Changes in membrane lipid composition in ethanol- and acid-adapted *Oenococcus oeni* cells: characterization of the *cfa* gene by heterologous complementation

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Cyclopropane fatty acid (CFA) synthesis was investigated in *Oenococcus oeni*. The data obtained demonstrated that acid-grown cells or cells harvested in the stationary growth phase showed changes in fatty acid composition similar to those of ethanol-grown cells. An increase of the CFA content and a decrease of the oleic acid content were observed. The biosynthesis of CFAs from unsaturated fatty acid phospholipids is catalysed by CFA synthases. Quantitative real-time-PCR experiments were performed on the *cfa* gene of *O. oeni*, which encodes a putative CFA synthase. The level of *cfa* transcripts increased when cells were harvested in stationary phase and when cells were grown in the presence of ethanol or at low pH, suggesting transcriptional regulation of the *cfa* gene under different stress conditions. In contrast to *Escherichia coli*, only one functional promoter was identified upstream of the *cfa* gene of *O. oeni*. The function of the *cfa* gene was confirmed by complementation of a *cfa*-deficient *E. coli* strain. Nevertheless, the complementation remained partial because the conversion percentage of unsaturated fatty acids into CFA of the complemented strain was much lower than that of the wild-type strain. Moreover, a prevalence of cycC19 : 0 was observed in the membrane of the complemented strain. This could be due to a specific affinity of the CFA synthase from *O. oeni*. In spite of this partial complementation, the complemented strain of *E. coli* totally recovered its viability after ethanol shock (10 %, v/v) whereas its viability was only partly recovered after an acid shock at pH 3.0.

INTRODUCTION

Most prokaryotes are able to adapt to and survive fluctuations of environmental conditions by using multiple strategies that can operate simultaneously. To survive and function in wine, *Oenococcus oeni* requires the activation of a proton-extruding ATPase (Drici-Cachon et al., 1996; Salema et al., 1996) and the proton-motive force generated by malolactic fermentation. Nevertheless, two main strategies are also required and these seem to be conserved in most bacteria. The first one involves the induction of the expression of specific genes called heat-shock genes (*hsp*). The second strategy leads to membrane fluidity adjustments by modifications in membrane composition, generally affecting phospholipids and their fatty acid composition. Indeed, the cell membrane constitutes one of the first barriers against environmental stresses and consequently plays a major role in homeostasis and in adaptation to stress conditions (Jones, 1989; Sajbidor, 1997; Weber & de Bont, 1996). Bacteria can modify their fatty acid composition in response to atypical conditions (Cronan, 2002). The lipid structure and the portion of saturated, unsaturated, branched or cyclic fatty acids in individual phospholipids influences the fluidity of biological membranes.

Many studies have focused on the deleterious effect of ethanol on membrane modifications in micro-organisms (Dombek & Ingram, 1984; Guzzo et al., 2000; Svobodova & Svoboda, 1988; Swan & Watson, 1997). In *Escherichia coli*, one of the changes that occur in membrane lipid composition:

**Abbreviations:** CFA, cyclopropane fatty acid; QRT-PCR, quantitative reverse transcriptase PCR.
composition in response to ethanol is an increase in the amount of unsaturated fatty acid (Ingram, 1976). During acetone-butanol fermentation, modifications in the unsaturated/saturated fatty acid ratio were found in Clostridium acetobutylicum cell membranes (Lepage et al., 1987). The unsaturated fatty acid acyl chains of bacterial membrane phospholipids have a major influence on membrane properties. In cis–trans isomerization, catalysed by a cis–trans isomerase, the double bond is reconfigured. The cis unsaturated chain contains a bond which increases membrane fluidity, whereas the trans isomer increases membrane rigidity. Loffeld & Keweloh (1996) suggested that the isomerization of cis into trans unsaturated fatty acids is an emergency action of cells of Pseudomonas putida to adapt membrane fluidity to drastic changes in environmental conditions.

An opposite effect in response to ethanol is observed in other micro-organisms (Rigomier et al., 1980; Teixeira et al., 2002). An increase in the content of saturated fatty acids is observed in Bacillus subtilis (Rigomier et al., 1980). A mechanism involved in the increase of saturated fatty acids is the conversion of monounsaturated fatty acids to cyclopropane fatty acids (CFAs). CFAs have been detected in membrane phospholipids of a variety of eubacteria (Grogn & Cronan, 1997). These CFAs are synthesized in situ by the transfer of a methylene group from S-adenosyl-L-methionine to a double bond of unsaturated fatty acid chains of membrane phospholipids by CFA synthase. Conversion of monounsaturated fatty acids to CFAs has been reported in many Gram-negative bacteria when the growth rate of cultures is markedly slowed, i.e. during the stationary phase of growth. In E. coli, the synthesis of CFAs is generally regarded as a means to reduce membrane fluidity and prevent the penetration of undesirable molecules in order to adapt the cells to adverse conditions (Chang & Cronan, 1999; Grogn & Cronan, 1997). The positive roles of CFAs have also been demonstrated in bacterial cells adapted to high acidity (Brown et al., 1989; Grogn & Cronan, 1997). The positive roles of CFAs have also been demonstrated in bacterial cells adapted to high acidity (Brown et al., 1989; Grogn & Cronan, 1997).

In E. coli, the onset of CFA synthesis as cultures enter stationary phase is due to increased transcription of cfa from the RpoS-dependent promoter, whereas a standard RpoD-dependent promoter is responsible for the low level of CFA synthesis in exponentially growing cultures (Chang & Cronan, 1999). In Lactococcus lactis, transcriptional fusion experiments have demonstrated high induction of cfa gene expression by acidity as well as during entry into the stationary phase of growth (Budin-Verneuil et al., 2005). The cfa gene of C. acetobutylicum appears to form an independent operon with a marR-homologous gene. The MarR-like gene product may act to reduce expression of the cfa gene directly or indirectly, based on the observation that the overexpression of marR resulted in decreased CFA accumulation (Zhao et al., 2003).

In this work, we analysed the membrane fatty acid composition of O. oeni in three conditions of stress: entry into the stationary phase of growth, and growth in the presence of ethanol or in acidic conditions. In all three conditions, we observed a decrease of the ratio of unsaturated to saturated fatty acids and an increase of CFA content. These results led us to study the level of transcription of the cfa gene of O. oeni in stress conditions. By complementation of an E. coli cfa mutant, we investigated the functionality of the cfa gene of O. oeni.

**METHODS**

**Bacterial strains and media.** O. oeni ATCC BAA-1163 (formerly O. oeni IOB 8413) was cultured at 30 °C in modified FT80 (mFT80) medium (Cavin et al., 1989) at pH 5.3. The E. coli strains used were derivatives of E. coli K-12. E. coli ER2738 [pE. coli lacZΔM15 zff::Tn10(TetR)lacZ Δlac-proAB Δ(hsd−/−)S30 (New England Biolabs) was used for cloning procedures. E. coli MG1655 (F− Δ lacI− Δ rfb−50 Δ rph−1) and E. coli YC1273 (MG1655 Δ cfa−kan) were used to confirm the function of the O. oeni cfa gene (Chang & Cronan, 1999; Jensen, 1993). E. coli strains were grown aerobically at 37 °C in luria–Bertani (LB) medium or in tryptone soya broth medium (TSB, Biokar) (Bertani, 1951). For recombinant strains, the medium was appropriately supplemented with ampicillin (100 μg ml⁻¹) or kanamycin (25 μg ml⁻¹).

**Growth in sublethal stress conditions, and acid and ethanol shocks.** Precultures of O. oeni were used to inoculate mFT80 medium at an initial OD₆₀₀ of 0.1. To obtain control cells, exponential-phase cells were harvested when an OD₆₀₀ of 0.7 was reached at pH 5.3. Stationary-phase cells were harvested after 36 h incubation in the same medium. For ethanol- and acid-grown cells, O. oeni was inoculated at the same OD₆₀₀ of 0.1 in mFT80 with 8 % (v/v) ethanol and at pH 3.5, respectively. Stress-grown cells were harvested from their exponential growth phase after 36 and 31 h of growth with 8 % ethanol and at pH 3.5, respectively.

To test resistance to ethanol and acidity, E. coli strains were cultivated in TSB medium to late-stationary phase (15 h) and 1 ml samples of cultures were harvested by centrifugation at room temperature. The cells were then washed with TSB medium and resuspended in 1 ml TSB medium at pH 3 (adjusted with HCl) or TSB supplemented with ethanol 10 % (v/v) for challenge. The cell suspensions were shaken at 37 °C and aliquots were collected at timed intervals (1, 2 and 3 h), and viable counts were measured by serial dilution and plating on LB agar supplemented with ampicillin. Survival is defined as the ratio of colonies (c.f.u.) formed on LB agar medium after challenges to the initial number of viable colonies.

**Lipid analysis.** Bacterial cells were taken from exponential-phase cultures under optimal conditions, in the presence of 8 % ethanol,
and at pH 3.5. Total lipids were extracted with chloroform/methanol according to the method described by Bligh & Dyer (1959). Phospholipids were purified by TLC on silica gel plates (Merck) with hexane/diethyl ether/methanol/acetic acid (90/20/3/2, by vol.) for development. The phospholipid band was scraped off and extracted from the silica gel with chloroform/methanol/water (45/45/10, by vol.). The fatty acids of total lipids and phospholipids were directly transesterified with methanol/H₂SO₄ (95/5, v/v) at 80 °C for 2 h. Total fatty acids were quantified by adding CitC7:0 (heptadecanoic acid) as an internal standard. The fatty acid methyl esters (FAMEs) were analysed by GLC using a Chrompack CP 9002 chromatograph equipped with a Varian Factor Four capillary column (30 m × 0.32 mm). The oven temperature increased after 1 min from 60 °C to 150 °C at 30 °C min⁻¹ for 3 min then to 220 °C at 2 °C min⁻¹. The FAMEs were identified by comparing retention times with those of authentic standards (Nu Chek Prep., Elysian, MN, USA).

**RNA extraction and analysis.** RNA extraction was performed using TRI Reagent (Sigma) according to the manufacturer’s instructions and 0.4 g of glass beads (70–100 μm) to disrupt cells with a FastPrep cell disintegrator (Bio 101). Samples were then treated as recommended by the manufacturer and used for Northern blotting, primer extension analysis, reverse transcriptase PCR (RT-PCR) or quantitative RT-PCR (QRT-PCR) experiments. Northern blotting was carried out as described by Sambrook et al. (1989). A DNA fragment corresponding to the O. oeni cfa gene was amplified by PCR using oligonucleotides L1 (TGGTATCATTGAGCGAGGAG) and R1 (GGATTATCGTGATCTCAAAGACG) and used as a probe in Northern hybridization experiments. PCR was performed in a final volume of 50 μl containing O. oeni genomic DNA (1 μg ml⁻¹), dNTPs (0.2 mM each), oligonucleotides (1 mM each), 10 U ml⁻¹ of Taq DNA polymerase (Bioline), and the buffer supplied with the enzyme. Amplification was performed for 35 cycles consisting of 30 s denaturation at 92 °C, 30 s annealing at 60 °C, and 30 s elongation at 72 °C. The PCR products were purified by using the Qiagen PCR purification kit (Qiagen) and probe was radiolabelled with [α-³²P]ATP using a random primers DNA labelling kit (Invitrogen). Primer extensions were performed as previously described (Grandvalet et al., 2005) with oligonucleotides cfa2C (TTTTGGCTTACCTGCCCATAAA) and cfa4C (GGGGTTTTATCAGTTTAAAG). The corresponding DNA-sequence reactions were carried out by using the same oligonucleotides and PCR-amplified DNA fragments with oligonucleotides cfa1C (CTTTTGGTTTTAATTTTCACTTTTTGAGG) and cfa2C, carrying the cfa promoter region. Nucleotide sequences were determined by the dyeoxy chain-termination method using the DNA sequencing cycle Reader kit (MBI Fermentas). RT-PCR and QRT-PCR were performed as previously described (Grandvalet et al., 2005) using the primer pair L1 and R1. The specificity of QRT-PCR products was determined with a melting curve. The efficiency of real-time amplification is calculated by the formula E=[10^((1/Ct)-1)]×100, where s is the slope of standard curve. Three independent experiments were performed and the results were calculated by the comparative critical threshold (ΔΔCt) method, in which the amount of target RNA is adjusted to a reference relative to an internal calibrated target RNA. The ldhD gene of O. oeni was chosen as an internal control for these experiments (Desroche et al., 2005).

**DNA isolation, manipulation and transformation**

**Cloning of the cfa gene from O. oeni.** The cfa gene was cloned by PCR amplification from O. oeni ATCC BAA-1163 chromosomal DNA using oligonucleotides cfa4M (GCCTGATCCTCCTTATTTAATTAAAAATAGAAATATT) and cfa5M (GAGGATCTTCTGTTCATTTTTTTTAGAAAT). BamH and EcoRI sites (italic) were included to aid subsequent manipulations. The PCR was performed by using Taq ADN polymerase high-fidelity Platinum (Invitrogen) as recommended by the manufacturer in order to minimize errors during polymerization. The resulting fragment carrying the whole cfa gene, including the promoter region and the terminator, was ligated to the corresponding cloning sites of pUC18 (Invitrogen) after digestion with BamHI and EcoRI, to form pMT1. This construct put the O. oeni cfa gene under control of its own promoter region. The sequence of the cloned PCR amplification product was confirmed by DNA sequencing (GENOME express). Plasmid pMT1 was used to transform the cfa-deficient E. coli strain YYY1273 and the wild-type E. coli strain MG1655. Transformation of E. coli was conducted by electroporation.

**Sequence and statistical analysis.** Sequence alignments were performed with CLUSTAL W (Kohli & Bachhawat, 2003). The significance of the difference between cell viability percentages and total fatty acid amounts was determined by a two-tailed Student’s t test. The confidence interval for a difference in the means was set at 95% (P<0.05) for all comparisons.

**RESULTS**

**Changes in membrane fatty acid composition in stationary-phase and in stress-grown O. oeni**

Two sublethal stress conditions were chosen to obtain stress-grown O. oeni cells: cultures in the presence of 8% (v/v) ethanol and at pH 3.5. The concentration of 8% ethanol was chosen as a hinge value: the main changes normally occurred in cells grown in the presence of at least 8% ethanol in the medium (Teixeira et al., 2002). The control cells were harvested in the exponential phase of growth, when an OD₆₀₀ of 0.7 was reached after 12 h of incubation. Stationary-phase cells were harvested after 36 h of incubation (maximal OD₆₀₀ of 1.6). Stress-grown cells were harvested from their exponential growth phase (OD₆₀₀ of 0.7) after 36 and 31 h of growth with 8% ethanol and at pH 3.5, respectively. The maximal OD₆₀₀ values reached by cultures in the presence of ethanol or at pH 3.5 were 1.0 and 1.2, respectively. The Neperian specific growth rate (μ) of cells cultured under optimal conditions was 0.16 h⁻¹ whereas that of cells cultured in the presence of 8% ethanol and at pH 3.5 significantly decreased to the same value of 0.05 h⁻¹. Nevertheless, the final biomass obtained by growth in sublethal stress conditions represented approximately 75% of the final biomass obtained in optimal conditions (data not shown).

We determined the fatty acid composition of the total lipids and the phospholipid fraction extracted from O. oeni cells grown under optimal conditions. The fatty acid profile of phospholipids was similar to that of total fatty acids and accounted for nearly 94% (w/w) of the total fatty acids. From then on, fatty acid analyses were carried out only on the total lipid extract. In O. oeni control cells (mid-exponential growth phase), eight main fatty acids were identified (Fig. 1); these represented 90 mol% of total fatty acids. The higher amount of oleic (C₁₈:1 n-9) and dihydrosterculic (cycC₁₉:0 n-9) acids compared to that of cис-vaecenic (C₁₈:1 n-7) and lactobacillic (cycC₁₉:0 n-7)
acids was in accordance with the presence of Tween 80 in the O. oeni culture medium (Guerrini et al., 2002; Lonvaud-Funel & Desens, 1990).

In the stationary phase of growth, the levels of major saturated fatty acids [myristic (C14:0) and palmitic (C16:0)] remained constant. In contrast, we observed a decrease in unsaturated fatty acids, particularly oleic acid, which is the main unsaturated fatty acid present in the medium. Moreover, the main effect on the fatty acid profile was an increase in the molar percentage of dihydrosterculic acid.

In cells grown in the presence of 8% ethanol, the membrane fatty acid profile dramatically altered compared to that of control cells. There was an increase in the molar percentage of the saturated palmitic (C16:0) and cyclopropane dihydrosterculic (cycC19:0 n-9) acids, and a decrease in that of the monounsaturated palmitoleic (C16:1) and oleic acids (Fig. 1). The amount of total fatty acids dropped by twofold in comparison with that of control cells (Table 1).

In cells grown under acid conditions (pH 3.5), we observed similar changes in membrane fatty acid profile as those observed in ethanol-grown cells but of smaller amplitude (Fig. 1). The ratio of unsaturated to saturated fatty acids dropped by fivefold compared to that of control cells. The total fatty acid content was only one-third of that of control cells (Table 1).

Expression of the O. oeni cfa gene increases at the onset of stationary phase and in stress growth conditions

The biosynthesis of CFAs from unsaturated fatty acid phospholipids is catalysed by CFA synthases (Grogan & Cronan, 1997). The genome sequence of O. oeni ATCC BAA-1163, (accession no. NZ_AAUV00000000) revealed an ORF (locus_tag: OENO64048) encoding a 45 kDa protein sharing 45% amino acid sequence identity with CFA synthase from Clostridium acetobutylicicum (Zhao et al., 2003) and 29% identity with CFA synthase from E. coli (Grogan & Cronan, 1984) and S. typhimurium (Kim et al., 2005). This putative O. oeni cfa gene is flanked by two genes (locus_tag OENO64049 and OENO64046) transcribed in the same orientation as cfa (Fig. 2b). The gene upstream of cfa (OENO64049) encodes a putative permease protein of an ABC transporter system, whereas the downstream gene (OENO64046 annotated ubiD) encodes a 3-octaprenyl-4-hydroxybenzoate carboxy-lyase. We noted that the genome sequence of O. oeni PSU-1 (accession no. NC_008528.1) contains an ORF (OEOE_1175) between cfa and ubiD, transcribed divergently. This putative gene encodes a 304 aa protein similar to a transcriptional regulator of the LysR family. This ORF is also present in the O. oeni ATCC BAA-1163 genome (OENO64047), but it has not been annotated because of the presence of a frameshift which is due to a sequencing

Table 1. Analysis of fatty acid profiles of O. oeni cells grown under different conditions

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Exponential-phase cells (control)</th>
<th>Stationary-phase cells (36 h)</th>
<th>Ethanol-grown cells</th>
<th>Acid-grown cells</th>
</tr>
</thead>
<tbody>
<tr>
<td>Saturation degree*</td>
<td>0.50</td>
<td>0.62</td>
<td>0.87</td>
<td>0.82</td>
</tr>
<tr>
<td>Unsaturated/saturated fatty acids†</td>
<td>0.99</td>
<td>0.61</td>
<td>0.15</td>
<td>0.23</td>
</tr>
<tr>
<td>Total fatty acids‡</td>
<td>5.6 ± 1.3</td>
<td>6.1</td>
<td>2.8 ± 0.2</td>
<td>1.8 ± 0.1</td>
</tr>
</tbody>
</table>

*Saturation degree = $\Sigma$(C14:0+C16:0+C18:0+cycC19:0)/100 (cycC19:0 is considered as a saturated fatty acid).
†Ratio of unsaturated to saturated fatty acids = $\Sigma$(C16:1+C18:1)/$\Sigma$(C14:0+C16:0+C18:0+cycC19:0).
‡The values represent quantities of total fatty acids (µg per OD600 unit of cells) and are means ± SD for three independent cultures. ND, Not determined.

Fig. 1. Fatty acid composition of O. oeni cells during growth in mFT80 medium under optimal conditions (exponential-phase cells, stationary-phase cells), in the presence of 8% (v/v) ethanol (ethanol-grown cells) or in medium at pH 3.5 (acid-grown cells). Stress-grown cells were harvested for analyses from their exponential growth phase. Means ± SD are presented (n=3).
expression of the \textit{O. oeni} gene by primer extension analysis. Total RNA was extracted from cells harvested in the exponential phase. (a) Primer extension product corresponding to the \textit{cfa} gene (lane ext) is shown alongside DNA-sequencing reaction products (lanes T, G, C and A). The corresponding nucleotide sequence is shown on the left. (b) Map of the \textit{cfa} genomic region. The transcriptional start site is indicated by an asterisk, the –10 sequence is boxed, the TG hexamer (Fig. 2b). To examine whether expression of \textit{cfa} is induced during growth in stress conditions, a QRT-PCR was set up. Total RNA was extracted from exponential- (control) and stationary-phase \textit{O. oeni} cells grown under optimal growth conditions and from exponential-phase cells grown in the presence of 8\% (v/v) ethanol (ethanol-grown cells) and at pH 3.5 (acid-grown cells). By using the comparative critical threshold (ΔΔC_{t}) method with the \textit{ldhD} gene of \textit{O. oeni} as an internal control (Desroche et al., 2005), we found that the \textit{cfa} mRNA levels increased by three-, six- and twofold in stationary-phase, ethanol- and acid-grown cells, respectively, in comparison with that of control cells.

\textbf{Expression of the \textit{O. oeni} cfa gene restores the synthesis of CFA in an \textit{E. coli} cfa mutant}

Because no genetic tool adapted to carry out gene inactivation in \textit{O. oeni} is yet available, the function of the \textit{O. oeni} \textit{cfa} gene was explored in the \textit{cfa}-deficient mutant \textit{E. coli} YYC1273 (Chang & Cronan, 1999). The \textit{O. oeni} \textit{cfa} gene, its promoter region included, was cloned into the pUC18 vector to generate pMT1, which was introduced into strain YYC1273 (YYC1273/pMT1). Before analysing the phenotype of the complemented strain, the heterologous expression of the \textit{O. oeni} \textit{cfa} gene in \textit{E. coli} was verified. \textit{cfa} transcripts were detected in \textit{E. coli} YYC1273/pMT1 (data not shown) by RT-PCR analysis. Moreover, primer extension analysis confirmed that the \textit{cfa} promoter of \textit{O. oeni} was recognized by the \textit{E. coli} transcriptional machinery (data not shown).

The viabilities of late-stationary-phase cultures of \textit{E. coli} strains exposed to ethanol shock (10\% v/v) and acid shock (pH 3.0) were measured. As previously described (Chang & Cronan, 1999; Grogan & Cronan, 1986), the \textit{E. coli} \textit{cfa}-deficient strain poorly survived ethanol or acid shock (Table 2). The control strains MG1655/pMT1 and YYC1273/pUC18 were also examined and no significant differences in percentage survival were noticed after

\begin{table}[h]
\centering
\begin{tabular}{|c|c|c|}
\hline
\textbf{E. coli strain} & \textbf{Survival (\%)} & \textbf{3 h after challenge*} \\
\hline
& 10\% (v/v) ethanol & pH 3.0 \\
\hline
MG1655 (wild-type) & 93.2 ± 7.7 & 70.6 ± 2.5 \\
YYC1273 (\textit{cfa}:: \textit{kan}) & 46.3 ± 5.2 & 11.0 ± 1.7 \\
YYC1273/pMT1 & 94.1 ± 11.5 & 43.3 ± 3.8 \\
\hline
\end{tabular}
\caption{Ethanol and acid survival of \textit{E. coli} strains}
\end{table}

\footnotesize{*Percentage survival was defined as [(c.f.u. ml^{-1} \times 3 h after challenge) / (c.f.u. ml^{-1} at \textit{t}_{0})] \times 100. The data represent the means ± SD of triplicate independent experiments.}
ethanol and acid shocks in comparison with strains MG1655 and YYC1273, respectively (data not shown). As shown in Table 2, pMT1 could complement the cfa-deficient strain of *E. coli* when cells were exposed to ethanol. However, the presence of pMT1 only partially restored the acid resistance observed in the wild-type strain.

Previous studies showed that *E. coli* strains carrying the *cfa::kan* mutation lacked detectable CFA synthase activity and made no CFA detectable by gas chromatography (Cronan *et al.*, 1974; Grogan & Cronan, 1986). So, to explore the capacity of the *O. oeni* CFA synthase to promote the cyclopropagation of double bonds of *E. coli* unsaturated fatty acids, the composition of membrane fatty acids of *E. coli* strains was analysed (Table 3). The analysis of fatty acid composition of the wild-type strain *E. coli* (MG1655) revealed the presence of myristic acid (C14:0), palmitic acid (C16:0), palmitoleic acid (C16:1) and *cis*-vaccenic acid (C18:1, n-7). We also noted the presence of CFAs such as cycC17:0 and lactobacillic acid (cycC19:0 n-7). Palmitic acid (C16:0) accounted for 58% of the total fatty acids identified whereas the monounsaturated fatty acid proportion was low (about 1%). The CFAs accounted for 31% of the total fatty acids identified; cycC17:0 alone accounted for more than 24% of the total. Consistent with previous reports, no CFA was detected in the *E. coli cfa*-deficient strain YYC1273 and the proportion of monounsaturated precursors was higher (41%) than in the wild-type strain (1%). Fatty acid analysis of the complemented strain YYC1273/pMT1 revealed a shift in the fatty acid composition of the cell membrane compared to the mutant strain. This result confirmed the capacity of the *O. oeni* CFA synthase to convert unsaturated fatty acids to CFAs in *E. coli*. However, the CFA level in the complemented strain (7%) was lower than that of the wild-type strain (31%). Thus, the incomplete restoration of acid resistance may be due to the deficiency of CFA in membranes of cells or to the modification of the unsaturated/saturated fatty acids ratio. Moreover, in contrast to the wild-type strain, the membrane of the complemented strain contained more cycC19:0 (n-7) than cycC17:0.

### DISCUSSION

In this study, we found that, like other bacteria, *O. oeni* produces CFAs at the beginning of the stationary phase. Moreover, we showed that environmental factors such as ethanol- and acid-growth conditions induce CFA synthesis. Biomembranes are the site of the primary contact of cells with their environment: the flexibility and the adaptation capability of the cells thus determine their survival ability. Membrane lipid and protein compositions are recognized as some of the main factors involved in stress tolerance (da Silveira *et al.*, 2003, 2004; Jones, 1989). Membrane lipid composition changes are induced in response to temperature, pH, solvents and other forms of stress (Dombek & Ingram, 1984; Gennis, 1989; Jones, 1989). In the present work, we observed significant increases in palmitic and dihydrosterculic acids in both ethanol- and acid-grown cells. According to the mechanisms for cyclopropane ring formation in membrane lipids proposed by Grogan & Cronan (1997), we can suggest that oleic and vaccenic acids would be converted into cyclopropane dihydrosterculic and lactobacillic acids, respectively. In *E. coli*, strains with high levels of CFAs survived acid shock much better than those with low CFA levels (Brown *et al.*, 1997). The cyclization of fatty acyl chains is generally considered a means of reducing membrane fluidity, thereby reducing proton permeability and preventing the penetration of undesirable molecules in order to adapt the cells to adverse conditions (Chang & Cronan, 1999; Cronan, 2002; Grogan & Cronan, 1997). Teixeira *et al.* (2002) observed an increase in the proportion of lactobacillic acid at the expense of *cis*-vaccenic acid in *O. oeni*. This increase protected *O. oeni* against the toxic effect of ethanol, balancing the increase in membrane fluidity normally

### Table 3. Effect of *cfa*-bearing plasmid pMT1 on *E. coli* fatty acid composition

<table>
<thead>
<tr>
<th>Fatty acid</th>
<th>MG1655 (wild-type)</th>
<th>YYC1273 (<em>cfa::kan</em>)</th>
<th>YYC1273/pMT1</th>
</tr>
</thead>
<tbody>
<tr>
<td>C14:0</td>
<td>9.1 ± 0.8</td>
<td>6.6 ± 0.3</td>
<td>7.8 ± 0.1</td>
</tr>
<tr>
<td>C16:0</td>
<td>58.2 ± 0.8</td>
<td>52.0 ± 1.9</td>
<td>53.9 ± 0.4</td>
</tr>
<tr>
<td>C16:1</td>
<td>0.4 ± 0.1</td>
<td>31.1 ± 1.9</td>
<td>27.5 ± 0.7</td>
</tr>
<tr>
<td>cycC17:0</td>
<td>24.1 ± 0.9</td>
<td>0</td>
<td>2.4 ± 0.7</td>
</tr>
<tr>
<td>C18:1 (n-7)</td>
<td>0.7 ± 0.4</td>
<td>10.3 ± 0.3</td>
<td>3.7 ± 0.5</td>
</tr>
<tr>
<td>cycC19:0 (n-7)</td>
<td>7.5 ± 0.6</td>
<td>0</td>
<td>4.7 ± 0.9</td>
</tr>
<tr>
<td>U/S ratio*</td>
<td>0.01</td>
<td>0.71</td>
<td>0.45</td>
</tr>
<tr>
<td>CFA conversion (%)†</td>
<td>96.7</td>
<td>0</td>
<td>18.5</td>
</tr>
</tbody>
</table>

*U/S ratio: unsaturated to saturated fatty acids ratio.
†Percentage conversion was calculated by the ratio (% CFA)/(% CFA + % monounsaturated fatty acid precursors).
The data represent the means ± SD of triplicate independent experiments.
attributed to ethanol. In our study, the increases in palmitic and dihydrosterculic acids led to an increased degree of fatty acid saturation in both ethanol- and acid-grown cells. It should be noted that da Silveira et al. (2003) observed an increase in the degree of unsaturation in cells grown with ethanol. However, in that work, CFAs were not detected. This discrepancy could reflect the variability among O. oeni strains, with other resistance mechanisms to the presence of ethanol as previously observed in E. coli (Ingram, 1976) and Saccharomyces cerevisiae (Swan & Watson, 1997).

We cloned a cfa gene, predicted to encode a CFA synthase, from O. oeni. To understand the mechanisms involved in the conversion of monounsaturated fatty acids to CFAs in stationary-phase or in stress-grown cells, we quantified the mRNA of the cfa gene in O. oeni at two phases of growth in optimal conditions (exponential and stationary phases) and in cells grown in the presence of ethanol (8 %, v/v) and at low pH (pH 3.5). The increased amounts of cfa mRNA transcripts correlated with the increased amount of CFA in the membrane and suggest that the expression of this gene could be regulated at the transcriptional level as previously described in E. coli (Chang & Cronan, 1999). The E. coli cfa gene is controlled by the σ^7 factor, which governs the general stress response to a number of environmental stimuli, including starvation, acid shock or osmotic stress. In L. lactis, the expression of cfa is induced by acidity as well as during entry into the stationary phase of growth (Budin-Verneuil et al., 2005). The mechanism involved in the control of cfa expression has not yet been elucidated. In C. acetobutylicum, Zhao et al. (2003) identified a marR homologous gene preceding cfa whose overexpression resulted in reduced CFA accumulation in cell membranes. The majority of MarR protein family members are transcriptional repressors. So, the cfa gene of C. acetobutylicum could be controlled by the product of the marR-like gene. Analysis of the O. oeni cfa promoter did not identify a putative −35 hexamer at an appropriate distance from the putative −10 hexamer that was identified. Nevertheless, a supplementary sequence element, 5′-TG-3′, is located one base upstream of the −10 hexamer. A number of activator-independent promoters have been reported where specific −35 hexamer contacts are not required for transcription initiation (Barné et al., 1997). Transcription initiation at these promoters is dependent on an ‘extended’ −10 element, 5′-TGTATAAT-3′, which appears to create alternative contact points for the σ subunit of RNA polymerase. In O. oeni ATCC BAA-1163, the ORF downstream of cfa (locus tag OENO6_64047 vs OOE1175 in O. oeni PSU-1), transcribed divergently, encodes a putative transcriptional regulator similar to LysR family members. This ORF could constitute a potential transcriptional regulator of cfa. Future studies will focus on the characterization of this gene.

No genetic tool adapted to carry out gene inactivation in O. oeni is yet available. In order to confirm the functionality of the O. oeni cfa gene, complementation experiments with an E. coli cfa-deficient mutant were conducted. The presence of CFAs significantly increased stress tolerance of the complemented strain in comparison to the cfa-deficient strain. The complemented strain totally recovered its viability after ethanol shock, whereas its viability was only partly recovered for acid shock. These results suggest that the stabilizing effect of CFAs on cell membranes could differ depending on the nature of the shock. Kim et al. (2005) suggested that the incomplete restoration of acid resistance they observed in S. typhimurium might have been due to a deficiency of unsaturated fatty acids (UFAs) in the cell membrane due to the overexpression of CFA synthase. We considered this hypothesis for O. oeni. Nevertheless, our results suggest that the complementation in our experiments remained partial because the percentage conversion of UFAs into CFAs of the complemented strain was much lower than that of the wild-type strain. This could be explained by several factors. (i) The CFA synthase level was too low for a total conversion of UFAs into CFAs. The reduced level of CFA synthase could be caused by the expression of a heterologous gene in E. coli cells. (ii) Another explanation could be linked to substrate specificity. In the E. coli mutant strain complemented with the O. oeni cfa gene, the major CFA of the membrane was lactobacilliacidic (cycC19:0 n-7) whereas the major membrane CFA of the wild-type E. coli strain was cycC17:0. We did not detect the presence of cycC17:0 in the O. oeni membrane. Its unsaturated fatty acid precursor (C16:1) was converted preferentially into the corresponding saturated fatty acid (C16:0), most probably by a saturase enzyme. It is noteworthy that cycC19:0 was the major CFA in the O. oeni membrane; it could account for 25% of membrane fatty acids of O. oeni cells cultured under stress conditions. In contrast, cycC17:0 was the major CFA in E. coli; most palmitoleic acid (C16:1) was cyclized into cycC17:0 (Brown et al., 1997). We detected two CFAs in O. oeni (cycC19:0 and cycC17:0), of which cycC19:0 accounted for the major part. In spite of the high proportion of C16:1, only a low amount of cycC17:0 was produced by the O. oeni CFA synthase. The prevalence of cycC19:0 in the membrane of the complemented strain could be due to a higher affinity of the O. oeni enzyme for its natural substrate.

This study demonstrates clearly the functionality of the cfa gene and suggests that it is regulated at the transcriptional level. Further investigation is needed in order to identify the regulators involved. The substrate specificity of the CFA synthase in O. oeni also needs to be elucidated.

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