

1 **Impact of the timing and the nature of nitrogen additions on the production kinetics of**
2 **fermentative aromas by *Saccharomyces cerevisiae* during winemaking fermentation in**
3 **synthetic media**

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19

20 Abstract

21 During alcoholic fermentation, many parameters, including the nitrogen composition of the
22 must, can affect aroma production. The aim of this study was to examine the impact of several
23 types of nitrogen sources added at different times during fermentation. Nitrogen was added as
24 ammonium or a mixture of amino acids at the beginning of fermentation or at the start of the
25 stationary phase. These conditions were tested with two *Saccharomyces cerevisiae* strains that
26 have different nitrogen requirements. The additions systematically reduced the fermentation
27 duration. The aroma production was impacted by both the timing of the addition and the
28 composition of the nitrogen source. Propanol appeared to be a metabolic marker of the
29 presence of assimilable nitrogen in the must. The production of ethyl esters was slightly
30 higher after the addition of any type of nitrogen; the production of higher alcohols other than
31 propanol was unchanged, and acetate esters were overproduced due to the overexpression of
32 the genes *ATF1* and *ATF2*. Finally the parameter affecting the most the synthesis of beneficial
33 aromas was the addition timing: The supply of organic nitrogen at the beginning of the
34 stationary phase was more favorable for the synthesis of beneficial aromas.

36 Keywords

37 Wine fermentation; aroma compounds; nitrogen; alcohol acetyltransferase; online monitoring;
38 *Saccharomyces cerevisiae*

39

40 1. Introduction

41 Currently, the market offers a wide variety of wines. The main characteristic to discriminate
42 these wines is their sensorial profile constituted by wine aromas (Swiegers et al., 2005;
43 Ugliano et al., 2010). One of the main challenges for wine producers is to control the wine
44 aromatic profile to meet consumer expectations. Among the different volatile molecules
45 involved in wine organoleptic properties, fermentative aromas – generated by the yeast
46 secondary metabolism during alcoholic fermentation – have been identified to be involved in
47 the fruity flavor (Ugliano et al., 2010). Their production depends on many parameters such as
48 the yeast strain (Lambrechts and Pretorius, 2000; Manginot et al., 1998), the must
49 composition in lipids (Rollero et al., 2016; Saerens et al., 2008), the assimilable nitrogen
50 (Barbosa et al., 2012; Hernandez-Orte et al., 2006; Vilanova et al., 2007), or the fermentation
51 temperature (Molina et al., 2007; Mouret et al., 2014b; Rollero et al., 2015).

52 The nitrogen composition of the must is highly important for aroma synthesis (Swiegers et al.,
53 2005). It has been shown that adding nitrogen to must with a low nitrogen content increases
54 the production of higher alcohols (Barbosa et al., 2009). However, when the assimilable
55 nitrogen concentration exceeds 200 to 300 mgN/L, the production of higher alcohols
56 decreases (Mouret et al., 2014b; Vilanova et al., 2007). Propanol does not have the same
57 behavior as the other higher alcohols. Its production is proportional to the initial amount of
58 nitrogen (Mouret et al., 2014b). Finally, the concentration of acetate esters and ethyl esters
59 increases with the initial quantity of assimilable nitrogen (Hernandez-Orte et al., 2006; Torrea
60 et al., 2011).

61 The effects observed after nitrogen addition in the stationary phase differ depending on the
62 studies, probably because of the use of different fermentation conditions. For example,
63 Hernandez-Orte et al. (2006) showed that addition at mid-fermentation had no significant
64 impact on the production of higher alcohols but led to greater increases in the production of

65 esters than addition at the beginning of the process. In contrast, Jiménez-Martí et al. (2007)
66 observed a decrease in higher alcohol production after addition during the stationary phase,
67 but there was no effect on the production of acetate esters.

68 The effect of the type of nitrogen on aroma production also depends on the yeast strain and
69 fermentation conditions. Webster et al. (1993) demonstrated that addition of amino acids led
70 to an increased production of higher alcohols compared to addition of ammonium, but
71 Barbosa et al. (2012) found that isoamyl alcohol production is higher when ammonium is
72 added. Contradictory observations were also observed for acetate and ethyl esters (Barbosa et
73 al., 2012; Torrea et al., 2011), indicating that no simple relationship can be established
74 between the nature of the nitrogen supply and the production of esters. It is thus difficult to
75 draw conclusions on the effect of nitrogen addition on aroma production, and much remains
76 unknown about the impact of nitrogen on yeast metabolism.

77 The aim of this study was to fully characterize the impact of nitrogen addition on the
78 formation of volatile compounds during alcoholic fermentation by utilizing innovative
79 strategies such as the online monitoring of aroma production. We studied two types of
80 nitrogen: ammonium and amino acids. The additions were made either at the beginning of
81 fermentation or at the start of the stationary phase. We also investigated the impact of these
82 additions on the metabolic pathways of the aroma production and their regulation.

83 Understanding the impact of nitrogen on the metabolism of *S. cerevisiae* in alcoholic
84 fermentation allows better management of this nutrient to produce volatile compounds.

85

86 **2. Materials & Methods**

87 2.1. Yeast strains

88 The *S. cerevisiae* yeast strains used in this study are the commercial strains Lalvin EC1118®
89 and Lalvin CY3079® (Lallemand SA, Montreal, Canada). These two strains have different

90 nitrogen requirements, with Lalvin EC1118® requiring less nitrogen than Lalvin CY3079®.
91 Fermentation tanks were inoculated with 10 g/hL active dry yeast previously rehydrated for
92 30 minutes at 37°C in a 50 g/L glucose solution (1 g of dry yeast diluted in 10 mL of this
93 solution).

94

95 2.2. Fermentation media

96 Fermentation was carried out in synthetic medium (SM) that simulates standard grape juice
97 (Bely et al., 1990). The SM used in this study contained 200 g/L of sugar (100 g/L of glucose
98 and 100 g/L of fructose). The concentrations of weak acids, salts and vitamins were identical
99 to those described by Rollero et al. (2016). The pH of the medium was adjusted to 3.3 with 10
100 M NaOH.

101 The must contained 100 mg/L of assimilable nitrogen. The nitrogen source was composed of
102 ammonium chloride and amino acids. The composition of the stock solution of amino acids
103 was the same to that described by Rollero et al. (2016).

104 The SM medium was initially supplemented with 2 mg/L of phytosterols (85451, Sigma
105 Aldrich) to satisfy the lipid requirements of yeast cells during anaerobic growth. The stock
106 solution was the same to the one described by Rollero et al. (2016).

107 Different types of nitrogen were added to this synthetic must: di-ammonium phosphate (DAP)
108 or a mixture of amino acids to a concentration of 70 mg N/L. These additions were performed
109 initially or during the stationary phase (at 85 g/L of consumed sugar).

110

111 2.3. Fermentation conditions

112 Fermentations were carried out in 10 L stainless steel tanks at 24°C. The amount of CO₂
113 released was measured accurately and automatically with a gas mass flow meter to calculate

114 the rate of CO₂ production (dCO₂/dt). Anaerobiosis was obtained by bubbling argon into the
115 medium.

116 Each fermentation was performed once. However, we previously determined that experiments
117 conducted with this online monitoring system yield highly reproducible results (Mouret et al.,
118 2012; Mouret et al., 2014b).

119 For the quantitative PCR, fermentations were achieved in 1 L fermenters at 24°C in triplicate.

120 As described by Rollero (2015), fermenters of 1 L and 10 L were designed to allow scale-up
121 without any effect on the outcome of fermentation. The fermenters were equipped with
122 fermentation locks to maintain anaerobiosis with continuous magnetic stirring (500 rpm). The
123 CO₂ release was followed by automatic measurement of fermenter weight loss every 20
124 minutes. The rate of CO₂ production was calculated by polynomial smoothing of the last ten
125 values of CO₂ production. The frequent acquisition of CO₂ release values and highly precise
126 bioreactor weighing enabled accurate CO₂ production rates to be calculated with good
127 reproducibility and a small variation coefficient: $(dCO_2/dt)_{max} = 0.8\%$ (Bely et al., 1990).

129 2.4. Cell population

130 During fermentation, the cell population was determined by using a Coulter counter (Model
131 Z2, Beckman-Coulter, Margency, France) fitted with a 100 µm aperture probe.

133 2.5. Measurement of assimilable nitrogen

134 The ammonium concentration was determined enzymatically (R-Biopharm, Darmstadt,
135 Germany).

136 The free amino acid content of the must was determined by cation exchange chromatography
137 with post-column ninhydrin derivatization (Biochrom 30, Biochrom, Cambridge, UK) as
138 described by Crepin et al. (2012).

139

140 2.6. Analysis of volatile compounds

141 The concentrations of volatile compounds in the headspace of the tank were measured with an
142 online GC device. Headspace gas was pumped from the tank at a flow rate of 14 mL/min
143 through a heated transfer line. Carbon compounds were concentrated in a cold trap (Tenax
144 TM) for 6 minutes, desorbed at 160°C for 1 minute, and analyzed with a Perichrom PR2100
145 GC coupled to a flame ionization detector (Alpha MOS, Toulouse, France). The GC method
146 and the calibration procedure were performed as described previously by Mouret et al. (2014a
147 and b).

148 The results are expressed as total production, representing the sum of the concentration
149 measured in the gas phase and the concentration in the liquid phase as described by Mouret et
150 al. (2014a and b). The total production value represents the capability of the yeast to produce
151 a volatile compound, independently of whether the subsequent fate of this compound was
152 accumulation in the liquid phase or evaporation.

153 2.7. Data processing and statistical analyses

154 Statistical analysis was performed with R software, version 3.1.1.

155 We obtained two datasets in which each variable of interest is a curve along time (h) that we
156 expressed in terms of consumed sugar (g/L). We chose to summarize these two datasets by
157 modeling each curve with an adequate model and then extracting criteria of interest.

158 First, for each condition, the biomass was modeled with a Weibull model using the drc
159 package (Ritz and Streibig, 2005). The four-parameter Weibull model is written as follows:

160

$$161 \quad f(x) = c + (d - c) \left[1 - \exp^{-\exp^{[b(\ln(x) - \ln(e))]}]} \right] \quad (\text{Equation 1})$$

162

163 This four-parameter ascending function is asymmetric with an inflection point at time e . For
164 each modeled function, we extracted several criteria of interest: μ_{max} , defined as the
165 maximum of the ratio $f'(t)/f(t)$ for each t expressed in h^{-1} , the inflection point, expressed in
166 terms of consumed sugar g/L , and the maximum biomass, expressed in 10^6 cells.
167 For this parametric model, the normality of residual distributions and homogeneity of
168 variance were studied with standard diagnostic graphs. No violation of the assumptions was
169 detected.
170 Each volatile compound under each condition was then modeled with a non-parametric model
171 using the cellGrowth package (Gagneur and Neudecker, 2012). The model used is a local
172 regression and allows for the extraction of the inflection point expressed in consumed sugar
173 (g/L), the maximal production in mg/L and the maximal rate (maximum of the first derivative
174 in $mg/L/h$). To calculate the specific rate, we divided the first derivative of the model (the
175 rate) by the population as estimated above.
176 To provide an overview of the dataset, principal component analysis (PCA) was carried out
177 with the FactoMineR package (Le et al., 2008).

178

179 2.8. RNA extraction

180 For each fermentation condition, 1×10^9 cells were harvested by centrifugation at 1,000g for
181 5 min at 4 °C. The cell pellets were washed with DEPC-treated water and then frozen in
182 methanol at -80 °C. Total RNA was extracted with the TRIzol reagent (Gibco BRL, Life
183 Technologies) and purified with an RNeasy kit (Qiagen).

184

185 2.9. Retro-transcription

186 First-strand cDNA was synthesized using 0.5 μg of total RNA by priming with an oligo(dT)
187 anchor at 42 °C for 50 min using Superscript-II reverse transcriptase (Invitrogen) according to
188 the manufacturer's instructions.

189 2.10. Primers and quantitative PCR

190 All of the primers were designed using Primer 3 software. The amplification efficiency was
191 calculated using the dilution method (Rasmussen, 2001). A description of the genes, primers,
192 and efficiencies are shown in Table 1.

193 Real-time PCR was performed in 96-well plates on an Applied Biosystems 7300 instrument
194 (Applied Biosystems, Foster City, CA, USA) using SYBR Green as the fluorophore.

195 Reactions were carried out in a 20 μ L volume that contained 5 μ L of cDNA, 3 μ M forward
196 and reverse primers, and 12.5 μ L of 2x Power SYBR Green PCR Master Mix. Each sample
197 was analyzed in triplicate, and a no-template control for each primer was included in all real-
198 time plates. Amplifications were performed under the following conditions: 50 °C for 2 min,
199 95 °C for 10 min, 40 cycles of 95 °C for 10 s, and 60 °C for 1 min. At the end of the
200 amplification cycle, a melting analysis was carried out to verify the absence of non-specific
201 amplification. The expression level of a given gene was reported as the quantification cycle
202 (Cq), corresponding to the number of cycles required to reach the pre-determined threshold
203 fluorescence. The threshold values were obtained using the automated setting of the
204 instrument software (baseline subtracted curve fit data). The data, expressed as Cq, were
205 imported into a Microsoft Excel data sheet for subsequent analysis.

207 2.11. Analysis of target genes

208 The expression of two target genes, *ATF1* and *ATF2*, was analyzed (Table 1). The genes were
209 chosen for their involvement in the conversion of higher alcohols into acetate esters. The
210 relative quantification of the mRNA was performed by normalizing the expression value
211 transformed in relative copy numbers (obtained from Cq values and considering the
212 efficiency) to the geometric mean of the value of a reporter gene. The reporter gene was
213 *SCR1*, a structural component of the signal recognition particle (Hann and Walter, 1991). In

214 the calculation of the relative copy number from raw Cq, amplification efficiencies were
215 considered.

216

217 **3. Results and discussion**

218 We investigated the impact of the addition of 70 mg/L of YAN on the fermentation kinetics
219 and on the main volatile compound production. We tested two different sources of nitrogen: a
220 mineral source as di-ammonium phosphate (DAP) and an organic one in the form of an amino
221 acid mixture. Additions were performed either at the beginning of fermentation or at the start
222 of the stationary phase (approximately 85 g/L of sugar consumed). The fermentative kinetic
223 and the production rate of eight aroma compounds were monitored online. These compounds
224 are propanol, isoamyl alcohol, isobutanol, isoamyl acetate, isobutyl acetate, ethyl acetate,
225 ethyl hexanoate, and ethyl octanoate.

226 The nitrogen and sugars were exhausted at the end of all of the fermentations. Final
227 concentrations of ethanol, glycerol and acetate were identical for all the conditions (data not
228 shown).

229

230 3.1. Effect of nitrogen addition on the fermentation kinetics

231 We compared the impact of different additions of nitrogen on the fermentation kinetics
232 (Figure 1).

233 The length of the lag phase was not impacted by the nitrogen content of the medium. In
234 addition, the growth phases of the fermentations in which nitrogen was added in the stationary
235 phase were the same as those of the control fermentation. This confirms that the fermentations
236 are very reproducible.

237 As expected (Bely et al., 1990; Mendes-Ferreira et al., 2004), nitrogen addition at the
238 beginning of fermentation led to an increase of the maximal CO₂ production rate. Regardless
239 of the nature of the added source, this value was equal to 0.79 g/L/h for the control
240 fermentation and increased to 1.4 g/L/h with an initial addition of nitrogen. We compared the
241 impact of different nitrogen additions on the fermentation kinetics (Figure 1).

242 The production of biomass was also 1.3-fold higher when more nitrogen was provided in the
243 must (Bell and Henschke, 2005; Bely et al., 1990).

244 The consequences of nitrogen addition during the stationary phase were very different from
245 those observed following an initial addition to the must. Adding nitrogen at the start of the
246 stationary phase resulted in an immediate increase of the fermentation activity up to a
247 maximum of 0.9 g/L/h of CO₂ produced, measured when all of the nitrogen added was
248 exhausted. However, the number of cells remained the same after the addition, as previously
249 observed by Bely et al. (1990). Overall, the additions of nitrogen substantially reduced the
250 fermentation duration (Table 2), as reported previously (Bell and Henschke, 2005). It should
251 be noted that the lowest fermentation times were obtained when nitrogen was added during
252 the stationary phase. This last observation confirms the value of adding nitrogen during this
253 phase, especially in the case of musts with low levels of phytosterols. Thus, adding nitrogen
254 after the cell growth phase activates the yeast metabolism without increasing the cell
255 population and consequently without diluting the lipid content of the yeasts. Therefore, the
256 improved fermentation performances obtained with addition of nitrogen at the beginning of
257 the stationary phase compared with an initial addition are likely due to a better resistance of
258 yeasts to ethanol at the end of fermentation (Sablayrolles et al., 1996).

259 In summary, both the fermentative kinetics (Figure 1) and the biomass production are only
260 modulated by the timing of the addition of nitrogen, regardless of the nature of the source
261 added (Figure 1 and Table 2).

262

263 3.2. Impact of nitrogen addition on volatile compound production

264 The data presented for aroma compounds are the total production, *i.e.*, the sum of the liquid
265 concentration and losses in the gas, because it is representative of the yeast metabolism
266 (Mouret et al., 2014a).

267 *3.2.1 Ethyl esters*

268 We followed the production rate of two ethyl esters: ethyl hexanoate and ethyl octanoate
269 (Figure 2a, b, c and d).

270 After nitrogen addition at the beginning of the fermentation, the total production of ethyl
271 hexanoate and octanoate increased moderately (+15% on average for the different conditions).
272 These variations are consistent with a mathematic model developed by Rollero et al. (2015)
273 for ammonium additions. This model predicts the production of the principal aroma
274 compounds depending on the temperature and the amount of lipid and nitrogen in the must.
275 With our parameters, this model predicts an increase of 10% for these two compounds from
276 100 to 170 mg/N/L.

277 We showed that the consequences of nitrogen supply in the must were comparable for the two
278 ethyl esters studied. However, when the nitrogen is added during the stationary phase, the
279 behavior of each ester was different. An addition during the stationary phase increased the
280 final concentration of ethyl hexanoate to the same extent as an initial addition. A higher
281 synthesis of ethyl hexanoate following the addition of nitrogen was clearly visible in the
282 evolution of the specific production rate of this ester (Figure 3). After the addition, this rate
283 doubled compared to the control fermentation. In contrast, the addition of nitrogen in the
284 stationary phase had no impact on the production of ethyl octanoate (Figure 2d).

285 The low impact of the addition of nitrogen on ethyl ester production is likely due to the
286 absence of causal relationships between the metabolic pathways of ethyl ester synthesis and
287 nitrogen metabolism. However, the nitrogen availability, inducing changes in the redox
288 balance of the cell, could modify the intracellular level of precursors, especially acetyl-coA
289 and further acyl-CoA derivatives (Bloem et al., 2016) or lipid synthesis due to the biomass
290 increase following the addition of nitrogen (Daum et al., 1998). This could explain the
291 variation of ethyl ester production depending on the time of the addition of nitrogen, as
292 adding nitrogen during the stationary phase resulted in a reduced increase in the final
293 population compared to an initial supplementation and consequently resulted in limited
294 changes in acyl-CoA availability.

295 Furthermore, these modifications could be too small to be sufficient to trigger an increase of
296 ethyl octanoate synthesis, which requires the addition of two additional carbons compared to
297 ethyl hexanoate.

298 *3.2.2. Higher alcohols*

299 **3.2.2.1 Propanol**

300 Propanol production is different than that of the other higher alcohols, as it is strongly
301 associated with the concentration of available nitrogen in the must (Mouret et al., 2014b).
302 During the control fermentation or fermentations with nitrogen added initially, propanol
303 production ended when the assimilable nitrogen was exhausted (Figure 4). The production of
304 propanol re-started immediately after nitrogen addition during the stationary phase and
305 stopped again when there was no more nitrogen in the medium.

306 These observations, confirming that propanol is a marker of nitrogen availability in the must
307 (Mouret et al., 2014b), also provided new insights on the activity of the metabolic pathway
308 involved in the synthesis of this compound. We first observed that the nature of added
309 nitrogen source, whether mineral or organic, has a direct impact on the amount of propanol

310 produced. An ammonium addition induced greater production of propanol than an amino acid
311 addition (Figure 2e and f). This phenomenon was especially pronounced during additions in
312 the stationary phase: the final propanol production was increased 4.3-fold after an ammonium
313 addition in the stationary phase, compared to a 2-fold increase after the addition of amino
314 acids (Table 2). These results could be explained by a different management of nitrogen by
315 cells depending on whether the source was organic or mineral. Thus, In particular, the
316 assimilated ammonium is entirely directed toward the common nitrogen pool, where it is
317 combined with α -ketoacids to produce the amino acids required for cell growth (Magasanik
318 and Kaiser, 2002). Amino acids are also largely directed toward the common nitrogen pool,
319 but part of it is directly assimilated without transformation (Crépin et al., 2014). Therefore,
320 for a given quantity of assimilable nitrogen, the nitrogen content incorporated into the
321 common pool is lower when organic nitrogen is added compared to a similar addition of
322 ammonium. This causes a reduction of the synthesis of the ketoacid precursor of propanol and
323 thus results in a lower production of propanol. These data demonstrate that propanol can also
324 be considered as a marker of the quality of available nitrogen (mineral or organic).

325 Then, we observed that propanol production was higher after nitrogen addition during the
326 stationary phase than at the beginning of the fermentation (Figure 2f). This likely reflects a
327 different management of the nitrogen resources depending on the timing of the addition.

328 Propanol is synthesized from α -ketobutyrate derived from threonine. However, α -ketobutyrate
329 is also a precursor of isoleucine. Propanol synthesis could be a way to degrade unused α -
330 ketobutyrate (Bisson, 1991). During cell growth, the demand for protein synthesis is high,
331 especially since the nitrogen addition at the beginning of the fermentation leads to an increase
332 in biomass production. A large part of α -ketobutyrate is used to produce isoleucine. In
333 contrast, the immediate demand of proteins is lower during the stationary phase when cell

334 growth has stopped. Because the isoleucine needs are lower, the α -ketobutyrate flux could be
335 re-oriented to the production of propanol.

336 **3.2.2.2 Other higher alcohols**

337 The impact of nitrogen addition on the other higher alcohols was different from that on
338 propanol.

339 In contrast to propanol, after a nitrogen addition at the beginning of fermentation, the total
340 productions of isoamyl alcohol and isobutanol were almost the same as those reached during
341 control fermentation (Figure 2g and i). These results are consistent with the predictions of the
342 mathematical model developed by Rollero et al. (2015), which predicted that the total final
343 concentrations obtained for the two higher alcohols studied would be identical with 100
344 mgN/L and 170 mgN/L of assimilable nitrogen.

345 In addition, the total productions of isoamyl alcohol and isobutanol were almost identical to
346 those obtained during the control fermentation regardless of the time or type of nitrogen
347 addition (Table 2, Figure 2g, h, i and j).

348 This absence of a difference could be explained by the fact that α -ketoacids that are
349 isobutanol and isoamyl alcohol precursors are produced from both central carbon metabolism
350 (CCM) and the catabolism of amino acids by the Ehrlich pathway (Bell and Henschke, 2005;
351 Hazelwood et al., 2008). Previous studies have demonstrated that the CCM contribution to the
352 synthesis of higher alcohols is much more important than the contribution of the amino acids
353 (Rollero, 2015). We can assume that there is a balance between the amount of α -ketoacids
354 supplied by CCM and the amount of α -ketoacids converted into amino acids for the synthesis
355 of proteins. Therefore, during an addition of nitrogen, the supplementary flux of α -ketoacids
356 related to the addition would be negligible compared to the flux from CCM (Crépin et al.,

2017; Rollero et al., 2017). The α -ketoacid pool available would then remain the same and would not change the final production of higher alcohols.

3.2.3. Acetate esters

Despite their very limited incidence in the production of branched alcohols, nitrogen supplementation, regardless of the nature of the added compound and the times of addition, resulted in a large overproduction of acetate esters (Figure 2i and j). This impact was especially pronounced when adding nitrogen at the beginning of the stationary phase: the final concentration of isoamyl acetate was 2.69 mg/L after a DAP initial addition but 4.09 mg/L after a DAP addition at the beginning of the stationary phase (Table 2). Furthermore, an addition of amino acids at the beginning of the stationary phase led to an increase of 20% of the production of isoamyl acetate in comparison with an addition of DAP (Figure 2j). However, the most important parameter for the production of acetate esters in our study was the timing of the addition (Table 2).

This systematic increase of the synthesis of acetate esters as a consequence of nitrogen addition while the concentration of the corresponding higher alcohol precursors remained unchanged was surprising. Thus, we focused on the bioconversion between these two types of molecules. A significant increase of the conversion yields of higher alcohols into corresponding acetate esters was noted when nitrogen was added (Figure 5a and b). After the addition of nitrogen at the beginning of the fermentation (either ammonium or amino acids) (Figure 5a), the yields were multiplied by 2 and by 10 after addition during the stationary phase (Figure 5b). These observations suggest that the effect of nitrogen is focused on the enzymes of the group of alcohol acetyltransferases (Atf1p and Atf2p) that catalyze the conversion of higher alcohols into acetate esters (Verstrepen et al., 2003).

380 To identify whether the genes coding for these enzymes are up-regulated as a consequence of
381 nitrogen addition, we measured the transcription level of the genes *ATF1* and *ATF2* by real-
382 time PCR experiments to investigate the impact of the addition of nitrogen in the form of
383 DAP or a mixture of amino acids during the stationary phase on their expression.

384 As a consequence of nitrogen addition, the transcription of *ATF1* and *ATF2* was significantly
385 increased in comparison with the control (Figure 6). The overexpression was greater for *ATF2*
386 than for *ATF1*. For the amino acid addition, the expression ratio compared to the reference
387 gene was equal to 234% for *ATF2* and 184% for *ATF1*.

388 A difference in the levels and kinetics of expression of these two genes was observed
389 depending on the nature of the nitrogen source added. The addition of DAP caused only a
390 small increase in the expression of the gene *ATF1* (141%), which remained constant during
391 the five hours following this addition (Figure 6a). In contrast, the addition of a mixture of
392 amino acids led to a peak of expression of this gene two hours after the addition. We observed
393 a strong increase in the expression of the gene *ATF2* 30 min after the nitrogen addition for
394 both nitrogen sources (Figure 6b). Nevertheless, this expression level was maintained for the
395 addition of DAP but decreased sharply after five hours following the addition of amino acids.
396 These differences according to the types of nitrogen sources added could explain the
397 differences in the production of esters acetate observed when adding amino acids or DAP
398 (Figure 2i and j).

399 The transcription of the gene *ATF1* is regulated by different environmental parameters
400 (Fujiwara et al., 1999) (Figure 7). In particular, it was shown that the promoter of the gene
401 *ATF1* contains a binding site for the Rap1p protein. This protein is known to be a target of the
402 Ras/cAMP/PKA pathway, which is the main glucose signaling pathway in yeast (Fujiwara et
403 al., 1999). However, another signaling pathway is known to target the same genes: the FGM
404 (fermentable-growth-medium-induced) pathway, which is active when all of the nutrients

405 needed for growth, including nitrogen, are present in the culture medium. The main protein
406 involved in this pathway is the protein kinase Sch9p, which has similarities with the catalytic
407 subunit of the cAMP-dependent protein kinases present in the Ras/cAMP/PKA pathway
408 (Verstrepen et al., 2003). It has been shown that the Sch9p protein plays a role in the
409 expression of *ATF1*, as its deletion leads to a decrease in the expression of the gene (Fujiwara
410 et al., 1999). These authors suggested that Sch9p would act on the activity of Rap1p and
411 therefore on the transcription of *ATF1*. With the results we obtained in RT-PCR, we
412 confirmed the nitrogen effect on the transcription of the gene *ATF1*, and we highlighted that
413 this effect also exists even more strongly for the gene *ATF2*. We can thus suggest that the
414 regulation of transcription of this gene was carried out via the same signaling pathway as for
415 *ATF1*. Moreover, it seems that *ATF2* is more sensitive to sudden changes in nitrogen
416 availability during fermentation than *ATF1*, as its activity increased more significantly.
417 Finally, the implication of nitrogen addition on the availability of acetyl-coA, which is
418 required for the synthesis of acetate esters (Bell and Henschke, 2005), can also be discussed.
419 Indeed, the Michaelis constant K_m of Atf1p for acetyl-coA is very low (0.025 mM) (Mason
420 and Dufour, 2000). Therefore, a slight change of acetyl-coA availability could have an
421 important effect on ester synthesis by Atf1p. This could explain why more acetate esters are
422 produced during the stationary phase than at the beginning of fermentation. During the growth
423 phase, acetyl-coA would mainly be used for biomass synthesis. In contrast, after nitrogen
424 addition in the stationary phase, acetyl-coA would be more available for aroma production
425 because there is no more biomass production.

426

427 3.3. Impact of nitrogen on different yeast strains

428 Fermentations were conducted with two *S. cerevisiae* strains having different nitrogen
429 requirements, which correspond to the amount of nitrogen that must be added during

430 fermentation to maintain a constant fermentation rate (Julien et al., 2000). The production of
431 the aromas studied by these two strains is represented on a PCA (Figure 8). The two first PCA
432 axes accounted for 80.9% of the total variation for Lalvin EC1118® (Figure 8a) and 80.4% for
433 Lalvin CY3079® (Figure 8b). For the two strains, the repartitions of the fermentation
434 conditions on the PCA were comparable, indicating that the effects of the nitrogen
435 management on the synthesis of fermentative aromas are similar for Lalvin EC1118® and
436 Lalvin CY3079®. However, it should be noted that the effect of the type of nitrogen added at
437 the beginning of fermentation was less visible with Lalvin CY3079®, as the individuals are
438 closer on the PCA. The principal parameter discriminating the fermentation conditions was
439 the timing of the addition, and the compounds most impacted were propanol and acetate
440 esters.

441

442 4. Conclusion

443 The objective of this study was to examine the impact of the nitrogen source (ammonium or
444 amino acids) and the timing of the addition of nitrogen on the aroma production of two
445 *Saccharomyces cerevisiae* strains during winemaking conditions.

446 The two *S. cerevisiae* strains had different nitrogen requirements and aromatic profiles, but
447 the impacts of nitrogen supply on their aroma metabolism were quite similar. From a general
448 point of view, the impact of the timing of the addition of nitrogen on aroma production was
449 higher than that of the nitrogen composition, even if adding organic nitrogen slightly
450 increased the acetate ester synthesis compared to the supply of ammonium.

451 We confirmed that propanol is a metabolic marker of the presence of available nitrogen in the
452 must and, more precisely, of the amount of intracellular nitrogen available for the *de novo*
453 synthesis of amino acids. In contrast, the production of other higher alcohols was not affected

454 by the additions of nitrogen. Ethyl ester production was slightly increased after the addition of
455 nitrogen, perhaps because of a change in the availability of acetyl-coA. The strongest impact
456 of the nitrogen could be observed for the acetate esters. In particular, their production
457 increased greatly after the addition of nitrogen, especially during the stationary phase. We
458 showed that the overproduction of these specific volatile compounds was due to an increase
459 of the production yields of acetate esters from corresponding higher alcohols resulting from
460 an overexpression of the genes *ATF1* and *ATF2* that encode for this enzymatic bioconversion
461 activity.

462 In the future, it would be interesting to confirm the effect of nitrogen management on other
463 strains to evaluate the generic aspect of the results obtained. In addition, these experiments
464 should be reproduced on natural must to validate that the differences in aroma concentrations
465 observed in this study have a perceptible impact on the sensory profile of the wine. Different
466 addition quantities could be tested, as the nitrogen concentration has an important impact on
467 the aroma production. It would also be interesting to study the metabolic fluxes impacted by
468 nitrogen addition in detail, especially the production of propanol from threonine, to explain
469 the production differences observed depending on the nitrogen source. However, these
470 findings open up new perspectives for the development of innovative strategies aimed at
471 maximizing the production of positive aromas through adapted nitrogen management.

472

473 **5. Acknowledgments**

474 We thank Evelyne Aguera, Magaly Angenieux, Christian Picou and Martine Pradal for
475 technical assistance.

476

477 **6. Conflict of interest**

478 The authors declare to not have conflict of interest.

479

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- 609

610

611 **Tables**

612 Table 1: Target genes used in qPCR.

Genes	Molecular function (SGD curate)	Reference	Primer sequence (5' -> 3')
<i>ATF1</i>	Alcohol acetyltransferase activity	(Fujii et al., 1994)	F: ATGATTCAGAATGGGCATGCT R: CTCCATATGTGCAGAAGTTTCGA
<i>ATF2</i>	Alcohol acetyltransferase activity	(Nagasawa et al., 1998)	F: TTCATTCAAGCGTGCTTTCTTG R: CGTTGCTTGGGAATAGCCACAT
<i>SCR1</i>	RNA subunit of the Signal Recognition Particle	(Felici et al., 1989)	F: TCTGGTGCGGCAAGGTAGTT R: CACCTTTGCTGACGCTGGAT

613

614

Table 2: Fermentation parameters and final aroma concentrations measured for fermentations with Lalvin EC1118®.

		Fermentation duration (h)	Maximal population (C/mL)	First peak of dCO ₂ /dt (g/L/h)	Second peak of dCO ₂ /dt (g/L/h)	Final concentration (total production) (mg/L)							
						Propanol	Isoamyl alcohol	Isobutanol	Isoamyl acetate	Isobutyl acetate	Ethyl acetate	Ethyl hexanoate	Ethyl octanoate
Control		310	5.02E+07	0.79	-	5.60	193.76	24.28	1.38	0.10	32.15	1.78	2.73
Addition at T₀	DAP	270	6.79E+07	1.36	-	10.65	199.33	27.69	2.69	0.22	36.80	1.94	3.25
	AA	270	6.78E+07	1.40	-	8.26	163.56	25.06	2.93	0.38	38.73	2.07	2.98
Addition in stationary phase	DAP	215	5.33E+07	0.75	0.91	24.17	189.31	19.57	4.09	0.24	49.12	2.17	2.62
	AA	220	5.35E+07	0.75	0.90	11.67	195.63	23.13	4.92	0.28	48.40	2.02	2.48

Figures

Figure 1: Changes in the fermentation kinetics depending on the addition of nitrogen with Lalvin EC1118[®]: control without addition (green curve); addition at the beginning of fermentation of DAP (dark blue curve) or amino acids (red curve); addition during the stationary phase of DAP (light blue curve) or amino acids (orange curve). The arrow indicates the timing of addition during the stationary phase.

Figure 2: Total production by Lalvin EC1118[®] of ethyl hexanoate, ethyl octanoate, propanol, isoamyl alcohol and isoamyl acetate during the fermentation with nitrogen additions at the beginning of the fermentation (respectively, a, c, e, g and i) and during the stationary phase (b, d, f, h and j). Control fermentation (green curve); addition of DAP at the beginning of the fermentation (dark blue curve); addition of DAP during the stationary phase (light blue curve); addition of amino acids at the beginning of the fermentation (red curve); addition of amino acids during the stationary phase (orange curve); Arrows represent the additions during the stationary phase.

Figure 3: Changes in the specific rate of ethyl hexanoate production after an addition during the stationary phase. Control fermentation (green curve); addition of DAP (light blue curve); addition of amino acids (orange curve). The arrow indicates the timing of addition during the stationary phase.

Figure 4: Propanol production (orange curve) and assimilable nitrogen consumption (purple crosses) by Lalvin EC1118[®] during a fermentation with the addition of amino acids in the stationary phase. The arrow represents the addition during the stationary phase.

Figure 5: Changes in the total production of isoamyl acetate as a function of the total production of isoamyl alcohol after nitrogen addition at the beginning of fermentation (a) or in the stationary phase (b) with Lalvin EC1118[®]. Control without addition (green curve); addition at the beginning of fermentation of DAP (dark blue curve) or amino acids (red curve); addition during the stationary phase of DAP (light blue curve) or amino acids (orange curve). The arrow indicates the timing of addition during the stationary phase.

Figure 6: *ATF1* (a) and *ATF2* (b) expression of Lalvin EC1118[®] after nitrogen addition measured by qPCR. Control (green bar); addition of DAP (light blue bar); addition of amino acids (orange bar).

Figure 7: Diagram of the transcriptional regulation of *ATF1* by glucose and nitrogen (from Fujiwara et al., 1999).

Figure 8: Principal component analysis of total aroma production at 180 g/L of consumed sugar for the strains Lalvin EC1118[®] (a) and Lalvin CY3079[®] (b). Control fermentation (green circle); initial additions (purple circle); addition during the stationary phase (blue circle). Addition of ammonium (NH₄) or amino acids (AA). EH = ethyl hexanoate, EO = ethyl octanoate, PR = propanol, IA = isoamyl alcohol, IB = isobutanol, IAA = isoamyl acetate, IBA = isobutyl acetate, EA = ethyl acetate.

Highlights

Nitrogen content of the must impacts aroma production in alcoholic fermentation.

The timing of addition and the source of nitrogen had an effect on aroma production.

Acetate esters were the most impacted by nitrogen addition.

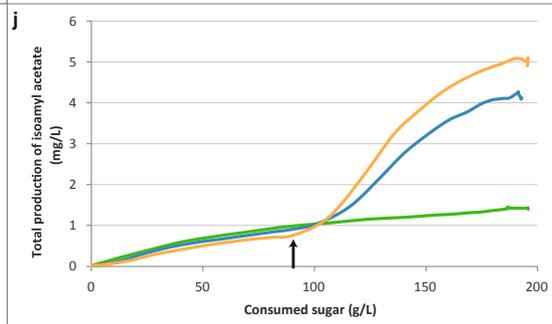
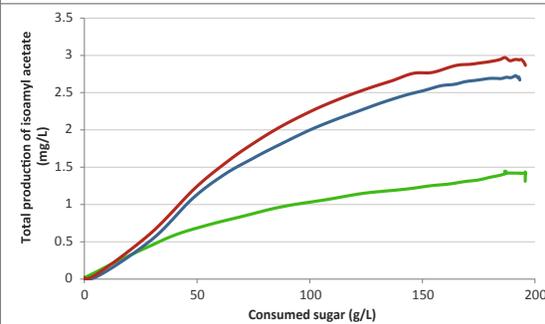
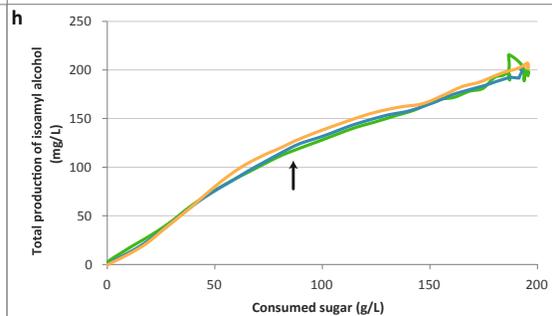
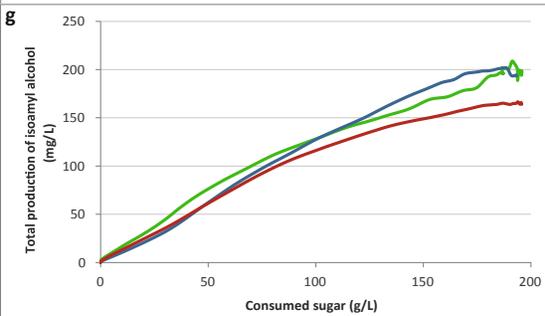
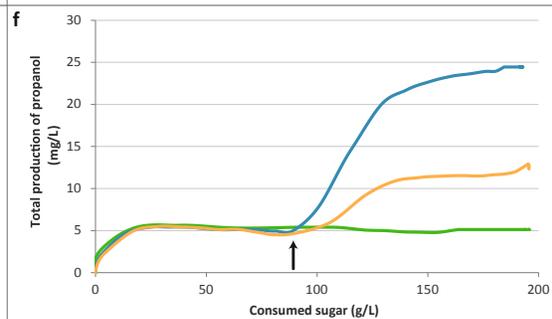
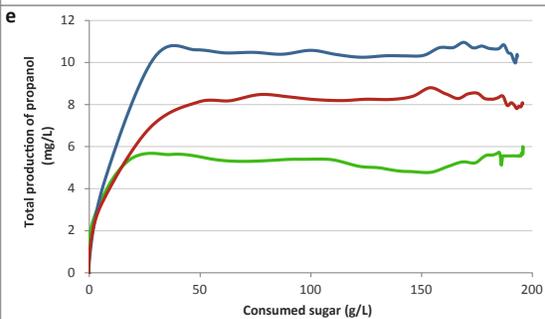
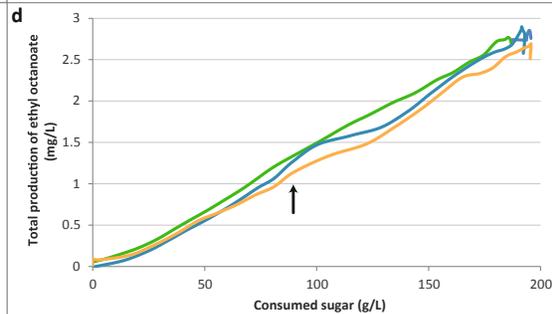
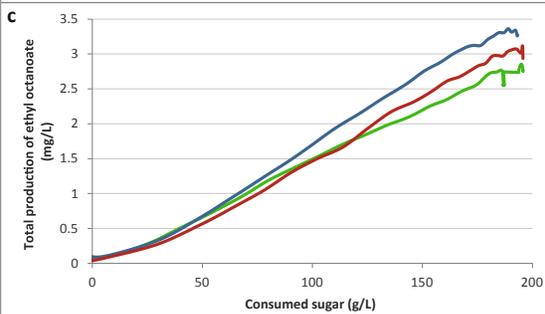
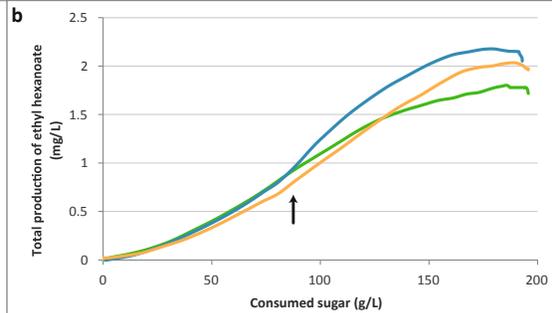
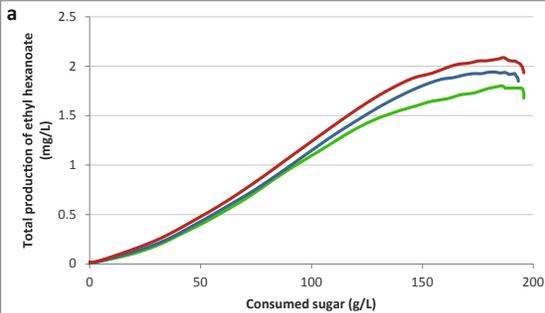
After a nitrogen addition in stationary phase, *ATF1* and *ATF2* were overexpressed.

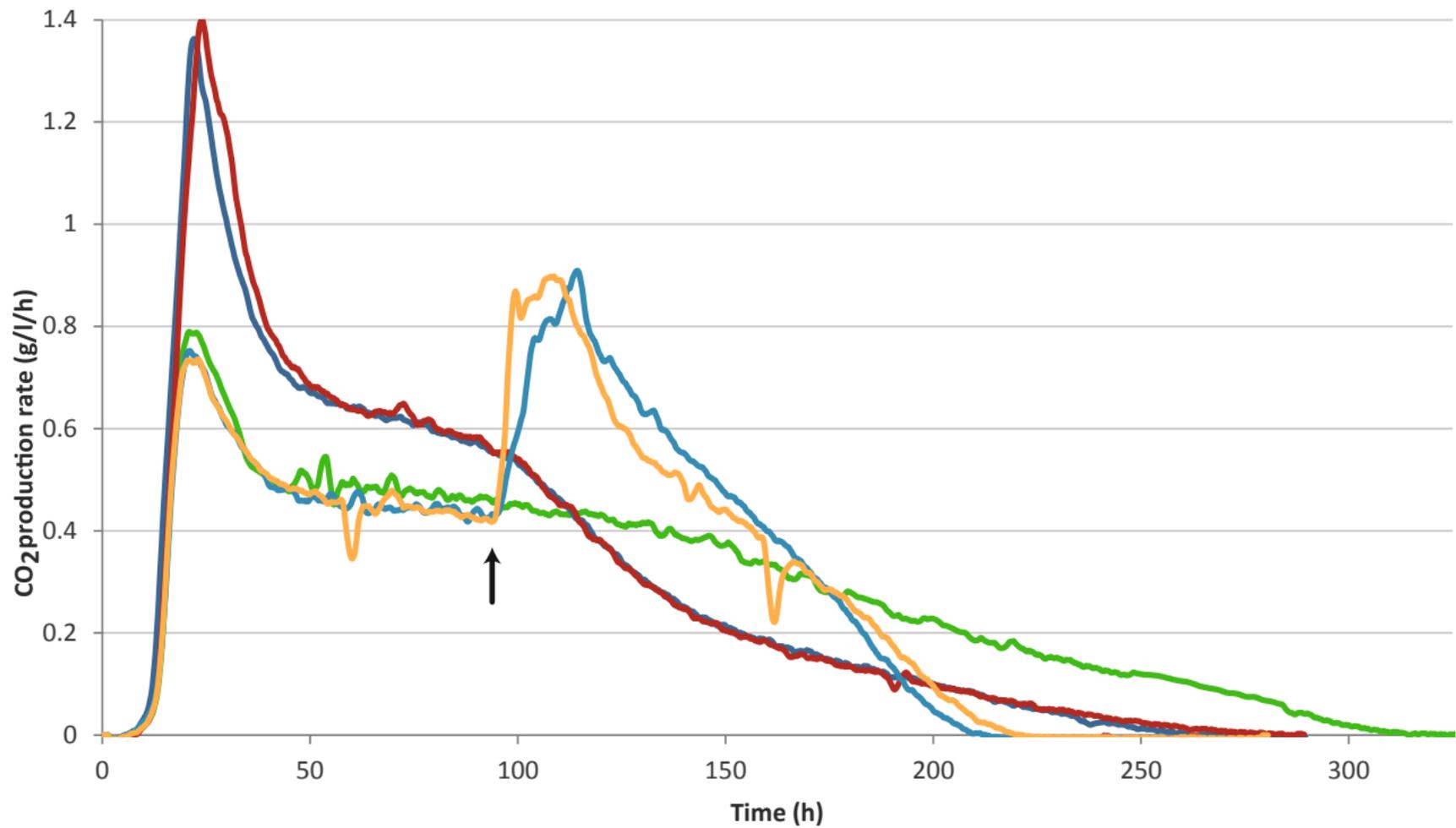
The best results were obtained when adding organic nitrogen in stationary phase.

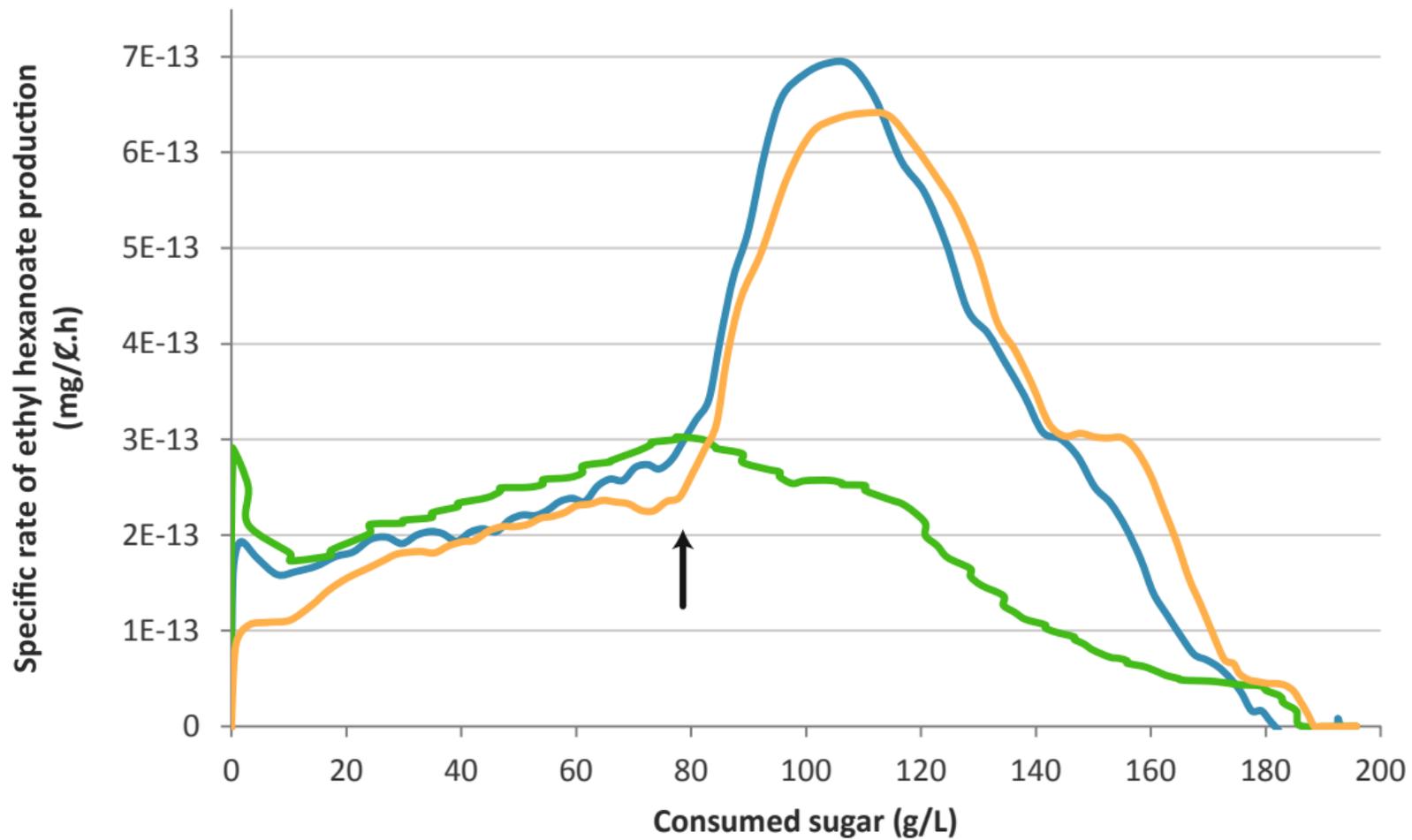
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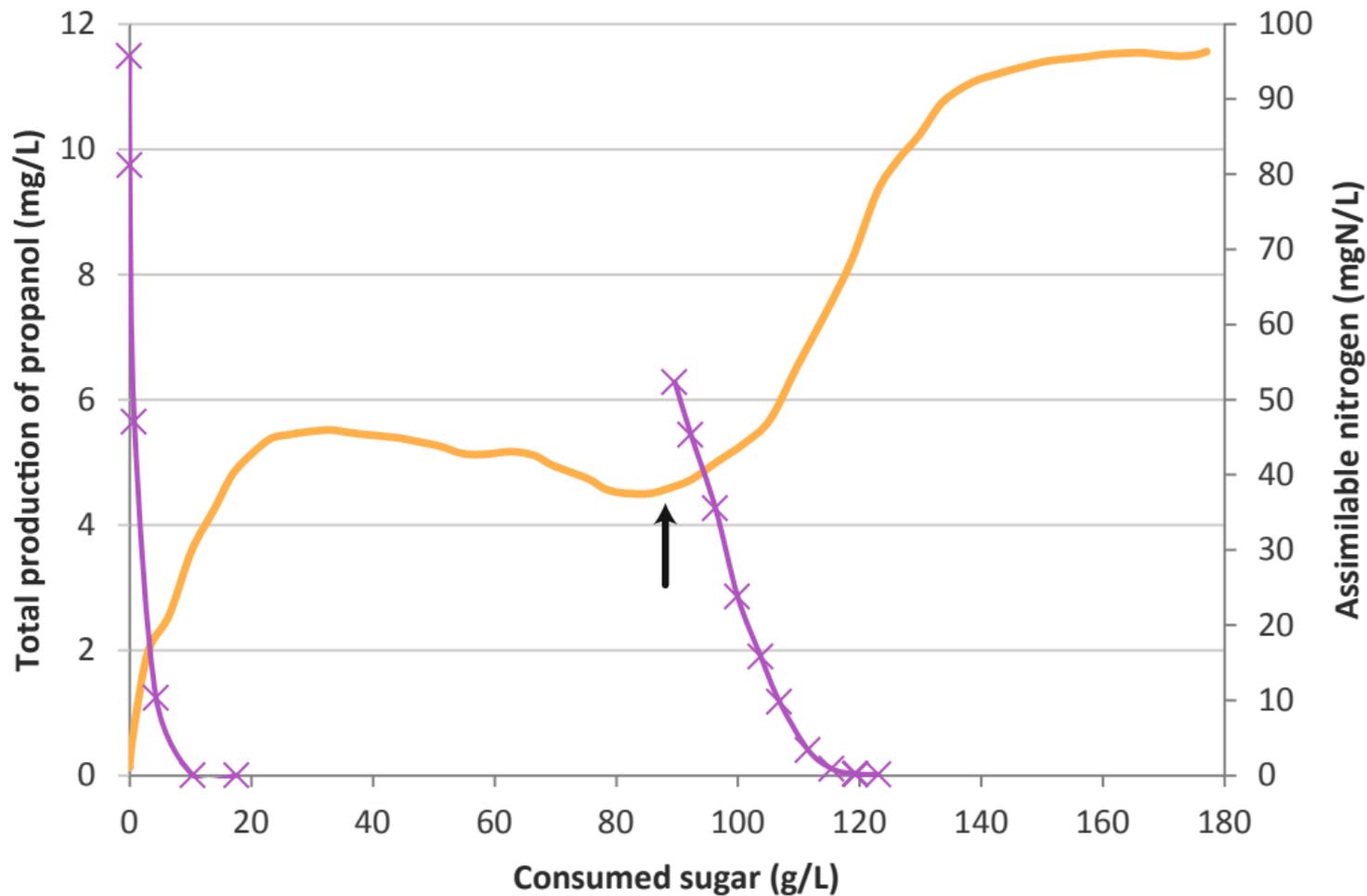
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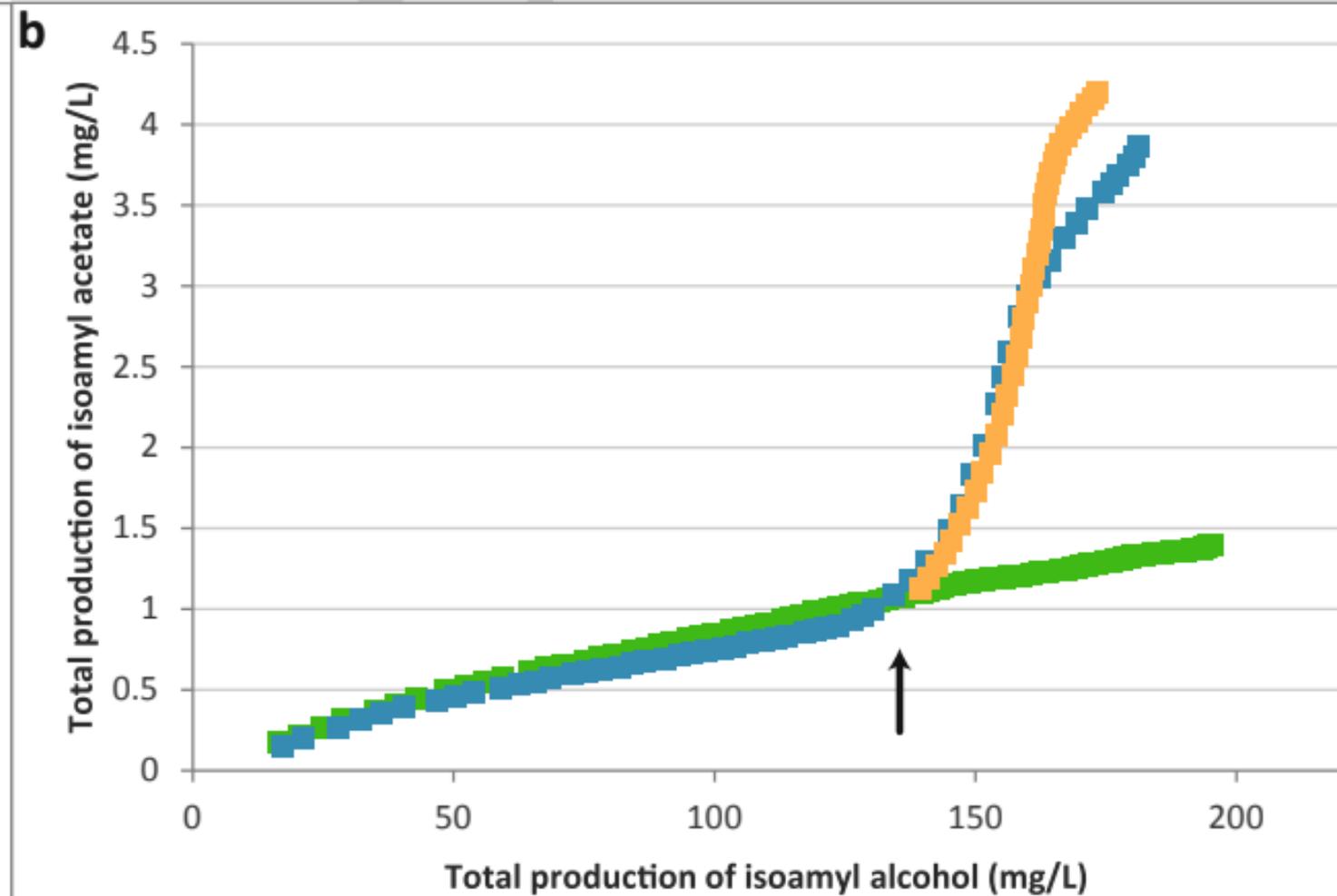
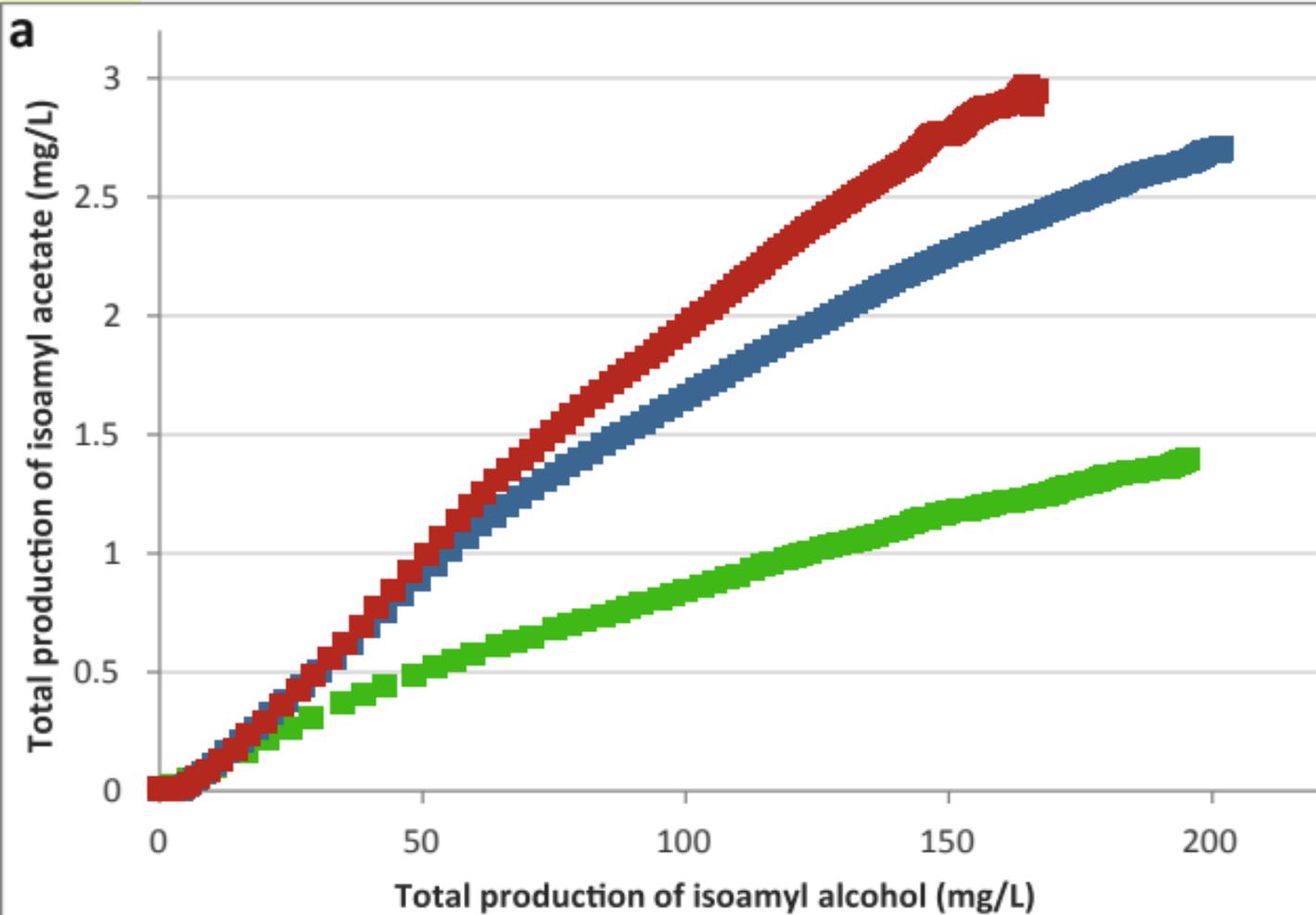
Seguinot, P., Rollero, S., Sanchez, I., Sablayrolles, J.-M., Ortiz-Julien, A., Camarasa, C., Mouret, J.-R. (2018). Impact of the timing and the nature of nitrogen additions on the production kinetics of fermentative aromas by *Saccharomyces cerevisiae* during winemaking fermentation in synthetic media. *Food Microbiology*, 76, 29-39. . DOI : 10.1016/i.fm.2018.04.005

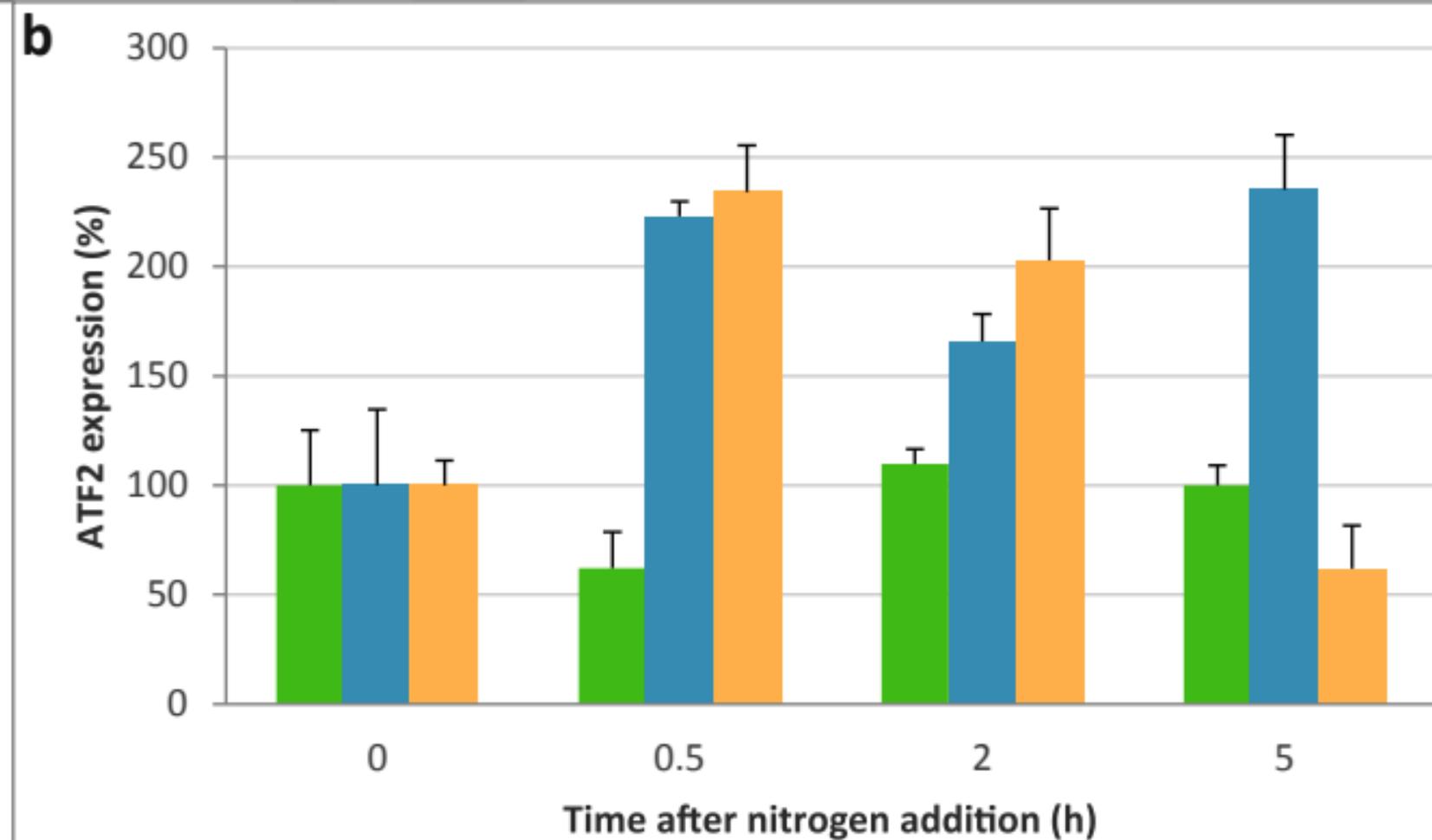
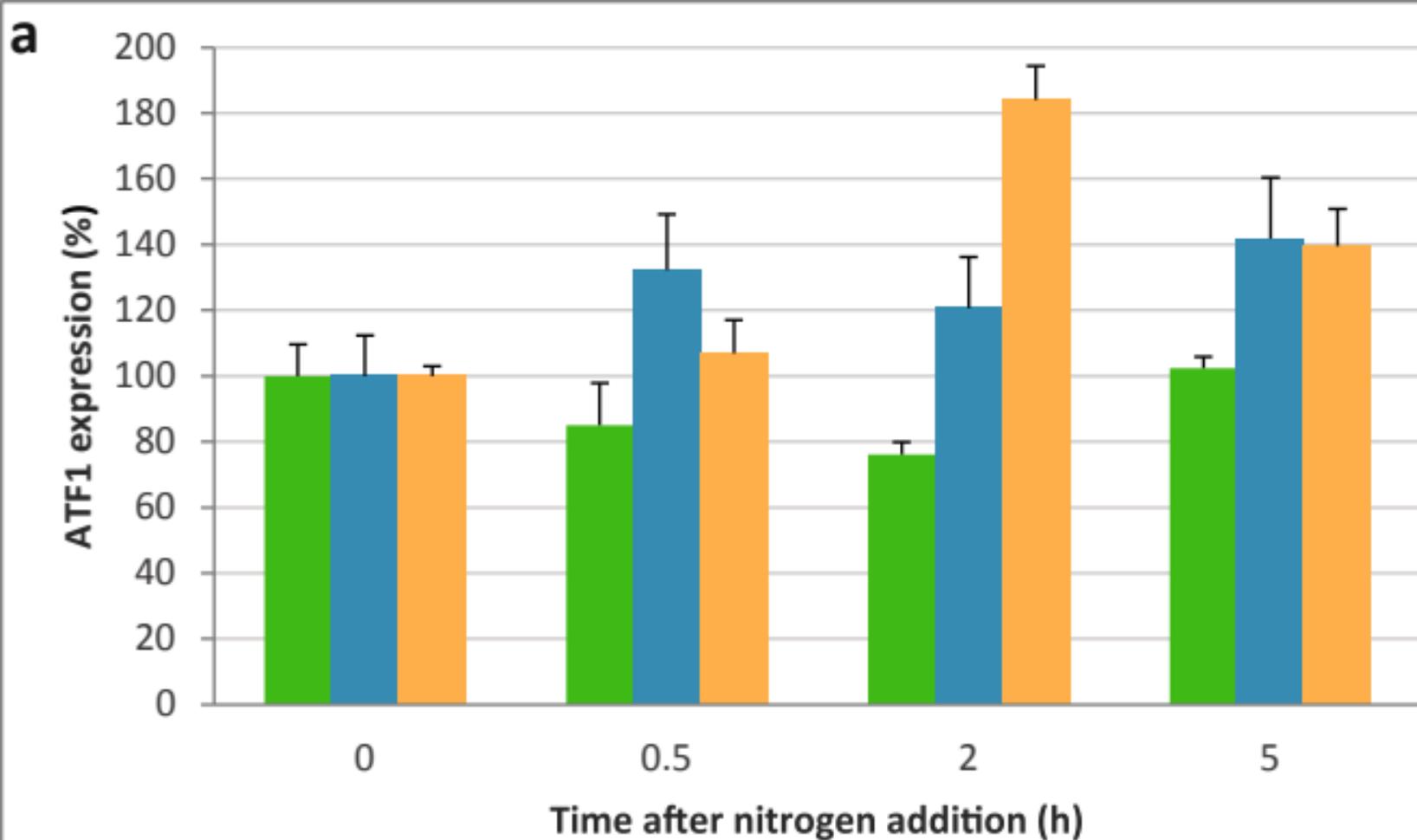


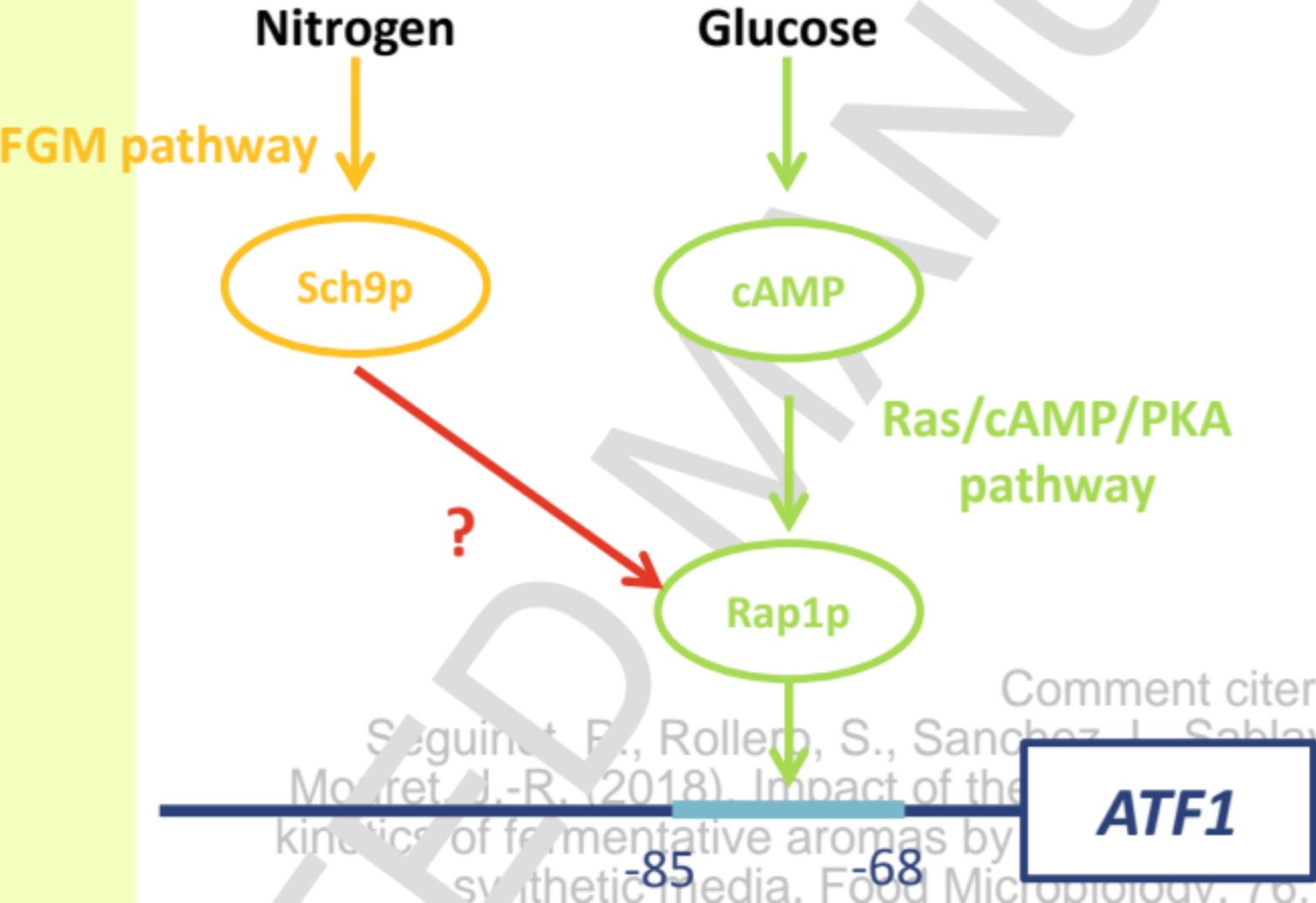


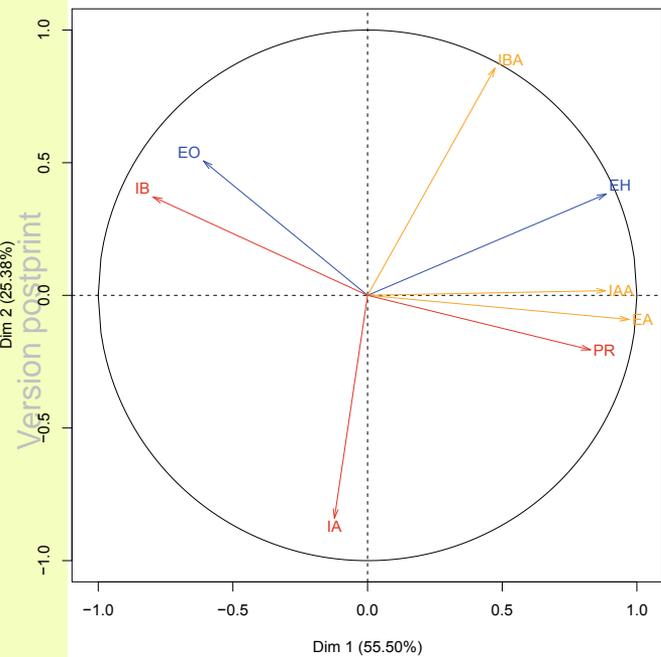
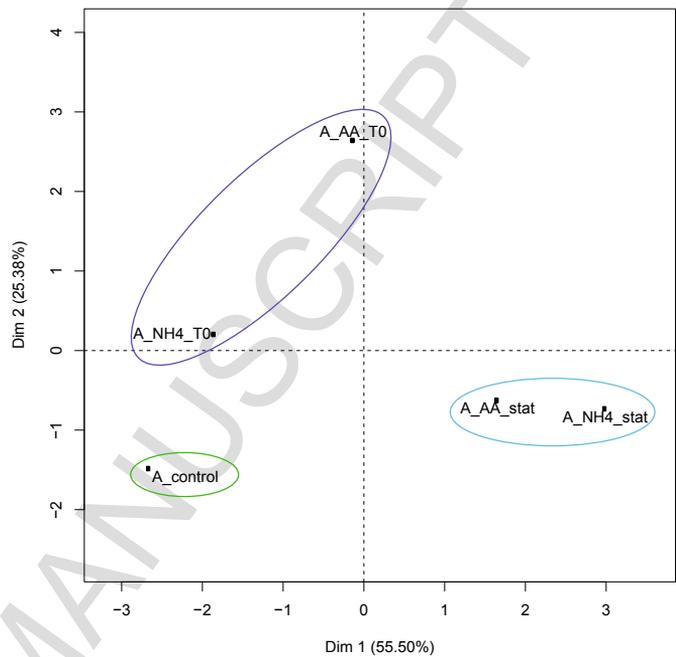
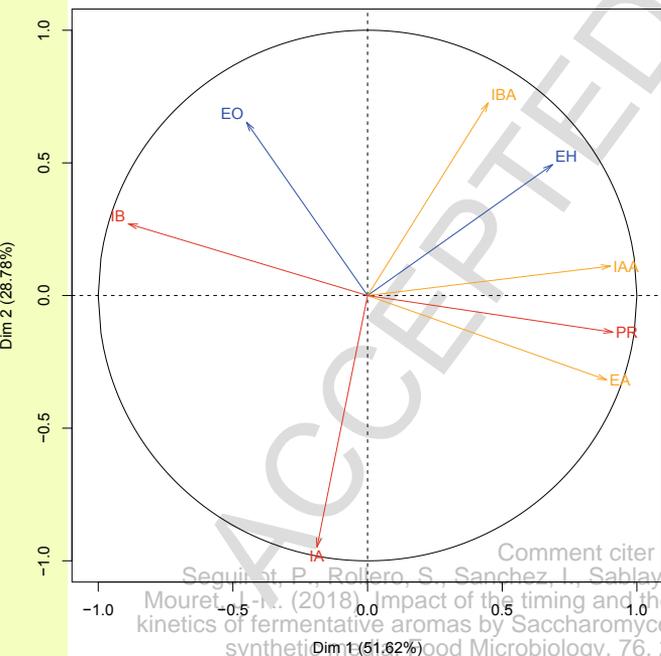










Variables factor map (PCA)**Individuals factor map (PCA)****b****Variables factor map (PCA)****Individuals factor map (PCA)**