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1 **Fine-tuning of process parameters modulates specific metabolic bacterial activities and aroma**
2 **compound production in semi-hard cheese**

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12 Abstract

13 The formation of cheese flavor mainly results from the production of volatile compounds by
14 microorganisms. We investigated how fine-tuning cheese-making process parameters changed the
15 cheese volatilome in a semi-hard cheese inoculated with *Lactococcus (L.) lactis*, *Lactiplantibacillus*
16 *(L.) plantarum*, and *Propionibacterium (P.) freudenreichii*. A standard (Std) cheese was compared
17 with three variants of technological itineraries: a shorter salting time (7h versus 10h, Salt7), a
18 shorter stirring time (15 min versus 30 min, Stir15min), or a higher ripening temperature (16°C
19 versus 13°C, Rip16°C). Bacterial counts were similar in the four cheese types, except for a 1.4 log₁₀
20 reduction of *L. lactis* counts in Rip16°C cheeses after 7 weeks of ripening. Compared to Std,
21 Stir15min and Rip16°C increased propionibacteria activity, causing higher concentrations of acetic,
22 succinic and propanoic acids and lower levels of lactic acid. Rip16 °C accelerated secondary
23 proteolysis and volatile production. We thus demonstrated that fine-tuning process parameters could
24 modulate the cheese volatilome by influencing specific bacterial metabolisms.

25

26 Figures and tables can be found at the end of the document.

27 **Introduction**

28 The quality of cheese is markedly dependent on the microorganisms used as starter, for both
29 acidification and aromatization purposes. The activity of microorganisms during cheese
30 manufacture and ripening induces modifications to all milk constituents (carbohydrates, proteins
31 and lipids), which in turn leads to the development of cheese flavor. Indeed, flavor development is a
32 dynamic biochemical process that is impacted by (i) milk composition; (ii) curd processing and
33 ripening conditions, and (iii) enzymes naturally present in cow milk and (iv) the indigenous
34 microorganisms or added as starter ¹. Cheese microorganisms are the primary source of the
35 enzymes that influence flavor development. Flavor compounds include sapid compounds (mainly
36 organic acids, peptides and amino acids), alongside added NaCl, and volatile aroma compounds.
37 The microbiological and biochemical processes involved in cheese aromatization have been well
38 deciphered in recent decades. In industrial cheeses, microorganisms developing aroma compounds
39 in cheeses essentially originates from selected strains inoculated as a starter culture in the milk at
40 the beginning of the cheese making. For example, in Cheddar and Emmental cheeses, the
41 production of diacetyl and propionic acid by *Lactococcus (L.) lactis* and *Propionibacterium (P.)*
42 *freudenreichii*, respectively, has been monitored during cheese making ^{2,3} and the corresponding
43 metabolic pathways have been established. The ability of microorganisms to produce aroma
44 compound is highly species and strain-dependent, as shown by the results of screening to select the
45 best producers ⁴. Many studies show the impact of starters and/or ripening cultures in the
46 differential production of aroma compounds in industrial cheeses: addition of different strains of *P.*
47 *freudenreichii* in Raclette cheese⁵, associations of different strains of *P. freudenreichii* and lactic
48 acid bacteria in Emmental cheese ^{6,7}, diversification of aroma compounds according to the strain of
49 *L. paracasei* in Cheddar cheese ⁸. However, little is known regarding the impact of process
50 implemented in the cheese manufacture on the metabolism of bacteria and thus on the production of
51 aroma compounds.

52 Environmental factors such as pH, salt and temperature are well known to influence the metabolism
53 of bacterial cells in a culture medium *in vitro*. In cheese, process parameters such as the salting step,
54 ripening temperature and duration of different stages can drastically influence the organoleptic
55 quality of cheeses. The effects of salt and temperature have been shown to modulate bacterial
56 growth and, as a consequence, the aroma compounds in cheeses⁹⁻¹¹. In Cheddar cheeses made with
57 raw milk, a ripening period at 8 °C instead of 1°C increased drastically volatiles compounds and
58 NSLAB growth⁹. In Caciocavallo Silano cheese, a traditional Italian cheese inoculated with an
59 undefined whey culture, an increase in the ripening temperature from 16°C to 20 °C promoted the
60 expression of genes related to proteolysis, lipolysis and amino acid and lipid catabolism and
61 significantly increased the cheese maturation rate and the aroma compounds content¹⁰.

62 The aim of the present study was to determine how certain variations in process parameters can
63 influence the metabolism of bacteria and therefore whether the choice of process parameters might
64 constitute a lever to modulate the volatilome of semi-hard cheeses.

65 Our strategy was first of all to develop a reproducible, standard semi-hard model cheese (Std) which
66 was inoculated with three strains: a *L. lactis* ssp *lactis* biovar *diacetylactis* strain for curd
67 acidification and diacetyl production, a *Lactiplantibacillus* (*L.*) *plantarum* strain to mimic the role
68 of a non-starter lactic acid bacterium, and a *P. freudenreichii* strain to produce diverse aroma
69 compounds during ripening. The second step was to establish how process parameters modulate the
70 formation of aroma compounds, by modifying three process parameters: reduced stirring time
71 (Stir15min), reduced salting time (Salt7h) or higher ripening temperature (Rip16°C), tested
72 independently. Sampling was performed throughout manufacture and ripening in order to assess the
73 effects of the technological changes versus the Std in terms of biochemistry, bacterial growth and
74 survival and aroma compound content. The relative contributions of time, changes to process
75 parameters were fully discussed.

76 MATERIALS AND METHODS

77 2.1 Microorganisms and culture conditions

78 The consortium used to manufacture the model cheese was composed of three bacterial strains
79 originating from the CIRM-BIA (INRAE, France) collection: *L. lactis* ssp *lactis* biovar *diacetylactis*
80 CIRM-BIA1206, *L. plantarum* CIRM-BIA465 and *P. freudenreichii* CIRM-BIA122.

81 The strains were stored at -80°C as glycerol stocks (15% v/v). All strains were grown without
82 agitation at 30°C in standard broths: the M17 broth containing 0.5% (w/v) lactose for *L. lactis*,
83 Man, Rogosa and Sharpe broth (MRS, pH 5.4) for *L. plantarum*, and YEL broth ¹² for
84 *P. freudenreichii*.

85 Before cheese making, the frozen strains were revived at 30°C for 2 days in broth media. *L. lactis*
86 and *L. plantarum* were then transferred three times at 1% (v/v) in commercial full-fat UHT cow's
87 milk (Delisse®, France). *L. lactis* was first inoculated in 10 mL milk for 48 h and then in 100 mL
88 milk for 24 h. The final culture of *L. lactis* was performed in 6 L milk and incubated for 41 h to
89 reach a targeted pH of between 5.3 and 5.5. Subcultures of *L. plantarum* were produced in the same
90 manner but in different milk volumes: 30 mL for the second culture and 2 L for the final culture
91 targeting a pH of between 6.3 and 6.4. The revived *P. freudenreichii* was subcultured twice at 1%
92 (v/v) in sterile milk ultrafiltrate supplemented with 10 g/L casein hydrolysate (Organotechnie, La
93 Courneuve, France) and 50 mM sodium L-lactate (Galaflo SL60; Société Arnaud, Paris, France)
94 (medium abbreviated as UF), prepared as previously described ¹³. The first subculture of *P.*
95 *freudenreichii* was performed in 10 mL UF for 72 h. It was then transferred into 0.5 L UF and
96 incubated for 60 h. Before cheese making, the cell concentration in the final culture of *P.*
97 *freudenreichii* was evaluated by spectrophotometry at 600 nm. An appropriate culture volume,
98 corresponding to a final population of 6.10^6 colony-forming units (CFU) per mL in the milk used
99 for cheese making, was centrifuged for 5 min at 6000 g. The cell pellet was then suspended in 10
100 mL UHT milk and inoculated into the cheese milk.

101 Plate counting was also used to control milk quality. The standardized milk was analyzed by plate
102 count agar (PCA) and VRBL agar to check for an absence of contamination. Around 10^3 CFU/mL
103 mesophilic bacteria, $\sim 10^2$ CFU/mL thermophilic bacteria and <1 CFU/mL coliforms were detected
104 after each pasteurization and each standardization. These levels were judged to be acceptable for
105 cheese making.

106

107

108 **2.2 Semi-hard cheese manufacture**

109 Four biological repetitions of cheese production were performed at the pilot scale. The repeatability
110 and reproducibility of the standard cheeses were assessed by making them in two or three different
111 vats, respectively, in order to generate duplicates or triplicates. The standard and three variant
112 itineraries were all performed twice in parallel in three different vats. The choice of vat was
113 randomized to prevent a potential ‘vat effect’.

114 To make each cheese, cow’s milk was freshly collected (Entremont, Montauban de Bretagne,
115 France) and treated in batches as follows (**Figure 1**). The cow’s milk was pasteurized at 76°C for
116 20 s, skimmed and standardized to 30 g fat and 36 mg calcium per kg of milk by adding fat and
117 CaCl_2 solution, as described by Leyva Salas et al. (2018) ¹⁴. Final cultures of *L. lactis* and *L.*
118 *plantarum* were inoculated in the standardized milk at $\sim 10^5$ CFU/mL. The inoculated milk then
119 underwent prematuration at 14°C for 18 h before cheese manufacture. *P. freudenreichii* was added
120 at a rate of $6 \cdot 10^6$ CFU/mL in matured milk and stirred for 20 min. The milk was then pumped into
121 vats (180 kg/vat) for cheese production.

122

123

124 The standard itinerary for cheese making (**Std**), represented schematically in **Figure 1**, was
125 modified from a previously described method ¹⁴. Briefly, the matured milk was warmed at 33°C for
126 around 30 min. When the pH reached 6.5, 0.25 mL/kg of commercial rennet (520 mg/L chymosin,
127 Carlina 145/80, Dupont Danisco, Dangé, Saint Romain, France) was added to the milk. Gelation
128 time was approximately 20 minutes and firming time was 10 minutes, for a total clotting time of 30
129 minutes. After cutting the coagulum to the size of corn grains (5x5x5 mm), the curd was stirred for
130 30 min at 33°C, followed by washing and draining steps. Washing was carried out by replacing
131 25% of the whey with water at the same temperature (33°C). The washed coagulum was then
132 transferred by gravity into a 56 x 44 cm container and was pre-pressed at 1.96 kPa for 30 min. After
133 pre-pressing, the curd was cut into six pieces (22 x 14 x 12 cm), each weighing around 3.7 kg,
134 which were then molded into cylinders (Ø= 39.6 cm, h = 13.1 cm) and placed on a horizontal press
135 for pressing. This involved three steps: 50 kPa for 30 min, 70 kPa for 1.5 h and then 120 kPa for 2
136 h. The cheeses were left in their molds overnight at room temperature (the curd temperature falling
137 from 27°C to 23°C during this period) and then demolded on the third day of cheese making, when
138 each cheese weighed around 2.5 kg. The demolded cheeses were then salted by immersion at 12°C
139 for 10 h in saturated brine. After overnight drying at the same temperature, the cheeses were
140 vacuum-packed in plastic bags (La Bovida, France) on the fourth day of cheese making and ripened
141 at 13°C for 7 weeks.

142 Three variant cheese making itineraries, namely, **Stir15min**, **Salt7h** and **Rip16°C** (**Figure 1**), were
143 also followed. These variants differed from the standard itinerary by only one parameter for each
144 variant. Stirring time was reduced from 30 min to 15 min under the **Stir15min** itinerary; salting
145 time was reduced from 10 h to 7 h under the **Salt7h** itinerary and ripening temperature was raised
146 from 13°C to 16°C under the **Rip16°C** itinerary. All other production steps were the same as in the
147 standard itinerary.

148 **2.2 Sample collection**

149 Samples were collected at nine different production stages, ranging from the inoculated milk to
150 cheese ripened for 7 weeks (**Figure 1, Table 1**). Fresh cheese curds were collected at 0, 2 h and 4 h
151 after the start of molding (C_m , C_{m+2h} , C_{m+4h}) and at the demolding stage (C_{dm}). During the ripening
152 period, cheeses were sampled at the start of ripening (C_{0w}) and after 4 and 7 weeks of ripening (C_{4w} ,
153 C_{7w}).

154 The samples were subjected to microbiological, physicochemical and biochemical analyses as
155 detailed in **Table 1**. After pH measurements, the milk samples were aliquoted into sterile jars.
156 Cheese samples were cut with a sterile knife to eliminate the rind (1 cm thick around the cheese
157 surface). Then core samples of around 20 g were cut aseptically for microbial enumeration. The rest
158 of the cheese was mixed using a blender to obtain small cubes with dimensions of less than 1 cm³
159 and then aliquoted into sterile jars.

160 Samples for microbial enumeration were stored at 4°C and analyzed within 24 h. Samples destined
161 for physicochemical (except pH) and biochemical analyses (except volatile compounds) were stored
162 at -20°C. For the analysis of volatile compounds, 2.5 ± 0.1 g of samples were added, in triplicate, to
163 22 mL PerkinElmer vials and stored at -80°C until analysis.

164

165 **2.3 Microbiological enumeration**

166 Before enumeration, 10 g of curd or cheese samples were added to the filter stomacher bag
167 (Humeau, Treillière, France), and blended in 90 g 2% (w/v) trisodium citrate (45°C) for 3 min at
168 maximum speed. Ten-fold serial dilutions of milk samples or citrate-cheese solutions were then
169 prepared in peptone salt water. The populations of *L. lactis*, *L. plantarum* and *P. freudenreichii* in
170 the samples were determined using the pour plate technique on M17 agar, MRS agar (pH 5.4) and
171 YEL agar, respectively. The *L. lactis* strain was grown aerobically at 30°C for 24 h, while anaerobic
172 incubation at 30°C was implemented for *L. plantarum* and *P. freudenreichii* for 48 h and 1 week,
173 respectively, as described previously¹⁵.

174 Counting results were noted as CFU per gram of sample (CFU/g). The bacterial populations at each
175 production stage were expressed as means \pm standard deviation for four biological replicates under
176 the standard itinerary, and for two replicates using the three variant itineraries.

177 **2.4 Physicochemical characterization**

178 pH was measured using a pH meter (WTW pH 3100, Weilheim, Germany) equipped with a
179 puncture electrode (LoT406-M6-DXK GmbH, Mettler Toledo, Urdorf, Switzerland) and
180 temperature probe (WTW 325/HC), by direct insertion into the fresh milk and cheese samples.
181 Other analyses were performed on samples after being thawed and equilibrated for 3 h at room
182 temperature. The dry matter content was determined by drying samples for 7 h at $102 \pm 2^\circ\text{C}$ ^{16,17}.
183 Fat content was measured using the Gerber–Van Gulik method with a butyrometer ¹⁸. The calcium
184 content was assessed by atomic absorption spectroscopy ¹⁹, results being first expressed as g/100 g
185 of cheese and then converted into the content in dry matter (g/100g DM). Chloride concentrations
186 were determined using a chloridometer based on coulometric titration (Corning 926 Chloride
187 Analyzer, Humeau Laboratoires, La Chapelle-sur-Erdre, France); the results were first expressed as
188 g/100g of cheese and then converted into the content in moisture (g/100g moisture).

189 **2.5 Evaluation of proteolysis**

190 The frozen samples were thawed and equilibrated for 3h at room temperature before nitrogen
191 determinations. Total nitrogen (TN) was determined using the Kjeldahl method ²⁰; it was then
192 converted to total protein content by multiplying by a factor of 6.38 ²¹. The degree of proteolysis
193 was characterized from the non-casein nitrogen content (NCN) (which corresponds to the nitrogen
194 fraction soluble at pH4.6) and from the nitrogen content (NPN), corresponding to the nitrogen
195 fraction soluble in 12% trichloroacetic acid. NCN and NPN were measured according to the method
196 described by Gaucher et al. ²².

197 **2.6 Extraction and quantitation of sugars and organic acids by HPLC**

198 Sugars and organic acids in the samples were quantified using high performance liquid
199 chromatography (HPLC). The extraction method was adapted from that described by Leyva Salas et
200 al.²³. Briefly, frozen samples were first thawed and equilibrated for 3 h at room temperature. Then
201 milk samples were directly diluted 40-fold in the H₂SO₄ solution (0.005 M) and filtered in
202 Vivaspin® 2 (10 kDa MWCO) by centrifugation at 9000 g for 20 min. Curd and cheese samples
203 were first blended in deionized water at 40°C (1:4 w/w) in a filter bag and incubated at 40°C for 1
204 h. The suspensions were then centrifuged (3000 g, 30 min, 4°C) and the supernatants filtered on
205 Whatmann 40 paper. The filtrates were diluted in the H₂SO₄ solution (0.005 M): 6-fold for C_m
206 curds, 4-fold for C_{dm} curds and C_{ow} cheeses, and 2-fold for ripened cheeses (C_{4w} and C_{7w}). The
207 diluted filtrates were then filtered once more (CHROMAFIL® Xtra PVDF-45/13, 0.45 µm pore
208 size, Machery-Nagel GmbH & Co. KG, Germany). HPLC analysis and the identification of
209 metabolites were performed according to the method described by Leyva Salas et al. (2019)²³.

210 **2.7 Analysis of volatile compounds by GC-MS**

211 Volatile compounds were analyzed using headspace (HS) trap extraction coupled to gas
212 chromatography-mass spectrometry (GC-MS). The principle of HS-CGMS has been described
213 elsewhere in detail, including the linearity ranges and limit of detection of 6 of the compounds
214 identified in the present study²⁴. The samples were injected in a random order, with standards
215 (mixture of nine volatiles: four esters (ethyl acetate, ethyl propanoate, ethyl butanoate and ethyl
216 hexanoate), two aldehydes (3-methylbutanal and benzaldehyde), two ketones (2-heptanone and 2-
217 nonanone), 2,3-butanedione, dimethyl disulfide and 3-methylbutanol) and blank samples (boiled
218 deionized water) to monitor possible MS drift and carryover. Compounds were eluted on an Elite-
219 WAX ETR (30 m x 0.25 mm ID x 0.25 µm, PerkinElmer USA) column. They were identified by
220 comparing their mass spectral data and linear retention indexes (LRI) calculated on a polar column
221 with that of reference standard compounds, and with data from Library NIST 2008 (Scientific
222 Instrument Services, Ringoes, NJ, USA) and PubChem. The data were processed as described
223 elsewhere²⁴. Briefly, raw data files were converted to time- and mass-aligned chromatographic

224 peaks areas, using the XCMS open source package implemented with the R statistical language²⁵.
225 The volatile compounds were semi-quantified using the abundance of one selected mass fragment
226 (m/z), in arbitrary units. Moreover, previous calibration curves of diacetyl spiked in cream²³ were
227 used to calculate approximate concentrations of diacetyl in milk after prematuration step.

228 **2.8 Statistical analysis**

229 The effect of ripening time, process parameters and their interactions were considered to
230 quantitatively identify, without bias, levers for organoleptic quality. Data were analyzed in a mixed
231 model framework, which explicitly accounted for the correlations between repeated measurements
232 within each type of cheese making, as follows:

$$233 \quad y_{ijkl} = \mu + I_i + SS_j + (I * SS)_{ij} + CM_k + \epsilon_{ijkl} \quad (1)$$

234 where y_{ijkl} is the observed quantity of metabolites l under itinerary i (Std, Stir15min, Salt7h,
235 Rip16°C) at the sampling stage j (M_{LAB} , M_{LAB+P} , C_m , C_{dm} , C_{0w} , C_{4w} , C_{7w}) for cheese making k (1, 2,
236 3, 4). The symbols I and SS represent the fixed effects due to the itinerary and the sampling stage,
237 respectively. $(I * SS)$ is the interaction effect between the itinerary and the sampling stage. The
238 symbol CM refers to the random effects of cheese making, and accounts for the correlation between
239 repeated measurements within each cheese making cycle. We assumed that CM_k are independent
240 and normally distributed and that ϵ_{ijkl} followed the normal probability distribution with a mean
241 equal to zero. We also assumed the independence between these random effects and ϵ_{ijkl} .

242 Three models of mixed analysis of variance were performed depending on the question and
243 available data and were fitted by maximizing the log-likelihood using the *nlme* R package.

244 - *Effect of milk maturation on milk composition*

245 We first analyzed four variables (two bacterial counts, pH, dry matter and 10 metabolites and
246 volatile compounds, see above) measured at the first two sampling stages under the standard
247 itinerary. Model (1) was simplified into a model with a single fixed effect due to the sampling stage
248 (M_{LAB} , M_{LAB+P}) and the cheese making random effect. From the test of the fixed effect, we

249 considered metabolites and volatile compounds with p-values lower than 0.05 as being statistically
250 different between the M_{LAB+P} and M_{LAB} sampling stages.

251 - *Comparison of the four itineraries during ripening*

252 We focused on the compounds measured during all four itineraries (standard + three variants) at the
253 three last sampling stages (C_{0w} , C_{4w} , C_{7w}). For each compound, we first of all tested the significance
254 of the interaction term in the model (1) using a likelihood ratio test, and only retained it in the
255 model if the p-value was greater than 0.05. In a second step, we computed estimated marginal
256 means for the itinerary fixed effect and performed comparisons between each variant in the itinerary
257 (Stir15min, Salt7h and Rip16°C) and the standard itinerary (Std) using the *emmeans* R package.
258 Raw p-values were adjusted for multiple comparisons using the Tuckey method and the level of
259 significance was fixed at 0.05. For the ($I \times PS$) interaction, the sum of the values for the five
260 production stages was divided by 5, and the results were subsequently referred to as the “global
261 mean” of all production stages. For the ($I \times RS$) interaction, the sum of the values for the three
262 ripening stages was divided by 3 and the results were subsequently referred to as the “global mean”
263 for ripening stages (2). The global means under the variant conditions were then compared to the
264 standard.

265 Plate counts, pH and dry matter content at each production stage were expressed as means in four
266 biological replicates for the standard itinerary, and two replicates for the variant itineraries. Other
267 concentrations were expressed as means in two biological replicates for both the standard and
268 variant itineraries.

269 - *Impact of sampling stages*

270 We analyzed 27 variables (three bacterial counts, pH, salt, dry matter and 21 metabolites and
271 volatile compounds) from the five last sampling stages (C_m , C_{dm} , C_{0w} , C_{4w} , C_{7w}) under the
272 Stir15min and Std itineraries. We followed the same two-step procedure as described in the
273 paragraph above.

274 All these analyses were implemented using R software version 3.6.1.

275 - *Principal Component Analysis*

276 A principal component analysis (PCA) was performed with 31 centered and scaled variables (three
277 bacterial counts, expressed as log-transformed data, pH, dry matter, MFFB, Ca₂, Cl, NCN, NPN
278 and 21 metabolites and volatile compounds) for the 32 cheese samples, using XLSstat for Microsoft
279 Excel (Addinsoft 2019, <https://www.xlstat.com>).

280

281 **3 RESULTS**

282 **3.1- Evolution of composition during cheese manufacture and ripening**

283 Dry matter (DM) and pH were chosen as physicochemical indicators to assess the repeatability and
284 reproducibility of the **Std** cheese. These parameters were monitored in four biological repetitions of
285 the cheese (**Figure 2**). Before cheese making, the M_{LAB} milk contained 11.65 ± 0.26 g/100 g DM
286 and the pH was 6.59 ± 0.02 . At the molding stage, the DM content in cheese was around $40.53 \pm$
287 3.21 g/100 g. It then rose progressively with pressing to reach 52.03 ± 1.37 g/100 g at demolding.
288 The DM content remained stable thereafter. The pH in cheese fell from 6.36 ± 0.05 to 5.45 ± 0.07
289 during molding and remained at around 5.19 ± 0.06 until the end of ripening. For the DM content
290 and pH, the standard deviation (SD) was less than 3% of the mean value at all stages, thus
291 confirming the repeatability and reproducibility of Std cheese manufacture. The only exception was
292 observed regarding DM at molding, where the SD was 8%. This relatively high SD value was due
293 to the non-homogeneity of the fresh cheese sample at that time.

294 In order to evaluate the influence of variant itineraries on the physicochemical evolution of cheese,
295 six composition parameters (i.e., DM, pH, protein, fat, calcium and chloride) were monitored
296 throughout the production of cheeses under both the standard and variant itineraries.

297 The physicochemical composition of cheeses at each production stage is summarized in Table 3.

298 The evolution of pH in variant cheeses displayed similar behavior and no significant differences

299 were found compared to the Std cheese. The global mean DM content in Stir15min cheese was
300 3.9% lower than in the Std cheese, which corresponded to a difference of 1.98 g/100g cheese
301 ($p < 0.05$). Salt7h cheese also contained significantly less DM than the Std cheese and the difference
302 was 1.5% ($p < 0.05$).

303 The total protein and fat contents in dry matter did not vary during production regardless of the
304 itinerary. Their contents were around 42.6 g/100g DM for total protein and 47.9 g/100 g DM for fat.
305 However, the moisture content in the fat-free basis (MFFB) of cheese was significantly higher in
306 Stir15min cheese than in the Std cheese ($p < 0.001$), with a difference of 2.4%. This was due to a
307 lower DM content in **Stir15min** cheese.

308 The calcium content in Std cheese increased gradually from 0.61 ± 0.09 g/100g cheese at molding
309 to 0.74 ± 0.04 g/100g at the end of ripening. Compared to **Std**, the **Stir15min** itinerary induced a
310 significantly lower calcium content in cheese (-5.9%, $p < 0.05$). However, the calcium content in dry
311 matter did not differ significantly ($p > 0.1$). The chloride level in the core of the **Std** cheese were
312 initially 0.35 ± 0.05 g/100g, corresponding to 0.72 ± 0.08 g/100g moisture. This increased over time
313 to reach 0.83 ± 0.03 g/100 g cheese at four weeks of ripening, and was then maintained at around
314 0.8 g/100g (1.8 g/100g moisture) during the later ripening period. Chloride levels in cheese and in
315 the moisture fraction were both significantly affected by the interaction between the ripening stage
316 and the itinerary ($I \times RS$). **Stir15min** cheese displayed a much more rapid rise in the chloride
317 content during the early ripening period and this was ultimately 10.9% higher than in the cheese
318 ($p < 0.05$). Compared to the **Std** cheese, the **Salt7h** cheese contained 8.6% less chloride in the cheese
319 ($p = 0.054$) and 10.9% less chloride in moisture ($p < 0.05$).

320 **3.2- Overview of bacterial evolution during cheese manufacture and ripening**

321 During the present study, the kinetic growth of the bacterial consortium was monitored during
322 cheese production according to the standard itinerary (**Std**). This enabled an assessment of the
323 repeatability and reproducibility of the **Std** cheese and the construction of a standard profile for

324 microbial evolution in a model cheese (**Figure 2**). The standard deviation of population values was
325 less than 0.5 log₁₀ units for all bacterial strains at all stages, thus confirming the repeatability and
326 reproducibility of the **Std** cheese.

327 The *L. lactis* and *L. plantarum* strains were inoculated in standardized milk at 5.7 and 5.2 log₁₀
328 CFU/g, respectively, while *P. freudenreichii* was inoculated at 6.1 log₁₀ CFU/g in matured milk.
329 During the prematuration step (14°C for 18 h), the *L. lactis* population increased significantly
330 (p<0.001) to reach 7.5 log₁₀ CFU/mL in the mature milk with an average doubling time (DT)
331 estimated at 3.1 h, while *L. plantarum* grew very slowly (DT = 19.7 h). Following molding, the
332 bacteria in milk were concentrated by approximately ten-fold in curd, so that *L. lactis*, *L. plantarum*
333 and *P. freudenreichii* levels in molded cheese (C_m) reached at 8.6, 6.4 and 7.0 log₁₀ CFU/g,
334 respectively. The *L. lactis* population reached the highest level before ripening (9.2 log₁₀ CFU/g)
335 and then fell slightly to reach 8.5 log₁₀ CFU/g at the end of ripening. *L. plantarum* grew rapidly
336 during molding (DT = 5.4 h); the highest population was reached at four weeks of ripening (8.4
337 log₁₀ CFU/g) and remained stable thereafter. The growth of *P. freudenreichii* occurred during
338 molding (DT = 5.4 h) and the first four weeks of ripening. The final population of *P. freudenreichii*
339 reached 8.5 log₁₀ CFU/g.

340 **Table 2** summarizes the populations of each strain and in the four cheese types. In **Stir15min**
341 cheese, the global mean of the *L. lactis* population was significantly lower than in **Std** cheese
342 (p<0.05). However, the difference was less than 0.5 log₁₀ units at each production stage. During the
343 ripening period, a significant (I × RS) interaction effect was detected for *L. lactis* (p<0.001), which
344 means that the course of its evolution during ripening stages was dependent on the itinerary.
345 Between 0 to 7 weeks of ripening, the population of *L. lactis* decreased under both **Std** and
346 **Rip16°C** itineraries, but this fall was more marked under **Rip16 °C** than **Std** (-1.43 and -0.61 log₁₀
347 CFU/g, respectively). After seven weeks of ripening, the *L. lactis* population in Rip16°C cheese
348 was significantly lower than in **Std** cheese (p<0.001) with a difference of 0.8 log₁₀ units.

350 **3.3- Evolution of nitrogen fractions**

351 **Figure 3** shows the evolution of nitrogen fractions under all itineraries. In standard conditions,
352 NCN represented less than 6% of total nitrogen (TN) before ripening, and NPN was lower than 2%
353 TN. At the start of ripening, the nitrogen fractions in cheese at 13°C increased rapidly and reached
354 $14.3 \pm 0.6\%$ for NCN and $5.8 \pm 0.1\%$ for NPN at four weeks of ripening. Thereafter, the nitrogen
355 fraction contents continued to increase but at a lower rate. By seven weeks of ripening, the Std
356 cheese contained $16.7 \pm 0.1\%$ NCN and $7.2 \pm 0.2\%$ NPN.

357 The nitrogen fractions in **Stir15min** and **Salt7h** cheeses did not differ from those in the **Std**.
358 However, cheese ripened at 16°C (**Rip16°C**) displayed significantly higher levels of proteolysis
359 ($p < 0.05$) when compared to the **Std** cheese, with an NCN content of $18.06 \pm 0.69\%$ (+ 8.2%) and a
360 NPN content of $8.90 \pm 0.08\%$ (+23.2%) after seven weeks of ripening. An interaction between the
361 effects of ripening stage and itinerary was observed for the NPN content, which increased much
362 more rapidly at a higher ripening temperature.

363 **3.4- Evolution of sugar and organic acid levels in milk and cheese during production**

364 The complete metabolome of milk before and after prematuration can be seen in **Table 4**. Lactose
365 and citric acid (48 and 2 g/L, respectively) were the two main carbon sources in milk and did not
366 vary significantly after prematuration. Lactic acid was only detected in matured milk. The acetic
367 acid content increased significantly by 3.4-fold ($p = 0.09$) during prematuration. Notable changes to
368 the volatile profile were also observed, with an increase in several compounds in mature milk:
369 hexanoic acid (1.2-fold), octanoic acid (1.7-fold), diacetyl (17.6-fold) ($p < 0.05$) and acetoin (6.2-
370 fold, $p = 0.054$).

371 Overall, 12 molecules were detected, including two sugars (lactose and galactose) and eight organic
372 acids (pyruvic, citric, succinic, lactic, acetic, propanoic, butanoic and phenyllactic acids), as well as
373 two ketones (diacetyl and acetoin). However, the levels of diacetyl and acetoin were too low to be

374 reliably quantified by HPLC, so instead they were semi-quantified from GC-MS data. According to
375 the previously published calibration curve ²⁶ diacetyl reached between 300 and 400 ng/g of milk
376 during the prematuration step.

377 **Table 5** presents the concentrations of ten compounds in both standard and variant cheeses
378 throughout manufacture and ripening. All molecules displayed significant variations in their
379 concentrations in the cheeses during production ($p < 0.001$). Based on the trends in evolution, three
380 groups of molecules were distinguished: (a) lactose and citric acid were consumed over time, (b)
381 galactose and lactic acid were first produced during cheese manufacture and then consumed, and (c)
382 pyruvic, succinic, acetic, propanoic, butanoic, phylactic acids were produced and accumulated over
383 time (**Figure 4**). During the standard cheese manufacture, lactose levels fell rapidly during molding
384 to reach less than 10 g/kg by demolding. Lactose continued to be consumed thereafter and the level
385 was at 0.79 ± 0.06 g/kg by seven weeks of ripening. Citric acid concentrations decreased to $0.15 \pm$
386 0.01 g/kg in cheese before ripening and were not detectable in ripened cheeses. Levels of other
387 organic acids rose throughout production, especially during the ripening period.

388
389 The **Stir15min** itinerary was compared with the standard itinerary throughout the production cycle
390 (**Table 5**). The interaction effect between itinerary and production stage ($I \times PS$) was significant for
391 citric, succinic, lactic and acetic acids ($p < 0.05$). **Stir15min** cheese had a lower citric acid content at
392 the molding stage (-16.5%), and a lower lactic acid content during the middle stages of cheese
393 production (around -10%). At the end of the ripening, it had a higher content in succinic (+ 40.2%)
394 and acetic acids (+18.3%). Other molecules did not display any significant ($I \times PS$) interaction
395 effect. However, the global mean of lactose contents was higher in **Stir15min** cheese (+43.5%),
396 while that of pyruvic and butanoic acids was lower (around -20%). Propanoic acid could only be
397 detected by HPLC during the ripening phase. The itinerary by ripening stage ($I \times RS$) interaction
398 effect was significant for propanoic acid because of its higher content in **Stir15min** cheese at seven
399 weeks of ripening (+13.6%). When all itineraries were compared during ripening, the ($I \times RS$)

400 interaction effect was significant for all molecules except galactose. The only difference between
401 the **Salt7h** cheese and **Std** cheese was the succinic acid content, which was +57.0% higher in the
402 latter. The **Rip16°C** cheese was the most contrasted sample. The levels of ten molecules differed
403 significantly from those in the **Std** cheese ($p < 0.05$). Six organic acids accumulated during ripening
404 (pyruvic, succinic, acetic, propanoic, butanoic and phenyllactic acids) and were produced more
405 rapidly in **Rip16°C** than in **Std** (**Figure 4 A-F**). The differences in concentration ranged from
406 34.1% to 158.7%, depending on the molecule ($p < 0.001$). The contents of these acids were also the
407 highest among all cheese types. By contrast, the lactic acid content in **Rip16°C** cheese by seven
408 weeks of ripening was 45.3% ($p < 0.001$) lower than in the **Std** cheese and the lowest among all
409 cheese types.

410 **3.5-Volatile compound profile in cheese**

411 A total of 14 volatile compounds was detected (**Table 6**), including four ketones (acetone, butan-2-
412 one, diacetyl, acetoin), six acids (acetic, propanoic, butanoic, hexanoic, octanoic, and
413 methylbutanoic acids), three alcohols (propan-1-ol, 2-methylbutan-1-ol and 1-hydroxypropan-2-
414 one), and one sulfur compound (dimethyl disulfide). All compounds were detectable in cheese from
415 the molding stage, but they varied in abundance over manufacture and ripening. Propan-1-ol, 2-
416 methylbutan-1-ol, DMDS and the acids were produced abundantly during ripening and their
417 abundance increased as a function of ripening time. In cheeses ripened for four and seven weeks the
418 high concentrations in acetic, propanoic and butanoic acids induced an overloading of the GC
419 capillary column, thus impairing the accuracy of their quantification. These three acids were
420 therefore quantified using HPLC and only their later concentrations were considered for statistical
421 analyses (**Table 5**).

422 The comparison between **Std** and **Stir15min** cheeses showed a significant ($I \times PS$) interaction
423 effect for 2-methylbutanol, 2-methylbutanoic acid ($p < 0.05$). **Stir15min** cheese always contained
424 higher levels of those two molecules during the ripening period, while the difference *versus* the **Std**
425 cheese diminished with ripening time (**Figure 4G and 4H**). After seven weeks of ripening, the 2-

426 methylbutanol and 2-methylbutanoic acid contents in **Stir15min** cheese were more than 10% higher
427 than in Std. **DMDS** was significant in both (I × PS) and (I × RS) interaction effects, as the
428 **Stir15min** cheese contained 51.8% (p<0.001) less DMDS than **Std** at the end of ripening. As for
429 molecules where the interactions were not significant, the global mean of diacetyl and acetol
430 intensities in ripened cheese was lower in **Stir15min** cheese, the difference being -47.0% (p<0.1)
431 and -35.8% (p=0.056), respectively.

432 During ripening, the volatile compound profile of **Salt7h** cheese did not differ from that of **Std**.
433 Concerning the **Rip16°C** cheese, the (RS × I) interaction effect was significant for 2-methylbutanol,
434 2-methylbutanoic and hexanoic acids (p<0.001). Compared to the **Std** cheese, the contents in 2-
435 methylbutanol (p<0.001), 2-methylbutanoic (p<0.05) and hexanoic acids (p<0.1) were higher at
436 four weeks of ripening (**Figure 4G-I**). At the end of ripening, the **Rip16°C** cheese contained
437 +82.7% 2-methylbutanol, +60.4% 2-methylbutanoic and +49.8% hexanoic acids (p<0.001).

438 **3.6- Global analysis of the cheese curd profile during cheese production**

439 As shown in **Figure 5**, PCA was performed on 31 variables describing the microbial and
440 biochemical composition of the cheeses. The first two principal components (F1 and F2) accounted
441 for 83.04% of total variability. F1, which described 62.65% of variability, was positively associated
442 with proteolysis parameters, the NaCl content, viable counts of *L. plantarum* and *P. freudenreichii*
443 and most acids and alcohols (**Figure 5A**). By contrast, F1 was negatively associated with viable
444 counts of *L. lactis*, pH, and the contents in sugars and citric acid, two ketones (acetone, butan-2-
445 one) and MFFB. F2, which accounted for 20.38% of variability, was positively correlated with
446 contents in diacetyl, acetoin, lactic acid and acetol, and viable counts of *L. lactis*.

447 The observation map (**Figure 5B**), showed five cheese groups distinguished as a function of
448 ripening stages. Fresh cheese curds collected at the molding stage (C_m) appeared in the low left
449 quadrant. At the manufacturing steps, the points corresponding to demoulding (D) and after salting
450 (C0w) moved vertically and positively along F2 axis concomitantly to *L. lactis* growth, lactate,

451 acetol and diacetyl production. Cheeses after demolding (D) and at the start of ripening (C_{0w})
452 showed similar profiles and were located together in the upper left quadrant. During ripening, points
453 progressively moved positively along F1 axis and negatively along F2 axis concomitantly with *L.*
454 *plantarum* and *P. freudenreichii* growth, reduction of lactate, acetol, diacetyl and production of
455 esters and proteolysis. Cheeses ripened for four weeks (C_{4w}) and seven weeks (C_{7w}) were mainly in
456 the upper right and lower right quadrants, respectively. Fresh curds were negatively associated with
457 F1 and were therefore characterized by higher pH values, moisture and lactose contents, and viable
458 *L. lactis* counts. Ripened cheeses (C_{4w} and C_{7w}) were mainly associated with higher counts of *L.*
459 *plantarum* and *P. freudenreichii*, higher proteolysis levels and higher contents in most flavor
460 compounds. Demolded cheeses (C_{dm}) and young-aged cheeses (C_{0w}) were separated from cheeses
461 at molding (C_m) and old-aged cheeses on the F2 and were characterized by high *L. lactis* counts and
462 higher contents in acetoin, diacetyl, lactic acid, and acetol. In order to facilitate comparison of the
463 four cheese types, the cheeses samples were color-coded relative to the itinerary applied (**Figure**
464 **5B**). In the groups of cheeses before ripening, the cheeses produced with variant processes were not
465 differentiated from the Std cheese. However, during ripening, cheese ripened at 16°C for four
466 weeks displayed the same profile as the cheese ripened at 13°C for seven weeks. The accelerated
467 ripening at higher temperature was more obvious among cheeses ripened at 16°C for seven weeks.
468 Their profiles contrasted with other cheeses, revealing the highest aroma content and more
469 advanced proteolysis.

470 **4- Discussion**

471 **4.1- Standard cheeses as a model cheese**

472 In this work, we developed a model semi-hard cheese with high reproducibility (less than 3% of
473 variation) in terms of moisture (54%), fat/dry matter (48%), protein/dry matter (42%) and growth of
474 starter and ripening bacterial species. For that purpose, we focused in particularly on optimizing the
475 cutting size of curd before stirring, the molding step, the pressing step using a horizontal press and
476 progressive pressing, and the use of plastic vacuum bags to prevent any microbial contamination of

477 the cheese surface during ripening. We grew our home-made starter cultures using publicly
478 available strains obtained from the CIRM-BIA collection. The ability of *L. lactis* ssp. *lactis* biovar.
479 *diacetylactis* CIRM-BIA1026 to produce diacetyl, and the previous observation of low lysis under
480 carbon source deficiency conditions (data not shown) were features of interest in this work. *L.*
481 *plantarum* and *P. freudenreichii* were chosen as adjunct bacteria as they contribute to cheese texture
482 and flavor by proteolysis and the production of flavor components²⁷. Compliance with the schedule
483 guaranteed a highly reproducible growth of each strain separately during preparation of the
484 inoculum and overall in the milk during the prematuration step and in cheeses. We suggest that this
485 model cheese could be reproduced by other scientists interested in the biochemistry of semi-hard
486 cheeses. Until now, most scientific studies performed on cheese have used Cheddar cheese^{2,28,29}
487 which is produced in large quantities throughout the world but which includes a specific step of dry
488 salting (salt is added directly to the grains: cheddarization). The production of our model cheese,
489 which includes a brine salting step, is representative of a broader panel of semi-hard cheeses such as
490 Tommes, Raclette, Edam, Gouda, Manchego, Provolone and Castelmagno cheeses.

491

492 **4.2 - Microbial and biochemical changes in Std cheese**

493 The activity of microorganisms during cheese making and ripening induces modifications to all
494 curd constituents which in turn leads to the development of cheese flavor. Flavor development is a
495 dynamic biochemical process that is influenced by (i) the type and composition of milk, (ii)
496 processing parameters, and (iii) the microorganisms and enzymes present in the cheese matrix. The
497 cheese microbiota is the primary source of enzymes that influence flavor development through the
498 degradation of carbon sources, proteins and lipids.

499 **4.2.1- Utilization of lactose, production of lactic and acetic acids by LAB**

500 The conversion of lactose to lactic acid is essential for the production of all types of cheeses
501 involving a bacterial acidification step. Lactic acid causes acidification and a refreshing acid taste,
502 which is particularly noticeable in young cheeses. In the **Std** cheese we followed the degradation of

503 lactose in milk, in curd and in cheeses up to seven-week ripened cheeses. As expected, the
504 utilization of lactose was very rapid during the acidification of milk and curd and was concomitant
505 with *L. lactis* growth. It occurred during the prematuration step and the acidification of curd during
506 pressing (**Figure 1; Table 5**) and 80% of lactose was consumed at the demolding step. The *L.*
507 *plantarum* strain was also able to use lactose (API gallery results, data not shown) and to produce
508 lactic acid. Lactose levels were very low (nearly zero) as from the fourth week of ripening.
509 Acidification was progressive during ripening because no fungi used the lactic and acetic acids
510 released by lactic acid bacteria. Acetic acid could be produced by all three strains and probably
511 resulted from the successive fermentations by *L. lactis*, *L. plantarum* and then *P. freudenreichii*
512 during ripening, the latter being the main contributor, as suggested by the time-course of production
513 (**Figure 4C**).

514

515 **4.2.2- Utilization of citric acid, production of diacetyl and acetoin by *L. lactis***

516 Citric acid is another carbon source for certain lactic acid bacteria strains. The strain of *L. lactis*
517 used during the present study belongs to the biovar *diacetylactis*. As early as the prematuration step
518 in the milk tank at 14°C (M_{LAB+P}), it produced high levels of diacetyl (**Table 4**, fold change × 17.6)
519 and consumed high levels of citric acid (**Table 4**, 90% at the demolding step) in line with the
520 findings of Passerini et al.³⁰. The high production of diacetyl during the early stage of cheese
521 production imparts the formation of a buttery flavor. Oxygen is required for this synthesis³¹.
522 Diacetyl production could also be explained by the introduction of oxygen being pumped and
523 stirred in the prematuration tank³². The production of diacetyl reached its highest level after four
524 weeks of ripening. The diacetyl content had fallen by the end of the ripening, which probably
525 resulted from its reduction into acetoin by lactic acid bacteria. Acetoin is generally produced in
526 much larger quantities, *i.e.* 10- to 50-fold higher than diacetyl concentrations³³. It is noteworthy
527 that the partial removal of lactoserum, which was replaced by warm water before molding, led to
528 the loss of one quarter of the diacetyl (and other soluble metabolites) produced before this step.

4.2.3- Primary and secondary proteolysis, a necessary step for volatile production by the bacterial consortium

Proteolysis is essential to flavor formation. The production of small peptides and free amino acids results from the activity of the added coagulant and/or of milk plasmin, in conjunction with cell envelope microbial proteinases and cytoplasmic peptidases³⁴. Short peptides and amino acids contribute to the basic flavor of cheeses. Free amino acids are further catabolized into many soluble and volatile compounds. Some of these compounds impact cheese aroma, such as volatile carboxylic acids, aldehydes and alcohols. A range of amino acid-converting enzymes are involved in their formation^{35,36}.

Primary and secondary proteolysis principally occurred during the four first weeks of ripening (**Figure 3**). According the literature, the primary proteolysis (**Figure 3**, NCN raising from 6 to 16 % of nitrogen fraction) is ensured by surface exposed protease from *L. lactis*, combined with those of *L. plantarum*. The secondary proteolysis (**Figure 3**, NPN) is difficult to attribute. Three aroma compounds derived from the catabolism of amino acids: 2-methylbutan-1-ol and 2-methylbutanoic acid likely resulted from the catabolism of isoleucine by *P. freudenreichii*.^{37,38} All of the corresponding pathways have been described as being expressed in *P. freudenreichii*³⁹. DMDS results from the catabolism of methionine³⁶.

4.2.4-Production of volatiles resulting from *P. freudenreichii* metabolism

P. freudenreichii produced aroma compounds via three main pathways: the fermentation of lactic acid, lipolysis, and branched-chain amino acid catabolism.

Lactic acid can be metabolized by a number of pathways to various compounds which may contribute to cheese flavor. *P. freudenreichii* is a ripening culture that is widely used in the manufacture of Swiss-type cheeses, where it uses lactic acid as the main carbon source⁴⁰.

Consequently, its growth is reliant on the consumption of lactic acid only. *P. freudenreichii*

554 converts lactic acid into propanoic acid, acetic acid and carbon dioxide. Unlike acetic acid and
555 carbon dioxide, which are also produced by LAB, propanoic acid was only produced by *P.*
556 *freudenreichii*. It accumulated gradually in the cheese during ripening.

557 Milk fat is another essential source for the development of cheese flavor during ripening. Lipolysis,
558 i.e. the hydrolysis of milk fat by lipolytic esterases, results in the formation of free fatty acids
559 (FFAs, namely acids in **Table 6** and **Figure 5**), which even at low concentrations will contribute to
560 cheese flavor, either positively (desirable pungent notes) or negatively (rancid notes), depending on
561 the type of cheese^{41,42}. FFAs also act as precursors for certain flavor compounds such as
562 methylketones, secondary alcohols, esters, and lactones³⁴.

563 Microorganisms are the principal sources of lipolytic enzymes in cheese. In ripened cheese
564 involving *P. freudenreichii* fermentation, the species is considered to be the main actor in milk fat
565 lipolysis. It has been demonstrated that *P. freudenreichii* is responsible for the formation of up to
566 96% of FFAs in Emmental cheeses⁴³, thanks to the activity of an extracellular lipolytic esterase⁴⁴.
567 By contrast, LAB esterases have received much less attention because they are mainly intracellular
568 and have weak lipolytic activity on milk fat^{41,42}. In our model cheese, the butanoic and hexanoic
569 acids generated during ripening likely resulted from lipolysis by *P. freudenreichii*.

570

571 **4.3- Influence of the fine-tuning of process parameters on the profile of aroma compounds**

572 **4.3.1- Effect of a reduced salting time on the formation of aroma compounds**

573 The **Sal7h** itinerary differed from **Std** by a 10.9% reduction in the salt concentration of the water
574 phase of cheese. It also resulted in a significant rise in succinic acid levels after seven weeks of
575 ripening (57%, **Table**). This delayed effect on succinic acid could be explained by the slow
576 diffusion of salt (sodium chloride) to the cheese core. Indeed, in pressed and brine-salted cheeses,
577 diffusion rates range from 0.1 to 0.45 cm²/day⁴⁵. The results of chloride measurements showed
578 that NaCl was only dispersed homogeneously in the core of the cheese after four weeks of ripening,

579 in line with the size of the model cheeses (see 2.2). We can hypothesize that a lower salt
580 concentration in the core might activate bacterial metabolic activity and cause an accumulation of
581 succinic acid that cannot be degraded by any of the three inoculated species which do not possess a
582 complete tricarboxylic acid pathway capable of metabolizing succinic acid. To the best of our
583 knowledge, succinic acid exerts no influence on cheese flavor, but the lower salt level might
584 directly impact cheese taste (not tested). Therefore, under the conditions of the present study, the
585 reduction in salt did not modify the profile of aroma compounds. It is likely that the salt reduction
586 applied was not sufficiently contrasted; salt levels can affect both bacterial growth and metabolic
587 activities in a strain-dependent manner, as previously illustrated on *L. lactis*^{46,47} and *P.*
588 *freudenreichii* in Swiss-type cheeses^{48,49}.

589

590 **4.3.2- Effect of a reduced stirring time on the formation of aroma compounds**

591 A reduction in stirring time selectively reduced the buttery flavor-associated compounds produced
592 by *L. lactis* and increased the amounts of some compounds that are associated with “aged-cheese”
593 and ‘Swiss-cheese related flavor’ notes, and resulted from the activities of *P. freudenreichii*. At
594 both ripening times (after four and seven weeks), the reduction in stirring time that we applied
595 increased i) the lactose content throughout manufacture and ripening (**Table 4 and 5**), ii) the NaCl
596 content (**Table 3**), iii) the secondary proteolysis during ripening (**Figure 3**), iv) moisture during
597 cheese making (**Table 3**).

598 Because of the higher contents in lactose (>50 %) and MFFB, we expected that the LAB would
599 produce more lactic acid. However lactic acid content of **Stir15min** was not significantly higher
600 than in the **Std** cheeses. One explanation might be the counter-effect of salt (+10.9%) on the
601 overall equilibrium of the metabolic ecosystem, thus illustrating the complexity of predictive
602 microbiology when one process parameter exerts pleiotropic effects (salt, lactose, MFFB).

603 The slightly higher secondary proteolysis during ripening, currently attributed to higher bacterial
604 metabolic activities -since no lysis was observed- might rather have resulted from the proteolytic
605 activity of *L. plantarum*, as previously demonstrated for some *L. plantarum* strains in Cheddar
606 cheese^{50,51}. Moreover, Stir15min decreased DMDS (-52%, $p < 0.001$), diacetyl and acetol
607 concentrations (-47% and -36%; $p < 0.1$). The higher level of MFFB (+2.4% in ripened cheeses)
608 caused a positive effect on *P. freudenreichii* activity and significantly increased levels of aroma
609 compounds such as propanoic, acetic, butanoic and succinic acids (from +14% up to +159%;
610 $p < 0.05$), and 2-methylbutanol and 2- methylbutanoic acid, during the ripening period (+15% and
611 +16% at C7w, $p < 0.001$ and $p < 0.1$) (**Table 5**). It is noteworthy that the fine-tuning of stirring time
612 on the day of cheese making can lead to a drastic rise (+40.2%) in succinic acid levels, two months
613 after production.

614

615 **4.3.3- Effect of a higher ripening temperature on aroma compound formation**

616 After both periods of ripening, a higher ripening temperature significantly increased secondary
617 proteolysis ($p < 0.05$, **Figure 4**), the contents in aroma compounds (2-methylbutanol and carboxylic
618 acids such as acetic and propanoic acids) and lipolysis, as indicated by butanoic and hexanoic acids
619 (**Table**). The rise in acids seen during ripening (from +34% to 159%; $p < 0.001$ at 7 weeks of
620 ripening, **Table** , **Figure 4**) arose from *P. freudenreichii* metabolism. A higher lactic acid
621 consumption (-45.3 %, $p < 0.05$) was also a sign of more pronounced *P. freudenreichii* activity. The
622 ACP built from the global metabolome of cheeses (**Figure 5**) showed that cheeses ripened at 16°C
623 for four weeks displayed the same profile as the cheeses ripened at 13°C for seven weeks,
624 indicating that a three degree rise in the ripening temperature accelerated the maturing process by
625 three weeks. Similarly, in traditional Italian cheeses, an increase of 4°C in the ripening temperature
626 has been seen to promote the expression of genes related to proteolysis, lipolysis and amino
627 acid/lipid catabolism, and significantly increase the cheese maturation rate¹⁰. These authors
628 suggested the contribution of non-starter lactic acid bacteria to the aroma profile of cheeses.

629

630 **4.4 Bacterial populations little affected by process parameters**

631 The changes observed in the metabolome resulted from changes to bacterial activity and not from
632 differences in cultivable cell counts.

633 The variant itineraries modified the aromatic profile of cheese by modulating the metabolic activity
634 of the cheese community. This modulation could either be direct, *i.e.*, temperature changing the
635 metabolic activities of bacteria, and/or indirect, *i.e.*, stirring and salting time initially changed the
636 physicochemical composition of the cheese matrix, which in turn influenced bacterial activity.

637 It is generally accepted that process parameters can impact the growth of bacterial species during
638 food fermentation. Surprisingly, during our study, the changes made in variant itineraries did not
639 affect growth kinetics, probably because we only adjusted the process parameters to a minor and
640 insufficient extent. The only effect observed was a significant loss of the cultivability of *L. lactis*
641 during ripening, which might have resulted from both cell lysis and/or the switch from a cultivable
642 state to a viable but non-cultivable (VBNC) state^{52,53}. But although *L. lactis* cells are in a VBNC
643 state, their metabolic activity may still influence the aromatic profile of cheeses.

644

645 **4.5 Fine-tuning of process parameters to produce more healthy and hedonic cheeses**

646 Our aim during this work was to evaluate how fine-tuning of process parameters during the
647 production process modulate bacterial aroma compounds of cheese. The conclusions are that, even
648 without impact on microbial growth, fine-tuning of process parameters, like stirring time or
649 ripening temperature influence the final organoleptic quality of cheese by promoting specific
650 bacterial metabolisms. A higher ripening temperature and a shorter stirring time increased the
651 content in *Propionibacterium*-related aroma compounds. It would have been interesting to perform
652 sensory evaluations of the cheeses in order to determine whether the differences in flavor were
653 perceived and appreciated or not. However, a 10.9% reduction in salt content did not influence the

654 amount of quantified metabolites in the cheeses, excepted for succinic acid. It nevertheless remains
655 noteworthy that this shorter salting step would be beneficial to consumer health. Indeed, there have
656 been calls for decades for less salt in the diet in order to improve public health. The WHO
657 recommends a daily salt intake of less than 5 g/day⁵⁴, but in 2017 the global average salt intake
658 remained high and is still estimated at around 15 g/day⁵⁵. A shorter salting time that does not affect
659 aromatic profiles might offer an ideal solution for manufacturers to produce low-salt cheeses with a
660 shorter production time. Similar studies on reducing the salt content in cheese showed that Na-
661 reduced cheeses tasted bitter and were therefore organoleptically unsatisfactory⁵⁶. Further sensory
662 analyses involving less salty cheeses are necessary to confirm their organoleptic quality and
663 conclude as to the positive effects of a shorter salting time.

664

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671

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- 838

839 **Figure 1: Schematic representation of the standard cheese making itinerary and three variant**
840 **itineraries, and kinetic sampling throughout production.**

841

842 **Figure 2 Kinetic evolutions during cheese manufacture and ripening under the standard itinerary**
843 **regarding (A) viable counts of the three bacterial species, (B) dry matter and (C) pH. M_{LAB}: milk**
844 **containing lactic acid bacteria (*L. lactis* and *L. plantarum*); M_{LAB-P}: milk containing lactic acid bacteria**
845 **and *P. freudenreichii*; C_m: molded cheese; C_{dm}: demolded cheese; C_{0w}: cheese ripened for 0 weeks; C_{4w}:**
846 **cheese ripened for 4 weeks; C_{7w}: cheese ripened for 7 weeks. Values are the means of four biological**
847 **replicates of cheese production.**

848

849 **Figure 3: Evolution of (A) the non-casein nitrogen fraction (NPN) and (B) the non-protein nitrogen**
850 **fraction (NPN) throughout cheese production under the standard and variant itineraries. Std in black,**
851 **Stir15min in yellow, Salt7h in green, Rip16°C in red. Values are the means of four and two biological**
852 **replicates of cheese production for Std and others respectively.**

853

854 **Figure 4: Accumulation of pyruvic (A), succinic (B), acetic (C), propanoic (D), butanoic (E) and**
855 **phenyllactic acids (F), 2-methylbutanol (G), 2-methylbutanoic (H) and hexanoic acids (I) throughout**
856 **cheese production. ND: not detected. Std in black, Stir15min in yellow, Salt7h in green, Rip16°C in**
857 **red. Values are the means of four and two biological replicates of cheese production for Std and others**
858 **respectively.**

859

860 **Figure 5: Principal component analyses of microbial, physicochemical and biochemical components in**
861 **cheeses throughout production under the standard and variant itineraries. A: variables, B:**
862 **observations. Std in black, Stir15min in yellow, Salt7h in green, Rip16°C in red. M: molded cheese; D:**
863 **demolded cheese; C_{0w}: cheese ripened for 0 weeks; C_{4w}: cheese ripened for 4 weeks; C_{7w}: cheese**
864 **ripened for 7 weeks. Values are the means of four and two biological replicates of cheese production**
865 **for Std and others respectively. Ellipses were arbitrarily drawn to delimit group of samples to**
866 **facilitate reading.**

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1 **Table 1: Samples collected throughout cheese production and their corresponding analysis.**

Collection time	Sampling stage	Sample label	Microbial analysis	Physicochemical analysis					Biochemical analysis		
			Enumeration	pH	DM ⁽¹⁾	Ca ²⁺	Fat	NaCl	Protein (TP, NCN, NPN) ⁽²⁾	Sugars and organic acids	Volatile compounds
0.5 h	Milk inoculated with LAB	M _{LAB}	X	X	X	X	X	X	X	X	X
18 h	Milk inoculated with <i>P. freudenreichii</i>	M _{LAB+P}	X	X	X	X	X	X	X	X	X
19.5 h	Cheese at molding	C _m	X	X	X	X	X	X	X	X	X
21.5 h	Cheese molded for 2h	C _{m+2h}		X	X	X					
23.5 h	Cheese molded for 4h	C _{m+4h}		X	X	X					
2 nd day	Cheese at demolding	C _{dm}	X	X	X	X	X		X	X	X
3 rd day	Cheese before ripening	C _{0w}	X	X	X	X	X	X	X	X	X
4 weeks	Cheese ripened for 4 weeks	C _{4w}	X	X	X	X	X	X	X	X	X
7 weeks	Cheese ripened for 7 weeks	C _{7w}	X	X	X	X	X	X	X	X	X

2 (1) DM: Dry matter

3 (2) TP: Total protein; NCN: Non-casein nitrogen; NPN: Non-protein nitrogen.

4

5

1 **Table 2. Evolution of the populations of the three bacterial species during the production of model semi-hard cheeses manufactured according to one standard**
2 **and three variant itineraries ^a. These values are the means of two biological replicates. The last four columns present (I X PS) and (I X RS) interactions, as well as**
3 **the global mean of the bacterial population under the itinerary analyzed.**

4

Bacteria	Itinerary	Cheese production					Comparison between		Comparison between all	
		Manufacturing stage		Ripening stage			Stir15min and Standard at		variant itineraries and	
		C _m	C _{dm}	C _{0w}	C _{4w}	C _{7w}	all production stages		Standard at ripening stages	
						I × PS ^c	Global mean ^d	I × RS ^e	Global mean	
L. lactis	Standard	8.78 ± 0.07	9.12 ± 0.05	9.06 ± 0.00	8.95 ± 0.01	8.45 ± 0.02	NS ^f	8.87 ± 0.26	– ^h	
CIRM-BIA1206	Stir15min	8.66 ± 0.02	9.03 ± 0.12	9.05 ± 0.04	8.76 ± 0.15	8.39 ± 0.00		8.78 ± 0.27**	*** ^g	–
	Salt7h			9.01 ± 0.08	8.97 ± 0.03	8.52 ± 0.17		–		–
	Rip16°C			9.08 ± 0.02	8.76 ± 0.03	7.65 ± 0.08***		–		–
L. plantarum	Standard	6.49 ± 0.09	7.53 ± 0.03	7.92 ± 0.05	8.47 ± 0.02	8.47 ± 0.02	NS	0.26 ± 7.78	8.29 ± 0.29	
CRIM-BIA465	Stir15min	6.47 ± 0.10	7.41 ± 0.05	7.90 ± 0.10	8.42 ± 0.03	8.47 ± 0.13		0.27 ± 7.74	NS	8.27 ± 0.29
	Salt7h			7.96 ± 0.04	8.48 ± 0.07	8.52 ± 0.09		–		8.32 ± 0.28
	Rip16°C			8.00 ± 0.00	8.53 ± 0.01	8.56 ± 0.15		–		8.36 ± 0.29
P. freudenreichii	Standard	7.16 ± 0.09	8.04 ± 0.05	8.11 ± 0.03	8.56 ± 0.07	8.59 ± 0.00	NS	7.78 ± 0.78	8.42 ± 0.24	
CIRM-BIA122	Stir15min	7.08 ± 0.05	7.99 ± 0.05	8.20 ± 0.02	8.59 ± 0.07	8.63 ± 0.21		7.74 ± 0.78	NS	8.47 ± 0.23
	Salt7h			8.05 ± 0.11	8.57 ± 0.03	8.65 ± 0.11		–		8.42 ± 0.30
	Rip16°C			8.14 ± 0.00	8.67 ± 0.06	8.62 ± 0.08		–		8.48 ± 0.27

5 ^aA description of the itineraries is available in Figure 1

6 ^cI, itinerary; PS, all production stages.

7 ^dglobal mean is the estimated marginal mean

8 ^eRS, ripening stage.

9 ^fNS, not significant.

10 ^g*, p ≤ 0.1; **, p ≤ 0.05; ***, p ≤ 0.001.

11 ^h–, not relevant

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2 **Table 3. Physicochemical evolution of cheeses during the production of model semi-hard cheeses manufactured according to one standard and three variant**
3 **itineraries ^a. Reported values are the means of two biological replicates. The last four columns present (I X PS) and (I X RS) interactions, as well as the global**
4 **means of each composition under the analyzed itinerary.**

Parameters	Itinerary	Cheese production					Comparison between Stir15min and Standard at all production stages		Comparison between all variant processes and Standard at ripening stages	
		Manufacturing stages		Ripening stages			I × PS ^b	Global mean ^c	I × RS ^d	Global mean
		C _m	C _{dm}	C _{ow}	C _{aw}	C _{7w}				
pH	Std	6.36 ± 0.08	5.46 ± 0.12	5.32 ± 0.03	5.12 ± 0.05	5.14 ± 0.02	NS ^e	5.48 ± 0.48	NS	5.19 ± 0.11
	Stir15min	6.37 ± 0.01	5.50 ± 0.08	5.33 ± 0.07	5.13 ± 0.05	5.15 ± 0.02				
	Salt7h			5.32 ± 0.05	5.19 ± 0.06	5.14 ± 0.01				
	Rip16°C			5.33 ± 0.09	5.09 ± 0.01	5.18 ± 0.02				
Dry matter in cheese (g/100 g)	Std	40.53 ± 4.81	51.44 ± 0.15	52.28 ± 1.41	53.41 ± 0.03	53.55 ± 0.26	NS	50.24 ± 5.45	NS	53.08 ± 0.90
	Stir15min	37.39 ± 4.61	50.36 ± 0.15	50.85 ± 1.99	51.34 ± 1.13	51.39 ± 1.00				
	Salt7h			51.83 ± 1.48	52.59 ± 0.63	52.39 ± 1.70				
	Rip16°C			52.15 ± 1.93	53.41 ± 0.73	53.23 ± 0.42				
Protein in dry matter (g/100 g)	Std		41.59 ± 1.32	43.34 ± 0.13	42.41 ± 0.66	42.32 ± 0.17	– ^g	–	NS	42.69 ± 0.59
	Stir15min		42.91 ± 0.23	43.60 ± 0.45	41.91 ± 0.95	42.25 ± 0.58				
	Salt7h			43.26 ± 0.54	42.43 ± 0.53	42.33 ± 0.32				
	Rip16°C			42.66 ± 1.41	42.31 ± 0.69	42.84 ± 0.14				
Fat in dry matter (g/100 g)	Std		46.78 ± 1.42	48.15 ± 2.92	48.41 ± 0.03	47.50 ± 1.72	–	–	NS	48.02 ± 1.57
	Stir15min		47.90 ± 1.61	49.29 ± 0.03	47.54 ± 1.80	45.62 ± 0.72				
	Salt7h			48.71 ± 0.65	48.48 ± 0.09	46.31 ± 0.46				
	Rip16°C			48.86 ± 2.26	49.23 ± 1.44	46.50 ± 0.70				
MFFB ^h (g/100 g)	Std		63.96 ± 0.48	63.79 ± 0.00	62.84 ± 0.01	62.30 ± 1.02	–	–	NS	62.98 ± 0.82
	Stir15min		65.43 ± 0.56	65.58 ± 1.81	64.37 ± 1.82	63.50 ± 1.24				
	Salt7h			64.43 ± 1.07	63.63 ± 0.54	62.39 ± 0.74				
	Rip16°C			64.22 ± 0.76	63.21 ± 1.35	62.16 ± 0.70				
Calcium in cheese (g/100 g)	Std	0.61 ± 0.09	0.70 ± 0.03	0.73 ± 0.01	0.71 ± 0.01	0.74 ± 0.04	NS	0.70 ± 0.06	**	–
	Stir15min	0.55 ± 0.08	0.68 ± 0.03	0.67 ± 0.02 (-7.8%)**	0.67 ± 0.03	0.72 ± 0.02				
	Salt7h			0.73 ± 0.01	0.70 ± 0.01	0.72 ± 0.00				

	Rip16°C			0.75 ± 0.00	0.70 ± 0.01	0.71 ± 0.02		–		–
Calcium	Std	1.50 ± 0.04	1.36 ± 0.05	1.40 ± 0.02	1.33 ± 0.02	1.38 ± 0.08	NS	1.40 ± 0.07	**	–
in dry	Stir15min	1.46 ± 0.04	1.35 ± 0.07	1.33 ± 0.02	1.31 ± 0.02	1.40 ± 0.07		1.37 ± 0.07		–
matter	Salt7h			1.41 ± 0.03	1.33 ± 0.01	1.37 ± 0.04		–		–
(g/100 g)	Rip16°C			1.44 ± 0.05	1.31 ± 0.01	1.34 ± 0.04		–		–
Chloride	Std			0.35 ± 0.05	0.83 ± 0.03	0.85 ± 0.04	–	–	**	–
in cheese	Stir15min			0.41 ± 0.07	0.96 ± 0.08 (+16.7%)*	0.94 ± 0.03 (+10.9%)*		–		–
(g/100 g)	Salt7h			0.32 ± 0.03	0.76 ± 0.03	0.78 ± 0.07 (-8.6%)*		–		–
	Rip16°C			0.37 ± 0.10	0.85 ± 0.09	0.85 ± 0.03		–		–
Chloride	Std			0.72 ± 0.08	1.77 ± 0.07	1.83 ± 0.08	–	–	**	–
in water	Stir15min			0.83 ± 0.11	1.98 ± 0.12 (+11.6%)*	1.94 ± 0.02		–		–
(g/100 g)	Salt7h			0.66 ± 0.04	1.61 ± 0.03 (-9.3%)*	1.63 ± 0.08 (-10.9%)*		–		–
	Rip16°C			0.77 ± 0.18	1.82 ± 0.16	1.82 ± 0.05		–		–

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^a A description of the itineraries is available in Figure1

^b I, itinerary; PS, all production stages.

^c Global mean is the estimated marginal mean

^d RS, ripening stage.

^e NS, not significant.

^f *, $p \leq 0.1$; **, $p \leq 0.05$; ***, $p \leq 0.001$.

^g –, not analyzed

^h MFFB, moisture content in the fat-free basis of cheese.

1 **Table 4, Concentrations of sugars, organic acids and volatiles in milk before and after prematuration at 14°C for 18 h ^a**

Compounds	Before prematuration	After prematuration	Comparison	p-value
Lactose (g/kg milk)	48.44 ± 0.27	47.47 ± 0.52	– ^b	p>0.1
Galactose (g/kg milk)	0.22 ± 0.02	0.21 ± 0.04	–	p>0.1
Citric acid (g/kg milk)	2.23 ± 0.04	2.28 ± 0.02	–	p>0.1
Lactic acid (g/kg milk)	ND ^c	0.15 ± 0.01	–	p>0.1
Acetic acid (g/kg milk)	0.01 ± 0.00	0.04 ± 0.00	× 3.4	p = 0.090
propan-2-one (a.u. ^d)	5.01E+08	4.97E+08	–	p>0.1
butan-2-one (a.u. ^d)	1.42E+09	1.31E+09	–	p>0.1
Butane-2,3-dione (a.u. ^d) (diacetyl)	2.56E+07	4.50E+08	× 17.6	p = 0.049
3-Hydroxybutan-2-one (a.u. ^d)	5.39E+07	3.34E+08	× 6.2	p = 0.054
Hexanoic acid (a.u. ^d)	3.24E+07	3.72E+07	× 1.2	p = 0.046
Octanoic acid (a.u. ^d)	1.67E+04	2.77E+04	× 1.7	p = 0.026

2 ^a Reported values are the means of two biological replicates.

3 ^b –, not analyzed

4 ^c ND, not detected

5 ^d arbitrary units: volatile compounds were semi-quantified using the abundance of one selected mass fragment (m/z)

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1 **Table 5, Concentrations of sugars and organic acids during the production of model semi-hard cheeses manufactured according to one standard and three**
 2 **variant itineraries ^a.**

		Cheese production					Comparison between Stir15min and Standard throughout production		Comparison between all variant processes and Standard throughout ripening			
Compounds, g/kg	itinerary	Manufacturing stages		Ripening stages			I × PS ^b	Global mean ^c	I × RS ^d	Global mean		
		C _m	C _{dm}	C _{0w}	C _{4w}	C _{7w}						
Lactose	Std	22.19 ± 1.17	8.27 ± 0.10	6.24 ± 1.07	1.14 ± 0.09	0.79 ± 0.06	NS ^e	7.73 ± 8.22	– ^g	–		
	Stir15min	25.32 ± 5.72	11.79 ± 0.63	10.23 ± 1.26 (+63.8%)***	4.62 ± 0.97 (+306.1%)***	3.46 ± 0.44 (+337.7%)***		11.08 ± 8.45 (+43.5%) *** ^f			**	–
	Salt7h			6.98 ± 0.18	1.11 ± 0.27	0.59 ± 0.57		–			–	–
	Rip16°C			7.28 ± 0.77	0.71 ± 0.53	0.18 ± 0.15		–			–	–
Galactose	Std	0.77 ± 0.30	0.70 ± 0.07	0.44 ± 0.20	0.21 ± 0.03	0.16 ± 0.01	NS	0.45 ± 0.29	NS	0.27 ± 0.16		
	Stir15min	0.59 ± 0.24	0.60 ± 0.04	0.46 ± 0.16	0.18 ± 0.00	0.10 ± 0.01		0.38 ± 0.24		0.24 ± 0.18		
	Salt7h			0.44 ± 0.21	0.23 ± 0.03	0.11 ± 0.03		–		0.26 ± 0.18		
	Rip16°C			0.46 ± 0.20	0.15 ± 0.02	0.07 ± 0.02		–		0.22 ± 0.20		
Pyruvic acid	Std	0.06 ± 0.01	0.24 ± 0.05	0.34 ± 0.06	0.45 ± 0.14	0.64 ± 0.03	NS	0.35 ± 0.21	NS	–		
	Stir15min	0.05 ± 0.02	0.19 ± 0.03	0.26 ± 0.06	0.41 ± 0.04	0.53 ± 0.13		0.29 ± 0.19 (-16.5%)*		–		
	Salt7h			0.32 ± 0.07	0.41 ± 0.09	0.62 ± 0.09		–		–		
	Rip16°C			0.33 ± 0.07	0.61 ± 0.02	0.91 ± 0.12 (+40.3%)**		–		–		
Citric acid	Std	1.28 ± 0.03	0.25 ± 0.04	0.15 ± 0.01	0.00 ± 0.00	0.00 ± 0.00	***	–	NS	0.48 ± 0.15		
	Stir15min	1.50 ± 0.11 (-16.5%)***	0.26 ± 0.04	0.15 ± 0.01	0.00 ± 0.00	0.00 ± 0.00		–		0.40 ± 0.14		
	Salt7h			0.11 ± 0.05	0.00 ± 0.00	0.00 ± 0.00		–		0.45 ± 0.15		
	Rip16°C			0.16 ± 0.00	0.00 ± 0.00	0.00 ± 0.00		–		0.62 ± 0.27		
Succinic acid	Std	0.09 ± 0.01	0.20 ± 0.01	0.17 ± 0.04	0.29 ± 0.04	0.35 ± 0.06	**	–	***	–		
	Stir15min	0.09 ± 0.00	0.17 ± 0.02	0.16 ± 0.01	0.33 ± 0.01	0.49 ± 0.07 (+40.2%)**		–		–		
	Salt7h			0.12 ± 0.02	0.32 ± 0.01	0.55 ± 0.06 (+57.0%)**		–		–		
	Rip16°C			0.15 ± 0.02	0.50 ± 0.01 (+73.0%)***	0.91 ± 0.01 (+158.7%)***		–		–		
Lactic acid	Std	4.16 ± 0.16	10.38 ± 0.38	11.65 ± 0.20	13.05 ± 0.20	10.35 ± 0.38	**	–	***	–		
	Stir15min	3.43 ± 0.25	9.50 ± 0.87 (-8.5%)*	10.13 ± 0.10 (-13.0%)**	11.25 ± 1.02 (-13.8%)**	9.98 ± 0.01		–		–		
	Salt7h			10.89 ± 0.14	13.79 ± 0.03	10.87 ± 0.22		–		–		
	Rip16°C			10.78 ± 0.59	10.29 ± 1.16 (-21.1%)***	5.66 ± 0.58 (-45.3%)***		–		–		
Acetic acid	Std	0.40 ± 0.05	0.86 ± 0.08	1.01 ± 0.05	1.89 ± 0.16	2.56 ± 0.05	**	–	***	–		
	Stir15min	0.36 ± 0.03	0.91 ± 0.10	0.98 ± 0.05	1.88 ± 0.04	3.02 ± 0.42 (+18.3%)**		–		–		
	Salt7h			0.98 ± 0.05	1.97 ± 0.09	2.65 ± 0.40		–		–		
	Rip16°C			0.94 ± 0.10	2.53 ± 0.05 (+34.2%)**	3.43 ± 0.13 (+34.1%)***		–		–		
Propanoic	Std	ND ^h	ND	0.11 ± 0.01	3.13 ± 0.24	4.98 ± 0.02	–	–	***	–		

acid									
	Stir15min	ND	ND	0.14 ± 0.01	3.33 ± 0.25	5.65 ± 0.20 (+13.6%)**		–	–
	Salt7h			0.13 ± 0.00	3.57 ± 0.03	5.17 ± 0.57		–	–
	Rip16°C			0.15 ± 0.00	5.14 ± 0.15 (+63.9%***)	7.91 ± 0.23 (+58.9%***)		–	–
Butanoic acid	Std	0.13 ± 0.01	0.21 ± 0.02	0.27 ± 0.03	0.66 ± 0.22	0.68 ± 0.09	NS	0.39 ± 0.26	–
	Stir15min	0.12 ± 0.01	0.17 ± 0.01	0.23 ± 0.02	0.40 ± 0.16	0.59 ± 0.00		0.30 ± 0.19 (-23.1%)*	***
	Salt7h			0.24 ± 0.02	0.48 ± 0.03	0.61 ± 0.00		–	–
	Rip16°C			0.22 ± 0.00	0.72 ± 0.14	1.24 ± 0.15 (+82.3%***)		–	–
Phenyllactic acid	Std	0.01 ± 0.00	0.04 ± 0.00	0.04 ± 0.00	0.04 ± 0.00	0.06 ± 0.00	NS	0.04 ± 0.02	–
	Stir15min	0.01 ± 0.00	0.04 ± 0.01	0.04 ± 0.00	0.04 ± 0.00	0.07 ± 0.00		0.04 ± 0.02	***
	Salt7h			0.04 ± 0.00	0.04 ± 0.00	0.06 ± 0.00		–	–
	Rip16°C			0.04 ± 0.00	0.06 ± 0.00 (+34.5%**)	0.10 ± 0.02 (+65.6%***)		–	–

1 ^a Values are the means of two biological replicates.

2 ^b I, itinerary; PS, all production stages.

3 ^c Global mean is the estimated marginal mean

4 ^d RS, ripening stage.

5 ^e NS, not significant.

6 ^f *, p ≤ 0.1; **, p ≤ 0.05; ***, p ≤ 0.001.

7 ^g –, not analyzed

8 ^h ND, not detected

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1 **Table 6: Volatile compounds detected by GC-MS in cheese during the production of model semi-hard cheeses**

Chemical class	CAS Number	Volatile compounds ^a (abbreviated code or trivial name)	Identification ^b	LRI	m/z	Odor descriptor ^c
Ketones	67-64-1	Propan-2-one (acetone)	LRI, DB, S	804	58	Solvent; ethereal; apple; pear
	78-93-3	Butan-2-one	LRI, DB, S	892	72	Acetone-like ethereal fruity camphor
	431-03-8	Butane-2,3-dione (diacetyl)	LRI, DB, S	979	86	Strong butter sweet creamy pungent caramel
	513-86-0	3-Hydroxybutan-2-one (acetoin)	LRI, DB, S	1284	88	Sweet buttery creamy dairy milky fatty
	116-09-6	1-hydroxypropan-2-one (acetol)	LRI, DB	1298	43	Pungent sweet caramellic ethereal
Alcohols	71-23-8	Propan-1-ol	LRI, DB, S	1054	59	Alcoholic fermented fusel musty
	137-32-6	2-methylbutan-1-ol	LRI, DB, S	1231	70	Roasted wine onion fruity fusel alcoholic whiskey
Sulfur compounds	624-92-0	(Methyldisulfanyl)methane (DMDS: dimethyl disulfide)	LRI, DB, S	1068	94	Sulfurous vegetable cabbage onion
Acids	64-19-7	Acetic acid (C2)	LRI, DB, S	1448	60	Sharp pungent sour vinegar
	79-09-4	Propanoic acid (C3)	LRI, DB, S	1533	74	Pungent acidic cheesy vinegar
	107-92-6	Butanoic acid (C4)	LRI, DB, S	1631	60	Sharp acetic cheese butter fruit
	116-53-0	2-Methylbutanoic acid	LRI, DB, S	1674	87	Pungent acid roquefort cheese
	142-62-1	Hexanoic acid (C6)	LRI, DB, S	1829	60	Sour fatty sweat cheese
	124-07-2	Octanoic acid (C8)	LRI, DB, S	1933	60	Fatty waxy rancid oily vegetable cheesy

2 ^a IUPAC name

3 ^b Identification based on: LRI, calculated linear retention index; DB, mass spectral data from Library NIST 2008, and S, Standard.

4 ^c Odor descriptions from thegoodscentscompany.com and foodb. ca (2020).

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1 Figures

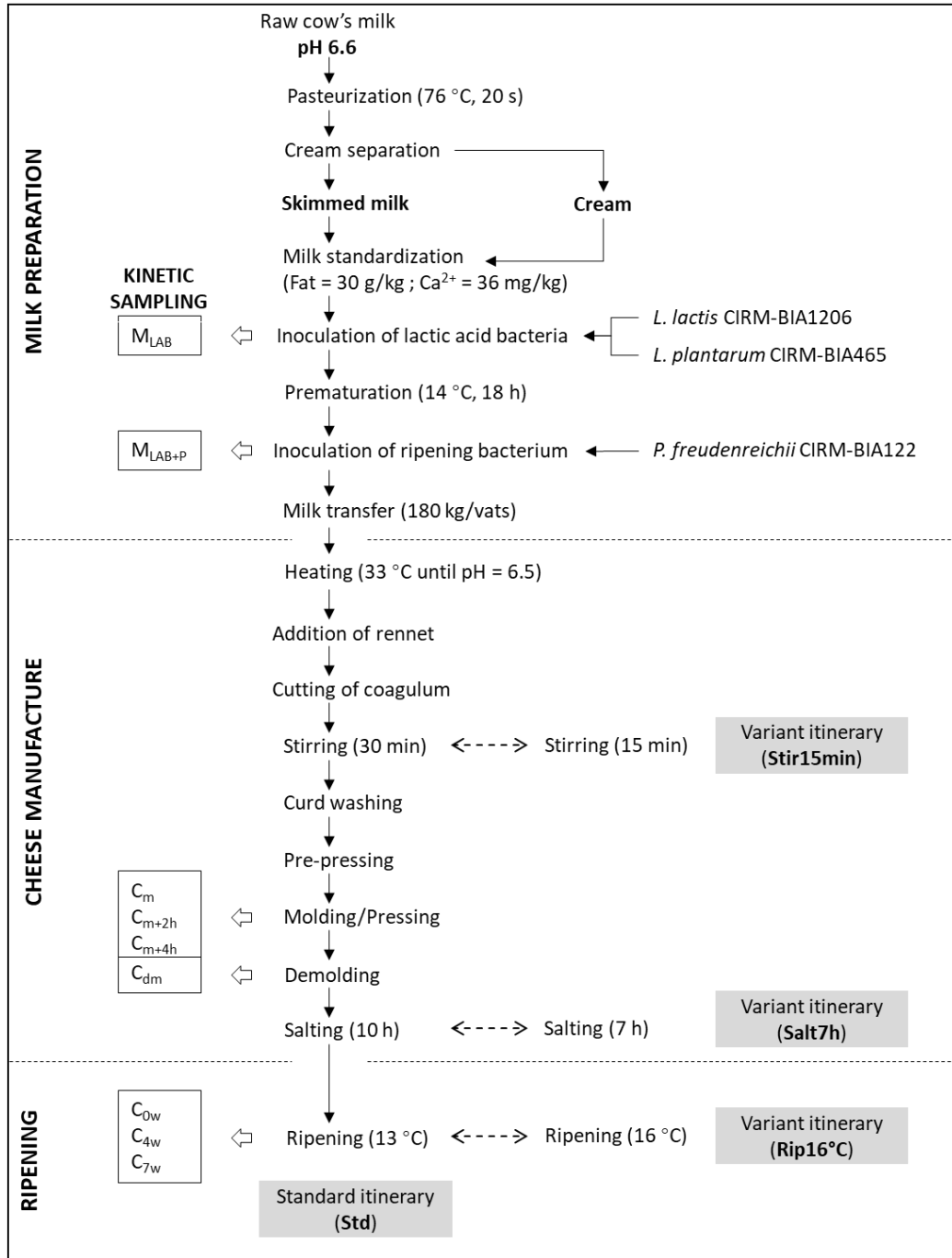


Figure 1

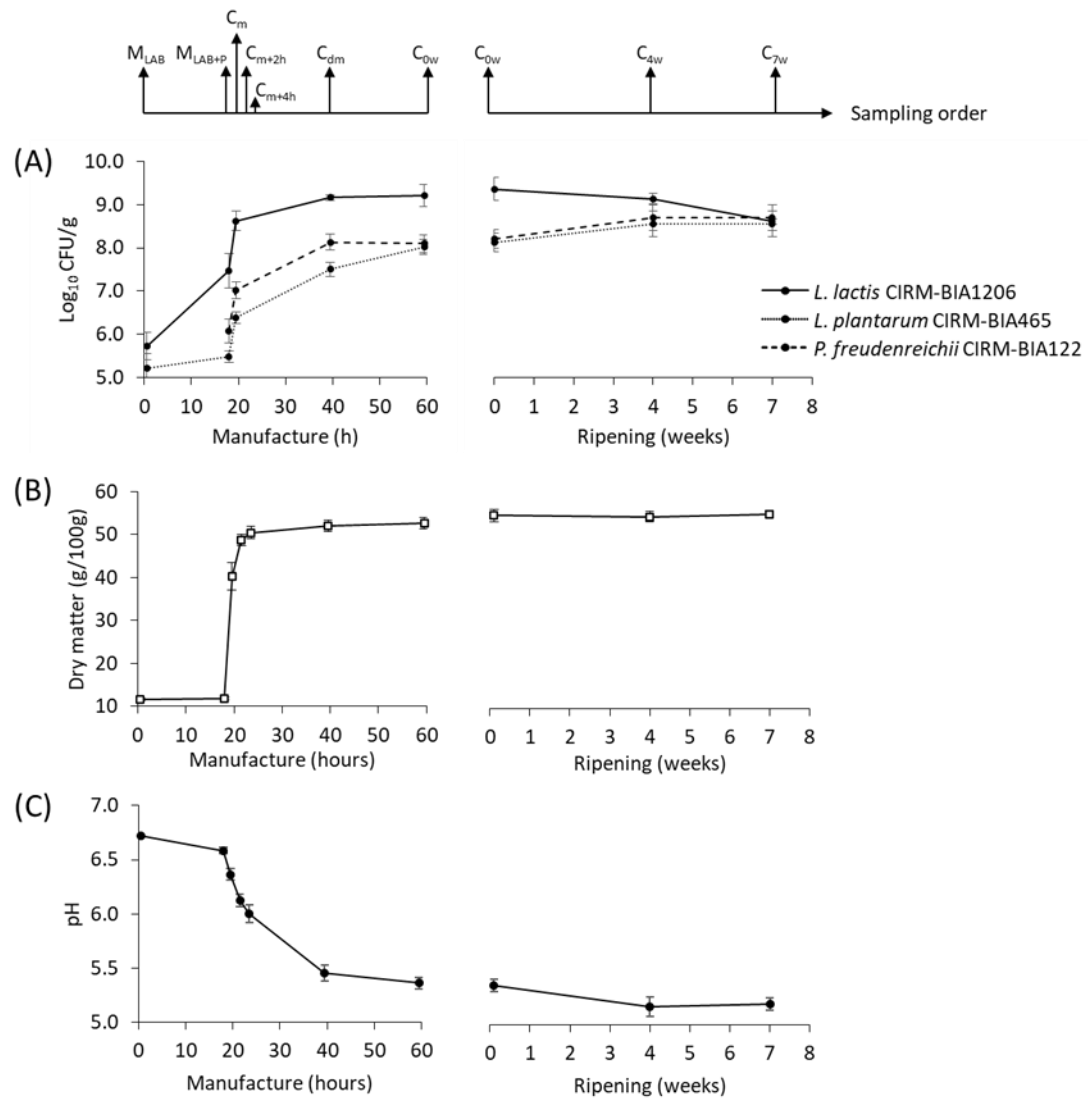


Figure 2

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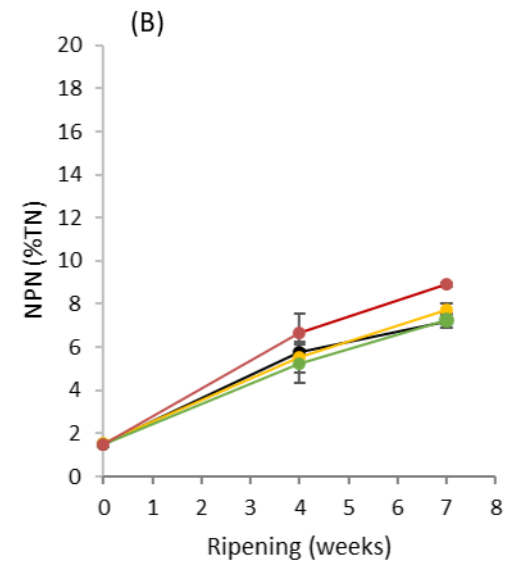
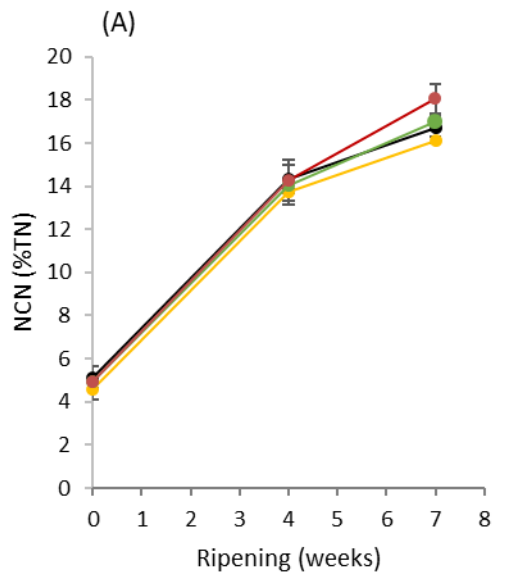
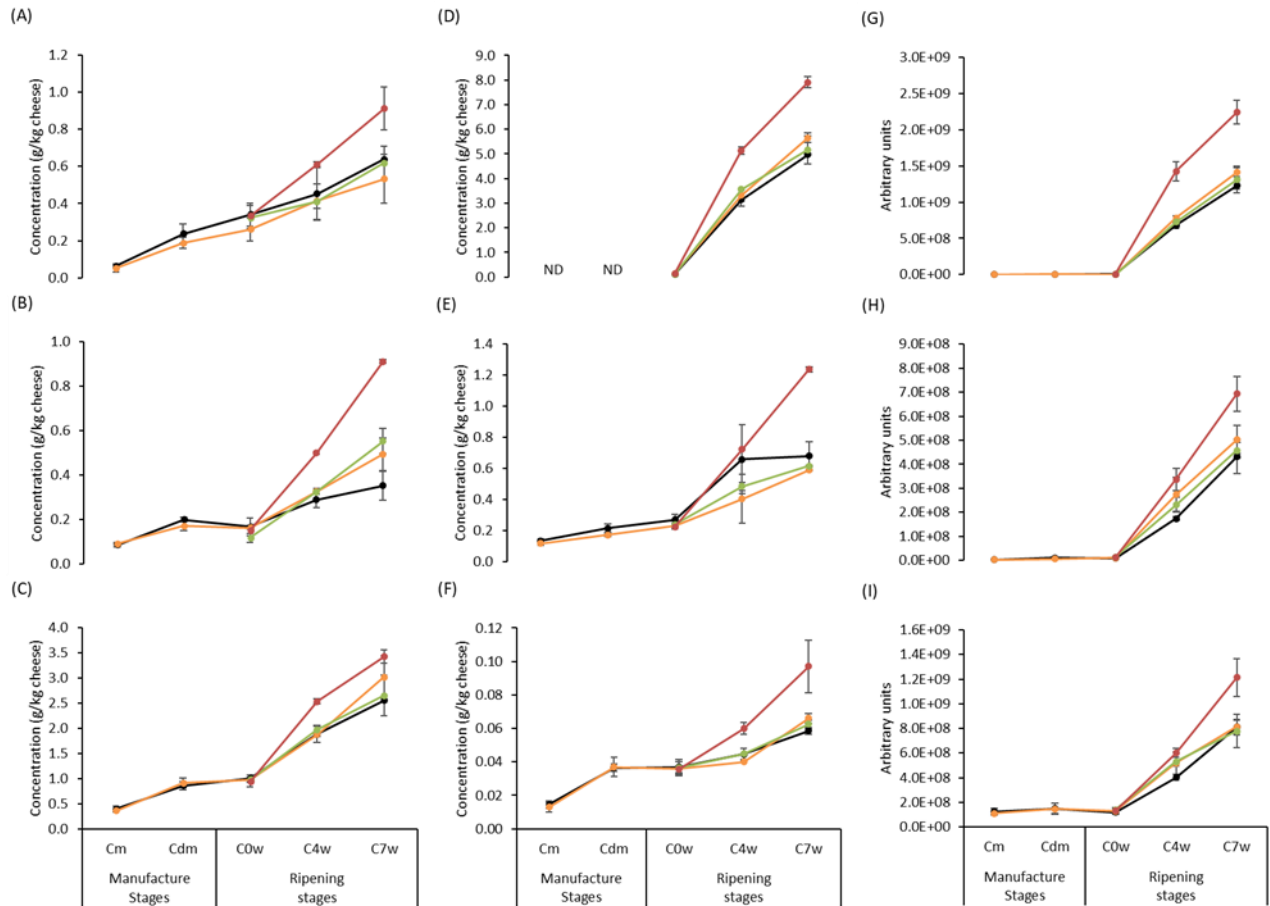


Figure 3

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Figure 4

(A)

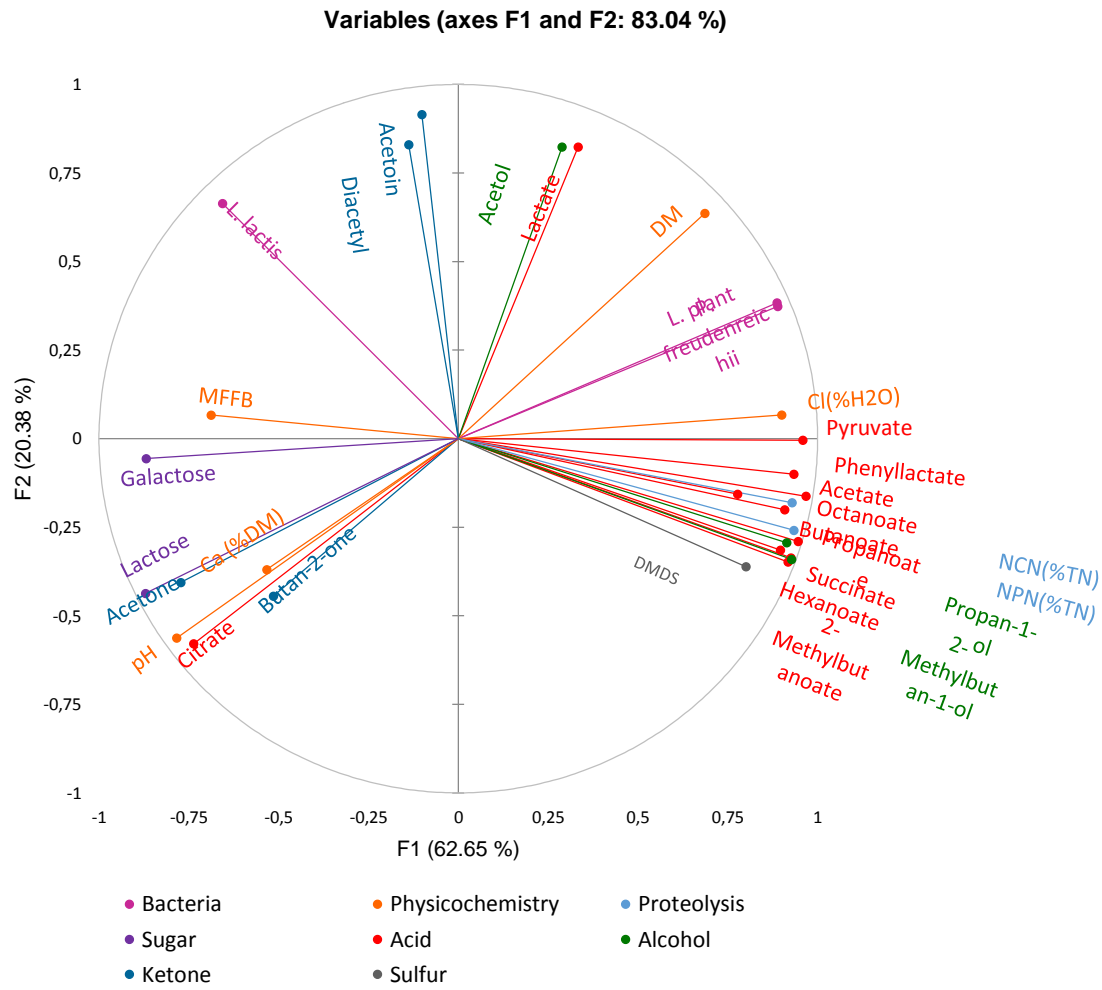
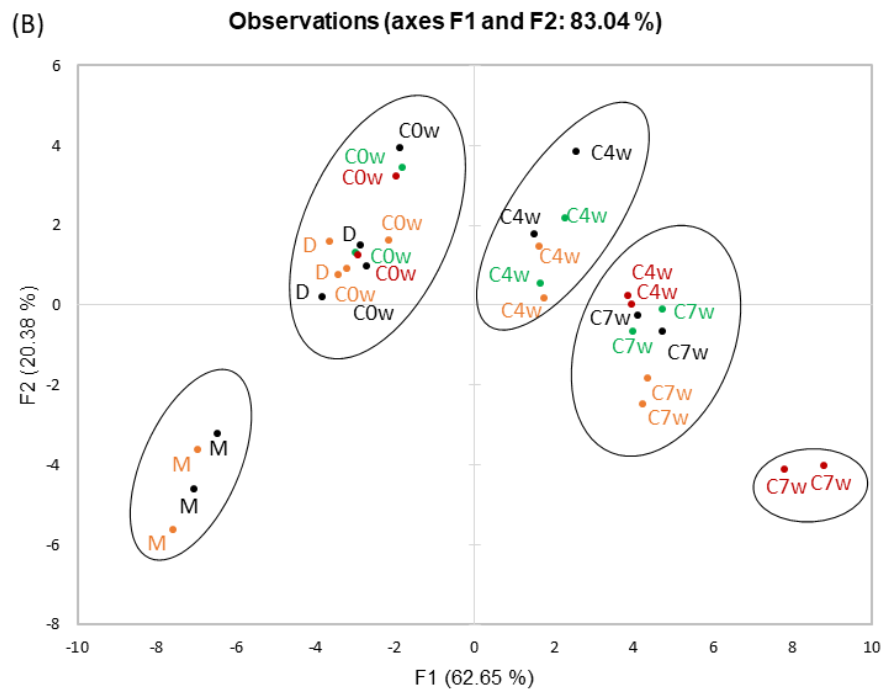


Figure 5A

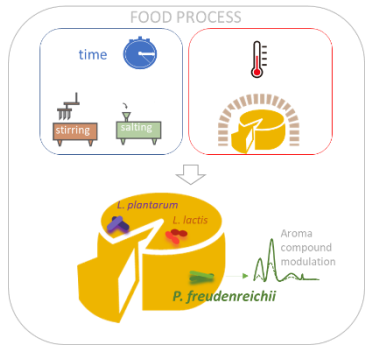


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Figure 5B

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3 TOC graphic



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