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5 **Microbial Interactions Within a Cheese Microbial Community**

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12 **Abstract**

13

14 The interactions that occur during the ripening of smear cheeses are not well understood.
15 Yeast-yeast interactions and yeast-bacteria interactions were investigated within a microbial
16 community composed of three yeasts and six bacteria found in cheese. The growth dynamics
17 of this community was precisely described during the ripening of a model cheese, and the
18 Lotka-Volterra model was used to evaluate species interactions. Subsequently, the effects of
19 yeast omissions in the microbial community on ecosystem functioning were evaluated. It was
20 found both in the Lotka-Volterra model and in the omission study that negative interactions
21 occurred between yeasts. *Yarrowia lipolytica* inhibited mycelial expansion of *Geotrichum*
22 *candidum*, and *Y. lipolytica,* and *G. candidum* inhibited *Debaryomyces hansenii* cell viability
23 during the stationary phase. However, the mechanisms involved in these interactions remain
24 unclear. It was also shown that yeast-bacteria interactions played a significant role in the
25 establishment of this multi-species ecosystem on the cheese surface. Yeasts were key species
26 in bacterial development, but their influence on the bacteria differed. It appeared that the
27 growth of *Arthrobacter arilaitensis* or *Hafnia alvei* relied less on a specific yeast function
28 because these species dominated the bacterial flora, regardless of which yeasts were present in
29 the ecosystem. For other bacteria such as *Leucobacter* sp. or *Brevibacterium aurantiacum*,
30 their growth relied on a specific yeast, *i.e.*, *G. candidum*. Furthermore, *B. aurantiacum*,
31 *Corynebacterium casei* and *Staphylococcus xylosus* showed a reduced colonization capacity
32 compared with the other bacteria in this model cheese. Bacteria/bacteria interactions could not
33 be clearly identified.

34

35

36 **Introduction**

37 Little is known about yeast-bacteria interactions, and smear ripened cheeses offer an
38 interesting model to investigate them. Indeed, the smear cheese microbial community is
39 composed of both yeast and bacteria, is of a known specific composition that constitutes the
40 "inoculum", and shows a reduced diversity and a high stability (12, 13, 25, 27, 34).

41 The smear is a red-orange, often viscous, microbial mat which is characterized by a
42 succession of microbial communities including both yeast and bacteria. For example, the
43 surface microflora of bacterial smear-ripened cheeses such as Reblochon, Tilsit and
44 Limburger is composed of yeast, mainly *Debaryomyces hansenii* and *Geotrichum candidum*,
45 and Gram-positive catalase-positive organisms such as coryneform bacteria and staphylococci
46 (2, 9, 10, 35). During the first days of ripening, yeasts colonize the cheese surface and utilize
47 lactate. This utilization progressively leads to the deacidification of the cheese surface,
48 enabling the establishment of a bacterial community that is less acid-tolerant (8). These
49 communities are relatively simple compared with other microbial communities such as soil
50 communities. Indeed, they are composed of a limited number of mostly cultivable species,
51 *i.e.*, 10-20 species (12, 27). The microbial diversity of cheese was investigated using both
52 cultivable and non-cultivable approaches such as rep-PCR, FT-IR spectroscopy, 16S rDNA
53 sequencing, cloning and sequencing of 16S rDNA, SSCP, DGGE and TGGE (12, 13, 27, 28,
54 31).

55 While the succession of yeast and bacteria has been well described, the functional
56 interactions in cheese between yeast and/or bacteria is not yet understood, and only a few
57 interactions have been observed. An early study from Purko et al. (33) on the association
58 between yeasts and *Brevibacterium linens* showed that *B. linens* did not grow on a vitamin-
59 free agar medium. However, when the same medium was inoculated with yeast, it grew
60 around the yeast colonies. Some yeast and bacterial strains have been selected for use by the

61 cheese industry because of their interesting technological properties such as aroma production
62 or pigmentation. However, it has been shown that these commercial ripening cultures do not
63 necessarily implant on the cheese surface, despite their massive inoculation in the early stages
64 of ripening (7, 12, 27, 28). Mounier et al. (28) showed that the microorganisms that developed
65 on the cheese surface were an adventitious microflora from the cheese environment (brine,
66 ripening shelves and personnel), which rapidly outnumbered the commercial cultures. Several
67 hypotheses have been advanced to explain these findings. These ripening cultures may be
68 unfit for the cheese habitat, or negative interactions may occur between them and the
69 adventitious microflora. Bacterial and yeast strains have also been selected for their anti-
70 listerial activity (11, 25). Eppert et al. (11) found single strains of linocin-producing *B. linens*
71 (a bacteriocin-like substance), which reduced *Listeria* spp. populations in cheeses but did not
72 exert an inhibition comparable to that obtained with the ripening consortia from which these
73 strains were isolated. Inversely, none of the 400 isolates from an effective anti-listerial
74 ripening consortium evaluated in the study of Maoz et al. (25) exhibited anti-listerial activity
75 in agar diffusion assays. This implies that the anti-listerial effect is probably not related to the
76 production of inhibitory substances during growth.
77 In macrosystem ecology, several models that represent intra- and interspecies
78 interactions in food webs have been established (see (3) for a review). The multispecies
79 Lotka-Volterra model (22, 36) is a simple model used to measure interactions based on a
80 linear relationship for a given species between growth rate and the populations of each
81 member of the community. Such a model may be a good tool to investigate interactions
82 within a microbial community.
83 Bonaiti et al. (5), using a three-step dichotomous approach, simplified an ecosystem of
84 83 strains from Livarot cheese, to four sub-ecosystems composed of nine species based on
85 odor profile. One of these sub-ecosystems showed great similarities with the odor profile of

86 the 83-strain ecosystem, which had a very similar odor profile to the commercial cheese. This
87 sub-ecosystem of nine species was thought to be a good model ecosystem to reproduce cheese
88 surface diversity and to investigate microbial interactions.

89 The aim of this study was to identify interactions within this ecosystem in model
90 cheeses. In the first part of this study, the growth dynamics of each member of this
91 community were described, and the generalized Lotka-Volterra model (GLV) was used as a
92 preliminary approach to represent inter- and intraspecies interactions. In the second part,
93 specific strains of this community were omitted in order to evaluate the consequences of these
94 omissions on the further development of the rest of the community (species distribution,
95 substrate utilization, color of the cheese surface).

96 **Material and methods**

97

98 *Strains.* The starters used for cheese-making were frozen Flora Danica cultures (CHN 12 and
99 CHN 15, Chr Hansen, Arpajon, France). Flora Danica contains a mixture of *Lactococcus*
100 *lactis* ssp. *lactis*, *L. lactis* ssp. *cremoris*, citrate-positive strains of lactococci and *Leuconostoc*
101 *mesenteroides* ssp. *cremoris*.

102 The nine micrörganisms that composed the model ecosystem were *Arthrobacter arilaitensis*
103 3M03, *Brevibacterium aurantiacum* 2M23, *Corynebacterium casei* 2M01, *Hafnia alvei* 2E12,
104 *Leucobacter* sp. 1L36 and *Staphylococcus xylosus* 1L18 for the bacteria and, *Debaryomyces*
105 *hansenii* 1L25, *Geotrichum candidum* 3E17 and *Yarrowia lipolytica* 1E07 for the yeast. These
106 strains were obtained from the culture collection of the Food Microbiology Laboratory (LMA,
107 Caen, France). They were originally isolated from various batches of Livarot cheese.

108

109 *Growth properties of the microorganisms of the ecosystem on an agar-based media.* The
110 growth characteristics of the bacteria and yeast as a function of pH and NaCl were tested in a
111 media that contained 0.5 g yeast extract, 1 g casaminoacids, 0.1 g glucose and 1.5 g agar. Salt
112 content was 0, 30, 50, 100 and 150 g l^{-1}, while pH was 5, 5.5, 6, 6.5 and 7. Growth was
113 visually evaluated by checking for the presence of colonies after 2, 4 and 8 days incubation at
114 12°C.

115

116 *Growth properties of the microorganisms found in the cheese ecosystem*. In this study, two
117 independent experiments were conducted at a five-month interval. In the first part of the
118 study, the growth dynamics of the nine species that composed the model ecosystem were
119 investigated on model cheeses (Exp. I). The cheeses were sampled in duplicate every day for
120 21 days for microbial enumeration, lactose and lactate content, and pH.

121 In the second part of the study, the effects of single or multiple omissions of the yeast
122 strains that originally composed the ecosystem were evaluated on model cheeses (Exp. II). All
123 the possible combinations were tested. Cheeses were sampled in triplicate on day 0, 3, 11 and
124 21 for microbial enumeration, lactose, lactate ammonia and free amino acid content, surface-
125 pH and color development.

126

127 *Cheese production.* Pilot-scale cheese production (coagulation, cutting, draining and molding
128 of the curd) according to a process used for Livarot cheese was carried out under aseptic
129 conditions in a sterilized, 2-m^3 chamber as previously described by Leclercq-Perlat et al. (19).
130 The milk used (~100 L) was pasteurized full-fat milk, standardized at 29 g/l fat with skim
131 milk. The milk was pasteurized for 2.5 min at 75°C, and cooled at 37°C in the chamber. After
132 1 l of milk had been pumped into the tank, the milk was inoculated with the starter culture
133 (Flora Danica, Chr Hansen, Arpajon, France). A filter-sterilized 10% $CaCl_2$ solution (100 ml)
134 was added at the end of pasteurization. It was followed by the addition of the filter-sterilized
135 coagulant containing 520 mg/l of chymosin at 30 ml/100 l of milk. Coagulation time was 20
136 min, and cutting of the curds took place after 30 min of hardening. The curd was then
137 manually stirred for 5 min at a rate of 10 stirs/min. After standing for 15 min, 70 l of whey
138 were removed prior to molding. Cheeses were shaped in circular polyurethane molds with a
139 diameter of 9 cm and a height of 11 cm. Cheeses weighed approximately 350 g. The molds
140 were inverted four times after 10 min, 2 h, 5 h and 15.5 h, with a temperature of 20°C in the
141 chamber. After 17 h, cheeses were demolded, and after another hour, they were transferred to
142 sterile bags and stored at –80°C until use.

143

144 *Ripening culture.* The yeast and bacteria were first precultured in 10 ml of Potato Dextrose
145 Broth (PDB) or Brain Heart Infusion broth (BHI), respectively, in 50-ml flasks incubated at
146 25°C for 55 h at 150 rpm. 400 µl of each preculture were then used to inoculate 40 ml of PDB

147 or BHI in 150 ml flasks, which were incubated at 25°C for 66 h at 150 rpm. Five to 10 ml of
148 each preculture were centrifuged at room temperature for 10 min at 4000 rpm. The
149 supernatant was discarded and the cells resuspended in 9 g/l NaCl to obtain a concentration of
150 2 x 10^9 CFU/ml and 2 x 10^7 CFU/ml for the bacteria and the yeast, respectively.
151 Subsequently, 1280 µl of each suspension were mixed and supplemented to make 20 ml with
152 9 g/l NaCl in a volumetric flask. This suspension was used to inoculate the model cheeses.

153
154 *Curd inoculation.* Under sterile conditions, 57 ml of a saline solution containing 92 g/l NaCl
155 were added to 246 g of unsalted curd and mixed three times for 10 s at maximum speed using
156 a Warring blender. 2.4 ml of the ripening culture were then added and mixed, yielding 10^4
157 CFU/g and 10^6 CFU/g of cheese, for the yeast and the bacteria, respectively. Thirty grams
158 were then transferred to sterile crystallizing basins with a diameter of 5.6 cm, and incubated at
159 12°C for 21 days. Two or three cheeses were used at each time point analyzed. Salt content of
160 the cheeses was ~17 g/kg.

161

162 *Analyses.* Surface pH was measured using a surface electrode Blue line 27 (Schott). The pH
163 values were the arithmetic means of three measurements. Surface color was measured using a
164 CM-2002 spectrocolorimeter (Minolta, Carrières sur Seine, France) as described by Mounier
165 et al. (29). The data was processed using the three-dimensional *L* * *a* * *b* response, and logged
166 into the *L* * and *C* * system. *L* * ranges from 0 (black) to 100 (white) and indicates lightness,
167 *a* * and *b* * are the chromaticity coordinates indicating the color directions; + *a* * is the red
168 direction at 0°, - *a* * is the green direction at 180°, + *b* * is the yellow direction at 90° and – *b*
169 * is the blue direction at 270°. Cheese surfaces were photographed using a digital camera.
170 Lactose and lactate content were determined on the whole cheese using HPLC as previously
171 described by Leclercq-Perlat et al. (19). The release of free amino acids was measured on the
172 whole cheese as described by Grunau et al. (14). Ammonia content of the whole cheese was

173 measured using the Nessler reagent.

174

175 *Microbiological analyses.* Cheese was homogenized using a mortar and pestle, and ~1 g of
176 the cheeses was sampled and transferred into a sterile container. A sterile saline solution (8.5
177 g/l NaCl) was added to yield a 1:10 dilution, and the mixture was homogenized with an Ultra
178 Turrax® (Labortechnik) at 8000 rpm/min for 1 min. Total bacteria except lactic acid bacteria
179 were enumerated by surface plating in duplicate on BHI agar supplemented with 50 mg/l
180 amphotericin B after five days incubation at 25°C. Yeast population was determined by
181 surface plating in duplicate using Yeast-Glucose-Chloramphenicol agar (YGC) supplemented
182 with 0.01 g/l tetrazolium chloride (TTC) after three days incubation at 25°C. Lactic acid
183 bacteria were enumerated by surface-plating in duplicate on MRS agar after two days
184 incubation at 30°C.

185

186 *Enumeration of yeast and bacterial species.* Each yeast species had a distinct morphotype on
187 YGC supplemented with TTC, which allowed their direct enumeration. For the bacteria, 250
188 colonies of each cheese sample were removed at random with sterile toothpicks and
189 transferred onto 96-well microtiter plates containing 100 µl of BHI supplemented with 10%
190 (v/v) glycerol and incubated three days at 25°C. The plates were stored at -80°C until use. For
191 bacterial identification, the isolates that grew in microtiter plates were replicated onto five
192 media, *i.e.*, BHI agar containing 20 mg/l erythromycin, 1 or 5 mg/l novobiocin, 1 mg/l
193 vancomycin or 1 g/l TTC. After incubation for three days at 25°C, the isolates were checked
194 for their ability to grow in the presence of the various selective agents. The combination of the
195 five media was discriminative for each bacterium (Table 1). The counts of each bacterium
196 (C_i) were estimated as follows:

197

$$C_i\,(CFU/g) = \frac{N_i \times C_0}{N_t}$$

where C_0 is the total bacterial count in CFU/g, N_t is the number of clones replicated, and N_i is the number of clones identified as bacterium *i*.

Statistical analysis

The data with repeated measurements (bacterial and yeast population, pH, color, lactate) were compared and statistically assessed using an analysis of variance (ANOVA). When differences were detected by ANOVA, a Student-Newman-Keuls test was used to determine which means were different. Statistical significance was set at $P < 0.05$.

Lotka-Volterra modeling

The multispecies Lotka-Volterra model was used in this study. Taking *n* species, the dynamic of the species *i* ($i = 1, \ldots, n$) is the following:

$$\frac{dX_i}{dt} = X_i\left(\beta_i + \sum_{j=1}^{n} \alpha_{ij} X_j\right)$$

where β_i represents the intrinsic growth rate of the species *I*, and α_{ij} the influence of the species *j* on the growth rate of species *i*. This influence is positive or negative according to the sign of α_{ij}. In this model, the interactions are assumed constant for a given species *j* abundance. To determine the interaction coefficients, the multispecies Lotka-Volterra system can be expressed as a multi-linear regression:

$$\frac{d\log(X_i)}{dt} = \beta_i + \sum_{j=1}^{n} \alpha_{ij} X_j$$

The left part of this equation was obtained by deriving the logarithm of the species concentration according to time using the cubic spline function without smoothing (Matlab®).

221 In a linear regression model, the correlations between explicative variables have a high impact
222 on parameter identification. The design of experiments makes it possible to avoid the
223 correlations, but this approach is not possible in the present study. Consequently, to avoid too
224 many correlations, the model was not used on each species but on clusters that grouped the
225 different organisms obtained from a squared correlation coefficient with a 0.75 threshold
226 value. For a given cluster, the sum of abundance of the different species was used in the linear
227 model. Inside this simplified system, an interaction coefficient α_{ij} was considered to be
228 significant when $P(\alpha_{ij} \neq 0) > 90\%$.

229 **Results**

230 **Growth properties of the ecosystem microorganisms**

231 The growth characteristics of the bacteria as a function of NaCl content and pH on an agar-
232 based media are compared in Figure S1 (supplementary material). The bacteria could be
233 divided into three groups based on their growth abilities. The first group was comprised of *H.*
234 *alvei* and *S. xylosus,* which grew under all the conditions tested, except at pH 5 and 0% NaCl
235 in which *S. xylosus* did not grow. The second group was comprised of *A. arilaitensis,* which
236 grew at a pH equal or greater than 5.5, except in the presence of 0 and 30 g l^{-1} NaCl where it
237 grew at a pH equal or greater than 6.5 and 6, respectively. The third group was comprised of
238 *Leucobacter* sp., *B. aurantiacum* and *C. casei,* which only grew at a pH equal or greater than
239 6, except for *B. aurantiacum,* which grew in the presence of 100 and 150 g l^{-1} NaCl at pH 5.5.
240 In some cases, *C. casei* only grew at a pH equal or greater than 6.5. The bacteria generally
241 grew better in the presence of increased concentrations of NaCl. Yeast grew under all the
242 conditions tested (data not shown).

243

244 **Microbial and physico-chemical dynamics during the development of the ecosystem on**
245 **model cheese**

246 *Reproducibility of microbial dynamics.* The growth of the three yeasts and six bacteria
247 during cheese ripening are shown in Figures 1A and 1B, respectively. There was a good
248 reproducibility (a difference of less than 0.5 $\log_{10}$ units) between duplicates in the numbers of
249 the yeast and the three dominant bacterial species, *i.e.*, *A. arilaitensis*, *Leucobacter* sp. and *H.*
250 *alvei* (data not shown). The three other bacterial species were only detected occasionally on
251 one or two of the cheeses analyzed because these bacteria had numbers below the detection
252 limit of our method of analysis (approximately 2 $\log_{10}$ units below the total count). *S. xylosus*
253 was not isolated on day 12, 16, 17, 18 and 20; *B. aurantiacum* on day 10, 12, 14 and 20 and

254 *C. casei* on day 20.

255 *Yeast growth. D. hansenii* and *Y. lipolytica* grew during the first days of ripening and
256 had almost similar growth rates (Figure 1A); in contrast, *G. candidum* grew only after two
257 days. A possible explanation for the absence of the increase in cell numbers of *G. candidum*
258 may be that *G. candidum* had a longer lag phase or formed mycelium at the start of ripening.
259 Indeed, mycelium with hyphae consists of different cells but would give only 1 CFU per agar
260 plate. The growth of *G. candidum* coincided with a slowing down of *D. hansenii* and *Y.*
261 *lipolytica* growth. Overall, *D. hansenii* dominated the cheese surface until day 5; then,
262 between day 6 and 9, the three yeasts had similar cell numbers, after which *D. hansenii*
263 became progressively subdominant compared with *Y. lipolytica* and *G. candidum*. Indeed, *G.*
264 *candidum* and *Y. lipolytica* numbers remained constant or increased slightly, while the *D.*
265 *hansenii* population decreased by 1.5 $\log_{10}$ units between day 6 and day 21.

266 *Bacterial growth.* During the first days of ripening, the counts of *H. alvei*, *A.*
267 *arilaitensis*, *Leucobacter* sp. and *S. xylosus* remained constant, while the populations of *C.*
268 *casei* and *B. aurantiacum* decreased by approximately 1 log unit between day 0 and 4 (Figure
269 1B). Growth of all the organisms occurred after day 5-6. *A. arilaitensis*, followed by *H. alvei*,
270 dominated the cheese surface between day 6 and day 9. After day 9, *Leucobacter* sp. counts
271 increased, and this species also became dominant on the cheese surface. *S. xylosus, C. casei*
272 and *B. aurantiacum* remained subdominant throughout the entire ripening period. Lactic acid
273 bacteria counts decreased slightly from ~10^8 CFU/g on day 0 to 2 x 10^7 CFU/g at the end of
274 ripening (data not shown).

275 *Lactose, lactate and pH dynamics during ripening.* Lactose, lactate and pH variations
276 during ripening are shown in Figure 2. Lactose was used first and was totally depleted on day
277 8. After an increase during the first days of ripening, probably due to a slight acidification by
278 the lactic acid bacteria, lactate was consumed from day 5 to day 9, but was not depleted. Sixty

279 percent of the lactate was used during growth, which indicates that lactate was not a limiting
280 carbon source. The surface deacidification occurred between day 2 and day 6, with a pH
281 increase from approximately 5.0 to 8.0. This deacidification was highly correlated with the
282 utilization of lactate and the growth of *G. candidum* on the cheese surface (data not shown).

283 *Generalized Lotka-Volterra modeling.* The dendogram of the different species
284 according to their squared correlation coefficient during growth is shown in Figure S2
285 (supplementary material). With a threshold value of 0.75, each yeast was considered to have a
286 specific growth dynamic. In contrast, except for *Leucobacter* sp., the growth dynamics of the
287 bacteria were considered to be correlated. Consequently, GLV modeling was performed on
288 the growth dynamics of five distinct groups that comprised four individual species, *i.e.*, *Y.*
289 *lipolytica*, *G. candidum*, *D. hansenii* and *Leucobacter* sp., and a group of bacteria including *A.*
290 *arilaitensis*, *B. aurantiacum*, C. *casei*, *H. alvei* and *S. xylosus.*

291 The main interactions according to GLV modeling are shown in Figure 3. Yeast-yeast
292 interactions were found to be only negative, while yeast-bacteria interactions were found to be
293 only positive. *G. candidum* interacted negatively with *D. hansenii* and *Y. lipolytica,* while it
294 interacted positively with *Leucobacter sp*. and the group of bacteria. *D. hansenii* was found to
295 have a negative interaction with *Y. lipolytica,* while it had a positive interaction with the group
296 of bacteria. Self-inhibition of *G. candidum* and *D. hansenii* were also found in the model.

297 The model succeeded in representing the growth of the different microbial populations as
298 shown in Figures S3 and S4 (supplementary material), which compare measured and
299 estimated values for the two data sets. Total residual error between estimated and measured
300 values was 0.1 ± 0.4 log CFU/g for both data sets.

301

302 **Effects of single and multiple omissions of yeast in the ecosystem**

303 We aimed at identifying yeast-yeast or yeast-bacteria interactions by comparing the

304 growth of each individual microorganism in the absence or presence of one, two or three
305 yeasts. The utilization of lactose and lactate, the deacidification rate and the color
306 development of the cheese surface were also compared for each inoculum tested.

307 *Reproducibility.* There was good reproducibility between triplicates in terms of lactose and
308 lactate utilization, deacidification and the growth of the microorganisms of the ecosystem as
309 well (data not shown). There was also a good reproducibility between the data of the dynamic
310 study and the omission study in which all the members of the community were inoculated
311 (data not shown).

312

313 *Yeast-yeast interactions*. The viability of *D. hansenii* during the stationary phase was affected
314 in the presence of the other yeasts (see Figure S5 in supplementary material). Populations of
315 *D. hansenii* were significantly lower ($p<0.05$) on day 11 when *D. hansenii* was grown in the
316 presence of *G. candidum* or *G. candidum* and *Y. lipolytica*. Indeed, populations of *D. hansenii*
317 were 0.5 and 0.7 $\log_{10}$ units lower than the *D. hansenii* monoculture in the presence of *G.*
318 *candidum* or *G. candidum* and *Y. lipolytica*, respectively. Moreover, between day 11 and day
319 21, *D. hansenii* populations decreased from 1 to 1.7 $\log_{10}$ units when this organism was co-
320 cultivated with *G. candidum* and/or *Y. lipolytica,* whereas it remained constant in the
321 monoculture. This inhibitory effect was similar regardless of whether *Y. lipolytica* or *G.*
322 *candidum* were present, but was more pronounced in the presence of both species.
323 Populations of *Y. lipolytica* and, to a lesser extent, populations of *G. candidum*, were
324 significantly lower ($p<0.05$) on day 11 when they were grown in the presence of other yeasts
325 (data not shown). Their respective counts were 0.4 and 0.7 $\log_{10}$ units lower than those
326 observed in monoculture. However, there was not any loss in viability of *Y. lipolytica* and *G.*
327 *candidum* during the stationary phase.

328 Interestingly, *Y. lipolytica* but not *D. hansenii* greatly influenced the mycelium

329 formation of *G. candidum*. In the monoculture or in the sole presence of *D. hansenii*, *G.*
330 *candidum* grew in the form of white mycelium, which covered the surface of the model
331 cheeses (Figure 4A and 4B), whereas in the presence of *Y. lipolytica*, growth occurred as
332 spaghetti-like structures without formation of pseudohyphae (Figure 4C). This inhibition of
333 mycelial development did not influence cellular growth since only small differences in
334 numbers of *G. candidum* were found (Figure 4D). This phenomenon was also observed in the
335 presence of both *Y. lipolytica* and *D. hansenii*. The idea that an interaction of *Y. lipolytica* on
336 *G. candidum* occurred was also reinforced because the rate of utilization of lactate in the
337 cheese containing *G. candidum* and *Y. lipolytica* was decreased in the presence of *Y. lipolytica*
338 compared with the monoculture or in co-culture with *D. hansenii* (Figure 4D). Ninety percent
339 of the lactate was used after 21 days when *G. candidum* grew as the sole yeast or in the
340 presence of *D. hansenii*, while only 44% was used when this organism was co-cultivated with
341 *Y. lipolytica*.
342
343 *Chemical characteristics of the cheese.*
344 *G. candidum* showed the highest deacidification rate, followed by *D. hansenii* and *Y.*
345 *lipolytica,* which had similar deacidification rates (Figure 5A). The pH reached its maximal
346 value, *i.e.*, 8.0, after 11 days when *G. candidum* was present in the ecosystem, whereas pH
347 ranged from 6 to 6.5 for *D. hansenii* and *Y. lipolytica* (Figure 5A) or a combination of both
348 species (data not shown). After 21 days, pH ranged from 7.4 to 8.0. The higher pH of cheese
349 containing *G. candidum* may be attributable to the fact that *G. candidum* utilized more lactate
350 than *D. hansenii* between d 0 and 11. *D. hansenii* produced a small amount of NH_3 (data not
351 shown). *Y. lipolytica* did not utilize lactate but produced large amounts of NH_3 (data not
352 shown). Amino acids and compounds such as ornithine and γ-amino-n-butyric acid (GABA),
353 differed between cheeses (data not shown). After 21 d, the cheese inoculated with *Y. lipolytica*

354 had 2-15 times more free amino acids, depending on the amino acid considered, than the
355 cheeses inoculated with *D. hansenii* or *G. candidum* and the cheese with no yeast. Except for
356 asparagine, cysteine, ornithine and GABA, all amino acids were produced in large quantities
357 in the cheese inoculated with *Y. lipolytica* compared with the two other yeasts (data not
358 shown).

359

360 *Development of the bacterial community.*

361 The growth of the bacteria in the cheese model was considerably influenced by the yeasts that
362 were either present or not in the initial inocula. Growth of the bacteria did not occur when
363 yeasts were not inoculated (Figure 6A). After 11 and 21 days, the cheeses that contained *G.*
364 *candidum* showed significantly higher surface-pH than the cheeses inoculated with *D.*
365 *hansenii* and/or *Y. lipolytica.* The differences in surface pH between cheeses inoculated with
366 *D. hansenii* and/or *Y. lipolytica* were much lower when *D. hansenii* and *Y. lipolytica* were
367 combined than when they were the sole yeasts inoculated (Figures 6A and 6B). After 11 days,
368 the bacterial count of the cheese inoculated with *G. candidum* by itself was significantly
369 higher ($p<0.05$) than the cheese inoculated with *D. hansenii* or *Y. lipolytica* by itself (Figure
370 6A). In contrast, with two or three yeasts in the community, total bacterial counts were
371 statistically similar ($p<0.05$) despite the fact that surface pH was significantly lower ($p<0.05$)
372 on the cheese containing *D. hansenii* and *Y. lipolytica* (Figure 6B). After 21 days, total
373 bacterial counts were not statistically different in all cheeses except the cheeses that contained
374 *Y. lipolytica* as the sole yeast, and *D. hansenii* and *Y. lipolytica*, which had counts 1.5 and 1
375 $\log_{10}$ units lower, respectively (Figures 6A and 6B).
376 As shown in Figure 7, there were only small differences in the distribution of the bacterial
377 species on the different cheeses after 11 days, except for the cheese inoculated with *D.*
378 *hansenii* and *G. candidum*. Except in the cheese inoculated with *G. candidum* and *D.*

379 *hansenii*, the cheeses were dominated by *A. arilaitensis,* which represented between 66 and
380 86% of the total isolates, followed by *H. alvei* (5-25%), *Leucobacter* sp. (2-10%), *S. xylosus*
381 (3-10%), *C. casei* and *B. aurantiacum* (0.4-2%). *H. alvei* (70%), followed by *A. arilaitensis*
382 (26%) and *Leucobacter* sp. (11%), dominated the cheese inoculated with *D. hansenii* and *G.*
383 *candidum*. After 21 d, differences and common patterns were found in the distribution of the
384 bacterial community. *Leucobacter* sp. grew in all the cheeses inoculated with *G. candidum*
385 and represented between 26 and 60%, whereas this species was subdominant (less than 5% of
386 the total isolates) in all cheeses in which *G. candidum* was absent. *A. arilaitensis* dominated in
387 the cheese inoculated with *D. hansenii* or *G. candidum* as the sole yeast (70% of the isolates),
388 while *H. alvei* dominated in cheeses inoculated with *Y. lipolytica* or *Y. lipolytica* and *D.*
389 *hansenii* (70% of the isolates). After 21 days, *S. xylosus*, *B. aurantiacum* and *C. casei*
390 remained subdominant, except in the cheese inoculated with *G. candidum* as the sole yeast in
391 which *B. aurantiacum* represented 10% of the isolates taken in this cheese.
392
393 *Color development of the cheese surface.*
394 There were only small differences in the color development of all the cheeses after 11 days,
395 except the cheese inoculated with no yeast and the cheeses inoculated with *G. candidum* or *G.*
396 *candidum* and *D. hansenii,* which had a lower b* (yellow dimension) probably because *G.*
397 *candidum* formed white mycelia on the surface (data not shown). In contrast, all the cheeses
398 differed considerably in terms of color development after 21 days (Figure 8). The consortium
399 that contained the three yeasts showed the highest a* and b* values, followed by the two other
400 cheeses inoculated with *Y. lipolytica* and *D. hansenii* or *Y. lipolytica* and *G. candidum*. The
401 cheeses inoculated with *G. candidum* by itself and *G. candidum* and *D. hansenii* had high a*
402 but low b* values, while the cheeses inoculated with only *D. hansenii* or *Y. lipolytica* had
403 high b* but low a* values.

404 **Discussion**

405 In this study, the dynamics of a nine-species cheese ecosystem and the effects of the
406 omission of one, two or three yeasts on the growth of this community were investigated in
407 model cheeses. To our knowledge, all the studies about the growth behavior of
408 microorganisms isolated from cheese have been done on mixed cultures with only two
409 microorganisms, generally a yeast and a bacteria, on cheese agar (23, 24) or on curd made
410 under aseptic conditions (4, 20, 29). Despite the fact that such studies provide interesting
411 information on the individual growth characteristics of these organisms and their contribution
412 to ripening, they do not take account of the fact that the cheese microflora is much more
413 diverse and that interactions may exist between the members of these communities. These
414 interactions may strongly influence their implantation and colonizing capacity in cheese, as
415 shown in this study.

416

417 *Yeast-yeast interactions. G. candidum* was isolated from nearly all smear-ripened cheeses.
418 This organism imparts a uniform, white velvety coat on the surface of some cheeses such as
419 St. Marcellin, while on others such as Livarot, it is not the case (6). In this study, it was found
420 that when *Y. lipolytica* was grown in association with *G. candidum*, hyphal formation was
421 inhibited and that *G. candidum* grew as spaghetti-like structures instead (Figure 4). Numerous
422 chemical and environmental parameters have been reported to influence the yeast-mycelium
423 formation, such as temperature, glucose levels, pH, nitrogen sources and inoculum size (30).
424 Among these, ammonia and proline, which were produced in greater quantities by *Y.*
425 *lipolytica* than *D. hansenii*, may be an explanation for this observation. Palkova and Forstova
426 (32) showed that, between different yeast taxa, ammonia induction triggered changes in
427 colony morphology in which pseudohyphae decomposed into non-dividing yeast cells.
428 Kulkarni and Nickerson (17) showed that proline (10 mM) induced the yeast morphology in

429 *Ceratosystis ulmi* in defined liquid media, and that budding yeasts were only formed above
430 10^6 blastidiospores per ml. However, in our study, other factors may be involved, and further
431 investigations are being pursued to understand this interaction. *G. candidum* was also less
432 metabolically active or its metabolism was differently orientated in the presence of *Y.*
433 *lipolytica* because *G. candidum* was less effective in utilizing lactate in spaghetti-like
434 structures than in mold-like structures. Indeed, mycelium-like structures may provide a better
435 access to substrates in the cheese matrix.

436 The presence of other yeasts in the cheese had only a small effect on the growth of
437 each individual yeast. This may be explained by the fact that each yeast utilized different
438 energy sources for growth. Barnett et al. (1) showed that *D. hansenii* assimilates lactose and
439 lactate while *G. candidum* and *Y. lipolytica* only assimilate lactate. In this study, *Y. lipolytica*
440 did not utilize lactate. The energy source of *Y. lipolytica* remained unclear, but nitrogen
441 compounds are likely to be its main energy source. *D. hansenii* populations were found to
442 significantly decrease in the presence of other yeasts. This indicates that competition for
443 nutrients or negative interactions (inhibition) occurred between yeasts, which affected cell
444 maintenance of *D. hansenii* during its stationary phase.

445

446 *Yeast-bacteria interactions.* In this study, it was demonstrated that the bacterial development
447 and distribution of the different species were modified depending on the yeast present in the
448 ecosystem. It is obvious, because of the different levels of acid-sensitivity of the bacteria, that
449 the deacidification rate of the yeasts influenced the bacterial development on the cheese
450 surface. Indeed, in most cases, the bacteria reached higher population levels when the
451 deacidification was more rapid. The growth characteristics of each bacterial strain as a
452 function of pH determined in agar–based media gave us an insight into the growth ability of
453 each bacterium. For example, *Leucobacter* sp. was much more acid-sensitive than *H. alvei*

454 and developed later in the ripening process. *C. casei* and *B. aurantiacum* were also quite acid-
455 sensitive and did not hold up well under the acidic stress that occurred at the start of ripening,
456 compared to the other members of the bacterial community. This may be responsible for their
457 subdominance in almost all the cheeses.

458 Surface-pH was not the only factor that influenced bacterial development. For
459 example, *S. xylosus*, which is able to grow at relatively low pH on agar, did not well colonize
460 the cheese surface compared to *A. arilaitensis*, *H. alvei* or *Leucobacter* sp. This also indicates
461 that growth abilities obtained in pure culture on agar-based media cannot be extrapolated to
462 more complex media and multi-species ecosystems. *S. xylosus* may have a limited
463 colonization capacity in cheese because the nutrients available may not have been sufficient to
464 support growth, or competition may have occurred between this strain and the different yeasts
465 and bacteria. In biodiversity studies, it has been reported that *Staphylococcus* spp. were often
466 predominant in the early stages of ripening, but were rapidly outnumbered by other bacteria at
467 the later stages of ripening (15, 28, 34). However, in co-cultures studies, *S. saprophyticus* was
468 able to reach high numbers, *i.e.*, 10^{10} CFU/g with *D. hansenii* in model cheese curd (29),
469 while it did not reach such numbers in cheese (28). Therefore, *Staphylococcus* spp. strains
470 may have a limited colonization capacity of this type of cheese, especially when the
471 microflora is much more complex.

472 *Leucobacter* sp. only grew in the cheeses that contained *G. candidum.* This would imply that
473 *Leucobacter* sp. was highly dependent on *G. candidum* activities either because *G. candidum*
474 rapidly deacidified the surface or because it produced metabolites that enhanced *Leucobacter*
475 sp. growth. Similarly, B. *aurantiacum* represented ~10% of the clones isolated after 21 d in
476 the cheese inoculated with *G. candidum* as the sole yeast, whereas *B. aurantiacum* was
477 subdominant in the other microbial communities. It is possible that *G. candidum* detoxified
478 the environment and released substrates that promoted growth of *B. aurantiacum* under these

479 conditions.

480 *A. arilaitensis* and, in most cases, *H. alvei,* were found to represent a large part of the bacteria
481 under all the conditions tested. Therefore, these species may not be highly dependent on a
482 specific yeast interaction, with the exception of surface deacidification. *A. arilaitensis* has
483 been found to dominate the microflora of many European cheeses (12, 13, 16). This shows the
484 high colonization capacity of this species compared with others, such as *B. linens* or *B.*
485 *aurantiacum*.

486 *Color development of the cheese surface.* The color differentiation that occurred between d 11
487 and d 21 is probably due to the production of pigments by the bacteria. Interestingly, in some
488 cases, if we compare two cheeses with almost similar bacterial distribution and population,
489 such as the ecosystems that contained only *Y. lipolytica* or *Y. lipolytica* and *D. hansenii*, color
490 differed considerably between the two ecosystems. This would imply that, depending on the
491 yeasts present, species-specific bacterial pigmentation was different in these two cheeses. This
492 is in agreement with a previous study of Leclercq-Perlat et al. (18) in which it was shown that
493 *B. linens* pigmentation differed depending on the yeast used for deacidification. The
494 ecosystem that contained the three yeasts yielded the strongest color development. This
495 suggests that each yeast would have different ecosystem functions in terms of color
496 development and that the combination of the three yeasts led to the highest pigment
497 production by the bacteria.

498 *Lotka-Volterra modeling.* In this study, Lotka-Volterra modeling was used for the first time
499 on a microbial ecosystem as a preliminary approach to represent inter- and intraspecies
500 interactions. This approach made it possible to identify the positive interactions between the
501 bacteria and the yeast during ripening, *i.e.*, the positive effect of *G. candidum* on *Leucobacter*
502 sp. and on the rest of the bacteria that were confirmed in this study. Similarly, the negative
503 interaction between yeasts, such as the inhibition of *G. candidum* on *D. hansenii,* was also

504 found in the Lotka-Volterra model. However, this model showed interactions such as a
505 negative interaction of the bacteria on *D. hansenii,* which could not be explained by the
506 omission study. Inversely, other interactions such as a negative interaction from *Y. lipolytica*
507 on *D. hansenii* were not significant in the model but observed *in situ*. Further data would be
508 necessary to confirm or invalidate the interactions observed in the model. Because growth of
509 most of the bacteria was highly correlated, we could not measure interactions between each
510 individual bacterial species and the yeasts. Despite the limits of this approach, the use of the
511 GLV model on only one set of data provided us with an insight into the main interactions.
512 Therefore, GLV modeling may be useful as a preliminary step to orientate interaction studies.

513 The smear cheese microbial community is a beneficial biofilm because it is
514 responsible for the flavor and appearance of this type of cheese. For a better understanding of
515 the interactions that occur, it would be interesting to investigate the spatial distribution of
516 these microorganisms on the cheese surface using fluorescence *in situ* hybridization, for
517 example.

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522 **References.**

523 1. **Barnett, J. A., Payne, R. W. and D. Yarrow.** 2000. Yeasts: Characteristics and
524 Identification. 3rd ed. Cambridge University Press, Cambridge, UK.
525 2. **Bärtschi, C., Berthier, J. and G. Valla.** 1994. Inventaire et évolution des flores
526 fongiques de surface du reblochon de Savoie. Lait. **74**: 105-114.
527 3. **Berlow, E.L., Neutel, A.-M., Cohen, J. E., De Ruiter, P., Ebenman, B.,**
528 **Emmerson, M., Fox, J. W., Jansen, V. A. A., Jones, J. I., Kokkoris, G. D.,**
529 **Logofet, D. O., McKane, A. J., Montoya, J. and O. L. Petchey.** 2004. Interaction
530 strengths in food webs: issues and opportunities. J. Anim. Ecol. **73**:585-598.
531 4. **Bonaïti, C., Leclercq-Perlat, M. -N., Latrille E. and G. Corrieu.** 2004.
532 Deacidification by *Debaryomyces hansenii* of smear soft cheeses ripened under
533 controlled conditions: relative humidity and temperature influences. J. Dairy Sci. **87**:
534 3976-3988.
535 5. **Bonaïti, C., Irlinger, F., Spinnler, H. E. and E. Engel.** 2005. An iterative sensory
536 procedure to select odor-active associations in complex consortia of microorganisms:
537 application to the construction of a cheese model. J. Dairy Sci. **88**:1671-84.
538 6. **Boutrou, R. and M. Gueguen.** 2005. Interests in *Geotrichum candidum* for cheese
539 technology. Int. J. Food Microbiol. **102**: 1-20.
540 7. **Brennan, N. M, Ward, A. C, Beresford, T. P., Fox, T. P., Goodfellow, M. and**
541 **T.M. Cogan.** 2002. Biodiversity of the bacterial flora on the surface of a smear
542 cheese. Appl. Environ. Microbiol. **68**: 820-830.
543 8. **Corsetti, A., Rossi, J. and M. Gobbetti.** 2001. Interactions between yeasts and
544 bacteria in the smear surface-ripened cheeses. Int. J. Food Microbiol. **69**: 1-10.
545 9. **Eliskases-Lechner, F. and W. Ginzinger.** 1995**.** The bacterial flora of surface-
546 ripened cheeses with special regard to coryneforms. Lait. **75**: 571-584.

547 10. **Eliskases-Lechner, F. and W. Ginzinger.** 1995**.** The yeast flora of surface-ripened
548 cheeses. Milchwiss. **50**: 458-462.
549 11. **Eppert, L., Valdés-Stauber, N., Gotz, H., Busse, M., and S. Scherer.** 1997. Growth
550 reduction of *Listeria* spp. Caused by undefined industrial red smear cheese cultures
551 and bacteriocin-producing *Brevibacterium linens* as evaluated *in situ* on soft cheese.
552 Appl. Environ. Microbiol. **63**: 4812-4817.
553 12. **Feurer, C., Irlinger, F., Spinnler, H. E., Glaser, P. and T. Vallaeys.** 2004.
554 Assessment of the rind microbial diversity in a farmhouse-produced vs a pasteurized
555 industrially produced soft red-smear cheese using cultivation and rDNA-based
556 methods. J. Appl. Microbiol. **97**:546-556.
557 13. **Feurer, C., Vallaeys, T., Corrieu, G. and F. Irlinger.** 2004. Does smearing
558 inoculum reflect the bacterial composition of the smear at the end of the ripening of a
559 French soft, red-smear cheese? J. Dairy Sci. **87**: 3189-3197.
560 14. **Grunau, J. A. and J. M. Swiader.** 1992. Chromatography of 99 amino acids and
561 other ninhydrin-reactive compounds in the Pickering lithium gradient system. J.
562 Chromatogr. **594**: 165-171.
563 15. **Irlinger, F., Morvan, A., EL Solh, N. and J. L. Bergere.** 1997. Taxonomic
564 characterisation of coagulase-negative Staphylococci in ripening flora from traditional
565 French cheeses. System. Appl. Microbiol. **20**: 319-328.
566 16. **Irlinger, F., Bimet, F., Delettre, J., Lefevre, M. and P. A. D. Grimont.** 2005. Two
567 new coryneform species isolated from the surface of cheeses are species of the genus
568 *Arthrobacter*: *Arthrobacter bergerei* sp. nov. and *Arthrobacter arilaitensis* sp. nov.
569 Int. J. Syst. Bacteriol. **55**: 457-462.
570 17. **Kulkarni, R. K. and K. W. Nickerson.** 1981. Nutritional control of dimorphism in
571 *Ceratocystis ulmi.* Exp. Mycol. **5**: 148-154.

572 18. **Leclercq-Perlat, M. -N., Corrieu, G. and H. -E. Spinnler.** 2004. The color of
573 *Brevibacterium linens* depends on the yeast used for cheese deacidification. J. Dairy
574 Sci. **87**: 1536-1544.

575 19. **Leclercq-Perlat, M. -N., Oumer, A., Bergere, J. -L., Spinnler, H. -E and G.**
576 **Corrieu.** 1999. Growth of *Debaryomyces hansenii* on a bacterial surface-ripened soft
577 cheese. J. Dairy Sci. **66**: 271-281.

578 20. **Leclercq-Perlat, M. -N., Oumer, A., Bergere, J. -L., Spinnler, H. -E and G.**
579 **Corrieu.** 2000. Behavior of *Brevibacterium linens* and *Debaryomyces hansenii* as
580 ripening flora in controlled production of smear soft cheese from reconstituted milk:
581 growth and substrate consumption. J. Dairy Sci. **83**: 1665-73.

582 21. **Leclercq-Perlat, M. -N., Oumer, A., Bergere, J. -L., Spinnler, H. -E and G.**
583 **Corrieu.** 2000. Behavior of *Brevibacterium linens* and *Debaryomyces hansenii* as
584 ripening flora in controlled production of smear soft cheese from reconstituted milk:
585 protein degradation. J. Dairy Sci. **83:** 1674-83.

586 22. **Lotka, A. J.** 1925. Elements of physical biology. Williams and Wilkins, Baltimore.
587 [Reprinted in 1956: Elements of mathematical biology. Dover Publications, Inc., New
588 York, New York].

589 23. **Masoud, W. and M. Jakobsen** 2003. Surface ripened cheeses: the effects of
590 *Debaryomyces hansenii*, NaCl and pH on the intensity of pigmentation produced by
591 *Brevibacterium linens* and *Corynebacterium flavescens*. Int. Dairy J. **13**: 231-237.

592 24. **Masoud, W. and M. Jakobsen** 2005. The combined effects of pH, NaCl and
593 temperature on growth of cheese ripening cultures of *Debaryomyces hansenii* and
594 corynefom bacteria. Int. Dairy J. **15**: 69-77.

595 25. **Maoz, A., Mayr, R. and S. Scherer.** 2003. Temporal stability and biodiversity of two
596 complex antilisterial cheese-ripening microbial consortia. Appl. Environ. Microbiol.

597 **69**: 4012-4018.

598 26. **Michalski, J. and R. Arditi.** 1999. The complexity-stability problem in food web
599 theory. What can we learn from exploratory models? p. 91-119. *In* A. Weill (Ed),
600 Advances in Environmental and Ecological Modelling. Elsevier, Paris, France.

601 27. **Mounier, J., Gelsomino, R., Goerges, S., Vancanneyt, M., Vandemeulebroecke,**
602 **K., Hoste, B., Scherer, S., Swings, J., Fitzgerald, G. F. and T. M. Cogan.** 2005.
603 The surface microflora of four smear-ripened cheeses. Appl. Env. Microbiol. **71**:
604 6489-500.

605 28. **Mounier, J., Goerges, S., Gelsomino, R., Vancanneyt, R., Vandemeulebroecke,**
606 **K., Hoste B., Brennan, N. M., Scherer, S., Swings, J., Fitzgerald, G. F. and T.M.**
607 **Cogan.** 2006. The sources of the adventitious microflora of a smear-ripened cheese. J.
608 Appl. Microbiol. **101**: 668-681.

609 29. **Mounier, J., Irlinger, F., Leclercq-Perlat, M. -N., Sarthou, A. -S., Spinnler, H. -**
610 **E., Fitzgerald, G. F. and T.M. Cogan.** 2006. Growth and colour development of
611 some surface ripening bacteria with *Debaryomyces hansenii* on aseptic cheese curd. J.
612 Dairy Res. **73**: 441-448.

613 30. **Nickerson, K. W., Atkin, A. L. and J. M. Hornby.** 2006. Quorum sensing in
614 dimorphic fungi: farnesol and beyond. Appl. Environ. Microbiol. **72**: 3805-3813.

615 31. **Ogier, J.- C., Lafarge, V., Girard, V., Rault, A., Maladen, V., Gruss, A., Leveau**
616 **J. -Y. and A. Delacroix-Buchet.** 2004. Molecular fingerprinting of dairy microbial
617 ecosystems by use of temporal temperature and denaturing gradient gel
618 electrophoresis. Appl. Env. Microbiol. **70**: 5628-5643.

619 32. **Palkova, Z. and J. Forstova.** 2002. Yeast colonies synchronize their growth and
620 development. J. Cell Sci. **113**: 1923-1928.

621 33. **Purko, M., Nelson, W. O. and W. A. Wood.** 1951. The associative action between
622 certain yeast and *Bacterium linens.* J. Dairy Sci. **34**: 699-705.
623 34. **Rea, M. C., Goerges, S., Gelsomino, R., Brennan, N. M., Mounier, J.,**
624 **Vancanneyt, M., Scherer, S., Swings, J., T.M. Cogan.** 2007. Stability of the
625 biodiversity of the surface consortia of Gubbeen, a red-smear cheese. J. Dairy Sci. **90**:
626 2200-10.
627 35. **Valdés-Stauber, N., Scherer, S. and H. Seiler.** 1997. Identification of yeasts and
628 coryneform bacteria from the surface microflora of brick cheeses. Int. J. Food
629 Microbiol. **34**: 115-129.
630 36. **Volterra, V.** 1926. Variazioni e fluttuazioni del numero d'individui in specie animali
631 conviventi. Vol. 2., Mem. R. Accad. Naz. dei Lincei. Ser. VI.

632 **Table 1. Selective media used to identify the different bacterial clones.**

633

	Novobiocin		Erythromycin	Vancomycin	TTC[‡]
	1 mg/l	5 mg/l	20 mg/l	1 mg/l	0.1 g/l
Arthrobacter arilaitensis	-[†]	-	-	-	+
Brevibacterium aurantiacum	+	-	-	v	v
Corynebacterium casei	+	+	-	-	v
Hafnia alvei	+	+	+	+	+
Leucobacter sp.	-	-	-	+	+
Staphylococcus xylosus	+	+	-	+	+

634

635 [†] -, absence of growth; +, growth; v, variable growth.

636 [‡] TTC: Tetrazolium chloride

637

638

639

640

641 **Figure legends.**

642 **Figure 1.** Yeast (A) and bacterial (B) dynamics of the cheese ecosystem on model cheeses.
643 (A): ♦**,** *Debaryomyces hansenii*; ■**,** *Yarrowia lipolytica*; ▲, *Geotrichum candidum.* (B): ●,
644 *Arthrobacter arilaitensis;* ■**,** *Hafnia alvei***,** □, *Leucobacter* sp., ♦, *Corynebacterium casei;* ○,
645 *Brevibacterium aurantiacum*, ▲, *Staphylococcus xylosus.*

646

647 **Figure 2.** Lactose (△), lactate (■**)** and pH (●) variations during the growth of the cheese
648 ecosystem on model cheese.

649

650 **Figure 3.** Main interactions (⟶, positive; ⟶ , negative) according to generalized Lotka-
651 Volterra modeling between the members of the multi-species ecosystem. *Dh*, *Debaryomyces*
652 *hansenii*; *Yl*, *Yarrowia lipolytica*; *Gc*, *Geotrichum candidum*; *L*s, *Leucobacter* sp; C, group
653 including *Arthrobacter arilaitensis*, *Hafnia alvei***,** *Corynebacterium casei*, *Brevibacterium*
654 *aurantiacum* and *Staphylococcus xylosus*.

655

656 **Figure 4.** Macromorphology of *Geotrichum candidum* grown as a monoculture (A) or in the
657 presence of *Debaryomyces hansenii* (B) or *Yarrowia lipolytica* (C) and (D) Lactate utilization
658 (closed symbols) and *G. candidum* counts (open symbols) in model cheeses containing *G.*
659 *candidum* (●, ○), *G. candidum* and *D. hansenii* (■**,** □) or *G. candidum* and *Y. lipolytica* (▲,
660 △).

661

662 **Figure 5.** Lactate consumption (closed symbols) and pH increase (open symbols) during
663 ripening in cheeses inoculated with *Debaryomyces hansenii* (▲, △), *Geotrichum candidum* (●,
664 ○) or *Yarrowia lipolytica* (■**,** □).

665

666 **Figure 6.** Total bacterial growth and surface pH increase during ripening in cheeses
667 inoculated with (A) no yeast (○), *Debaryomyces hansenii* (■), *Yarrowia lipolytica* (♦),
668 *Geotrichum candidum* (▲) or (B) *D. hansenii* and *Y. lipolytica* (◊), *D. hansenii* and *G.*
669 *candidum* (△), *Y. lipolytica* and *G. candidum* (□), *D. hansenii, Y. lipolytica,* and *G. candidum*
670 (●).

671

672 **Figure 7.** Distribution of the bacterial species in the model cheese after 11 and 21 days as a
673 function of the yeast inoculated. DH, *Debaryomyces hansenii*; YL, *Yarrowia lipolytica;* GC,
674 *Geotrichum candidum*.

675

676 **Figure 8.** Color of the cheese surface after 21 d as a function of the chromaticity coordinate
677 a* (red dimension) and b* (yellow dimension) values. Cheeses were inoculated with no yeast
678 (♦), *Debaryomyces hansenii* (■), *Geotrichum candidum* (▲), *Yarrowia lipolytica* (●), *D.*
679 *hansenii* and *Y. lipolytica* (◊), *Y. lipolytica* and *G. candidum* (□) and *D. hansenii, Y. lipolytica,*
680 and *G. candidum* (○).

681 **Figure 1.**

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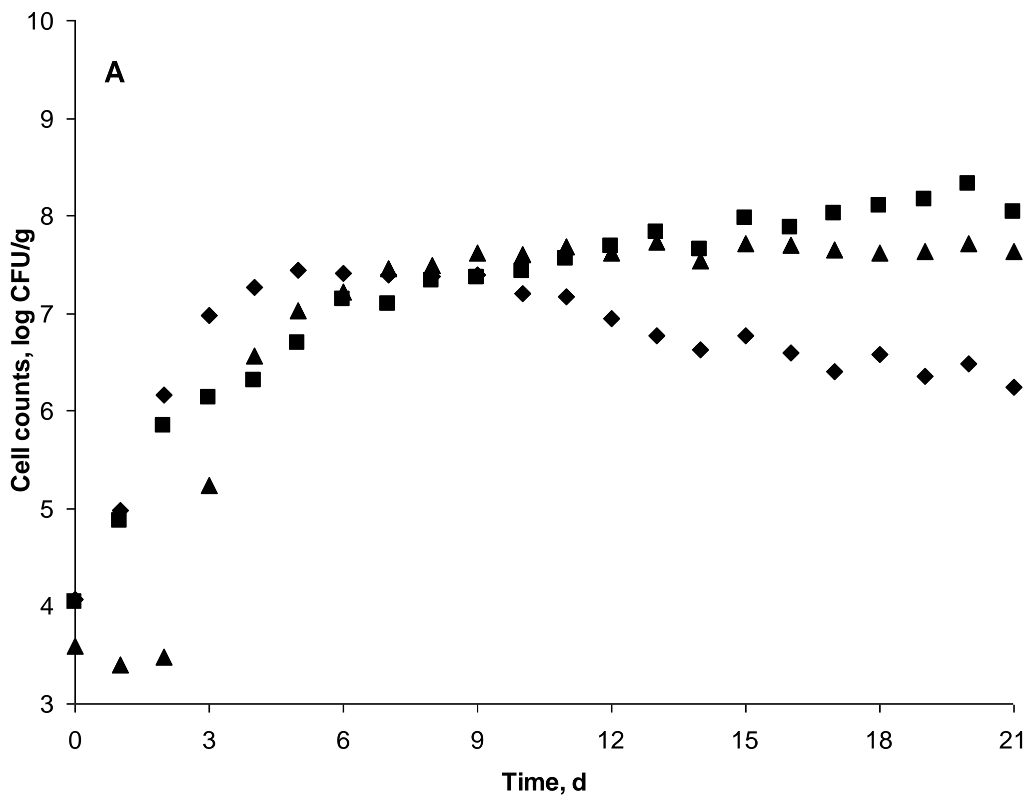

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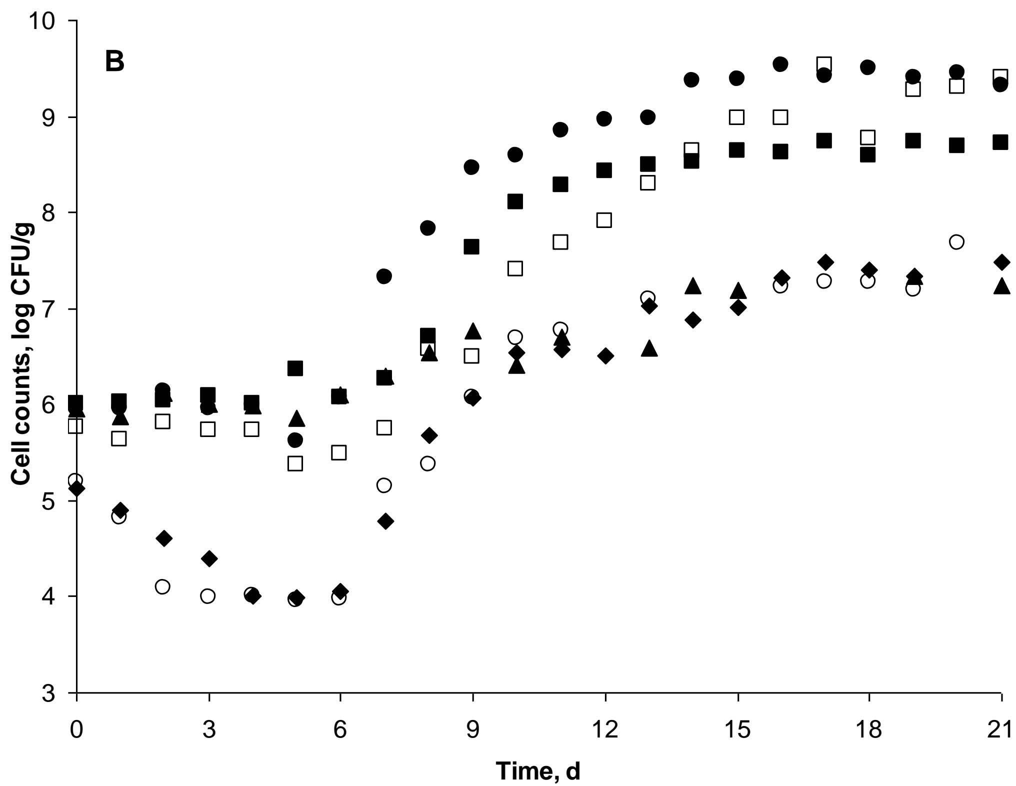

696 697 698 699 700 701 702 703 704 705

706 **Figure 2.**

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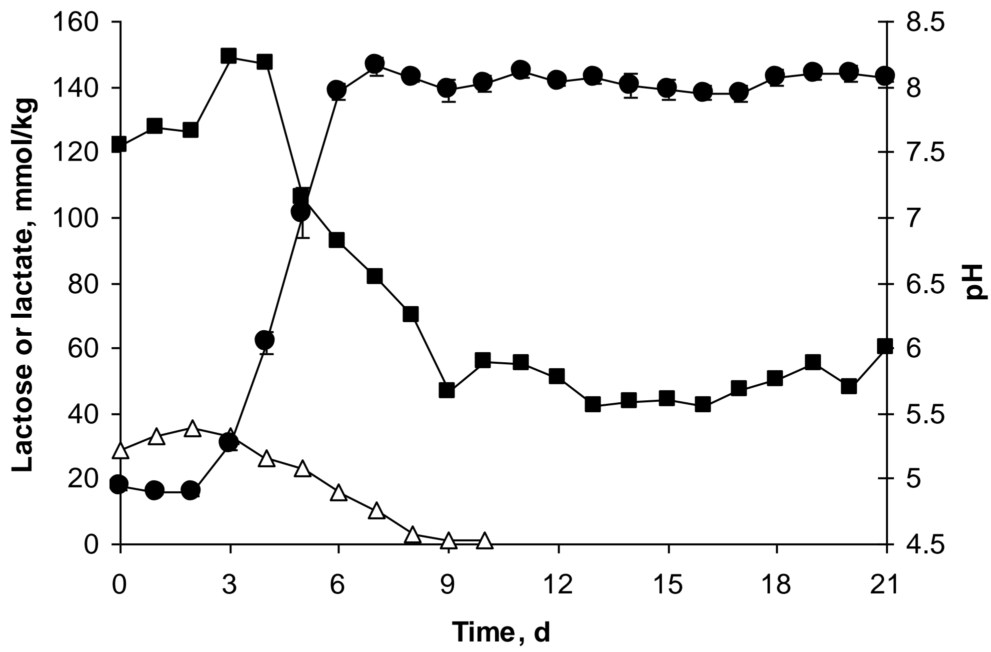

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722 **Figure 3.**

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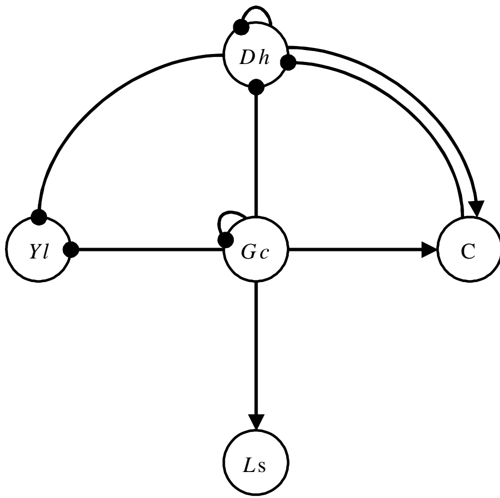

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725 **Figure 4.**

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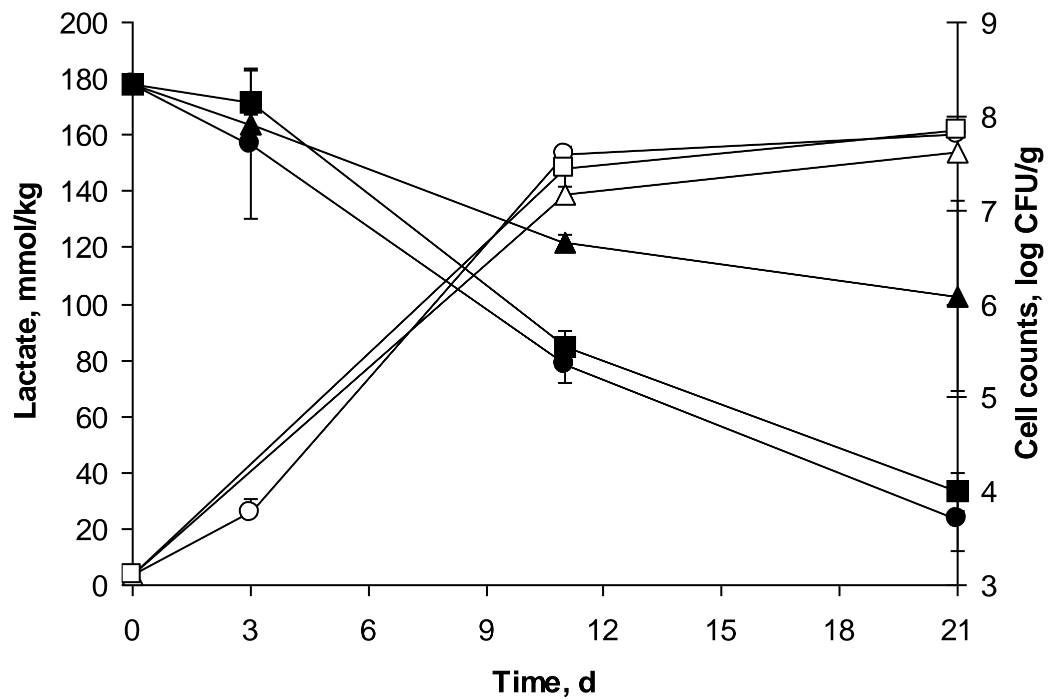

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736 **Figure 5.**

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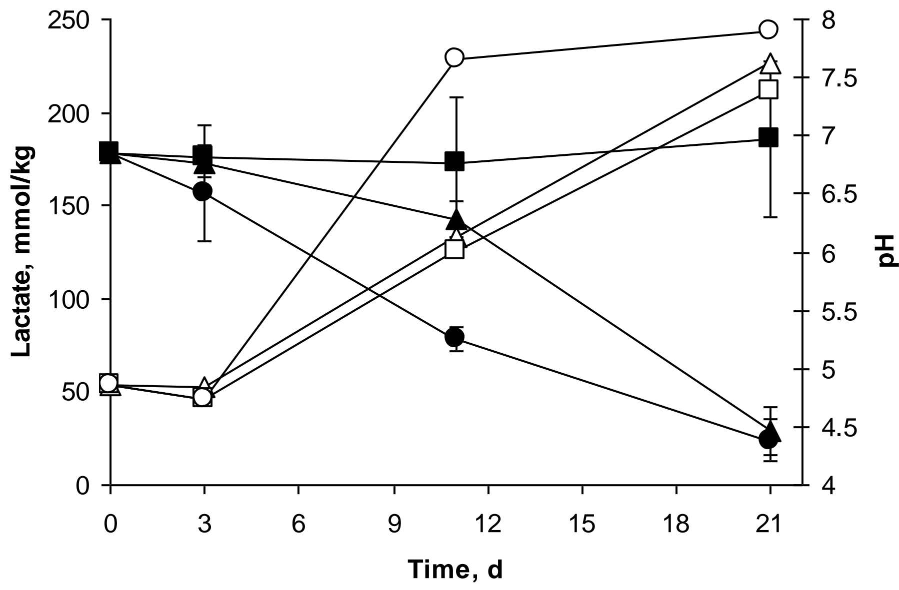

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753 **Figure 6.**

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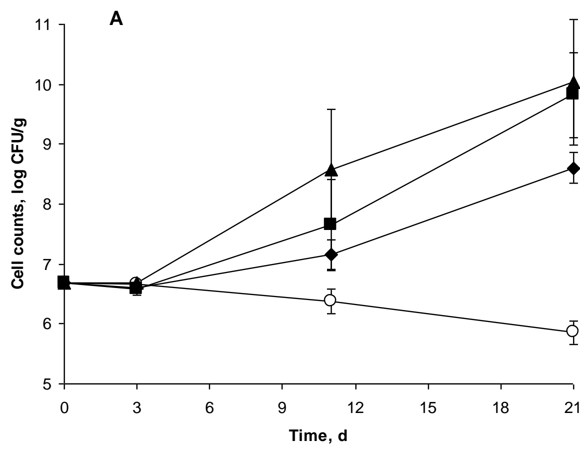

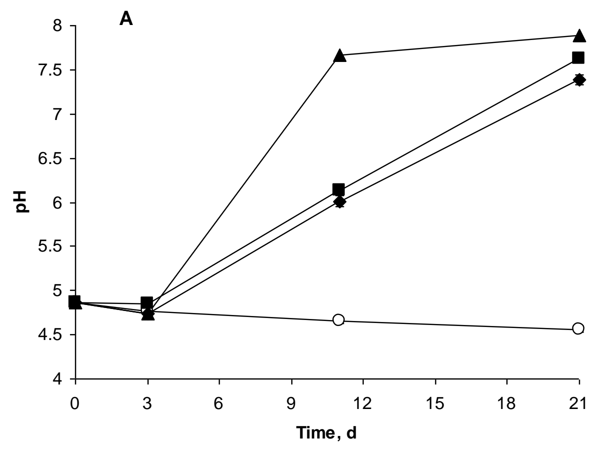

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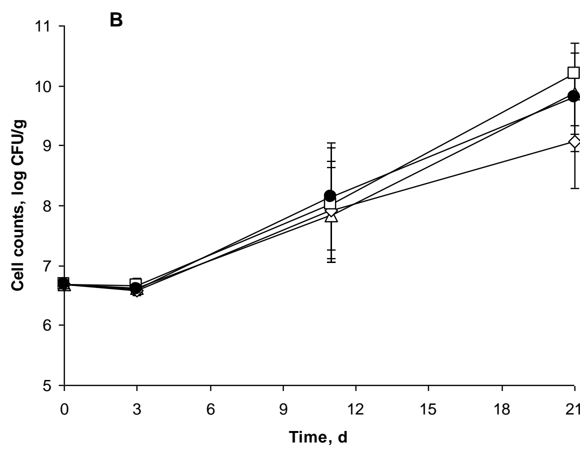

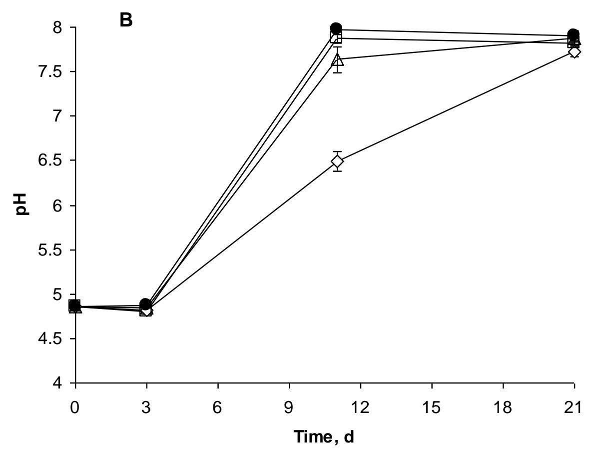

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778 **Figure 7.**

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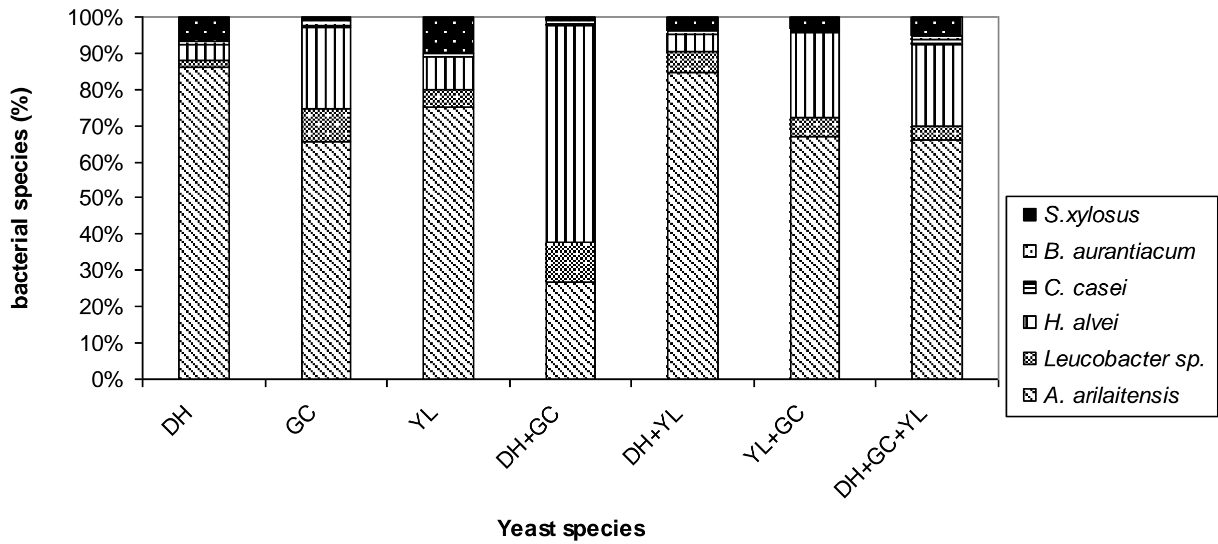

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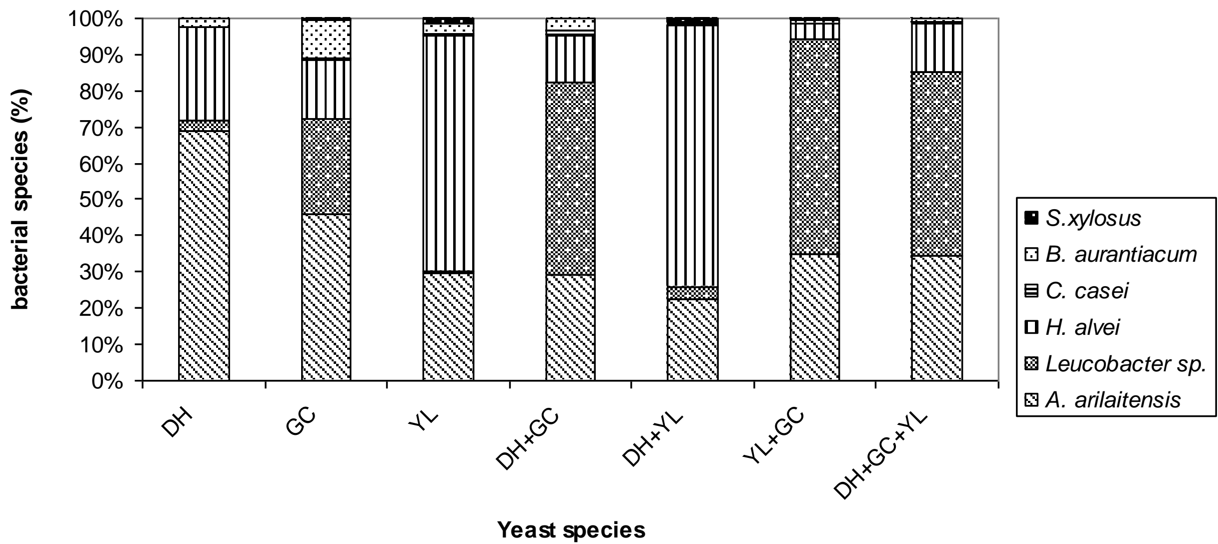

798 **Figure 8.**

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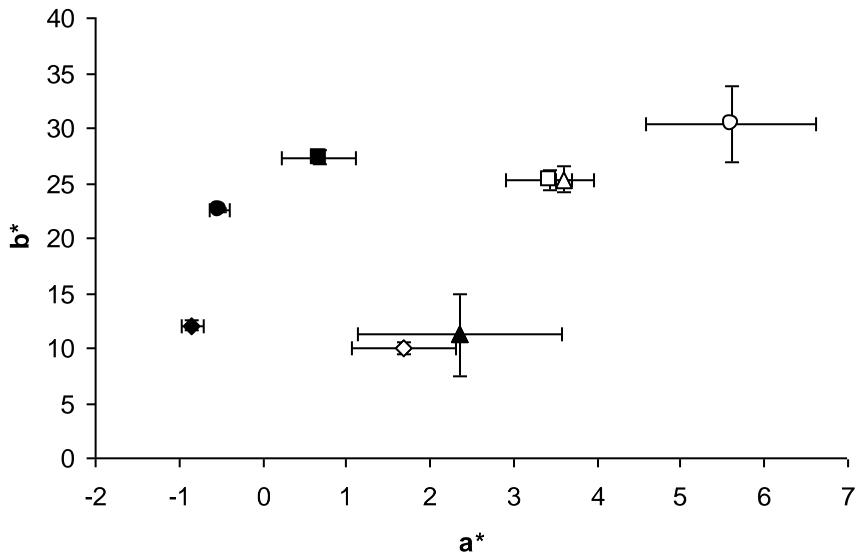

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801 **Supplementary material**

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803 **Figure legends.**

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805 **Figure S1**. Growth properties of the bacteria of the cheese ecosystem as a function of pH and
806 NaCl content at 12°C. Growth after ■ 2 days, ■ 4 days and □ absence of growth after
807 incubation for 8 days.

808 **Figure S2**. Dendrogram of the different species according to their squared correlation
809 coefficient during growth in model cheese used for Lotka-Volterra modelling.

810 **Figure S3**. Comparison of experimental populations (○) of experiment I and estimated
811 populations (▬) using Lotka-Volterra modelling of *Debaryomyces hansenii* (Dh), *Yarrowia*
812 *lipolytica* (Yl), *Geotrichum candidum* (Gc), *Leucobacter* sp. (Le) and a group including
813 *Arthrobacter arilaitensis*, *Hafnia alvei*, *Corynebacterium casei, Brevibacterium aurantiacum*
814 and *Staphylococcus xylosus* (C).

815 **Figure S4**. Comparison of experimental populations of experiment II (○) and estimated
816 populations (▬) using Lotka-Volterra modelling of *Debaryomyces hansenii* (Dh), *Yarrowia*
817 *lipolytica* (Yl), *Geotrichum candidum* (Gc), *Leucobacter* sp. (Le) and a group including
818 *Arthrobacter arilaitensis*, *Hafnia alvei*, *Corynebacterium casei, Brevibacterium aurantiacum*
819 and *Staphylococcus xylosus* (C).

820 **Figure S5.** Growth of *Debaryomyces hansenii* when cultivated as a monoculture (■) or in co-
821 culture with *Yarrowia lipolytica* (▲), *Geotrichum candidum* (○) or *Y. lipolytica* and *G.*
822 *candidum* (□).

823

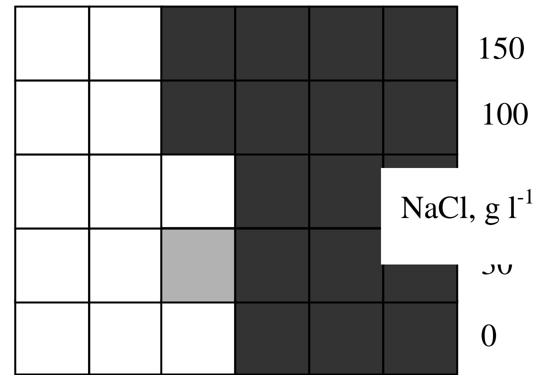
Figure S1.

Leucobacter sp., 12°C

150
100
NaCl, g l^{-1}
0

5 5.5 6 6.5 7 8
pH

C. casei, 12°C

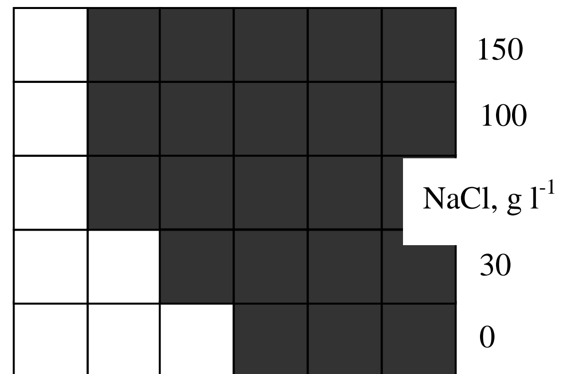


S. xylosus, 12°C

150
100
NaCl, g l^{-1}
30
0

5 5.5 6 6.5 7 8
pH

A. arilaitensis, 12°C



H. alvei, 12°C

150
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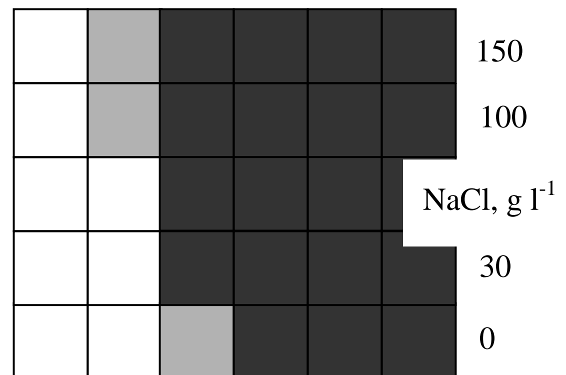
NaCl, g l^{-1}
30
0

5 5.5 6 6.5 7 8
pH

B. aurantiacum, 12°C



849 **Figure S2.**

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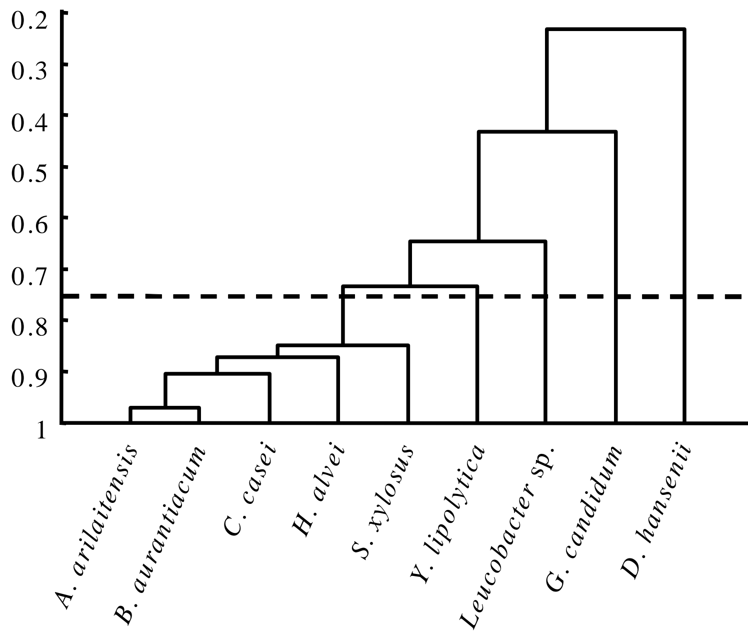

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869 **Figure S3.**

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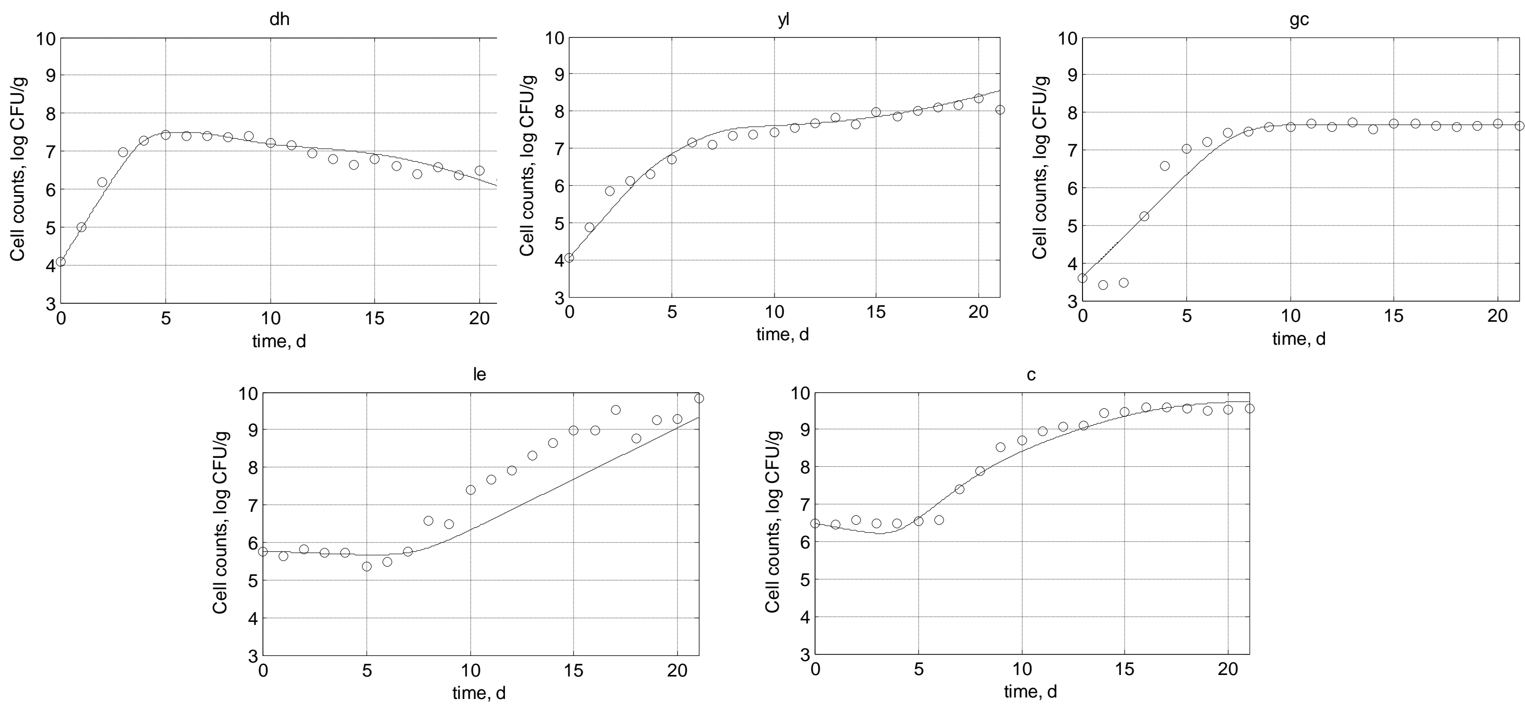
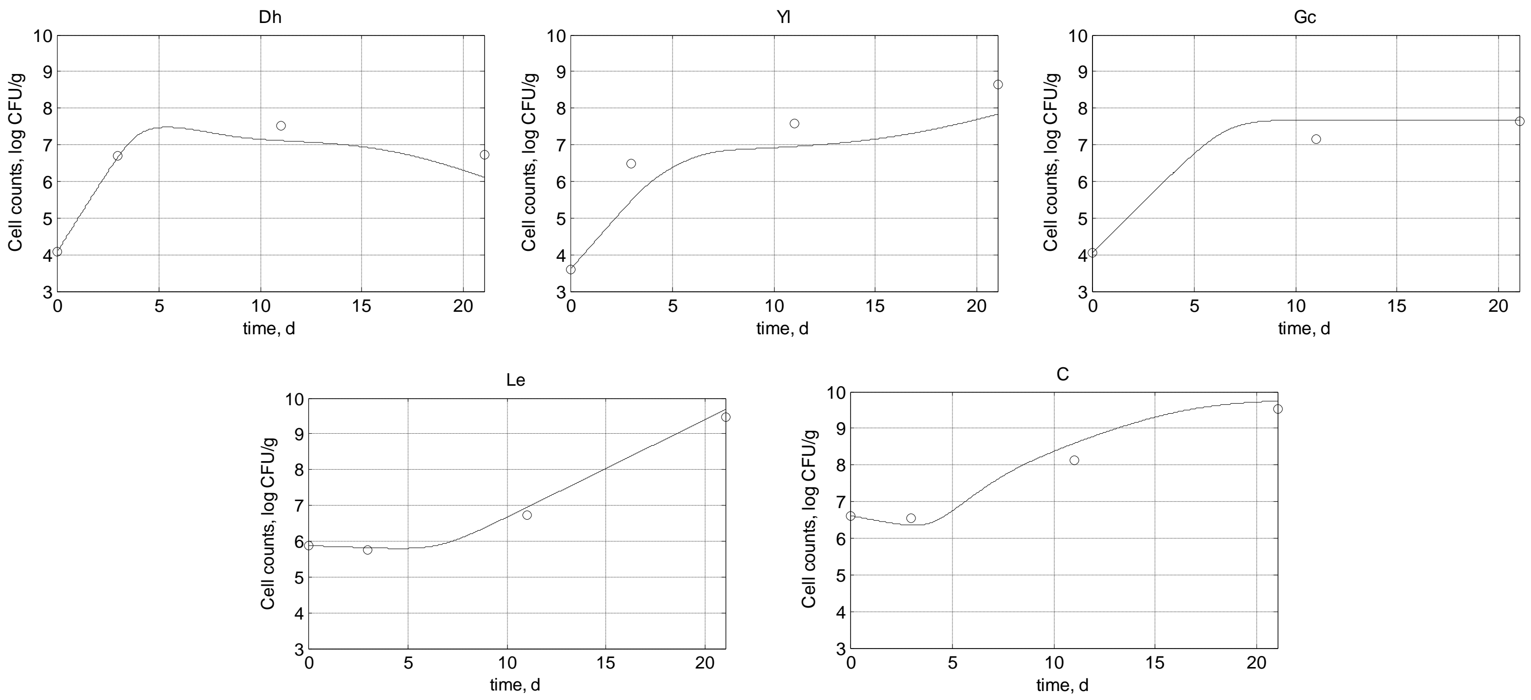
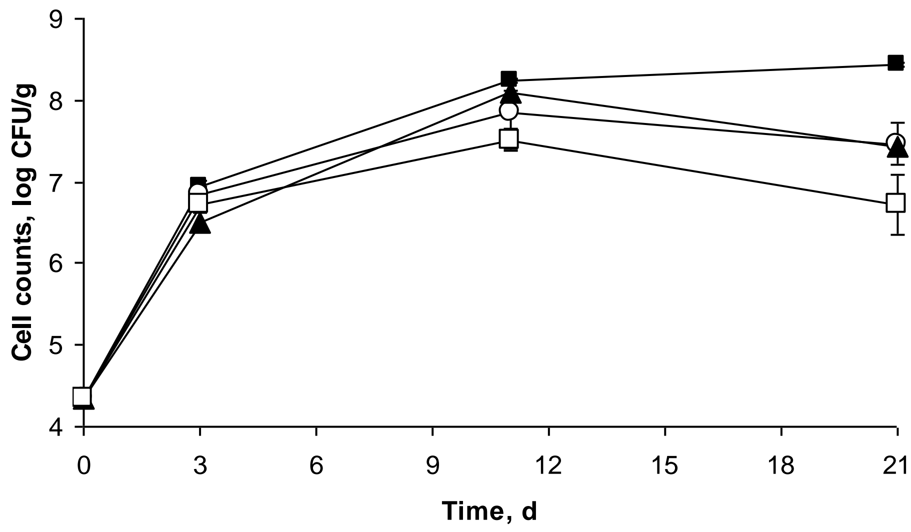


872 **Figure S4.**



875 **Figure S5.**



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