</td>
<td>9 ± 1</td>
<td>553 ± 100</td>
<td>9012 ± 721</td>
<td>1414 ± 48</td>
</tr>
<tr>
<td>CRL-2</td>
<td>6.82 ± 0.17</td>
<td>12 ± 4</td>
<td>827 ± 332</td>
<td>9711 ± 1883</td>
<td>1396 ± 70</td>
</tr>
<tr>
<td>CRL-19</td>
<td>6.91 ± 0.04</td>
<td>10 ± 8</td>
<td>842 ± 264</td>
<td>12396 ± 4254</td>
<td>1377 ± 0</td>
</tr>
<tr>
<td>CRL-49</td>
<td>6.96 ± 0.06</td>
<td>9 ± 3</td>
<td>407 ± 137</td>
<td>8518 ± 373</td>
<td>1260 ± 14</td>
</tr>
<tr>
<td>CRL-50</td>
<td>7.32 ± 0.39</td>
<td>16 ± 5</td>
<td>785 ± 17</td>
<td>3202 ± 1874</td>
<td>916 ± 140</td>
</tr>
</tbody>
</table>

Hop aroma conversion by Brettanomyces strains during secondary fermentation

A dry hopped commercial beer supplemented with glucose (1.2%, w/v) was inoculated with the respective strain of Brettanomyces, re-sealed in the ANKOM system and refermented for 14 days. At this point, the glucose had been consumed as shown by the CO2 accumulation curves (Fig. 4B) and between 6.8 and 7.3% (v/v) alcohol had been produced (Table 3). The total amount of monoterpenoid alcohols were higher in the secondary fermentations compared to the primary fermentations due to dry-hopping (Fig. 5B). However, bioconversion of monoterpene alcohols occurred to a similar extent as in the primary fermentation with, in both cases, the conversion of ca. 25 μg/L geraniol. As in the primary fermentations, Brettanomyces strains increased α-terpineol and β-citronellol content while reducing linalool and geraniol. There was no correlation between strain dependent beta-glucosidase activity (Fig. 4) and hop aromas, suggesting that the intracellular beta-glucosidase was
not available to release of aglycones from hops. In support of this, 
Takoi et al 2010 (3) reported the release of glycosidically bound 
precursors using added Sumizyme BGA, a commercial 
beta-glucosidase derived from *Aspergillus niger* (3). Nevertheless, 
a treatment at 50°C for 60 min was included, which is unsuitable 
for beer. Other studies have reported optimal activity at even 
higher temperatures (16). Other enzymes such as an extracellular 
exoglucanase protein encoded by *EXG1* gene have been related

**Table 3.** Ethanol production after fermentation of Pilsner wort with varying nitrate content.

<table>
<thead>
<tr>
<th>Yeast</th>
<th>Media</th>
<th>Hop contact time (min)</th>
<th>Initial nitrate content (mg/L)</th>
<th>Alcohol (% v/v)</th>
</tr>
</thead>
<tbody>
<tr>
<td>CRL-1</td>
<td>Pilsner Wort 1</td>
<td>0</td>
<td>1.8</td>
<td>7.04 ± 0.12</td>
</tr>
<tr>
<td>CRL-1</td>
<td>Pilsner Wort 2</td>
<td>30</td>
<td>11.7</td>
<td>7.02 ± 0.06</td>
</tr>
<tr>
<td>CRL-1</td>
<td>Pilsner Wort 3</td>
<td>60</td>
<td>22</td>
<td>6.89 ± 0.21</td>
</tr>
<tr>
<td>CRL-27</td>
<td>Pilsner Wort 1</td>
<td>0</td>
<td>1.8</td>
<td>7.2 ± 0.0</td>
</tr>
<tr>
<td>CRL-27</td>
<td>Pilsner Wort 2</td>
<td>30</td>
<td>11.7</td>
<td>7.1 ± 0.04</td>
</tr>
<tr>
<td>CRL-27</td>
<td>Pilsner Wort 3</td>
<td>60</td>
<td>22</td>
<td>6.96 ± 0.08</td>
</tr>
</tbody>
</table>

Figure 5. Monoterpene alcohols in beers after fermentation with *Brettanomyces* as primary (A) or secondary (B) yeasts. The sum of monoterpene alcohols by strain is indicated in µg/L. Standard deviation is shown by error bars (n=2).
to non-specific activity of sugar bound molecules (17,32,36,37). Further research is needed to evaluate the specific role of proteins in the release of hop aglycones and whether other compounds such as nerol or ergosterol derivatives contribute to the bioconversion.

**Effect of hop boiling time on the nitrate content in wort**

The transfer of nitrate from hops to wort was investigated by varying wort boiling time with 0, 0.5 and 1 hour of additional boiling. The concentration of nitrate in the worts was respectively 1.8, 11.7 and 22 mg/L. This linear ($R^2 = 0.9999$) increase in nitrate over time is in agreement with previous studies (19). The nitrate levels were below the maximum residual level in the EU (50 mg/L). However, this will be dependent on the hop variety and treatment during cultivation (38). These results confirm that hops are a significant source of nitrate in wort and confirm the risk that long contact times or large hop additions can result in the release of high concentrations of nitrate.

**Effect of fermentation by *Brettanomyces* strains on nitrate concentration**

Fermentations were conducted in wort containing different concentrations of nitrate with two strains of *Brettanomyces*. Strain CRL-1 contained all the nitrate assimilation genes whereas CRL-27 had none of these genes. Nitrate and ethanol concentrations were measured in final beers, harvested after 9 days of fermentation when CO₂ production had stopped (Fig. 6). The results in Fig. 7 show that the nitrate concentration was unaffected in the fermentation with CRL-27 (without the nitrate assimilation cluster). In contrast, nitrate was almost fully consumed in

![Figure 6](image_url)  
**Figure 6.** Fermentation of worts with varying nitrate content with *Brettanomyces* CRL-1 (+ nitrate assimilation) and CRL-27 (- nitrate assimilation). Curves represent the average values of duplicate fermentations. Wort 1 (W1) had no additional boiling, Wort 2 (W2) had additional hop boiling for 30 minutes, Wort 3 (W3) was boiled for 1 hour.

![Figure 7](image_url)  
**Figure 7.** Nitrate content after fermentation with different *B. bruxellensis* strains in worts W1, W2, W3 containing 1.8, 11.7 and 22 mg/ml NO₃ respectively. Wort 1 (W1) had no additional boiling, Wort 2 (W2) had additional hop boiling for 30 minutes, Wort 3 (W3) was boiled for 1 hour. CRL-1 contains the nitrate assimilation loci, CRL-27 does not.
fermentations with CRL-1, which contained all of the nitrate assimilation genes. Interestingly, ca. 2.5 mg/mL nitrate remained in the CRL-1 fermentations, independent of the starting concentration, suggesting that the capacity of the Brettanomyces strain for nitrate reduction is much higher. Furthermore, despite nitrite (NO2-) being the an intermediate in the pathway, it was not detected in any sample. This suggests that the enzyme nitrite reductase is efficient in reducing nitrite to ammonia (NH3).

Despite wort being rich in amino acids and the preferred nitrogen source in Brettanomyces (39), nitrate was efficiently assimilated during fermentation. This has been linked to the need of yeast to reoxidise NAD(P)H, to maintain the redox balance and enable cell growth (28). Examination of the fermentation data suggests that the fermentative metabolism was not affected by the assimilation of nitrate, in contrast to previous studies (28,29,40). This is presumably due to the content of nitrate in wort which was much lower than previously reported (>240 mg/L) (40), suggesting that the nitrate level transferred by hops was not significant enough to make an impact on yeast metabolism.

Conclusions

In this study, the interaction between hop derived compounds and yeast of the genus Brettanomyces was studied. In particular, beta-glucosidase activity was found to be highly strain dependent, with Brettanomyces ananas the most efficient in converting β-substrates. The beta-glucosidase activity of Brettanomyces strains is almost exclusively intracellular and therefore has little impact on the release of hop derived monoterpenes alcohols during fermentation. In addition, the conversion of geraniol into β-citronellol was substantially higher, most likely from a direct contribution of the oxidoreductase proteins BbHye2 and BbHye3. Furthermore, it was demonstrated that nitrate levels in wort increased linearly with time during wort boiling, but the level was reduced during subsequent Brettanomyces fermentation. No effect on nitrate levels was seen in a strain lacking the nitrate assimilation genes, confirming that YNR1, YNI1 and YNT are required for nitrate metabolism.

Author contributions

MSC designed, performed the experiments and wrote the manuscript, BF provided technical support, NS supported the experimental design, TJH supported writing the manuscript, JF supported the experimental design and overall supervision.

Acknowledgements

The authors would like to acknowledge Dr Rosa Garcia Sanchez for critical review of the manuscript, Dr Ross Fennessy for experimental discussion, Dr Anna Chailyan for bioinformatics support, the Brewing Science Department at CRL, Jacobsen Breweries for providing wort and beer and the Carlsberg Group Development for Analytics support. The project was supported by Innovationsfonden Denmark. MSC is a recipient of an Industrial PhD fellowship (project 5189-00057).

Conflict of interest

A patent application protecting some of this work has been submitted by Carlsberg Breweries.

References


wileyonlinelibrary.com/journal/jib © 2020 The Authors. Journal of the Institute of Brewing published by John Wiley & Sons Ltd on behalf of The Institute of Brewing & Distilling
Biotransformation of hopcompounds by Brettanomyces


