

## Microbial interactions within a cheese microbial community

Jérôme Mounier, Christophe Monnet, Tatiana Vallaeys, Roger Ardit, Anne-Sophie Sarthou, Arnaud Hélias, Françoise Irlinger

► **To cite this version:**

Jérôme Mounier, Christophe Monnet, Tatiana Vallaeys, Roger Ardit, Anne-Sophie Sarthou, et al.. Microbial interactions within a cheese microbial community. Applied and Environmental Microbiology, American Society for Microbiology, 2008, 74 (1), pp.172-181. 10.1128/AEM.01338-07 . hal-00556971

**HAL Id: hal-00556971**

**<https://hal.univ-brest.fr/hal-00556971>**

Submitted on 25 Jan 2011

**HAL** is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



1  
2  
3  
4  
5  
6  
7  
8  
9  
10  
11

**Microbial Interactions Within a Cheese Microbial Community**

Jérôme Mounier<sup>1</sup>, Christophe Monnet<sup>1</sup>, Tatiana Vallaes<sup>1</sup>, Roger Arditi<sup>2</sup>, Anne-Sophie Sarthou<sup>1</sup>, Arnaud Hélias<sup>1</sup> and Françoise Irlinger<sup>1\*</sup>

<sup>1</sup>UMR782 Génie et Microbiologie des Procédés Alimentaires, INRA, AgroParisTech, 78850 Thiverval Grignon, France.

<sup>2</sup>Ecologie des Populations et Communautés, AgroParisTech, 75000 Paris, France

---

\* Corresponding author. Mailing address: UMR782 Génie et Microbiologie des Procédés Alimentaires, INRA, AgroParisTech, 78850 Thiverval Grignon, France. Phone: +33 (0)1 30 81 54 91. Fax: +33 (0)1 30 81 55 97. E-mail: irlinger@grignon.inra.fr.

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 microorganisms 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<sup>-1</sup>, 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<sup>3</sup> 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<sub>2</sub> 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  $2 \times 10^9$  CFU/ml and  $2 \times 10^7$  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 spectrophotometer (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

198

$$C_0 = \sum_{i=1}^n \frac{N_i C_i}{N}$$

199

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

202

203 **Statistical analysis**

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

208

209 *Lotka-Volterra modeling*

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

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

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

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

219 The left part of this equation was obtained by deriving the logarithm of the species  
 220 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  $\alpha_{ij}$  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<sup>-1</sup> 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<sup>-1</sup> 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<sub>10</sub> 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<sub>10</sub> 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<sub>10</sub> 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<sup>8</sup> CFU/g on day 0 to 2 x 10<sup>7</sup> 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 dendrogram 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  $0.1 \pm 0.4$  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<sub>3</sub> (data not  
351 shown). *Y. lipolytica* did not utilize lactate but produced large amounts of NH<sub>3</sub> (data not  
352 shown). Amino acids and compounds such as ornithine and  $\gamma$ -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.



518 **Acknowledgements**

519 J. Mounier would like to thank INRA for awarding him a post-doc fellowship. The authors

520 thank M.-N. Leclercq-Perlat and F. Lecornue for cheese production under aseptic conditions.

521 The authors also thank A. Antoinette and A. Delile for their excellent technical assistance.

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. Vallaey.** 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., Vallaey, 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 coryneform 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., Spinner, 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<br>20 mg/l | Vancomycin<br>1 mg/l | TTC‡<br>0.1 g/l |
|-----------------------------------|------------|--------|-------------------------|----------------------|-----------------|
|                                   | 1 mg/l     | 5 mg/l |                         |                      |                 |
| <i>Arthrobacter arilaitensis</i>  | -†         | -      | -                       | -                    | +               |
| <i>Brevibacterium aurantiacum</i> | +          | -      | -                       | v                    | v               |
| <i>Corynebacterium casei</i>      | +          | +      | -                       | -                    | v               |
| <i>Hafnia alvei</i>               | +          | +      | +                       | +                    | +               |
| <i>Leucobacter</i> sp.            | -          | -      | -                       | +                    | +               |
| <i>Staphylococcus xylosus</i>     | +          | +      | -                       | +                    | +               |

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*; *Ls*, *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.**

682

683

684

685

686

687

688

689

690

691

692

693

694

695

696

697

698

699

700

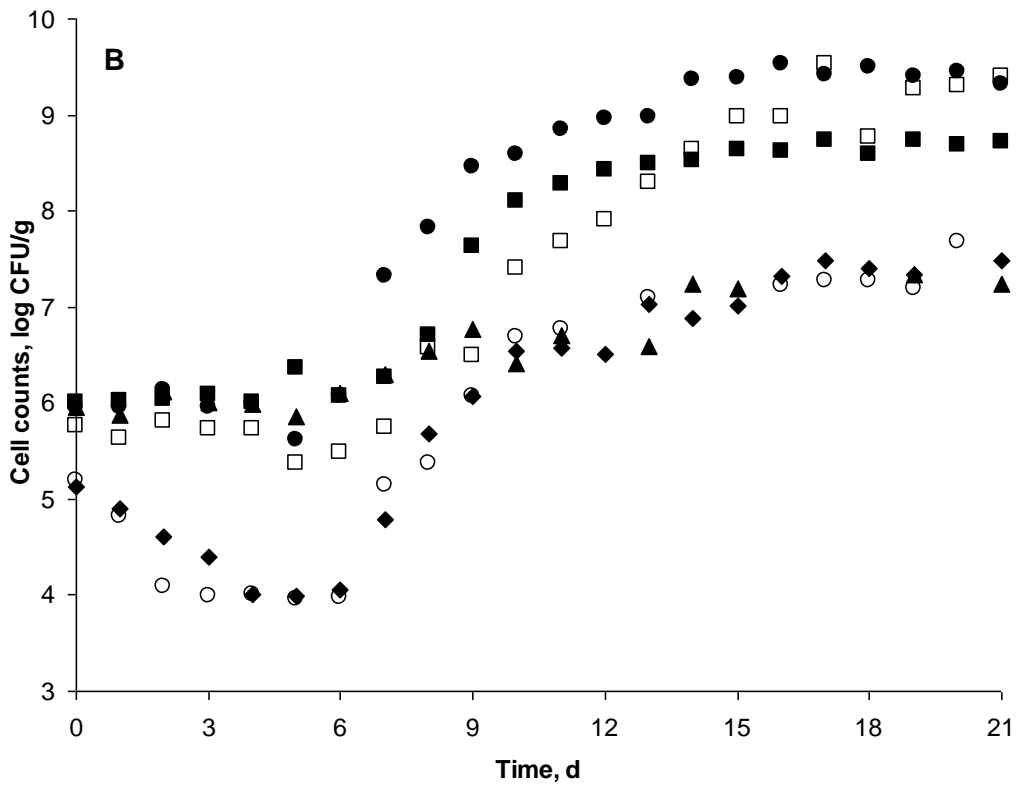
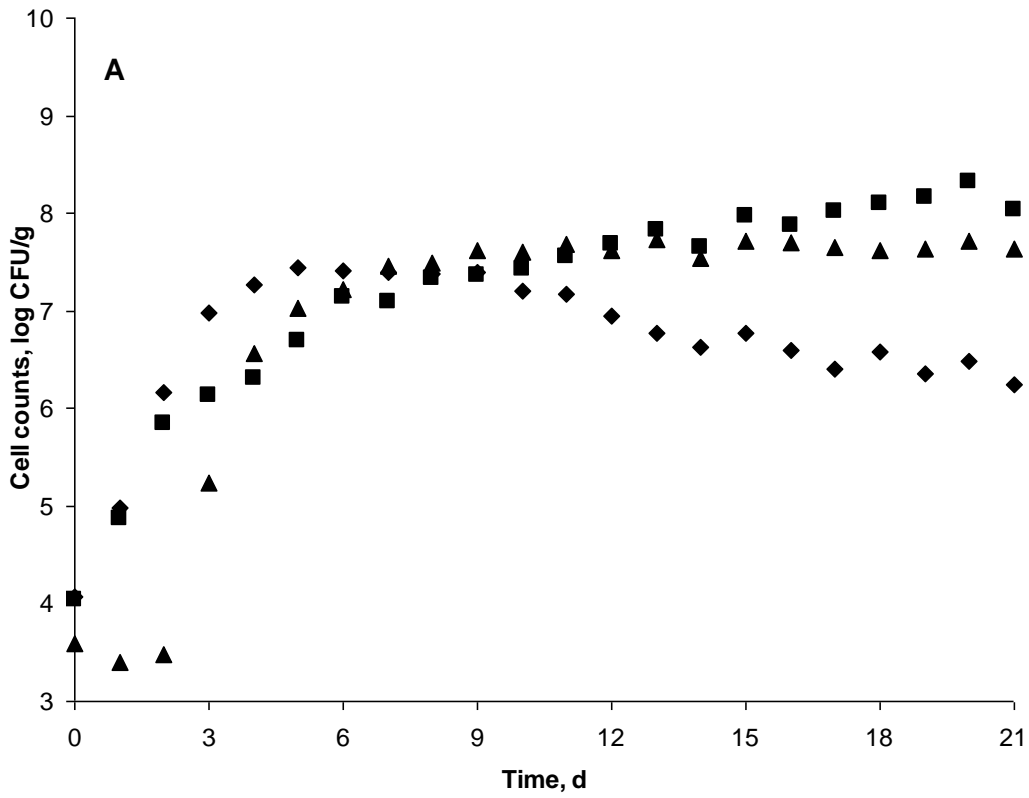
701

702

703

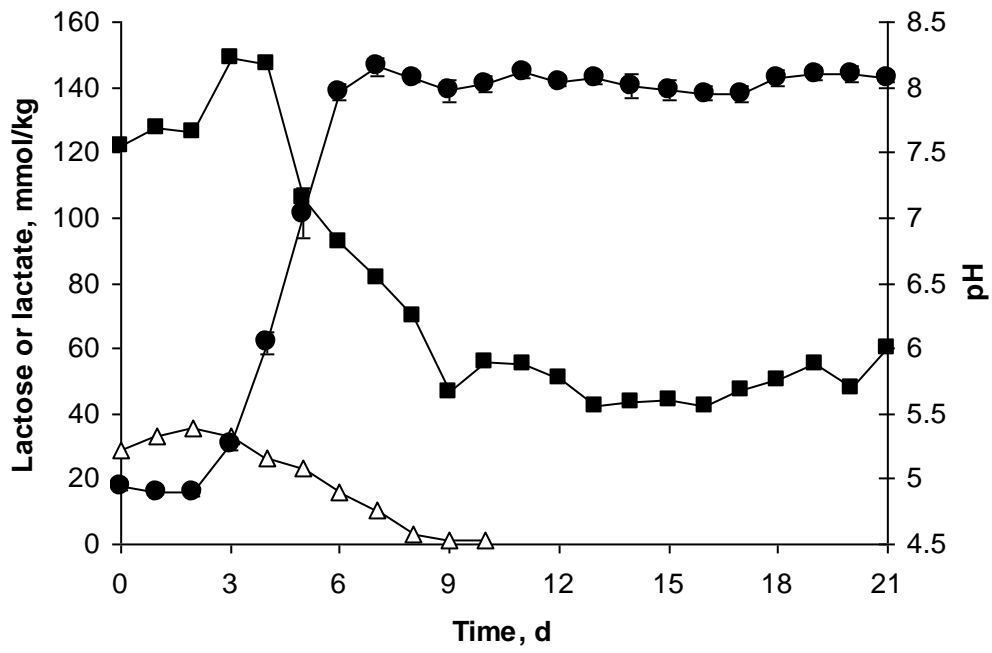
704

705



706 **Figure 2.**

707



708

709

710

711

712

713

714

715

716

717

718

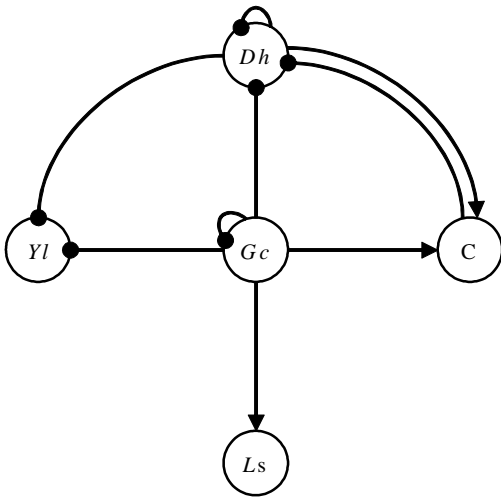
719

720

721

722 **Figure 3.**

723



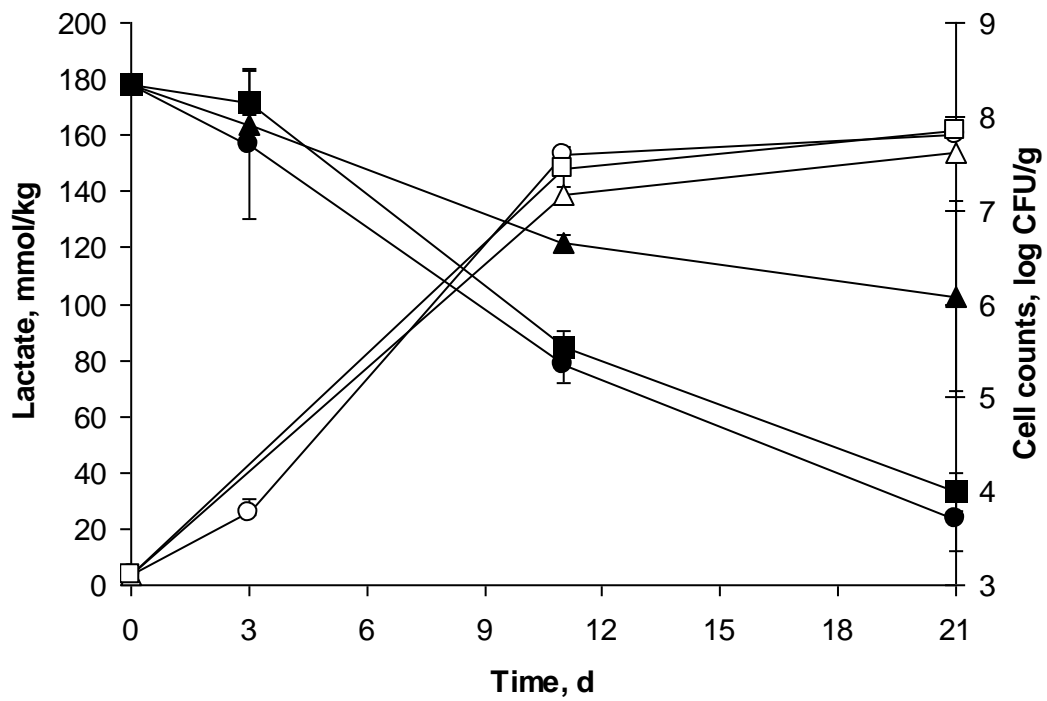
724

725 **Figure 4.**

726



727



728

729

730

731

732

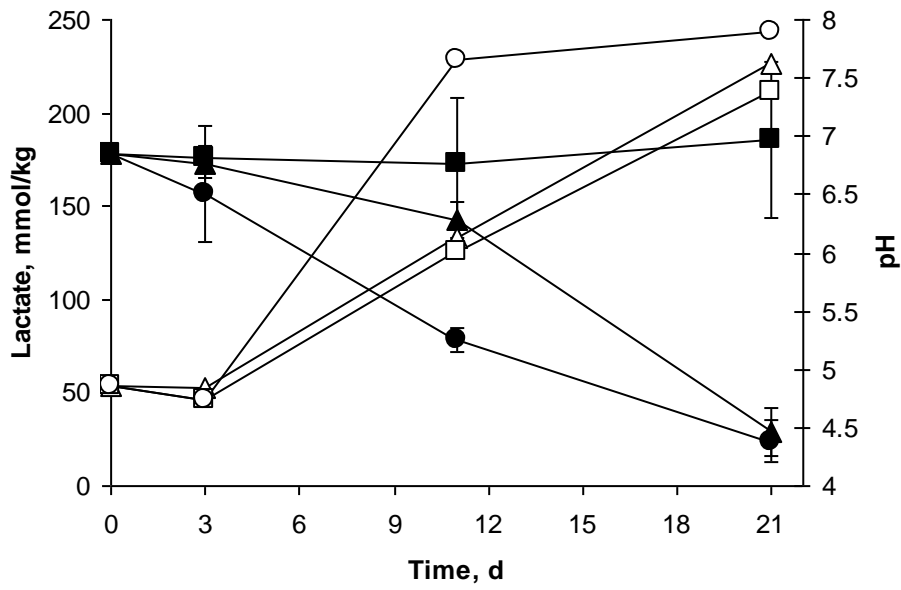
733

734

735

736 **Figure 5.**

737



738

739

740

741

742

743

744

745

746

747

748

749

750

751

752

753 **Figure 6.**

754

755

756

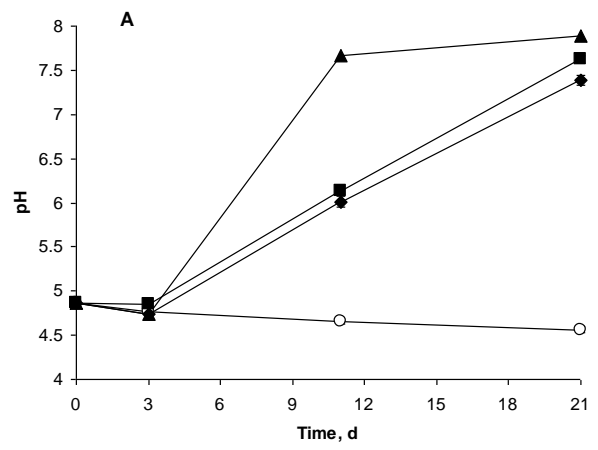
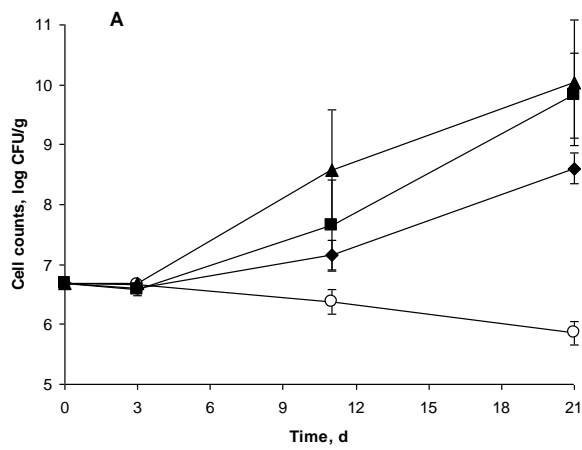
757

758

759

760

761



762

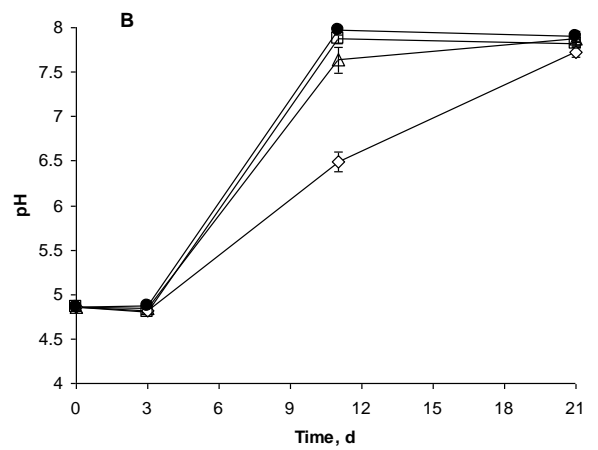
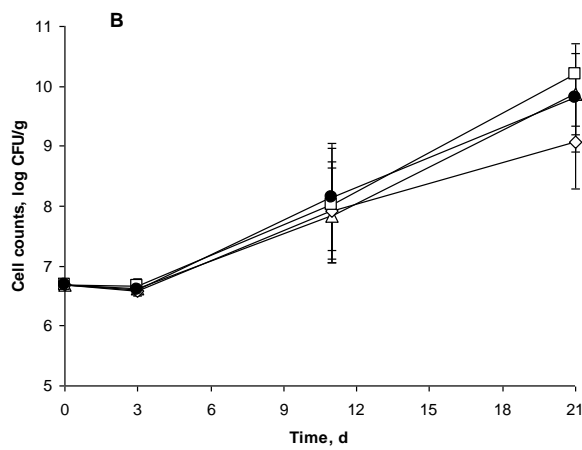
763

764

765

766

767



768

769

770

771

772

773

774

775

776

777

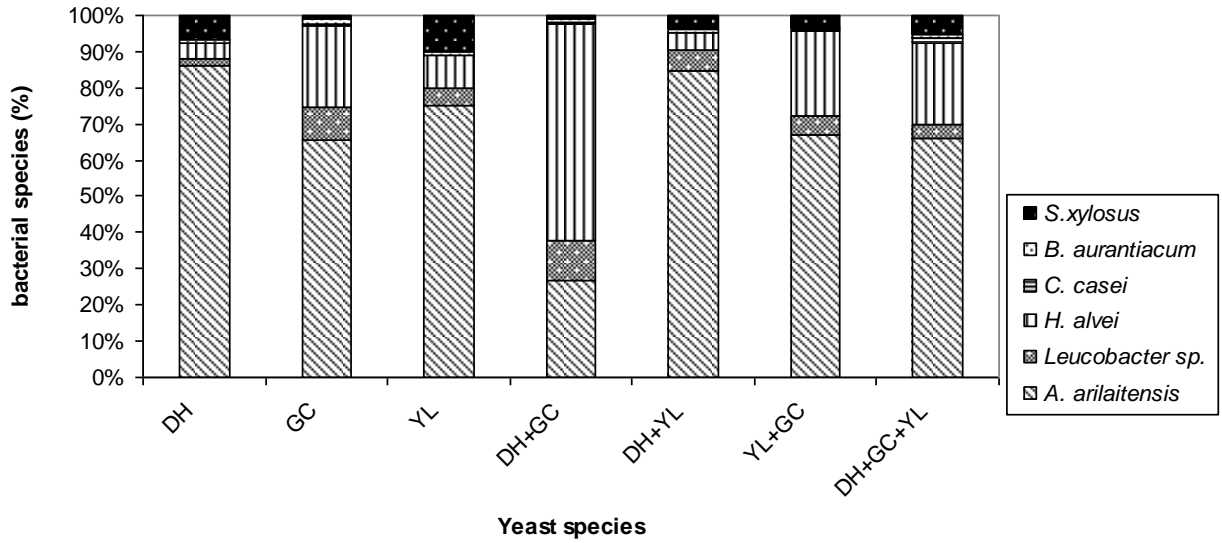
778 **Figure 7.**

779

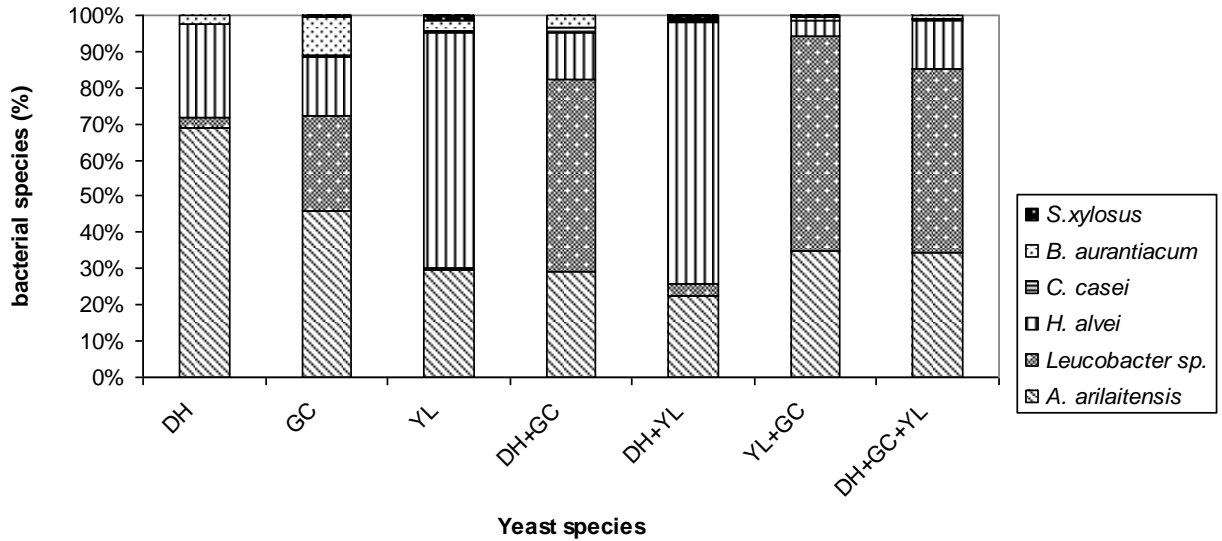
780

781

d 11



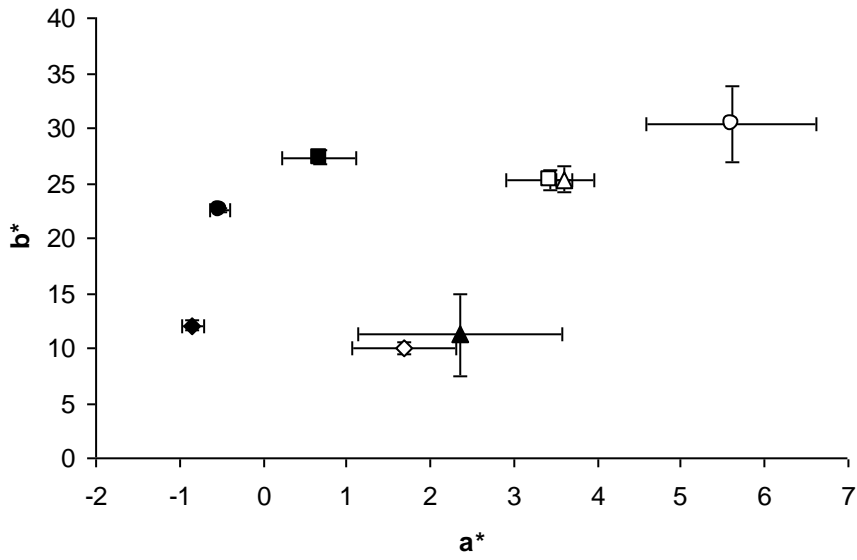
d 21





798 **Figure 8.**

799



800

801 **Supplementary material**

802

803 **Figure legends.**

804

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

824 **Figure S1.**

825

*Leucobacter* sp., 12°C

826

827

828

829

830

831

832

833

*S. xylosus*, 12°C

834

835

836

837

838

839

840

841

*H. alvei*, 12°C

842

843

844

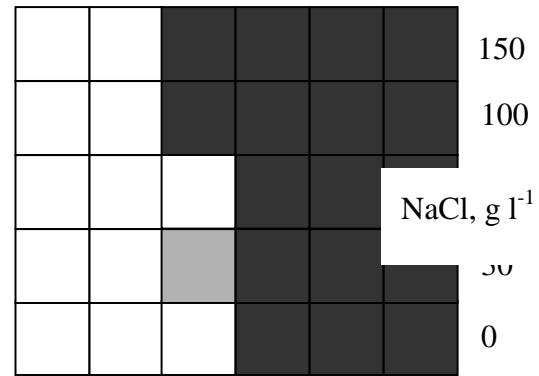
845

846

847

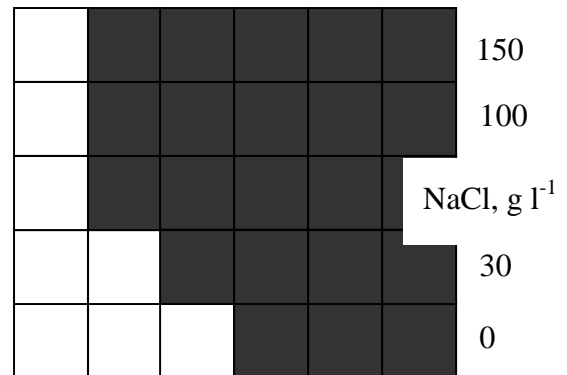
848

*C. casei*, 12°C



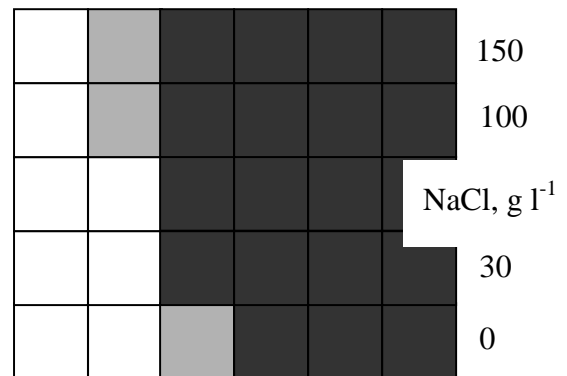
pH

*A. arilaitensis*, 12°C



pH

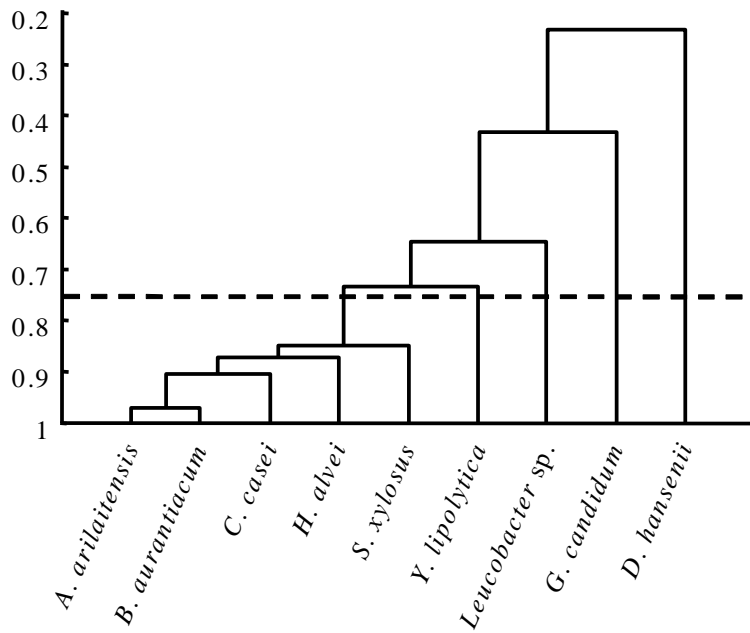
*B. aurantiacum*, 12°C



pH

849 **Figure S2.**

850



851

852

853

854

855

856

857

858

859

860

861

862

863

864

865

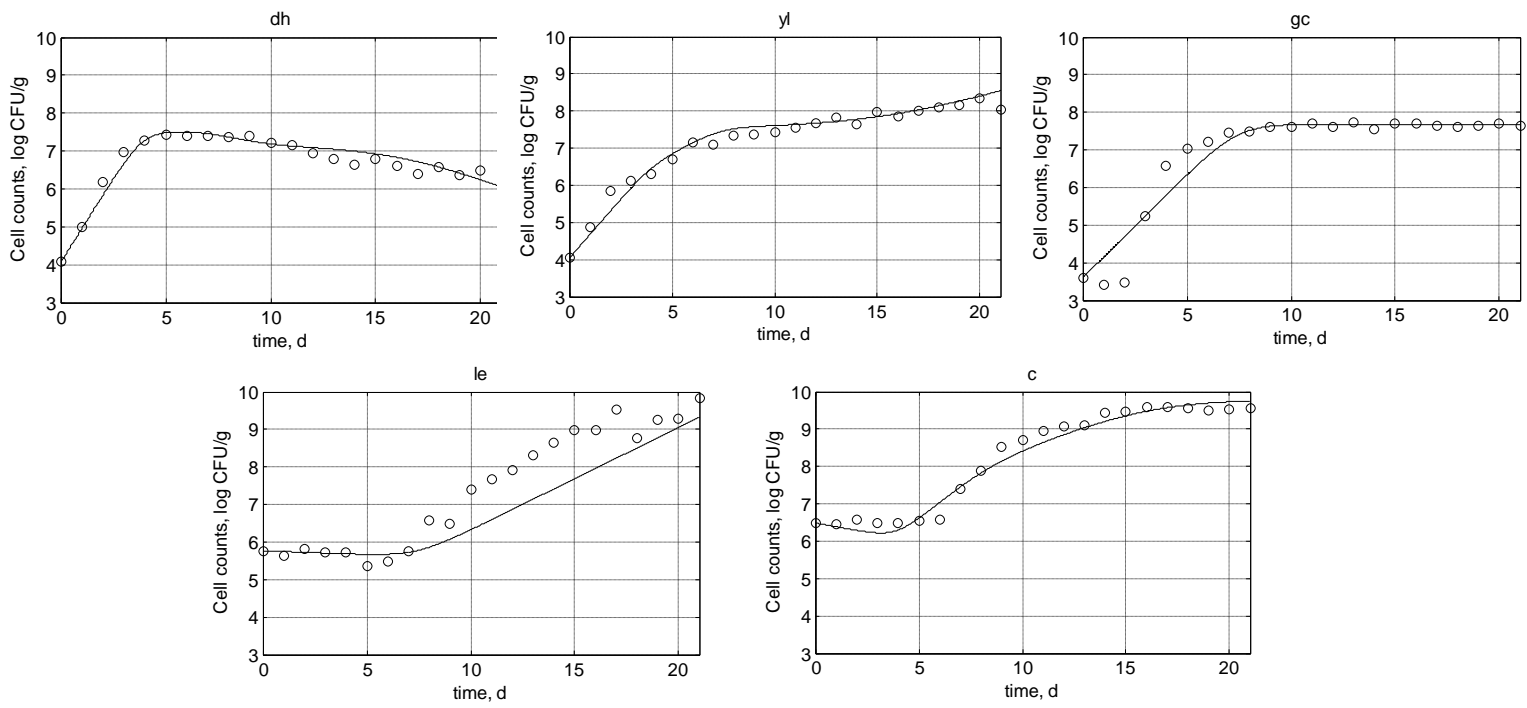
866

867

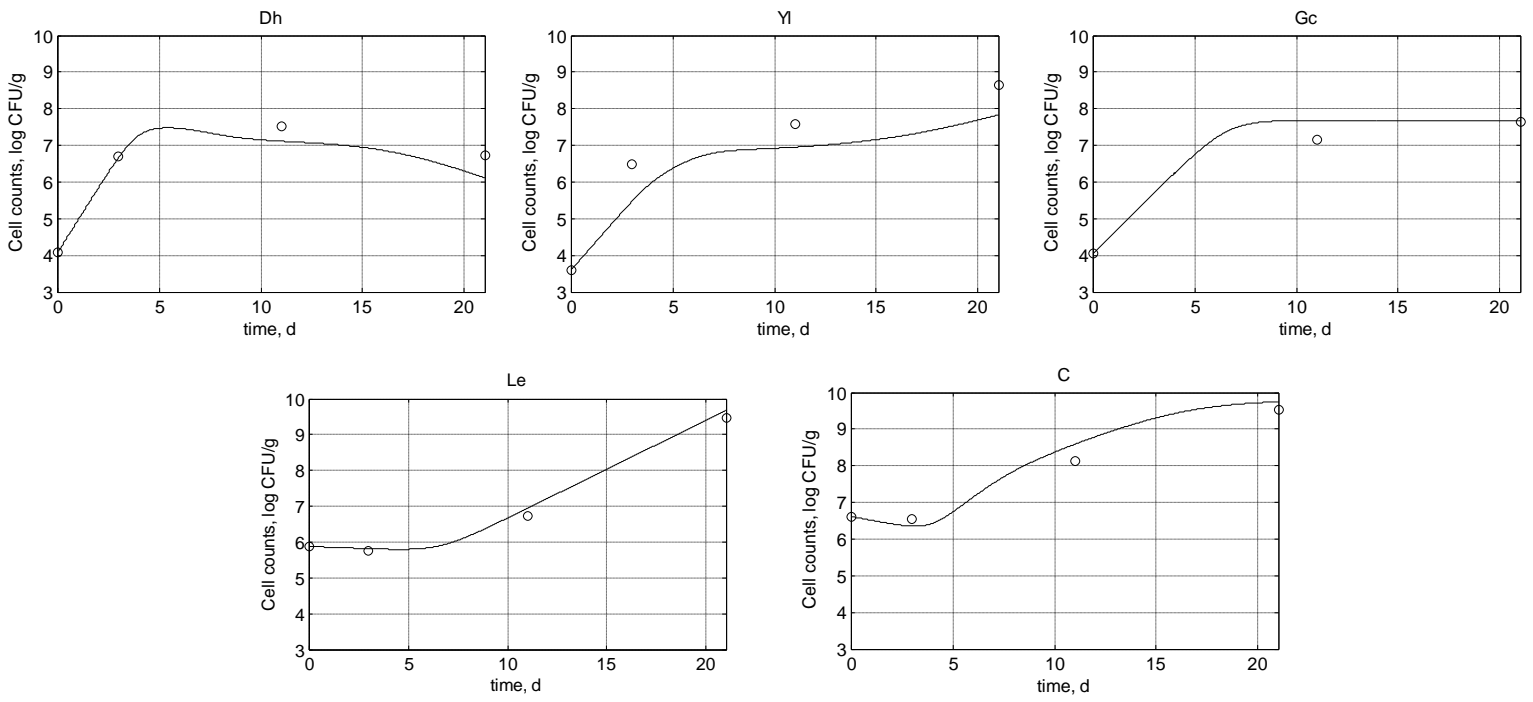
868

869 **Figure S3.**

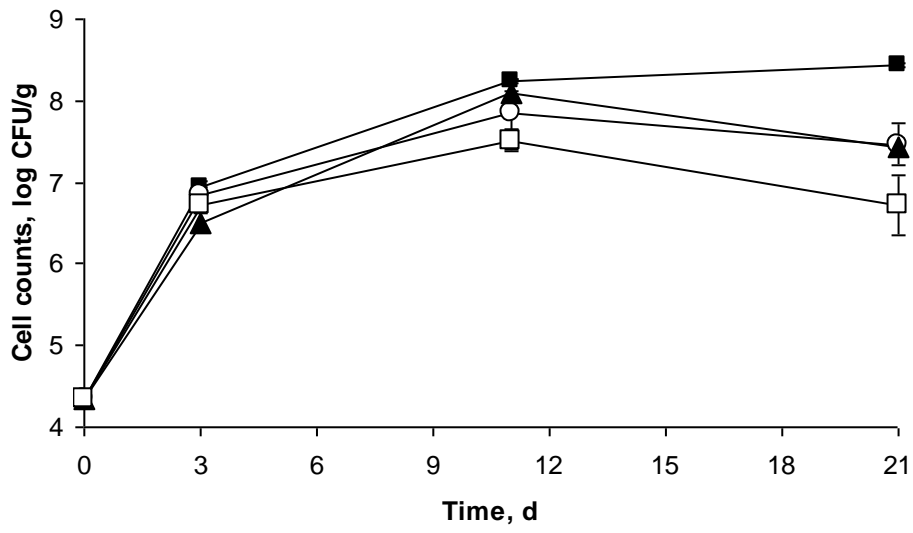
870



872 **Figure S4.**



875 **Figure S5.**



876

877

878

879

880

881

882

883

884

885

886

887

888

889

890

891

892