



UNIVERSITÀ DEGLI STUDI DI TORINO

AperTO - Archivio Istituzionale Open Access dell'Università di Torino

Starmerella bacillaris and Saccharomyces cerevisiae mixed fermentations to reduce ethanol content in wine

This is the author's manuscript Original Citation: Availability: This version is available http://hdl.handle.net/2318/1565180 since 2018-01-04T12:43:20Z Published version: DOI:10.1007/s00253-016-7413-z Terms of use: Open Access Anyone can freely access the full text of works made available as "Open Access". Works made available under a Creative Commons license can be used according to the terms and conditions of said license. Use of all other works requires consent of the right holder (author or publisher) if not exempted from copyright protection by the applicable law.

(Article begins on next page)





This is the author's final version of the contribution published as:

Vasileios Englezos, Starmerella bacillaris and Saccharomyces cerevisiae mixed fermentations to reduce ethanol content in wine, APPLIED MICROBIOLOGY AND BIOTECHNOLOGY,100, 2016, 5515-5526, 10.1007/s00253-016-7413-z

The publisher's version is available at: https://link.springer.com/article/10.1007/s00253-016-7413-z

When citing, please refer to the published version.

Link to this full text: http://hdl.handle.net/10.1007/s00253-016-7413-z

This full text was downloaded from iris-Aperto: https://iris.unito.it/

iris-AperTO

University of Turin's Institutional Research Information System and Open Access Institutional Repository

1	Starmerella bacillaris and Saccharomyces cerevisiae mixed fermentations to
2	reduce ethanol content in wine
3	
4	Vasileios Englezos', Kalliopi Rantsiou', Francesco Cravero', Fabrizio Torchio', Anne Ortiz-
5 6	Julien [°] , Vincenzo Gerbi [°] , Luca Rolle [°] , Luca Cocolin [°] .
7	¹ University of Torino, Dipartimento di Scienze Agrarie, Forestali e Alimentari, Agricultural
8	Microbiology and Food Technology Sector, Largo Paolo Braccini 2, 10095 Grugliasco,
9	Torino, Italy.
10	
11	² Istituto di Enologia e Ingegneria Agro-Alimentare, Università Cattolica del Sacro Cuore, Via
12	Emilia Parmense 84, 29122 Piacenza, Italy.
13	
14	³ Lallemand SAS, Blagnac, France.
15	
16	*Corresponding author: Luca Cocolin
17	Email: lucasimone.cocolin@unito.it.
18	
19	
20	
21	
21	
22	
23	
24	
25	
26	
27	
28	
20	
<i></i> }	
30	

31 Abstract

Decreasing the ethanol content in wine is a current challenge, mainly due to the global climate change and to the consumer preference for wines from grapes with increased maturity. In this study, a central composite design and response surface methodology approach was used to investigate the potential application of *Starmerella bacillaris* (synonym Candida zemplinina) in combination with Saccharomyces cerevisiae, in mixed (co-inoculated and sequential) cultures, to understand better the mechanism of co-habitation and achieve the objective of reducing the ethanol in wines. Laboratory scale fermentations demonstrated a decrease up to 0.7 % (v/v) of ethanol and an increase of about 4.2 g/L of glycerol when S. cerevisiae was inoculated with a delay of 48 h with respect to the inoculation of Starm. bacillaris. Pilot scale fermentations, carried out in winemaking conditions, confirmed the laboratory results. This study demonstrates that the combination of strains and inoculation protocol could help to reduce the ethanol content in wines. Keywords Non-Saccharomyces yeast; Starmerella bacillaris; Central Composite Design; Response Surface Methodology; Ethanol content reduction.

64 Introduction

65

66 In the last 20 years, there has been an increasing global attention for ethanol content in wines, 67 influenced mainly by the media and the government programs, due to the marketing, social 68 and health associated reasons (Saliba et al. 2013). Wine consumption, in light to moderate 69 amounts (1-2 glass of wine per day), has been well demonstrated to be beneficial for the 70 human health (German and Walzem 2000; Yoo et al. 2010). In opposition, high levels of 71 ethanol consumption and irregular drinking has been shown to be casually correlated with 72 more than sixty different medical conditions (Room et al. 2005). The production of well-73 structured and full bodied red wines nowadays, is more difficult than previously thought, 74 especially in warm climate wine regions (Jones et al. 2005). Usually, winemakers in order to 75 achieve the optimum phenolic maturation and tannin concentration, necessary for the quality 76 of these wines, postpone the harvest time, which results in a high, to excessive, sugar 77 concentration in the over ripe grapes (Mira de Orduňa 2010). As a consequence, the 78 excessive sugar content could be translated to wines with elevated levels of ethanol, 79 increasing the perception of bitterness, hotness and decreasing the perception of some wine aromas and flavour attributes (Goldner et al., 2009). 80

81 Facing the climate change, human health and the constant growing demand for full 82 bodied red wines, it is important to anticipate further increase. In this way, several 83 technological approaches have been proposed, to reduce ethanol content in wine (Pickering 84 2000), ranging mainly from pre-fermentation (selection of grapevine clones and vineyard 85 management) to post-fermentation approaches (spinning cone column, reverse osmosis etc.), 86 which however, could increase the production costs and affect negatively wine quality 87 (Pickering 2000). One the other hand, in recent years intervening on the yeast ecology during 88 must fermentation is gaining more attention and this is carried out mainly by decreasing the 89 sugar-ethanol yield transformation through the selection of wine yeasts (Contreras et al. 90 2015; Gobbi et al. 2014; Quirós et al. 2014). For non-Saccharomyces yeasts, the quantity of 91 sugar used to produce 1 % (v/v) of ethanol is higher (17.0 - 40.0 g/L) (Englezos et al. 2015; 92 Magyar and Tóth 2011) due to their ability to utilize the carbon to produce biomass and by-93 products. As a consequence, through their metabolism ethanol concentration does not 94 increase (Contreras et al. 2014; Contreras et al. 2015ab; Gobbi et al. 2015; Gonzalez et al. 95 2013; Morales et al. 2015; Quiros et al. 2014).

Among, the non-*Saccharomyces* species of oenological interest, *Starmerella bacillaris* (synonym *Candida zemplinina*) (Duarte et al. 2012) is considered as one of the

98 most promising species to achieve the objective described above. S. bacillaris is supposed to 99 be one of the best candidates, due to its ability to produce less ethanol from sugar consumed, 100 tolerate high concentrations of ethanol present in the wine and produce low levels of biogenic amines (Englezos et al. 2015; Magyar and Tóth 2011; Rantsiou et al. 2012; Suzzi et al. 2012; 101 102 Tristezza et al. 2013). These phenotypic characteristics support the potential use of this wine 103 yeast, in combination with S. cerevisiae either in co-inoculated or sequential inoculated 104 fermentations to reduce the potential ethanol content in wine (Giaramida et al. 2013; Gonzalez et al. 2013; Masneuf-Pomarede et al. 2015). However, strain selection and 105 106 establishment of inoculation protocols are essential in order to moderate yeast growth and 107 produce wines with the aspects described above.

In this context, the aim of this study was to understand the appropriate time of *S. cerevisiae* addition after *S. bacillaris* inoculation in order to achieve a high level of ethanol reduction. A central composite design (CCD) and response surface methodology approach (RSM) was used for this final goal, in order to optimize and find the appropriate inoculation protocol.

113

114 Materials and methods

115

116 Yeast strains

117

Two S. bacillaris (FC54 and C.z 03) and one S. cerevisiae (ScBa49) isolate were obtained 118 119 from the Yeast Culture Collection of the DISAFA (Dipartimento di Scienze Agrarie, 120 Forestali e Alimentari University of Torino, Italy). S. bacillaris MUT 5705 came from the Mycotheca Universitatis Taurinensis - MUT (DBIOS - University of Torino, Italy), while a 121 commercial S. cerevisiae wine yeast Uvaferm BC[®] (Lallemand SA, Montreal, Canada) was 122 123 used as a reference strain (Table 1). S. bacillaris strains were selected for their physiological 124 and enological performance (Englezos et al. 2015) and routinely cultivated on YPD slants (1% yeast extract, 2% bacteriological peptone, 2% glucose and 2% agar, all w/v) or stored at 125 126 -80 °C in YPD broth supplemented with 20% glycerol (Sigma, Milano, Italy).

127

128 Wine fermentations

129

130 Laboratory scale fermentations

Grape must of Barbera cultivar (Vitis vinifera L.) without the grape skin was obtained from 132 the experimental winery of the University of Torino. Grape must contained 233.2 g/L sugars 133 (116.4 g/L glucose, 116.8 g/L fructose), titratable acidity 8.20 g/L (expressed as tartaric acid), 134 135 pH 3.20 and absence of ethanol. The initial Yeast Available Nitrogen (YAN) was 197 mg/L 136 composed by the sum of 116 mg/L of AUG (ammonium + urea + L-arginine) and 81 mg/L of 137 PAN (primary amino nitrogen). The must was pasteurized in a water bath at 60°C for 1 hour 138 and the sterility was checked by plating 100 µL of must on WL Nutrient Agar medium (Biogenetics, Milano, Italy) and incubated them at 28 °C for 5 days. Under sterile conditions, 139 140 25 mL of the pasteurized must was distributed onto 50 mL tubes with loose screw cap for all 141 the fermentations performed in this work.

142

143 Pure fermentations

144

The oenological performance of the three S. bacillaris and two S. cerevisiae strains was 145 146 evaluated by micro-vinification trials in pure culture fermentations. The inoculum of the five 147 veast strains was prepared by pre-adaptation of the strains in the same must as described 148 above for 48 hours at 25 °C. Afterwards, the yeast cells were stained with methylene blue dye 149 and immediately the viable cell population was counted by using a Thoma hemocytometer 150 chamber (BRAND GMBH + CO KG, Wertheim, Germany). Before inoculation, appropriate 151 amounts of inoculum were calculated and subsequently used to inoculate the musts at an initial cell population of 1.0×10^6 cells/mL. All the fermentations were carried out in 152 duplicate under static conditions at 25 °C for 21 days. 153

- 154
- 155 Central Composite Design
- 156

157 Two factorial CCD were used to understand the appropriate experimental plan to model the delay of S. cerevisiae inoculation and the sampling time for the chemical analyses during the 158 159 fermentation period, as previously described by Torchio et al. (2011). A matrix was 160 generated with two factors, delay of S. cerevisiae inoculation (hours) and time of chemical 161 analyses (days of fermentation) at five levels (- α , -1, 0, +1, + α), where α was equal to 1.41 162 factorial units. The corresponding values were calculated in the decoded matrix based on the 163 limit of the design $-\alpha$ and $+\alpha$. In this study, it was decided that 0 (co-inoculation) and 48h 164 (sequential inoculation) delay would be the extreme values of the S. cerevisiae addition and 0 165 and 21 days for the time of chemical analyses (Table S1 in the Supplementary Material).

166

167 After running Response Surface Methodology (RSM), a second-order polynomial regression168 equation was fitted to the subsequent equation:

169

170 $Y = b_0 + b_1X_1 + b_2X_2 + b_{11}X_1^2 + b_{22}X_2^2 + b_{12}X_1X_2$

171

172 Where, Y is the predicted response of the dependent variable, X_1 (inoculation delay) and X_2 173 (sampling time) are the independent variables that correspond to the response of Y, b_0 is the 174 value in the central point conditions, b_1 and b_2 represent the linear regression coefficient 175 associated with each variable, b_{11} and b_{22} are the quadratic regression coefficient of each 176 independent value, while b_{12} is the regression coefficient of the interaction effect between the 177 two variables. The second-order polynomial equations used to generate the surface curves are 178 presented in Supplementary Material (Table S2 in the Supplementary Material).

179

180 Mixed fermentations

181

182 Mixed fermentations were carried out by inoculating the three S. bacillaris and two S. cerevisiae strains in combination, according to the X1 of CCD pattern. Five inoculation 183 184 strategies were carried out: inoculation of the two species simultaneously (co-inoculation) 185 and addition of the S. cerevisiae at 7, 24, 41 and 48 hours after S. bacillaris inoculation 186 (sequential inoculation). In each case, the musts were inoculated with 48 hours pre-adapted cultures grown in the same must, with the same cell relative density of 1:1 as described above 187 188 for the pure cultures. Fermentations were carried out in duplicate under static conditions at 25 189 °C for 21 days.

190

191 Pilot-scale fermentations

192

Fermentations were performed in 2-hL stainless-steel fermenters with Barbera grape, at the experimental winery of the University of Torino. The must composition was as follows: 250.4 g/L of sugars (126.1 g/L glucose, 124.3 g/L fructose), titratable acidity 10.21 g/L (expressed as tartaric acid), pH 3.09, total sulphur dioxide 20 mg/L. The initial YAN was 145 mg/L composed by the sum of 55 mg/L of AUG and 90 mg/L of PAN. The best performing couple and inoculation strategy according to the laboratory fermentations were selected for these trials: a pure culture fermentation of *S. cerevisiae* Uvaferm BC[®] was used as control

and a sequential mixed culture which S. cerevisiae Uvaferm BC[®] was inoculated with 48 200 hours delay after S. bacillaris MUT 5705 inoculation. Both strains were inoculated with an 201 initial cell population of 1.0×10^6 cells/mL as described above for the laboratory scale trials. 202 203 Fermentations were performed in duplicate at 25 ± 2 °C. Must was pumped up twice a day 204 and racking was carried out when residual sugars were less than 2 g/L. Malolactic fermentation was carried at 20 °C in stainless steel tanks, by inoculating the commercial 205 Oenococcus oeni Lalvin VP41[®] strain (Lallemand SA, Montreal, Canada), according the 206 207 manufacturer's instructions. At the end of the malolactic fermentation, wines were clarified, 208 supplemented with 50 mg/L of total SO₂ and then bottled and subjected to chemical analysis.

209

210 Microbiological and molecular analysis

211

212 Samples were collected in duplicate at 0, 1, 2, 4, 7, 14 and 21 days from the beginning of fermentation, serially diluted in Ringer's solution (Oxoid, Milan, Italy) and plated on WL 213 214 Nutrient Agar medium (Biogenetics). Plates were incubated at 28 °C for 5 days and the two 215 types of colonies were differentiated visually as described previously (Rantsiou et al. 2012) 216 and subsequently counted. The enumeration of non-Saccharomyces yeasts in the pilot-scale 217 fermentations was carried out using lysine agar medium (Oxoid, Milan, Italy). Concerning 218 pilot-scale trials, 5 putative colonies of S. bacillaris and S. cerevisiae from each sampling 219 point (30 for each ferment), were isolated and then subjected to molecular characterization by 220 Rep and interdelta-PCR, as suggested by Englezos et al. (2015) and Charpentier et al. (2002) 221 respectively, in order to understand strain dynamics over the fermentation process.

- 222
- 223 Chemical analysis
- 224

Ethanol, glycerol, acetic acid production, as well as the glucose and fructose consumption were determined by HPLC using an Agilent 1260 Infinity HPLC apparatus (Milford, MA, USA) as described by Rolle et al. (2012). The concentration of total YAN was determined by using two enzymatic kits (Megazyme International, Wicklow, Ireland) following the kit manufacturer instructions. In particular, total YAN concentration was calculated by the sum of ammonium, urea and L-arginine (AUG) and the concentration of the primary amino nitrogen (PAN).

- 232
- 233 Statistical analyses

234

The data obtained from the different inoculation strategies, were subjected to one-way analysis of variance (ANOVA) by using the statistical software package IBM SPSS Statistics (version 21.0. IBM Corp., Armonk. NY, USA). The ANOVA analysis was coupled by the Duncan test (p < 0.05), in order to evaluate the significant differences between the data obtained.

The RSM was performed with the statistical software STATISTICATM, program version 10.0 (StatSoft Inc. Tulsa, USA) to evaluate the results obtained by the CCD pattern applied. The regression models were performed only with R^2 values greater than 0.8 indicating that the variability could be explained by the second-order model equations.

244

245 **Results**

246

- 247 Laboratory scale fermentations
- 248
- 249 Growth dynamics
- 250

The growth dynamics of the *S. bacillaris* and *S. cerevisiae* strains when inoculated in pure cultures in Barbera must are presented in Fig. 1. The five strains grew similarly and reached a cell population of about 10^8 colony forming units (CFU)/mL on the second day of fermentation. On the seventh day, viable cell population started to decrease and no *S. bacillaris* population was observed at the last sampling point (<10 CFU/mL on WLN medium plates), while populations of the *S. cerevisiae* strains (ScBa49 and Uvaferm BC[®]) ranged from 10^6 to 10^7 CFU/mL, respectively.

258 In Fig. 2 the growth dynamics of the mixed fermentations with S. cerevisiae ScBa49 259 are illustrated. In the co-inoculated and sequential fermentation (7 hours delay), all S. bacillaris and S. cerevisiae couples showed comparable growth dynamics, reaching a 260 population of 10^7 to 10^8 CFU/mL in 2 days. Through the rest of the fermentation, S. 261 cerevisiae ScBa49 maintained this counts, while S. bacillaris populations started to decrease. 262 263 When the other three inoculation strategies (24, 41 and 48 hours delay) were carried out, all 264 S. bacillaris strains used in this study competed with S. cerevisiae ScBa49 during the first 7 days of fermentation. After this day, S. bacillaris started to decrease and the population 265 266 became undetectable (<10 CFU/mL on WLN medium plates) after 14 (24 hours delay) and 267 21 days (41 and 48 hours delay), while the viability of the *S. cerevisiae* cells remained stable 268 at 10^6 to 10^7 CFU/mL throughout the whole fermentation process.

269 The population dynamics for the mixed fermentations with S. cerevisiae Uvaferm BC[®] are shown in Fig. 3. Population dynamics within the first four days of fermentation, for 270 271 the co-inoculated and sequential inoculated trials (7 hours delay), were comparable to those 272 observed for *S. cerevisiae* ScBa49. Afterwards, the population of *S. cerevisiae* Uvaferm BC[®] started to decrease, with counts that ranged from 10^5 to 10^6 CFU/mL at the end of the 273 monitored period (21 days), in contrast with the S. cerevisiae ScBa49 population that 274 275 remained stable during all the monitored period. Interestingly, sequential inoculations with 276 the highest delay (24, 41 and 48 hours), showed similar population dynamics as for the 277 couples previously tested.

278

279 Chemical composition of the wines

280

281 The mean concentration of sugars, glycerol, organic acids and ethanol in the must and wines 282 obtained from the pure cultures of S. bacillaris and S. cerevisiae, after 21 days of 283 fermentation, are presented in Table 2. S. bacillaris in pure cultures produced partially 284 fermented wines with significant presence of residual sugars (up to 32.6 g/L glucose), while 285 the fructose was totally consumed (<1.0 g/L). Complete fermentation of the sugars was 286 observed only for S. cerevisiae strains in pure cultures. The chemical composition of these wines was characterized from the presence of lower levels of glycerol (7.8 - 8.3 g/L) and 287 higher levels of ethanol (13.8 - 14.0) % (v/v) compared to S. bacillaris pure cultures. 288 289 Compared to wines produced with S. cerevisiae in pure culture, wines fermented with S. 290 bacillaris presented significantly higher glycerol yields and lower potential ethanol 291 concentrations.

292 The chemical composition of the wines produced from mixed fermentations carried out with S. cerevisiae strains ScBa49 and Uvaferm BC[®] are presented in Tables 3 and 4, 293 294 respectively. In mixed fermentations with ScBa49, the five different inoculation protocols 295 resulted in a different consumption of sugars. As it can be seen, inoculation delay up to 7 296 hours, always allowed consumption of all sugars (< 2.9 g/L) from the must at day 21, 297 regardless of the S. bacillaris strain used. On the contrary, inoculation delays of 24, 41 and 298 48 hours, always performed poorly, leaving significant higher quantities of sugars (14.1 – 27.6 g/L), mainly glucose. A different behaviour was observed for the Uvaferm BC® 299

300 commercial strain, since all couples fermented all the sugars from the must (< 3.9 g/L) after 301 21 days from the beginning of fermentation, independently of the inoculation delay applied.

- 302 The glycerol production was also influenced by time of S. cerevisiae addition and the sampling time (Table 4). Compared to wines produced by *S. cerevisiae* Uvaferm BC[®] in pure 303 304 culture, wines produced by mixed yeast species contained more glycerol. In particular, with a 305 delay of 48 hours the glycerol content of the wines increased up to 4.2 g/L (Table 4). The 306 modeling of glycerol production with RSM reflects that its increase is correlated with the 307 increase of the inoculation delay of S. cerevisiae. The production of this metabolite was linearly increased when S. cerevisiae yeast strain Uvaferm BC[®] was inoculated in the first 24 308 hours (R²=0.985) after S. bacillaris addition. Conversely, minor differences were found by 309 increasing the sequential inoculation between 24 and 48 hours. Acetic acid production, was 310 311 also influenced by the inoculation strategy, however all the couples tested in this study 312 maintained values at levels lower than 0.50 g/L.
- 313 Regarding ethanol production, in sequentially inoculated fermentations, only the couple S. bacillaris MUT 5705 and S. cerevisiae Uvaferm BC[®] produced wine with 0.7 % 314 (v/v) less ethanol compared to S. cerevisiae Uvaferm BC[®] in pure culture (Tab. 4). In this 315 316 case, the must was initially inoculated with S. bacillaris followed by S. cerevisiae after 24, 41 317 and 48 hours. Additionally, an interesting observation was the increasing quantity of sugars 318 (g/L) consumed by these couples to produce 1% (v/v) of ethanol, with the increase of 319 inoculation delay. This was particularly evident when the inoculation delay moved to 48 320 hours, highlighting the contribution of S. bacillaris to the ethanol reduction. For all the 321 couples tested, the shape of the surface curves (Fig. 4, right panel) also confirmed this trend, 322 indicating a significant linear decrease of the ethanol content when S. cerevisiae was 323 inoculated with a delay of minimum 4 hours. However, this decrease was improved with the 324 inoculation delay, with a maximum value at 48 hours (maximum monitored). Taking in 325 consideration these findings and the results from growth dynamics, we hypothesized that the 326 most suitable protocol able to reduce the ethanol at industrial scale could be the sequential 327 inoculation with 48 hours delay. This is also in line with previous studies, in which 328 indigenous S. cerevisiae started to grow after 2 days from S. bacillaris inoculation 329 (Giaramida et al. 2013). Extended delays were not tested because considered not applicable 330 in real wine-making settings.
- 331
- 332 Pilot-scale fermentations
- 333

334 In order to validate the results obtained at laboratory scale, the best performing couple (MUT 5705 and Uvaferm BC[®]) and the inoculation strategy of 48 h delay were selected to ferment 335 Barbera must at pilot-scale fermentations at 25 °C. Pure fermentation with Uvaferm BC[®] was 336 used as control. Both inoculation rates and procedures were as close as possible to laboratory 337 338 scale fermentations, in order to obtain a better reproducibility. Molecular typing of S. bacillaris and S. cerevisiae isolates by Rep and interdelta-PCR amplification respectively, 339 340 revealed that these fermentations were guided by the inoculated strains (data not shown). The cell population of Uvaferm $BC^{\mathbb{R}}$ in pure culture reached a concentration of about 10^8 341 CFU/mL on the second day, which was maintained to these levels during the whole 342 343 fermentation period (Fig. S1 in the Supplemental Material, panel a). Indigenous non-Saccharomyces veasts were detected at concentration of $10^5 - 10^6$ CFU/mL during the first 344 two days, after which they rapidly decreased to undetectable levels (< 10 colonies on lysine 345 medium) on the fourth day. In addition, wild S. bacillaris strains, which were determined to 346 347 be different from the inoculated MUT 5706 by Rep-PCR profiling, were found in the must at concentrations up to 10⁶ CFU/mL during the first four days, after this point a remarkable 348 decrease of cell population was observed. When S. cerevisiae Uvaferm BC[®] was inoculated 349 with 48 hours delay after S. bacillaris MUT 5705 inoculation (Fig. S1 in the Supplemental 350 Material, panel b), Uvaferm BC[®] cell population was affected by MUT 5705 and it was not 351 able to reach counts of 10⁸ CFU/mL. This allowed MUT 5705 to maintain relative high cell 352 population (about $10^6 - 10^7$ CFU/mL) until the seventh day of fermentation. The same pattern 353 was seen for the non-Saccharomyces during the first four days, afterwards rapidly decreased 354 355 to undetectable levels.

356 The chemical composition of the wines produced from the pilot-scale fermentation is given in Table 5. Sequential fermentations consumed sugars slower than Uvaferm BC[®] in 357 pure culture (10 days vs 7 days). The wine produced from sequential inoculation contained 358 significantly more glycerol (13.4 g/L vs 12.0 g/L) than Uvaferm BC[®], while the ethanol 359 360 content was reduced by 0.5 % (v/v). On the contrary, acetic acid production after malolactic fermentation for the sequential inoculation was reduced compared to that observed for 361 Uvaferm BC[®] (0.34 g/L vs 0.47 g/L). A significant increase of 0.5 in total acidity was seen 362 363 for the sequentially inoculated wine, with a parallel decrease of pH.

364

365 **Discussion**

One possible approach to reduce the ethanol content of wines is by fine-tuning yeast ecology 367 368 during must fermentation. The selection and use of non-Saccharomyces wine yeasts can 369 potentially lead to a reduction of the overall sugar-ethanol yield during alcoholic 370 fermentation. In the study presented here, the possibility of using S. bacillaris in combination 371 with S. cerevisiae was investigated in order to regulate the ethanol production in a must with 372 a high initial sugar concentration (233.2 g/L). In order to find the appropriate time of S. 373 cerevisiae addition after S. bacillaris inoculation, a CCD approach was selected to model the 374 chemical composition of the wine produced with particular attention on the ethanol and 375 glycerol concentration. With RSM, several combinations of S. bacillaris/S. cerevisiae at 376 different inoculation times were tested simultaneously with a small number of experiments 377 able to generate large amounts of information, according to the CCD experiment plan, which 378 permits to uncover interactions between variables (Bezerra et al. 2008).

379 In pure fermentations, S. bacillaris strains produced wines with residual sugars, composed exclusively by glucose, confirming the preference of this species for fructose 380 381 (Englezos et al. 2015; Magyar and Tóth 2011). The impact of this non-Saccharomyces yeast 382 on the chemical composition of the wine was evident with a higher production of glycerol, in 383 agreement with previous studies (Englezos et al. 2015; Magyar and Tóth 2011; Magyar et al. 384 2014), higher amounts of sugars used to produce 1% of alcohol and slightly higher 385 production of acetic acid compared to the S. cerevisiae strains, in accordance with previous 386 studies (Sadoudi et al. 2012; Soden et al. 2000).

387 When mixed fermentation trials were performed, the co-inoculation of the two species 388 did not show a significant reduction of ethanol content and the chemical composition of these 389 wines was very similar to the control wines produced by the S. cerevisiae strains in pure 390 cultures. This behavior is confirming the high competitive ability of S. cerevisiae over non-391 Saccharomyces yeast cells, probably due to the depletion of nutrients present in the must, 392 cell-to-cell contact-mediated mechanisms or due to the production of toxic metabolites 393 (Andorrà et al. 2010; Nissen et al. 2003; Pérez-Nevado et al. 2006) and underlines the need to 394 understand better the mechanism of this co-habitation.

In this context, the early growth of *S. bacillaris* in the sequential inoculations with the highest delays (24, 41 and 48 hours) limited the subsequent growth of the two *S. cerevisiae* strains. One possible explanation for this behaviour is that *S. bacillaris* decreased the nutrient concentration by subtracting large quantities of organic nitrogen from the must (data not shown) (Andorrà et al. 2010; Medina et al. 2012). Indeed, since only the Uvaferm $BC^{\ensuremath{\mathbb{R}}}$ commercial strain totally consumed the sugars in these fermentations, it can be hypothesized that this strain has probably lower demands in nutrients (e.g. nitrogen) compared to ScBa49
wild strain. These results suggest that nutrient concentration and strain selection have a
fundamental role on the fermentation rate of the mixed fermentations with *S. bacillaris* and *S. cerevisiae*.

405 Sequential fermentations performed with the strain Uvaferm $BC^{\text{(B)}}$, changed positively 406 the chemical composition of the wines produced, especially in terms of glycerol. Glycerol 407 production was influenced by the time of *S. cerevisiae* addition and the sampling time (Table 408 4). The higher concentration of glycerol is in agreement with previous studies (Giaramida et 409 al. 2013; Suzzi et al. 2012),.

410 Interestingly, the inoculation delay changed dramatically the sugar to ethanol 411 conversion rate of alcoholic fermentation. More specifically, in the sequentially inoculated 412 fermentations, yeasts consumed more sugars to produce 1.0 % (v/v) of ethanol, compared to *S. cerevisiae* Uvaferm BC[®] in pure culture highlighting the impact of *S. bacillaris* for ethanol 413 reduction (Bely et al. 2013; Englezos et al. 2015; Giaramida et al. 2013). However, the 414 results revealed that only the couple MUT 5705 and Uvaferm BC[®] sequentially inoculated 415 416 with a minimum of 24 hours delay was able to consume up to 17.5 g/L of sugars to produce 417 1.0% of ethanol, while the official European Economic Community (EEC) ethanol 418 conversion factor is 16.83 g/L (Ribéreau Gayon et al. 2006). The coefficient of determination (R²) was 0.88 indicating a good correlation between the inoculation delay and fermentation 419 420 efficiency (g/L of sugar used for 1 % v/v ethanol production).

421 These results let us to hypothesize that S. bacillaris diverts carbon derived from the 422 glycolytic pathway away from ethanol production to the synthesis of biomass and production 423 of by-products, in order to maintain intracellular NADH/NAD+ redox balance ensuring 424 continuous operation of the metabolic processes. These products include glycerol, 425 monocarboxylic (acetic acid and pyruvic acid), dicarboxylic (succinic acid and α -ketoglutaric 426 acid) and tricarboxylic acids (citric acid and isocitric acid), and aroma volatile compounds 427 (van Dijken and Scheffers 1986). The overproduction of titratable acidity observed in the 428 pilot scale sequential fermentation could result from the swift of carbon flux towards organic 429 acid production, since S. bacillaris is considered high producer of α -ketoglutaric acid and 430 pyruvic acid (Magyar et al. 2014; Mangani et al. 2011).

In order to confirm laboratory scale fermentations, the best performing couple (MUT 5705 and Uvaferm $BC^{(R)}$) and inoculation strategy (48 hours delay) were used to ferment Barbera must in pilot scale fermentations. The presence and dominance of the inoculated yeast strains was confirmed using Rep-PCR and interdelta PCR amplification for the *S*.

bacillaris and S. cerevisiae, in order to exclude contributions of indigenous strains. Pilot-435 436 scale results confirmed the findings observed in laboratory settings, with the only exception 437 of acetic acid production, which was registered to be higher in pure culture fermentation. The 438 effect of MUT 5705 on wine composition was apparent. As in the laboratory scale 439 fermentation, production of glycerol was higher in the sequential trial than in pure culture 440 fermentation, while ethanol production showed a significant reduction. The pH was also 441 lower and the titratable acidity higher, for wine produced from sequential than this produced 442 from pure culture fermentation.

443 In summary, this study presents a fermentation protocol tested under both laboratory 444 and pilot scale conditions to reduce ethanol levels in wines. This protocol is based on the inoculation of the grape must with S. bacillaris MUT 5705 and S. cerevisiae Uvaferm BC® 445 446 after 48 hour from the beginning of the fermentation. Furthermore, the exploitation of this 447 inoculation protocol could be further investigated using other varieties of grape musts, in 448 order to understand the impact of the co-habitation of these species to wine composition in 449 terms of aroma and flavour. In the future, the decrease of ethanol as described here, could 450 help winemakers to decide the appropriate time to harvest their grapes, without the risk of 451 excessive sugar content, which can be converted in high levels of ethanol in wine.

452

Acknowledgments This work was funded by the (FP7/2007-2013) under grant agreement no. 315065 – WILDWINE (www.wildwine.eu). The information in this document reflects only the author's views and the Community is not liable for any use that may be made of the information contained herein.

- 457
- 458 **Compliance with ethical standards**
- 459

460 **Conflict of interest** The authors declare that there is no conflict of interest.

461

462 Ethical approval <u>This paper does not contain any studies with human participants or</u>
463 <u>animals.</u>

464

```
465 References
```

<sup>Andorrà I, Berradre M, Rozès N, Mas A, Guillamón JM, Esteve-Zarzoso B (2010) Effect of pure and mixed
cultures of the main wine yeast species on grape must fermentations. Eur Food Res Technol 231:215-224.
doi:10.1007/s00217-010-1272-0</sup>

- Bely M, Renault P, Da Silva T, Masneuf-Pomerade I, Albertin W, Moine V, Coulon J, Sicard D, De Vienne D,
 Marullo P (2013) Non-conventional yeasts and alcohol level reduction. In: Teissedre PL (eds) Alcohol level
 reduction in wine. Vigne et Vin Publications Internationales, France, pp 33-37
- Bezerra MA, Santelli RE, Oliveira EP, Villar LS, Escaleria LA (2008) Response surface methodology (RSM)
 as a tool for optimization in analytical chemistry. Talanta 76:965-977. doi:10.1016/j.talanta.2008.05.019
- 475 Charpentier C, Colin A, Alais A, Legras JL (2009) French Jura flor yeasts: genotype and technological
 476 diversity. Antoine van Leeuwenhoek 95: 263-273. doi: 10.1007/s10482-009-9309-8
- 477 Contreras A, Hidalgo C, Henschke PA, Chambers PJ, Curtin C, Varela C (2014) Evaluation of non478 *Saccharomyces* yeasts for the reduction of alcohol content in wine. Appl Environ Microbiol 80:1670-1678.
 479 doi: 10.1128/AEM.03780-13
- 480 Contreras A, Curtin C, Varela C (2015a) Yeast population dynamics reveal a potential "collaboration" between
 481 *Metschnikowia pulcherrima* and *Saccharomyces uvarum* for the production of reduced alcohol wines
 482 during Shiraz fermentation. Appl Microbiol Biotechnol 99:1885–1895. doi: 10.1007/s00253-014-6193-6
- 483 Contreras A, Hidalgo C, Schmidt S, Henschke PA, Curtin C, Varela C (2015b) The application of non484 Saccharomyces yeast in fermentations with limited aeration as a strategy for the production of wine with
 485 reduced alcohol content. Int J Food Microbiol 205:7-15. doi: 10.1016/j.ijfoodmicro.2015.03.027
- 486 Duarte FL, Pimentel NH, Teixeira A, Fonseca, Á (2012) Saccharomyces bacillaris is not a synonym of C.
 487 stellata: reinstatement as Starmerella bacillaris comb. nov. Antonie van Leeuwenhoek 102:653–658.
 488 doi:10.1007/s10482-012-9762-7
- 489 Englezos V, Rantsiou K, Torchio F, Rolle L, Gerbi V, Cocolin L (2015) Exploitation of the non-490 Saccharomyces yeast Starmerella bacillaris (synonym Candida zemplinina) in wine fermentation: 491 Physiological and molecular characterizations. Int J Food Microbiol 199:33-40. 492 doi:10.1016/j.ijfoodmicro.2015.01.009
- 493 German JB, Walzem RL (2000) The health benefits of the wine. Annu Rev Nutr 20:561-593.
 494 doi:10.1146/annurev.nutr.20.1.561
- Giaramida P, Ponticello G, Di Maio S, Squadrito M, Genna G, Barone E, Scacco A, Corona O, Amore G, Di
 Stefano R, Oliva D (2013) *Candida zemplinina* for production of wines with less alcohol and more
 glycerol. S Afr J Enol Vitic 34:204-211
- Gobbi M, De Vero L, Solieri L, Comitini F, Oro L, Giudici L, Ciani M (2014) Fermentative aptitude of
 non- Saccharomyces wine yeast for reduction in the ethanol content in wine. Eur Food Res Technol
 239:41-48. doi:10.1007/s00217-014-2187-y
- Goldner MC, Zamora MC, Di Leo Lira P, Gianninoto H, Bandoni A (2009) Effect of ethanol level in the
 perception of aroma attributes and the detection of volatile compounds in red wine. J Sens Stud 24:243-257.
 doi: 10.1111/j.1745-459X.2009.00208.x
- Gonzalez R, Quirós M, Morales P (2013) Yeast respiration of sugars by non-Saccharomyces yeast species: A
 promising and barely explored approach to lowering alcohol content of wines. Trends Food Sci Technol
 29:55-61. doi:10.1016/j.tifs.2012.06.015
- 507 Jones GV, White MA, Cooper OR, Storchmann K (2005) Climate change and global wine quality. Clim 508 Change 73:319-343. doi:10.1007/s10584-005-4704-2
- 509 Magyar I, Tóth T (2011) Comparative evaluation of some oenological properties in wine strains of Candida

- 510 stellata, Candida zemplinina, Saccharomyces uvarum and Saccharomyces cerevisiae. Food Microbiol
- 511 28:94-100. doi:10.1016/j.fm.2010.08.011
- Magyar I, Nyitrai-Sárdy D, Leskó A, Pomázi A, Kállay M (2014) Anaerobic organic acid metabolism of
 Candida zemplinina in comparison with *Saccharomyces* wine yeasts. Int J Food Microbiol 178:1-6.
 doi:10.1016/j.ijfoodmicro.2014.03.002
- Mangani S, Buscioni G, Collina L, Bocci E, Vincenzini M (2011) Effects of microbial populations on
 anthocyanin profile of Sangiovese wines produced in Tuscany, Italy. Am J Enol Vitic 62:487-494. doi:
 10.5344/ajev.2011.11047
- Masneuf-Pomarede I, Juquin E, Miot-Sertier C, Renault P, Laizet Y, Salin F, Alexandre H, Capozzi V, Cocolin
 L, Colonna-Ceccaldi B, Englezos V, Girard P, Gonzalez B, Lucas P, Mas A, Nisiotou A, Sipiczki M, Spano
- G, Tassou C, Bely M, Albertin W (2015) The yeast *Starmerella bacillaris* (synonym *Candida zemplinina*)
 shows high genetic diversity in winemaking environments. FEMS Yeast Res 15:fov045. doi: 10.1093/femsyr/fov045
- Medina K, Boido E, Dellacassa E, Carrau F (2012) Growth of non-*Saccharomyces* yeasts affects nutrient
 availability for *Saccharomyces cerevisiae* during wine fermentation. Int J Food Microbiol 157:245-250.
 doi:10.1016/j.ijfoodmicro.2012.05.012
- Mira de Orduňa R (2010) Climate change associated effects on grape and wine quality and production. Food
 Res Int 43:1844-1855. doi:10.1016/j.foodres.2010.05.001
- Morales P, Rojas V, Quirós M, Gonzalez R (2015) The impact of oxygen on the final alcohol content of wine
 fermented by a mixed starter culture. Appl Microbiol Biotechnol 99:3993-4003. doi: 10.1007/s00253-014 6321-3
- Nissen P, Nielsen D, Arneborg N (2003) Viable Saccharomyces cerevisiae cells at high concentrations cause
 early growth arrest of non-Saccharomyces yeasts in mixed cultures by a cell-cell contact-mediated
 mechanism. Yeast 20:331-341. doi:10.1002/yea.965
- Pérez-Nevado F, Albergaria H, Hogg T, Girio F (2006) Cellular death of two non-*Saccharomyces* wine-related
 yeasts during mixed fermentation with *Saccharomyces cerevisiae*. Int J Food Microbiol 108:336-345.
 doi:10.1016/j.ijfoodmicro.2005.12.012
- 537 Pickering GJ (2000) Low-and reduced-alcohol wine: a review. J Wine Res 11:129-144. doi:
 538 10.1080/09571260020001575
- Quirós M, Rojas V, Gonzalez R, Morales P (2014) Selection of non-*Saccharomyces* yeast strains for reducing
 alcohol levels in wine by sugar respiration. Int J Food Microbiol 181:85-91. doi:
 10.1016/j.ijfoodmicro.2014.04.024
- Rantsiou K, Dolci P, Giacosa S, Torchio F, Tofalo R, Torriani S, Suzzi G, Rolle L, Cocolin L (2012) *Candida zemplinina* can reduce acetic acid production by *Saccharomyces cerevisiae* in sweet wine fermentations.
 Appl Environ Microbiol 78:1987-1994. doi:10.1128/AEM.06768-11
- Ribéreau Gayon P, Dubourdieu D, Donèche B, Lonvaud A (2006) The microbiology of wine and vinifications.
 Handbook of enology, vol. 1, 2nd edn. Wiley, Chichester, England
- 547 Rolle L, Giordano M, Giacosa S, Vincenzi S, Río Segade S, Torchio F, Perrone B, Gerbi V (2012) CIEL*a*b*
- 548 parameters of white dehydrated grapes as quality markers according to chemical composition, volatile
- 549 profile and mechanical properties. Anal Chim Acta 732:105-112. doi:10.1016/j.aca.2011.11.043

- Room R, Babor T, Rehm J (2005) Alcohol and public health. The Lancet 365:519-30. doi: 10.1016/S0140 6736(05)17870-2
- Sadoudi M, Tourdot-Maréchal R, Rousseaux S, Steyer D, Gallardo-Chacón J, Ballester J, Vichi S, Guérin Schneider R, Caixach J, Alexandre H (2012) Yeast-yeast interactions revealed by aromatic profile analysis
 of Sauvignon Blanc wine fermented by single or co-culture of non-*Saccharomyces* and *Saccharomyces*
- 555 yeasts. Food Microbiol 32: 243-253. doi: 10.1016/j.fm.2012.06.006
- Saliba AJ, Ovington LA, Moren CC (2013) Consumer demand for low-alcohol wine in an Australian sample.
 Int J Wine Res 5:1-8. http://dx.doi.org/10.2147/IJWR.S41448
- Soden A, Francis IL, Oakey H, Henschke, PA (2000) Effects of co-fermentation with *Candida stellata* and
 Saccharomyces cerevisiae on the aroma and composition of Chardonnay wine. Wine Aust J Grape Wine
 Res 6:21-30. doi:10.1111/j.1755-0238.2000.tb00158.x
- Suzzi G, Schirone M, Sergi M, Marianella RM, Fasoli G, Aguzzi I, Tofalo R (2012) Multistarter from organic
 viticulture for red wine Montepulciano d'Abruzzo production. Front Microbiol 3:1-10.
 http://dx.doi.org/10.3389/fmicb.2012.00135
- Torchio F, Rio Segade S, Gerbi V, Cagnasso E, Rolle L (2011) Changes in chromatic characteristics and
 phenolic composition during winemaking and shelf-life of two types of red sweet sparkling wines. Food
 Res Int 44:729-738. doi:10.1016/j.foodres.2011.01.024
- Tristezza M, Vetrano C, Bleve G, Spano G, Capozzi V, Logrieco A, Mita G, Grieco F (2013) Biodiversity and
 safety aspects of yeast strains characterized from vineyards and spontaneous fermentations in the Apulia
 Region, Italy. Food Microbiol 36:335-342. doi: 10.1016/j.fm.2013.07.001
- Van Dijken JP, Scheffers WA (1986) Redox balances in the metabolism of sugars by yeasts. FEMS Microbiol
 Lett 32:199-224. DOI: 10.1111/j.1574-6968.1986.tb01194.x
- Yoo YJ, Saliba AJ, Prenzler PD (2010) Should red wine be considered a functional food? Comp Rev Food Sci
 Food Saf 5:530-551. doi:10.1111/j.1541-4337.2010.00125.x

Table 1 Strains used in this study

Strain	Species	Geographical region of isolation	Collection
FC54	S. bacillaris	Friuli Venezia Giulia (ITALY)	DISAFA
MUT 5705	S. bacillaris	Friuli Venezia Giulia (ITALY)	MUT ^a
C.z 03	S. bacillaris	Piedmont (ITALY)	DISAFA
ScBa49	S. cerevisiae	Piedmont (ITALY)	DISAFA
Uvaferm BC®	S. cerevisiae	France	LALLEMAND

^aMUT= Mycotheca Universitatis Taurinensis (DBIOS - University of Torino, Italy)

592 Table 2 Concentration of sugars, glycerol, organic acids and ethanol in the must and wines obtained from pure fermentations of S.

Treatment	Residual sugars (g/L)	Glucose (g/L)	Fructose (g/L)	Acetic acid (g/L)	Glycerol (g/L)	Ethanol (% v/v)	Fermentation efficiency ¹	Potential ethanol ² (% v/v)	Glycerol yield (g/L) ³
Must	233.2 ± 0.1	116.4 ± 0.1	116.8 ± 0.1	< 0.1	< 0.1	< 0.1	/	/	/
S. bacillaris									
FC54	$21.7\pm10.4^{\text{b}}$	21.5 ± 10.6	0.2 ± 0.2	0.40 ± 0.02	11.8 ± 0.8	12.1 ± 0.7	$18.1 \pm 0.7^{\circ}$	$13.4\pm0.0^{\rm a}$	$0.06\pm0.00^{\rm b}$
MUT 5705	$29.7\pm9.9^{\text{b}}$	29.7 ± 10.0	0.1 ± 0.1	0.41 ± 0.02	12.9 ± 0.3	12.0 ± 0.6	17.0 ± 0.1^{ab}	$13.7\pm0.0^{\rm b}$	$0.07\pm0.01^{\text{b}}$
C.z 03	32.6 ± 11.2^{b}	32.4 ± 11.4	0.2 ± 0.2	0.37 ± 0.03	12.6 ± 0.4	11.7 ± 0.7	17.1 ± 0.1^{b}	$13.7\pm0.0^{\rm b}$	$0.07\pm0.01^{\rm b}$
S. cerevisiae									
ScBa49	$1.0\pm0.2^{\mathrm{a}}$	0.3 ± 0.1	0.7 ± 0.0	0.26 ± 0.04	7.8 ± 0.1	13.8 ± 0.0	16.8 ± 0.0^{ab}	$13.9\pm0.0^{\circ}$	$0.03\pm0.00^{\text{a}}$
Uvaferm BC [®]	0.5 ± 0.1^{a}	0.1 ± 0.1	0.4 ± 0.0	0.14 ± 0.01	8.3 ± 0.3	14.0 ± 0.2	16.6 ± 0.2^{a}	$14.1\pm0.2^{\text{d}}$	$0.04\pm0.01^{\text{a}}$
Sig ⁴	***	/	/	/	/	/	***	***	***

593 *bacillaris* and *S. cerevisiae* strains

 1 Fermentation efficiency (sugars used to produce 1.0 % of ethanol (v/v)): initial and residual sugar concentrations were used to calculate

595 the fermentation efficiency

- ²Potential ethanol (% v/v) = ethanol produced + ((residual glucose + residual fructose) * 0.06)
- 3 Glycerol yield = glycerol produced / (initial sugar concentration final sugar concentration)
- 598 All data are expressed as average value \pm standard deviation (n = 2). Different superscript letters within the same column indicate
- 599 significant differences among the strains according to the Duncan test (p < 0.05)
- 600 ⁴Sig: *** indicate significance at p < 0.001

Table 3 Concentration of sugars, glycerol, organic acids and ethanol in the wines obtained from mixed fermentations using the S.

cerevisiae strain ScBa49

Strains and inoculation strategy	Residual sugars (g/L)	Glucose (g/L)	Fructose (g/L)	Acetic acid (g/L)	Glycerol (g/L)	Ethanol (% v/v)	Fermentation efficiency ¹
Pure fermentation ScBa49	$1.0\pm0.2^{aA\alpha}$	$0.3\pm0.1^{aA\alpha}$	0.7 ± 0.1	$0.26\pm0.05^{aA\alpha}$	$7.8\pm0.1^{aA\alpha}$	$13.8\pm0.1^{\rm bC\gamma}$	$16.6\pm0.3^{\rm A}$
Couple: FC54 and ScBa49							
Co-inoculation	$2.0\pm0.1^{\text{a}}$	$0.2\pm0.1^{\text{a}}$	1.7 ± 0.1	$0.34\pm0.02^{\rm b}$	$8.2\pm0.3^{\text{a}}$	$13.8\pm0.1^{\text{b}}$	16.6 ± 0.1
Inoculation delay: 7 h.	$2.4 \pm 1.4^{\mathrm{a}}$	$0.4\pm0.1^{\rm a}$	2.0 ± 1.3	$0.39\pm0.01^{\rm b}$	$9.6\pm0.3^{\rm b}$	$13.7\pm0.2^{\rm b}$	16.7 ± 0.2
Inoculation delay: 24 h.	$23.1\pm0.1^{\rm b}$	$22.6\pm0.9^{\text{b}}$	0.4 ± 0.1	$0.51\pm0.01^{\circ}$	$11.8 \pm 0.2^{\circ}$	$12.4\pm0.2^{\text{a}}$	16.8 ± 0.3
Inoculation delay: 41 h.	26.3 ± 7.9^{b}	26.2 ± 7.9^{b}	0.4 ± 0.1	$0.49\pm0.01^{\circ}$	$12.0 \pm 0.5^{\circ}$	$12.3\pm0.5^{\rm a}$	17.1 ± 0.1
Inoculation delay: 48 h.	$23.2\pm8.5^{\rm b}$	$23.2\pm8.5^{\text{b}}$	0.4 ± 0.1	$0.49\pm0.01^{\circ}$	$12.0 \pm 0.3^{\circ}$	$12.1\pm0.5^{\text{a}}$	17.1 ± 0.5
Sig ²	**	**	NS	* * *	***	**	NS
Couple: MUT 5705 and ScBa49							
Co-inoculation	$1.8\pm0.2^{\mathrm{A}}$	$0.3\pm0.1^{\rm A}$	1.5 ± 0.3	$0.32\pm0.06^{\rm AB}$	$8.5\pm0.2^{\rm B}$	$14.0\pm0.1^{\rm D}$	$16.4 \pm 0.1^{\text{A}}$
Inoculation delay: 7 h.	$2.9\pm0.1^{\rm A}$	$0.3\pm0.1^{\rm A}$	2.6 ± 0.1	$0.40\pm0.02^{\rm B}$	$9.5\pm0.1^{\rm C}$	$13.8 \pm 0.1^{\circ}$	$16.7\pm0.3^{\rm AB}$
Inoculation delay: 24 h.	$14.1 \pm 2.7^{\rm B}$	$13.5\pm2.9^{\rm B}$	0.5 ± 0.2	$0.50\pm0.01^{\rm C}$	$11.7\pm0.3^{\rm D}$	$12.8\pm0.1^{\rm B}$	$17.3\pm0.1^{\rm BC}$
Inoculation delay: 41 h.	$24.5 \pm 0.3^{\circ}$	$24.1 \pm 0.3^{\circ}$	0.4 ± 0.1	$0.51 \pm 0.01^{\circ}$	$12.2\pm0.1^{\mathrm{E}}$	$12.4 \pm 0.1^{\text{A}}$	$17.3\pm0.4^{\rm BC}$
Inoculation delay: 48 h.	27.6 ± 0.7^{D}	27.2 ± 0.1^{D}	0.6 ± 0.3	$0.51 \pm 0.05^{\circ}$	$12.8\pm0.1^{\rm F}$	12.3 ± 0.1^{A}	$17.5 \pm 0.2^{\circ}$
Sig ²	***	***	NS	**	***	***	*
Couple: C.z 03 and ScBa49							
Co-inoculation	0.9 ± 0.1^{lpha}	$0.3\pm0.1^{\alpha}$	0.7 ± 0.1	$0.34\pm0.02^{\beta}$	$8.5\pm0.1^{\beta}$	$13.9\pm0.2^{\gamma}$	16.8 ± 0.4
Inoculation delay: 7 h.	$1.3 \pm 0.1^{\alpha}$	$0.3\pm0.1^{\alpha}$	1.0 ± 0.1	$0.40\pm0.02^{\beta}$	$9.7\pm0.3^{\gamma}$	$13.8\pm0.1^{\gamma}$	16.7 ± 0.1
Inoculation delay: 24 h.	$20.0\pm1.4^{\beta}$	$19.6 \pm 1.4^{\beta}$	0.4 ± 0.1	$0.47\pm0.01^{\gamma}$	$12.5\pm0.2^{\delta}$	$12.6\pm0.1^{\beta}$	16.9 ± 0.3
Inoculation delay: 41 h.	$23.6 \pm 1.2^{\gamma}$	$23.6 \pm 1.2^{\gamma}$	0.4 ± 0.1	$0.49\pm0.01^{\gamma}$	$12.6\pm0.2^{\delta}$	$12.1 \pm 0.1^{\alpha}$	17.2 ± 0.1
Inoculation delay: 48 h.	$25.8\pm0.1^{\delta}$	$25.8\pm0.1^{\delta}$	0.4 ± 0.1	$0.47\pm0.02^{\gamma}$	$12.5\pm0.4^{\delta}$	$12.3 \pm 0.1^{\alpha}$	17.2 ± 0.1
Sig^2	***	***	NS	***	***	***	NS

605	fermentation efficiency
606	All data are expressed as average value \pm standard deviation (n = 2). Different superscript Latin, UPPER Latin and Greek letters within the
607	same column indicate significant differences among the couples FC54 and ScBa49, MUT 5705 and ScBa49 and C.z 03 and ScBa49
608	according to the Duncan test ($p < 0.05$) respectively
609	² Sig: *, **, *** and NS indicate significance at $p < 0.05$, $p < 0.01$, $p < 0.001$ and not significant respectively
610	
611	
612	
613	
614	
615	
616	
617	
618	
619	
620	

¹Fermentation efficiency (sugars used to produce 1.0 % of ethanol (v/v)): initial and residual sugar concentrations were used to calculate

604

Table 4 Mean concentration of sugars, glycerol, organic acids and ethanol in the wines obtained from mixed fermentations with the S.

cerevisiae strain Uvaferm $BC^{\mathbb{R}}$

Strains and inoculation strategy	Residual sugars (g/L)	Glucose (g/L)	Fructose (g/L)	Acetic acid (g/L)	Glycerol (g/L)	Ethanol (% v/v)	Fermentation efficiency ¹
Pure fermentation Uvaferm BC [®]	0.5 ± 0.1^{Aa}	$0.1\pm0.1^{\rm A\alpha}$	0.4 ± 0.1	$0.14\pm0.01^{aA\alpha}$	$8.3\pm0.3^{aA\alpha}$	$14.0\pm0.2^{\rm B}$	$16.6 \pm 0.2^{\text{A}}$
Couple: FC54 and Uvaferm BC [®]							
Co-inoculation	0.8 ± 0.1	0.4 ± 0.2	0.4 ± 0.1	0.19 ± 0.05^{a}	8.8 ± 0.1^{ab}	14.0 ± 0.1	16.6 ± 0.1
Inoculation delay: 7 h.	0.6 ± 0.1	0.2 ± 0.1	0.4 ± 0.1	$0.19\pm0.05^{\text{a}}$	$9.5\pm0.1^{\rm b}$	14.0 ± 0.2	16.7 ± 0.2
Inoculation delay: 24 h.	1.3 ± 0.6	1.0 ± 0.5	0.3 ± 0.1	$0.37\pm0.01^{\text{b}}$	$12.5\pm0.2^{\rm c}$	13.8 ± 0.3	16.8 ± 0.3
Inoculation delay: 41 h.	3.9 ± 2.5	3.6 ± 2.4	0.3 ± 0.1	$0.46\pm0.09^{\text{b}}$	$12.5\pm0.3^{\rm c}$	13.4 ± 0.2	17.1 ± 0.1
Inoculation delay: 48 h.	3.1 ± 1.9	2.8 ± 1.9	0.3 ± 0.1	$0.41\pm0.05^{\text{b}}$	$12.6\pm0.6^{\rm c}$	13.5 ± 0.3	17.0 ± 0.5
Sig ²	NS	NS	NS	**	***	NS	NS
Couple: MUT 5705 and Uvaferm BC^{\otimes}							
Co-inoculation	$0.7\pm0.1^{\rm AB}$	$0.2\pm0.1^{\rm A}$	0.5 ± 0.1	$0.19\pm0.05^{\rm A}$	$9.1\pm0.1^{\rm B}$	$14.1\pm0.1^{\rm B}$	$16.4\pm0.1^{\rm A}$
Inoculation delay: 7 h.	$0.6\pm0.1^{\rm A}$	$0.2\pm0.1^{\rm A}$	0.3 ± 0.1	$0.19\pm0.05^{\rm A}$	$9.9\pm0.1^{\rm C}$	$13.9\pm0.2^{\rm B}$	$16.7\pm0.3^{\rm AB}$
Inoculation delay: 24 h.	$0.8\pm0.2^{\rm AB}$	$0.5\pm0.2^{\rm AB}$	0.3 ± 0.1	$0.34\pm0.01^{\rm B}$	$12.5\pm0.2^{\rm D}$	$13.4\pm0.1^{\rm A}$	$17.3\pm0.1^{\rm BC}$
Inoculation delay: 41 h.	$1.7\pm0.4^{\mathrm{C}}$	$1.3 \pm 0.4^{\circ}$	0.4 ± 0.1	$0.42\pm0.03^{\rm B}$	$12.9\pm0.1^{\rm D}$	$13.4\pm0.3^{\rm A}$	$17.3\pm0.4^{\rm BC}$
Inoculation delay: 48 h.	$1.1\pm0.1^{\rm B}$	$0.9\pm0.0^{\rm B}$	0.3 ± 0.1	$0.42\pm0.04^{\rm B}$	$12.5\pm0.2^{\rm D}$	$13.3\pm0.1^{\rm A}$	$17.5 \pm 0.2^{\circ}$
Sig ²	**	**	NS	***	***	*	*
Couple: C.z 03 and Uvaferm $BC^{\mathbb{R}}$							
Co-inoculation	$0.7\pm0.1^{\beta}$	$0.2\pm0.1^{\alpha}$	0.5 ± 0.1	$0.17\pm0.05^{\alpha}$	$9.1\pm0.4^{\beta}$	13.9 ± 0.4	16.8 ± 0.4
Inoculation delay: 7 h.	$0.5\pm0.1^{\alpha}$	$0.2\pm0.1^{\alpha}$	0.4 ± 0.1	$0.19\pm0.04^{\alpha}$	$9.5\pm0.1^{\beta}$	13.9 ± 0.1	16.7 ± 0.1
Inoculation delay: 24 h.	$1.1\pm0.1^{\gamma}$	$0.7\pm0.1^{\beta}$	0.4 ± 0.1	$0.34\pm0.03^{\beta}$	$12.8\pm0.1^{\delta}$	13.7 ± 0.2	16.9 ± 0.3
Inoculation delay: 41 h.	$1.9\pm0.1^{\delta}$	$1.6\pm0.1^{\gamma}$	0.3 ± 0.1	$0.41\pm0.03^{\beta}$	$12.2\pm0.3^{\gamma\delta}$	13.5 ± 0.1	17.2 ± 0.1
Inoculation delay: 48 h.	$2.5\pm0.1^{\epsilon}$	$2.2\pm0.1^{\delta}$	0.3 ± 0.1	$0.40\pm0.01^{\beta}$	$12.0\pm0.2^{\gamma}$	13.4 ± 0.1	17.2 ± 0.1
Sig ²	***	***	NS	***	***	NS	NS

623	Fermentation efficiency:	(sugars used to produce	1.0 % of ethanol(v/v)): initial	and residual sugar concentrations	were used to calculate

624 fermentation efficiency

- 625 All data are expressed as average value \pm standard deviation (n = 2). Different superscript Latin, UPPER Latin and Greek letters within the
- 626 same column indicate significant differences among the couples FC54 and Uvaferm BC[®], MUT 5705 and Uvaferm BC[®] and C.z 03 and
- 627 Uvaferm BC[®] according to the Duncan test (p < 0.05) respectively

628 ²Sig: *, **, *** and NS indicate significance at p < 0.05, p < 0.01, p < 0.001 and not significant respectively

- - -

Table 5 Mean concentration of sugars, glycerol, organic acids and ethanol in the wines produced from pure (Uvaferm BC[®], control) and

643	sequential (MUT 5705 a	nd Uvaferm BC®) culture	fermentations at pilot scale (2hL)
-----	------------------------	-------------------------	------------------------------------

Parameter	Must	Control	Sequential	Sign ¹
Residual sugars (g/L)	250.4 ± 2.5	< 2.0	< 2.0	NS
Acetic acid (g/L)	< 0.1	0.47 ± 0.07	0.34 ± 0.04	**
Glycerol (g/L)	< 0.1	12.0 ± 0.4	13.4 ± 0.1	***
Ethanol (% v/v)	< 0.1	15.4 ± 0.0	14.9 ± 0.1	***
рН	3.09 ± 0.01	3.38 ± 0.00	3.35 ± 0.00	***
Titratable acidity (g/L)	10.21 ± 0.14	6.71 ± 0.04	7.18 ± 0.08	***

645 All data are expressed as average value \pm standard deviation (n = 2)

 1 Sig: **, *** and NS indicate significance at p < 0.01, p < 0.001 and not significant respectively, between control and sequential fermented

647 wines

- 650 Figures legends
- 651

Fig. 1 Growth dynamics of *S. bacillaris* (A) and *S. cerevisiae* (B) strains in pure cultures. *S. bacillaris* strains: FC54 (- \circ -), MUT 5705 (- \diamond -), C.z 03 (- \Box -) and *S. cerevisiae* strains: ScBa49 (- \diamond -) and Uvaferm BC[®] (- \diamond -). Counts are the mean CFU/mL values ± standard deviations of two independent experiments

656

Fig. 2 Growth dynamics of mixed fermentations performed with the three *S. bacillaris* strains and the *S. cerevisiae* strain ScBa49. *S. bacillaris/S. cerevisiae* couples: FC54 (- \circ -), ScBa49 (- \bullet -), MUT 5705 (- \diamond -) and ScBa49 (- \bullet -), C.z 03 (- \Box -) and ScBa49 (- \blacksquare -). Counts are the mean CFU/mL values \pm standard deviations of two independent experiments. The arrow indicates the *S. cerevisiae* inoculation

662

Fig. 3 Growth dynamics of mixed fermentations performed with the three *S. bacillaris* strains and the *S. cerevisiae* strain Uvaferm $BC^{\mathbb{R}}$. *S. bacillaris/S. cerevisiae* couples : FC54 (- \circ -) and Uvaferm $BC^{\mathbb{R}}$ (- \bullet -), MUT 5705 (- \diamond -) and Uvaferm $BC^{\mathbb{R}}$ (- \bullet -), C.z 03 (- \Box -) and Uvaferm $BC^{\mathbb{R}}$ (- \blacksquare -). Counts are the mean CFU/mL values \pm standard deviations of two independent experiments. The arrow indicates the *S. cerevisiae* inoculation

668

Fig. 4 Response surface curves fitted to experimental data points corresponding to the
glycerol (g/L) (left panel) and ethanol (% v/v) (right panel) production as a function of *S. cerevisiae* inoculation and time of the chemical analyses. *S. bacillaris/S. cerevisiae*couples: FC54 and Uvaferm BC[®] (panel A), MUT 5705 and Uvaferm BC[®] (panel B),
C.z 03 and Uvaferm BC[®] (panel C).

- 674
- 675
- 676
- 677
- 678
- 679
- 680
- 681

682 Fig.1





699 Fig. 2





702 Fig.3









10.00

Children (RV)







С



Experiments	Inoculation delay (hours)	Chemical analyses (days)	Inoculation delay (hours)	Chemical analyses (days)
1	-1	-1	7	3.0
2	1	-1	41	3.0
3	-1	1	7	18.0
4	1	1	41	18.0
5	-1.41	0	0	10.5
6	1.41	0	48	10.5
/ 8	0	-1.41	24	0.0
0 9-13	0	0	24	10.5

Table S1 Matrix used for the CCD analysis

733 Table S2. Second-order polynomial regression equations used to generate the surface

	Chemical compounds	Couples	\mathbf{b}_0	\mathbf{b}_1	b ₂	b ₁₁	b ₂₂	b ₁₂
•	•	FC54 and Uvaferm BC®	-4.941	0.2513	1.849	-5.217E-03	-6.280E-02	3.900E-03
	Glycerol	MUT 5705 and Uvaferm BC®	-4.767	0.2443	1.781	-5.167E-03	-6.036E-02	5.390E-03
		C.z03 and Uvaferm BC®	-4.941	0.2513	1.849	-5.217E-03	-6.281E-02	3.929E-03
		FC54 and Uvaferm BC®	3.238	-0.1163	1.563	7.870E-04	-4.892E-02	1.111E-03
	Ethanol	MUT 5705 and Uvaferm BC®	2.398	-0.0506	1.701	-4.563E-04	-5.708E-02	2.460E-03
725		C.z03 and Uvaterm BC®	2.256	-0.0301	1.721	-7.940E-04	-5.922E-02	2.939E-03
735								
/36								
737								
738								
739								
740								
741								
742								
743								
744								
745								
746								
740								
747								
748								
/49								
750								
751								
752								
753								
754								
755								
756								
757								

734 curves for the three couples of *S. bacillaris* and *S. cerevisiae*.

759 FigS1.



760

Fig. S1 Growth dynamics of yeast during pilot scale fermentations. (a) Control culture fermentation, (b) Sequential fermentation. *S. bacillaris* (- \circ -), *S. cerevisiae* (- \bullet -) and indigenous non-*Saccharomyces* yeasts (- \diamond -). Counts are the mean CFU/mL values ± standard deviations of two independent experiments. The arrow indicates the *S. cerevisiae* inoculation