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Marina Cretenet, Sébastien Nouaille, Jennifer Rivière, Lucie Gouffier, Ludwig Stenz, et al.. Staphylococcus aureus virulence and metabolism are dramatically affected by Lactococcus lactis in cheese matrix. Environmental Microbiology Reports, 2011, 3 (3), pp.340-351. 10.1111/j.1758-2229.2010.00230.x . hal-02291148

HAL Id: hal-02291148

<https://normandie-univ.hal.science/hal-02291148>

Submitted on 18 Sep 2019

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Journal:	<i>Environmental Microbiology and Environmental Microbiology Reports</i>
Manuscript ID:	Draft
Manuscript Type:	EMI - Research article
Journal:	Environmental Microbiology
Date Submitted by the Author:	n/a
Complete List of Authors:	Even, Sergine; INRA, UMR1253 STLO; Agrocampus Ouest, UMR1253 STLO Cretenet, Marina; INRA, UMR1253 STLO; Agrocampus Ouest, UMR1253 STLO Le Loir, Yves; INRA, UMR1253 STLO; Agrocampus Ouest, UMR1253 STLO
Keywords:	microbe:microbe interactions, environmental signal/stress responses



***Staphylococcus aureus* virulence and metabolism are dramatically affected
by *Lactococcus lactis* in cheese matrix**

Running title: *S. aureus* interaction with *L. lactis* in cheese matrix.

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34 **Keywords:** *Staphylococcus aureus*, cheese, virulence, enterotoxin, ecosystem, bacterial
35 interactions

36 **Summary**

37 In complex environments such as cheeses, the lack of relevant information on the physiology
38 and virulence expression of pathogenic bacteria and the impact of endogenous microbiota has
39 hindered progress in risk assessment and control. Here, we investigated the behaviour of
40 *Staphylococcus aureus*, a major foodborne pathogen, in a cheese matrix, either alone or in the
41 presence of *Lactococcus lactis*, as a dominant species of cheese ecosystems. The dynamics of
42 *S. aureus* was explored *in situ* by coupling a microbiological and, for the first time, a
43 transcriptomic approach. *L. lactis* affected the carbohydrate and nitrogen metabolisms and the
44 stress response of *S. aureus* by acidifying, proteolysing and decreasing the redox potential of
45 the cheese matrix. Enterotoxin expression was positively or negatively modulated by both *L.*
46 *lactis* and the cheese matrix itself, depending on the enterotoxin type. Among the main
47 enterotoxins involved in staphylococcal food poisoning, *sea* expression was slightly favoured
48 in the presence of *L. Lactis*, whereas a strong repression of *sec4* was observed in cheese
49 matrix, even in the absence of *L. lactis*, and correlated with a reduced *saeRS* expression.
50 Remarkably, the *agr* system was downregulated by the presence of *L. lactis*, in part because
51 of the decrease in pH. This study highlights the intimate link between environment,
52 metabolism and virulence, as illustrated by the influence of the cheese matrix context,
53 including the presence of *L. lactis*, on two major virulence regulators, the *agr* system and
54 *saeRS*.

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Introduction

Staphylococcus aureus is a major human pathogen, with clinical manifestations ranging from skin infections to sepsis (Wertheim et al., 2005). *S. aureus* is also a major causative agent of food poisonings, due to the production of staphylococcal enterotoxins (SE) by strains contaminating foodstuffs (Zhang et al., 1998; Tirado and Schmidt, 2001; Le Loir et al., 2003; Ikeda et al., 2005). Although symptoms are not life-threatening or only rarely so, staphylococcal food poisoning (SFP) outbreaks remain a persistent public health problem. Milk and milk products are often incriminated in SFP, especially in France (De Buyser et al., 2001; Jorgensen et al., 2005; Delbes et al., 2006).

The capacity of *S. aureus* to provoke one or another infection relies on a wide variety of virulence factors, the expression of which reportedly depends on the nature of the environment and stresses encountered. This intimate link between metabolic processes and virulence gene expression in *S. aureus* has been recently highlighted by Somerville and Proctor (Somerville and Proctor, 2009). In recent years, functional genomics, transcriptomics and proteomics have led to significant results on virulence gene expression and regulation and on the responses of *S. aureus* to different stressors (Dunman et al., 2001; Bischoff et al., 2004; Weinrick et al., 2004; Cui et al., 2005; Chang et al., 2006; Pane-Farre et al., 2006; Rogasch et al., 2006). However these studies were conducted either in laboratory conditions or in a setting relevant to the medical context and thus are hardly transferable to complex food environments.

S. aureus growth and enterotoxin detection have been reported for years in several foodstuffs including milk products (Vernozy-Rozand et al., 1998; Meyrand et al., 1998; Delbes et al., 2006; Poli et al., 2007; Cremonesi et al., 2007). More recently, a few studies have investigated *S. aureus* behaviour in milk, allowing relevant genes in this context to be pointed out (Lammers et al., 2000; Sharer et al., 2003; Borezee-Durant et al., 2009). Nevertheless, apart

from these few recent and targeted studies, the physiology of *S. aureus* and the mechanisms governing its virulence expression are poorly understood in the milk and cheese context. In particular, our knowledge of individual enterotoxin gene expression and regulation was mainly derived from studies performed in laboratory media and in planktonic growth conditions (Derzelle et al., 2009). Recently, technical bottlenecks have been overcome, allowing the measurement of gene expression, including expression of enterotoxin genes, in complex matrices such as cheeses (Ulve et al., 2008; Duquenne et al., 2010). As a consequence of these advances, *in situ* approaches can now be used to investigate *S. aureus* physiology, including virulence expression, in realistic environmental conditions.

Several factors can affect *S. aureus* behaviour in cheese. In particular, the presence of other microorganisms, especially lactic acid bacteria (LAB), reportedly limits *S. aureus* growth and enterotoxin production. However, again, most of our knowledge relies on observations or screenings for inhibitory activities, the molecular mechanisms of which remain unknown. LAB antagonism is a complex and multifactorial phenomenon, and various hypotheses have been advanced regarding its mechanisms, including production of inhibitory compounds (bacteriocin, hydrogen peroxide), acidification, and nutritional competition (Barber and Deibel, 1972; Haines and Harmon, 1973; Notermans and Heuvelman, 1983; Ammor et al., 2006; Delbes et al., 2006; Otero and Nader-Macias, 2006; Charlier et al., 2008a). Molecular and global approaches, including transcriptomics and proteomics, are powerful tools that have already allowed the mechanisms of action of one species of bacteria upon another to be deciphered (Mashburn et al., 2005; Laughton et al., 2006). Recently, we reported the first transcriptomic approach regarding the interaction between *S. aureus* and *L. lactis* in a chemically defined medium (CDM) (Even et al., 2009; Nouaille et al., 2009). We showed that *L. lactis* was able to strongly affect the expression of several regulatory systems and virulence

genes of *S. aureus*, including the accessory gene regulator (*agr*), a key regulator of bacterial virulence.

In this study, *S. aureus* MW2 growth was followed in cheese matrix for 7 days by coupling a microbiological and, for the first time, a transcriptomic approach. *S. aureus* was grown either alone or in the presence of *L. Lactis* in order to address the influence of this antagonistic flora. Results show that, in cheese matrix, expression of important *S. aureus* virulence genes was strongly altered by both the cheese matrix itself, as an abiotic environmental component, and by the presence of *L. lactis*.

Results

One log inhibition of *S. aureus* growth by *L. lactis* in cheese matrix. *S. aureus* MW2 was grown in ultra-filtrate (UF) retentate, a cheese matrix, as previously described (Ulve et al., 2008) to mimic the conditions encountered during the cheese-making process (i.e., immobilized growth in the colony in a dairy environment). UF retentate, the cheese matrix used for this study, is based on the MMV (Maubois-Moquot-Vassal) process and has been widely used in several cheese-making processes for soft to semi-hard cheeses (Mistry V.V. and Maubois J.L., 1993; Maubois J.L., 1997). MW2 was selected among all sequenced strains of *S. aureus* for its origin (community-acquired) and its content in enterotoxin genes (Baba et al., 2002). Two additional *S. aureus* field strains (kindly provided by AFSSA-Ierqap) involved in SFP outbreaks were tested in similar growth conditions to validate our results: *S. aureus* 257D (isolated from chocolate milk and carrying the *sea* gene) and *S. aureus* 253E (isolated from cheese and carrying the *sea* and *sed* genes).

S. aureus MW2 grew exponentially in the cheese matrix for the first 6 h of culture and entered into the stationary phase before the temperature shift at 10 h. The final population density was 2×10^9 cfu g⁻¹ at 24 h and was maintained until day 7 (Fig. 1). The kinetics of *S. aureus* MW2 growth in mixed culture revealed an inhibition of *S. aureus* by *L. lactis* from 6 h onwards, reaching one log at 7 days (Fig. 1A). Lactose was never depleted from the medium during the 7 days of culture (Fig. 1B). In *S. aureus* pure culture, small amounts of acetate were quantified by day 7, whereas lactate production was not observed (Fig. 1B). pH remained unchanged. In contrast, the presence of *L. lactis* caused a drop in pH values down to 5 by day 7, in accordance with lactate and acetate production (Fig. 1C). Similar inhibition by *L. lactis* was observed on *S. aureus* 257D and 253E, the two field strains. Both strains grew to a final density (10^9 cfu g⁻¹ by day 7) in pure culture in cheese matrix that was similar to that of the *S.*

aureus MW2 strain. Final populations of strains 257D and 253E after 7 days were 1.5- and 2-log lower, respectively, in mixed culture compared to pure culture (data not shown).

A severe decrease of the expression of genes involved in cellular machinery in the presence of *L. lactis*. The gene expression profiles of *S. aureus* in pure and mixed cultures with *L. lactis* in cheese matrix were analysed using microarrays and reverse transcription quantitative PCR (RT-qPCR) over 7 days. Expression of genes involved in cell division, transcription, translation, and cell envelope biosynthesis were maintained for 7 days in pure culture but were downregulated in mixed cultures (Table 1, Table S1). Indeed, the expression of genes involved in cell division (*ftsH*, *ftsZ*, *ftsL*) and cell envelope biosynthesis (*pbp4*, *gpsA*, *MW2013*) continuously decreased during the first 24 h in mixed culture but was not significantly modified in pure culture. Additionally, expression of genes involved in transcription (*rho*, *rpoC*) and translation (*fus*, *tufA*, *rpmI*) decreased in mixed culture at all times compared to 6 h. These results were confirmed by RT-qPCR and expanded to 7 days of culture for *ftsZ* and *pbp4* (Table 1). In conclusion, although *S. aureus* entered a stationary phase in pure culture after 24 h, cells retained an active metabolic status, as revealed by the maintenance of expression of several genes related to growth, transcription and translation. The presence of *L. lactis* provoked a premature arrest of *S. aureus* MW2 growth. Accordingly, expression of growth-related genes decreased in mixed compared to pure culture.

A major acid stress triggered by *L. lactis*. *S. aureus* did not undergo major stresses when grown in pure culture in cheese matrix (Table 1, Table S1). Indeed, no specific stress response was revealed by the transcriptomic profile in pure culture except the induction of the SigmaB regulon, in agreement with the transition to the stationary phase. Conversely, the presence of

166 *L. lactis* altered the expression of stress-related genes. In agreement with cheese matrix
167 acidification by *L. lactis*, genes associated with the acid stress response showed increased
168 expression in mixed culture, as revealed by both microarray and RT-qPCR data. The urease
169 (*ureD*) pathway, as well as part of the deaminase pathway (*arcC*, *arcR*) involved in the acid
170 stress response (Cotter and Hill, 2003), were overexpressed in mixed compared to pure
171 culture (Table 1). Accordingly, urea was consumed more rapidly in mixed culture than in pure
172 culture (Table S2). Urea can indeed only be consumed by *S. aureus*, as *L. lactis* does not
173 possess a urease-encoding gene. The *sodA* gene, encoding a superoxide dismutase and
174 reportedly involved in the response to oxidative stress generated by an acidic environment
175 (Clements et al., 1999), was also highly upregulated in mixed culture, with a ~4-fold increase
176 at 24 h and 7 days compared to pure culture (Table 1). In addition, expression of members of
177 the CtsR regulon, including the chaperone-encoding genes *dnaK* and *clpC*, as well as *ctsR*
178 itself, increased in mixed culture over 7 days (Table 1), as previously reported in response to
179 various stresses, including acid stress (Chastanet et al., 2003).

180 Apart from the induction of acid stress-related gene expression, *S. aureus* did not undergo
181 major stresses in the presence of *L. lactis*. Genes associated with the general stress response
182 were underexpressed in mixed culture. Notably, genes known to be under SigmaB control (eg,
183 *asp23*, MW1682 and MW0781, encoding, respectively, the alkaline shock protein 23 and two
184 general stress protein-like proteins) were underexpressed in mixed compared to pure cultures
185 (Table S1, Table 1). The expression of *sigB* itself had decreased in mixed culture by day 7
186 (Table 1). SigmaB activity is regulated at the protein rather than the transcriptional level
187 (Senn et al., 2005), and SigmaB response to stressful conditions is reportedly primarily
188 controlled by an induction of *rsbU* transcription (Pane-Farre et al., 2009). Here, *rsbU* was also
189 downregulated in mixed culture (Table S1), which may account for the reduced activity of
190 SigmaB and thus the lower expression of the SigmaB regulon.

Interestingly, genes known to be involved in the oxidative stress response (ie, *trxA*, encoding the thioredoxin, and *kata*, encoding a catalase) were down-expressed in the mixed compared to the pure culture (Table 1). Likewise, the expression of *ahpF*, encoding the alkyl hydroperoxide reductase subunit F, was induced in pure culture whereas it remained constant in mixed culture over 24 h (Table S1). Collectively, these data suggest that *S. aureus* cells sensed a lower redox potential in mixed culture, in accordance with the reducing activity of *L. lactis* (Tachon et al., 2010).

In conclusion, response to acid stress seemed predominant over any other stress-specific response encountered by *S. aureus* during growth in mixed culture with *L. lactis*.

Major changes in *S. aureus* carbohydrate metabolism. In cheese matrix, lactose concentration decreased only slightly by day 7 in pure culture, suggesting that *S. aureus* did not actively metabolize lactose as a carbon source (Fig. 1B). *S. aureus* can grow on amino acids, particularly glutamate (Mah et al., 1967; Borezee-Durant et al., 2009). Predictably, the glutamate concentration strongly decreased until 24 h in pure culture (Table S2). Whether glutamate was also used as a carbon source by *S. aureus* in mixed culture in cheese matrix can be assumed but not proved, because in mixed culture changes in free amino acid and carbohydrates resulted from both lactococcal and staphylococcal metabolisms. Indeed, several amino acids, including glutamate, accumulated from 6 h onwards in cheese matrix in mixed culture as a result of lactococcal proteolytic activity (Table S2). Glutamate was available in mixed culture to sustain *S. aureus* growth.

Strikingly, the presence of *L. lactis* provoked a shift of the expression of several genes related to pyruvate metabolism. The expression of *lctE* and *adh1*, encoding lactate dehydrogenase and alcohol dehydrogenase, was transiently induced in pure culture, whereas it decreased from 10 h onwards in mixed culture (Table 1). On the contrary, the expression of *pflA*,

encoding the pyruvate formate lyase, was higher in mixed culture from 24 h onwards. In the mixed culture, *alsS* and *butA*, encoding respectively the alpha acetolactate synthase and the acetoin reductase, were strongly over-expressed, at all time points in the case of *alsS* (Table 1). Of note, production of acetoin was detected in mixed culture (data not shown), although we cannot exclude, as previously mentioned for amino acids and carbohydrates, that it resulted from both lactococcal and staphylococcal activities. The expression of *alsS* is under the control of CidR, which has been shown to be induced by acetate and lactate, together with the *cid* and *lrg* operons (Yang et al., 2006). In addition, we found here that *cidA* and, to a lesser extent, *lrgA* were overexpressed in mixed culture (Table 1), which correlated well with the production of lactate and acetate by *L. lactis* in mixed culture (Fig. 1B).

***L. lactis* proteolysis relieved *S. aureus* amino acid limitation in cheese matrix.** Cheese matrices are reportedly poor in free amino acids, so the main source of amino acids is provided by proteolysis of caseins (Savijoki et al., 2006). Accordingly, a biochemical analysis revealed that very few amino acids were initially present in the UF retentate (Table S2). Most of them disappeared before 6 h in *S. aureus* pure culture, suggesting a free amino-acid limitation in cheese matrix similar to that previously observed in milk (Borezee-Durant et al., 2009). A few amino acids had accumulated in pure culture by day 7, yet at a low level, suggesting a limited but active proteolysis of *S. aureus* MW2 on caseins. Urea was also used as an alternative nitrogen source after 6 h (Table S2). Urease is known to be induced in the case of nitrogen starvation in *Bacillus subtilis* and *Corynebacterium glutamicum* (Schmid et al., 2000; Brandenburg et al., 2002; Beckers et al., 2004).

In contrast, in mixed culture free amino acids were released and were thus available for the growth of both lactococcal and staphylococcal populations (Table S2). Amino acid accumulation is likely to result mainly from lactococcal proteolytic activity. Amino acid

release might thus relieve the limitation observed in *S. aureus* pure culture. Indeed, the expression of *relA*, a gene involved in the stringent response, that is induced in the case of amino acid limitation (Anderson et al., 2006), was significantly reduced in mixed culture (ratios 0.2 at 24 h and 0.1 at day 7). Furthermore, several genes involved in nitrogen nutrition and amino acid biosynthesis were downregulated during mixed culture. Genes encoding peptidases such as *pepT* and MW1694 as well as *opp3*, the sole oligopeptide transport system used for growth in milk (Hiron et al., 2007), were downregulated in mixed culture (Table 1, Table S1). Expression of genes involved in the biosynthesis pathway of leucine (*leuA*) and isoleucine (*ilvD*) was also lower in mixed culture, especially at 24 h (Table 1). Biosynthesis of these branched-chain amino acids (BCAA: leucine, isoleucine and valine) is under the control of the CodY repressor (Pohl et al., 2009). Increased proteolytic activity in the mixed culture likely provided the necessary co-repressors (BCAA) for CodY-mediated repression of branched-chain amino acid biosynthesis. Collectively, these results suggest that, in mixed culture, lactococcal proteolysis deeply modified the expression of *S. aureus* genes involved in nitrogen nutrition and amino acid biosynthesis.

Downregulation of the expression of *S. aureus* agr system in mixed culture. *S. aureus* virulence expression is tightly controlled by several regulatory systems, of which the *agr* system, *sarA*, *saeRS* and *codY* are key elements (Novick, 2003; Bronner et al., 2004). A striking difference was noted in *agr* system expression when pure and mixed cultures were compared. In pure culture, both *agrA* and RNAIII (*agr* effector) expressions increased over time, especially at 24 h and 7 days, whereas these inductions were strongly attenuated in the presence of *L. lactis* (Table 1). Hence, in mixed culture, the expression of *agrA* and RNAIII increased slightly at 10 h but decreased afterward. As a result, the expression of RNAIII and *agrA* was strongly downregulated from 24h onward in mixed culture with *L. lactis* compared

266 to pure culture. Accordingly, expression of *rot*, which is normally repressed by RNAIII in the
267 stationary phase (Geisinger et al., 2006), was higher in mixed culture at 7 days (Table 1).
268 Likewise, expression of *sarA* and *mgrA*, both known as activators of the *agr* system (Chien et
269 al., 1998; Ingavale et al., 2005), were downregulated at 7 days in mixed compared to pure
270 cultures (Table 1). The downregulation of the *agr* system by *L. lactis* was confirmed in the
271 field strain *S. aureus* 257D: the expression of both *agrA* and RNAIII was strongly enhanced
272 in pure culture in cheese matrix and severely diminished in mixed culture (data not shown).
273 No transcripts of *agrA* and RNAIII were quantified in *S. aureus* 253E, indicating that this
274 strain was *agr* deficient.

275 Regarding virulence factors, differential expression of several genes occurred in the presence
276 of *L. lactis*. Some cell wall-associated virulence factors showed enhanced expression over 24
277 h in *S. aureus* pure cultures only (e.g. *fnb* (MW0764) and *ebpS*, encoding fibrinogen and
278 elastin-binding proteins, respectively; Table S1). Other genes were induced in both conditions
279 but earlier in pure culture, as observed for *clfA* (clumping factor A) and *cap8A* (involved in
280 the capsular polysaccharide synthesis), compared to mixed culture (Table 1). Additionally,
281 *ssaA* (staphylococcus secretory antigen SsaA homolog) was over-expressed in pure culture
282 from 6 h to 24 h (Table S1). Conversely, *fnb* (MW2421), *sdrD* and *sdrC* encoding fibrinogen-
283 binding proteins were over-expressed in mixed culture (Table 1, Table S1). Finally, the
284 biofilm-associated gene *icaA* was strongly downregulated in mixed compared to pure culture
285 (Table 1). Few secreted virulence factors showed differential expression in pure and mixed
286 cultures of *S. aureus*. The hemolysin III (MW2096)– and hemolysin (MW0802)–encoding
287 genes showed increased expression in pure culture from 6 h to 24 h, while their expression
288 remained constant in mixed culture during this period (Table S1). Conversely, *isaB*
289 (immunodominant antigen B) expression was induced earlier in pure culture but reached a
290 higher level in the mixed culture than in the pure culture at 7 days (14.3-fold) (Table 1).

In conclusion, few virulence genes showed differential expression between pure and mixed cultures, and no general trends were observed. Strikingly, downregulation of the *agr* system was provoked by *L. lactis*, as previously observed in a chemically defined medium under environmental conditions very different from those of the cheese matrix (Even et al., 2009).

CodY-independent inhibition of *S. aureus* virulence by *L. lactis*. Transcriptomic analysis of *S. aureus* MW2 suggested an increased CodY repression in mixed culture with *L. lactis*. Increased proteolytic activity in mixed culture was indeed likely to relieve the amino acid limitation that occurred in pure culture and to provide the co-repressors (valine, isoleucine and leucine) for CodY-mediated repression. Recently, it was shown that a mutation in *codY* was associated with an increased expression of both RNAII and RNAPIII (Majerczyk et al., 2008). We thus tested whether the higher CodY activity in mixed culture resulting from *L. lactis* proteolysis could be responsible for the downregulation of the *agr* system. To address this question, a *S. aureus* MW2 $\Delta codY$ mutant strain was constructed and tested in pure and mixed cultures. In pure culture, a higher expression of RNAPIII expression was observed in the *codY* mutant as previously described by Majerczyk et al. The downregulation of both *agrA* and RNAPIII by *L. lactis* occurred in the *codY* mutant as in the wild-type strain (Fig. 2). These results indicated that the downregulation of the *S. aureus agr* system by *L. lactis* was not mediated through CodY repression and thus was probably not related to the proteolytic activity of *L. lactis*; however, a CodY-independent regulation pathway could not be excluded.

Acidification by *L. lactis* is partially involved in *S. aureus* virulence inhibition. To further evaluate the mechanisms involved in inhibition of *S. aureus* growth and lack of induction of the *agr* system expression in mixed culture, the decrease in pH was dissociated from the presence of *L. lactis*. Glucono delta-lactone (GDL) was used to mimic acidification by *L.*

lactis. Compared to other acids, spontaneous GDL hydrolysis into gluconic acid is slow, occurs in the cheese matrix after curd formation and mimics the kinetics of the decrease in pH induced by *L. lactis* (Fig. 3B). *S. aureus* growth was not significantly affected by the addition of GDL (Fig. 3A). We investigated the effect of acidification on the expression of the *agr* system in the three environments and found dissimilar effects on the transcription of RNAII and RNAIII. Expression of *agrA* was decreased only in mixed culture, whereas RNAIII expression was reduced by both GDL acidification and mixed culture conditions (Fig. 3C and 3D). However, it must be noted that RNAIII reduction was only 4-fold in GDL conditions compared to 80-fold in mixed culture. These results demonstrate that, in cheese matrix, the decrease in pH in mixed culture could partially account for RNAIII downregulation. Finally, it should be noted that acidification directly inhibited the P3 promoter (RNAIII) independently of an effect on the autoinducing system (RNAII).

Downregulation of enterotoxin gene expression in cheese matrix. We especially focused on the production of enterotoxins because they are essential causative agents of SFP. Of the six enterotoxins possessed by *S. aureus* MW2, SEA, SEC, SEG and SEH have a demonstrated emetic activity, whereas SEIL and SEIK are non-emetic (Orwin et al., 2001; Thomas et al., 2007). The expression profiles of enterotoxin genes were heterogeneous with respect to time and *L. lactis* effect. In *S. aureus* pure culture in cheese matrix, *sea* and *seh* expression decreased with time (6-fold and 8-fold, respectively, between 6 h and 7 days; Table 1). In contrast, *sec4* expression did not vary significantly over 7 days, and expression of *seg2*, *sek2* and *sel2* decreased only slightly with time. While *seg2* and *sek2* were under-expressed in mixed culture from 10 h onwards, no significant variation was observed for *sec4* expression in the mixed vs the pure culture. On the contrary, both *sel2* and *seh* genes were over-expressed in the mixed compared to the pure culture, with a maximum ratio of 17-fold for *seh* at 7 days

(Table 1). The expression profile of *sea* was similar in mixed and pure cultures, and *sea* expression showed a slight increase in mixed culture. Results obtained with *S. aureus* field strains isolated from SFP confirmed that *sea* expression was not affected by the presence of *L. lactis* LD61 and even significantly increased in *S. aureus* 257D. Indeed, *sea* expression decreased with time in both pure and mixed cultures in the field strain *S. aureus* 253E, without any significant effect of the presence of *L. lactis*. An inductive effect of *L. lactis* on *sea* expression was observed in the field strain 257D: *sea* expression was higher in mixed compared to pure culture at both 9 h and 7 days (data not shown).

The kinetics of enterotoxin expression in pure *S. aureus* culture in cheese matrix were in agreement with previously published data obtained in BHI, a rich laboratory medium, for *sea*, *seg2* and *sek* (Derzelle et al., 2009). Under planktonic growth conditions in BHI, expression of *sec*, *seh* and *sel* was enhanced after the exponential growth phase (Derzelle et al., 2009), whereas in the cheese matrix expression of these genes did not change or was decreased (Table 1). Enterotoxin expression was further compared in *S. aureus* MW2 between growth in pure culture in cheese matrix and in chemically defined medium (CDM) under planktonic conditions over 24 h, corresponding to the late stationary phase (Table 2, (Even et al., 2009)). The influence of the cheese matrix clearly varied with the enterotoxin types. The expression profile of *sea* was similar in both conditions, and *seg2* and *sek2* expressions were slightly lower in cheese matrix compared to CDM during the exponential growth phase (2- to 3-fold at 8 h). Strikingly, the cheese matrix strongly altered both the level and dynamics of *sec4*, *seh* and *sel2* expression. *sec4*, *seh* and *sel2* expressions were higher in CDM compared to cheese matrix at all time-points, from 3- to 23-fold for *sec4*, 5- to 64-fold for *seh*, and from 4- to 42-fold for *sel2* (Table 2). Although *seh* expression remained constant in CDM over 24 h (Even et al., 2009), it strongly decreased in the stationary phase (24 h) in cheese matrix (Table 1). In addition, *sec4* and *sel2* expression strongly increased in CDM in the stationary phase (Even et

366 al., 2009) but remained constant in cheese matrix and even slightly decreased at 24 h (Table
367 1). The differences in *sec4* expression in cheese matrix versus CDM were validated by
368 immunological detection of SEC production. Production of $5.16 \mu\text{g ml}^{-1}$ of SEC by *S. aureus*
369 MW2 was detected after 24 h in CDM, whereas no SEC was detected at 24 h in cheese
370 matrix. In cheese matrix, SEC was detectable but not quantifiable (quantification limit: 0.021
371 ng ml^{-1}) at 7 days.

372 In conclusion, these results show that both the cheese matrix itself and the presence of *L.*
373 *lactis* modulated enterotoxin gene expression and that these modulations were strongly
374 dependent on enterotoxin type.

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Discussion

S. aureus physiology, including virulence expression and regulation, has been widely studied in the past decades by either targeted or global strategies. However, most of them have been done in laboratory growth conditions or in vivo conditions relevant to human or animal infectious contexts and far removed from the context of food such as cheese matrix. *S. aureus* growth conditions in cheese matrix differ from classical laboratory conditions in at least 2 major ways. Milk is a complex nutritional matrix that undergoes several physico-chemical modifications, in a concomitant or sequential way, including transition from liquid to solid state. As a consequence, *S. aureus* growth in liquid medium is planktonic, whereas in cheese matrix *S. aureus* is immobilised and grows as colonies. In addition, cheeses contain more or less complex microbial ecosystems, including acidifying flora such as LAB that have been shown to display antagonistic properties against *S. aureus*. In this study, we investigated for the first time the dynamics of *S. aureus* growth and global gene expression in a cheese matrix for 7 days, allowing a global understanding of *S. aureus* physiology in this particular context, with special attention paid to the influence of *L. lactis*, the model LAB species.

Premature arrest of *S. aureus* growth in the presence of *L. lactis*. The overall view of the *S. aureus* transcriptome in mixed culture with *L. lactis* showed a massive downregulation of genes involved in cell division, transcription, translation and cell envelope metabolism in comparison to the pure culture. Growth of *S. aureus* stopped earlier in mixed culture, resulting in one log inhibition at 24 h. Then, between 24 h and 7 days, the population remained viable. *S. aureus* growth slowed earlier (at 6 h) in mixed culture and at a non-limiting pH (6.3) since *S. aureus* can grow in a more acidic environment (Charlier et al., 2008b). Hence, acidification did not seem to be involved in the early inhibition of *S. aureus* growth. This was further reinforced by GDL experiments, which revealed that the decrease in

pH did not affect *S. aureus* growth during the course of the 7-day study. However, it must be noted that the acid used to mimic acidification was not lactate and that the nature of the acid used to adjust pH in the culture medium reportedly influences the impact of pH on *S. aureus* growth (Domenech et al., 1992). A previously reported early inhibition of *S. aureus* growth by *L. lactis* in liquid milk was not due to acidification but rather to unidentified nutrient-related phenomena (Charlier et al., 2008b). The early inhibition of *S. aureus* growth observed in the cheese matrix likely relied on similar mechanisms.

Major acid stress but no general stress. *S. aureus* did not undergo major stresses when cultivated alone in cheese matrix, whereas the acid stress response was major in the *S. aureus* transcriptomic profile in mixed culture, with induction of the expression of genes encoding detoxification enzymes (*ureD*, *sodA*), the arginine deaminase pathway (*arcC*, *arcR*) and the *ctsR* regulon (*ctsR*, *dnaK*, *clpC*).

S. aureus sensed not only the decrease in pH but also the production of lactate (and acetate) itself that triggered major changes in central metabolism. Acidification of the cheese matrix by *L. lactis* led to transcription of *S. aureus* genes involved in acetoin production (*alsS* and *butA*) instead of the gene encoding lactate dehydrogenase. The induction of *alsS* expression in the presence of lactate or acetate is mediated by CidR (Yang et al., 2006). Concomitantly, lactate and acetate induced the expression of *cid* and *lrg* operons in mixed culture. These two operons were shown to affect *S. aureus* murein hydrolase activity, autolysis, viability and biofilm formation (Rice et al., 2003; Rice et al., 2005; Rice et al., 2007). In particular, lactate was shown to promote a transition of cell physiology towards a “survival” state, in which cells remained viable with a reduced metabolic activity. Apart from acidic stress, no other major stress was revealed in the *S. aureus* transcriptome in mixed culture.

It should be noted that the presence of *L. lactis* relieved the amino acid limitation of *S. aureus* in cheese matrix. The high proteolytic activity of *L. lactis* in cheese matrix resulted in the release of free amino acids (especially branched-chain amino acids, co-factors of CodY) that were then available for *S. aureus*. In mixed culture, we observed a strong repression of leucine and isoleucine biosynthesis pathways, suggesting CodY-mediated activity (Pohl et al., 2009).

***S. aureus* sensed a lower redox potential in mixed culture.** Expression of genes belonging to various functional categories (stress, carbon metabolism and virulence) suggested the redox potential was lower in mixed culture. First, genes involved in oxidative stress response, including *trxA*, *katA*, and *ahpF*, were upregulated in pure compared to mixed culture. In addition, the expression of *clpL*, known to be under SigmaB control, was more than 7-fold higher in mixed culture than pure culture, whereas the expression of other SigmaB-dependent genes was reduced. The expression of *clpL* has been shown to be strongly induced in an anaerobic environment independently of any SigmaB induction (Fuchs et al., 2007). In our study, *lacG* (lactose transporter), *pflA* (involved in acetate formation) as well as *isaB* (immunodominant antigen B) were over-expressed in mixed compared to pure cultures. *lacA*, another gene belonging to the *lac* operon, *pflA* and *isaB* were also found to be induced in anaerobic conditions by Fuchs et al. Collectively, these results suggest that *S. aureus* cells sensed a lower redox potential in mixed compared to pure cultures, as might be expected given that the early steps of *L. lactis* growth reportedly result in oxygen exhaustion and reduction of the growth medium (Brasca et al., 2007; Tachon et al., 2010).

A biofilm-like behaviour in mixed culture? In mixed culture, *S. aureus* responded to a more acidic and anaerobic-like (lower redox potential) environment than in pure culture. These two

environmental parameters are often associated with biofilm formation. Many of the genes whose expression is induced in cheese matrix in mixed culture are associated with biofilm formation in the literature. Comparison of *S. aureus* transcriptomes in biofilm *versus* planktonic growth showed higher transcription of genes involved in the deiminase pathway (*arc* genes), genes coding for urease (*ureA-G*), and the pyruvate formate lyase (*plfA*) as well as a decreased expression of genes involved in nitrogen metabolism (*opp3*, *ilvE*) (Beenken et al., 2004; Resch et al., 2005). Enhanced expression of *isaB* can be related to anaerobic conditions (Fuchs et al., 2007) and enhanced expression of *sdrC* to mild acidic conditions (Weinrick et al., 2004). Both expressions were shown to be induced in biofilm compared to planktonic conditions (Resch et al., 2005). Of note, *cidA* was shown to contribute to biofilm adherence by affecting cell lysis and the release of genomic DNA. Extracellular DNA has been found in the biofilm matrix produced by *S. aureus* (Rice et al., 2007; Mann et al., 2009). All these genes associated with *S. aureus* biofilm formation were upregulated in mixed compared to pure cultures. Nevertheless, it should be noted that this biofilm-like behaviour of *S. aureus* in mixed culture was *ica*-independent as *icaA* expression was strongly downregulated in mixed culture. This strong downregulation of *icaA* expression in mixed culture may indeed be due to higher repression by CodY (Majerczyk et al., 2008). Collectively, our data suggest that the acidic and anaerobic environment generated by *L. lactis* triggered the same metabolic pathways involved in biofilm formation.

Inhibition of the expression of the *S. aureus agr* system. In mixed culture with *L. lactis*, a lack of induction of the *agr* system (both RNAII (*agrA*) and RNAlII) was observed in the post-exponential growth phase. Several mechanisms and signalling pathways have been shown to influence the expression of the *agr* system. Notably, growth in an acid environment has been reported to affect *S. aureus* RNAlII expression; however, this remains a matter of

debate (Regassa et al., 1992; Weinrick et al., 2004; Bore et al., 2007). Here, using GDL, we demonstrated that, in the cheese matrix context, a decrease in pH could, at least in part, account for RNAIII downregulation. The expression of *agrA* was not affected by the addition of GDL, showing that the decrease in pH affected RNAIII level directly and was not dependent for this effect on the autoinducing system (*agrABCD*). Such uncoupling between RNAII and RNAIII expression has been previously reported (Xiong et al., 2002; Garzoni et al., 2007). Interestingly, downregulation of the *agr* system (*agrA* and RNAIII) by *L. lactis* had been previously observed in a chemically defined medium under environmental conditions far removed from the cheese matrix context (Even et al., 2009). The mechanism(s) involved in *agr* system attenuation in CDM were not elucidated, but it was established that they are not related to acidification as pH was maintained at 6.6. Hence, although the ability of *L. lactis* to alter the *agr* system expression was not restricted to specific conditions, this ability appears to rely on multiple mechanisms acting on RNAII and or RNAIII.

In cheese matrix, one could hypothesize that lactococcal proteolysis acted on *agr* system expression through a CodY-mediated regulation in *S. aureus*. However, although CodY reportedly affects *agr* system expression (Majerczyk et al., 2008), it did not seem to be involved here since a *codY* mutant of *S. aureus* MW2 and the wild-type strain had similar expression profiles of the *agr* system.

What does enterotoxin expression in cheese matrix imply for food poisoning? In foodstuff, SE production is the main risk associated with *S. aureus*. Strikingly, three enterotoxins of *S. aureus*, namely *sec4*, *seh* and *sel2*, were strongly downregulated in cheese matrix compared to a chemically defined medium. This observation at the gene expression level was confirmed at the protein level by quantification of SEC. Our results on *sec4* expression and production were in agreement with those of previous studies, which failed to

503 detect SEC production in cheese by strains carrying *sec* genes and producing SEC in
504 laboratory media (Otero et al., 1990; Otero et al., 1993; Poli et al., 2007). In contrast, *sea*
505 expression was not affected in cheese matrix and the production of SEA was not inhibited,
506 perhaps accounting for its high frequency in SFP (Mossel and Van Netten, 1990; Lehn et al.,
507 1995; Omoe et al., 2005).

508 Regulation of SE genes is poorly understood and mainly restricted to classical SE such as
509 SEA and SEC. Expression of the *sec4* gene is reported to be under a positive control by the
510 *agr* system and *SaeRS* and to decrease in glucose-containing medium (independently of
511 medium acidification) and high salt concentration (Genigeorgis et al., 1971; Regassa et al.,
512 1992; Regassa and Betley, 1993; Voyich et al., 2009). The promoter of *saeRS* was shown to
513 be repressed by a high salt concentration, implying that water activity was also reduced
514 (Geiger et al., 2008). Taken together, these results establish a link between water activity and
515 expression of *sec4* via *SaeRS* regulation. In cheeses, water activity is lower than in a liquid
516 medium such as CDM (typical water activities of cheeses vary from 0.9 to 0.99) (Marcos,
517 1993). Here, water activity was estimated at 0.96 in UF retentate cheese matrix. In agreement,
518 *saeS* expression was found to be lower in cheese matrix than in CDM from 8 h onward (Table
519 2). Reduced water activity in the cheese matrix may thus partially account for the
520 downregulation of *saeRS*, which may in turn be responsible for low *sec4* expression.

521 In addition to the effect of the cheese matrix itself on SE expression, the presence of *L. lactis*
522 was able to alter SE production. Of note, the effect of *L. lactis* on SE expression differed
523 between CDM and cheese matrix, highlighting again the crucial role of environmental
524 conditions (Even et al., 2009). Among the main enterotoxins involved in SFP, *sea* expression
525 was slightly increased in cheese matrix in the *S. aureus* MW2 strain as well as in *S. aureus*
526 257D, by the presence of *L. lactis*. This higher *sea* expression in the presence of *L. lactis*
527 might be due to acidification, as was recently reported (Wallin-Carlquist et al., 2010). In this

study, addition of acetic acid provoked an increase of *sea* expression. This was related to the induction of the *sea*-encoding prophage and thus to an increase of intracellular *sea* gene copy number. The genetic context of enterotoxin genes is thus likely to play a major role in the control of enterotoxin gene expression. Enterotoxin genes are carried by different genetic determinants: *sea*, *seg2* and *sek2* are carried by the same prophage, *sel2* and *sec4* are located on the same genomic island and *seh* exists beyond the right boundary of the chromosome cassette *SCCmec*, carrying the methicillin resistance gene (Baba et al., 2002). The expression of SE genes might thus respond to various regulation mechanisms depending on their genetic support. If we are to better understand the variations observed here for SE expression, further studies will be required to unravel the impact of mixed culture conditions on *S. aureus* phage and mobile genetic element biology.

Conclusions.

The behaviour and dynamic response of *S. aureus* to *L. lactis* antagonism was explored through *in situ* gene-expression profiling in conditions mimicking the cheese-making process. This study provides new insights into how *S. aureus* adapts to a changing environment and during microbial competition. It also highlights the important role of environmental conditions, thus reinforcing the requirement for *in situ* approaches. In particular, this study showed that SFP occurrence in the cheese ecosystem is a multilayer problem involving both *S. aureus* metabolism and virulence expression in response to environmental changes driven by technological processes (temperature, renneting) and microbial activity (*L. lactis* growth and impact on the cheese matrix). Such parameters, individually or in combination, affect *S. aureus* behaviour through various regulatory pathways. Deciphering the molecular mechanisms underlying *S. aureus* response(s) to these multifactorial and dynamic

552 environmental changes in cheese matrix opens new avenues for the development of novel
553 prevention strategies against this major foodborne pathogen.

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Experimental procedures

Bacterial strain and growth conditions. *L. lactis* subsp. *lactis* biovar *diacetylactis* LD61 (kindly provided by R. Perrin, Soredab, La Boissière Ecole, France) and *S. aureus* MW2 were used throughout this work. Two additional *S. aureus* strains isolated from foodstuffs involved in food poisoning and kindly provided by AFSSA-Ierqap were used in complementary interaction experiments: *S. aureus* 257D (isolated from chocolate milk involved in SFP, contains *sea*), and 253E (isolated from cheese involved in SFP, contains *sea*, *sed*). *S. aureus* was grown in UF-cheeses in pure and mixed cultures with *L. lactis* LD61 as previously described (Ulve et al., 2008). Briefly, the UF retentate was heated to 30 °C and inoculated with *S. aureus* from subculture on Tryptic Soy Broth (TSB) at 10^6 cfu g⁻¹ for assessment of the worst-case scenario in case of contamination. When added, *L. lactis* LD61 was inoculated at 10^6 cfu g⁻¹ from subculture on M17. Rennet (Maxiren 180; DSM Food Specialities, Delft, The Netherlands) was added simultaneously at a concentration of 0.3 µl ml⁻¹. After incubation for 10 h at 30 °C, UF cheeses (20 g) were transferred to 12 °C to mimic the temperature shift encountered by *S. aureus* strains during the making of soft cheese. *S. aureus* and *L. lactis* populations were determined as previously described (Nouaille et al., 2009).

In order to investigate the effect of acidification on *S. aureus*, glucono-delta-lactone (GDL, Hansen, Arpagon, France) was added sequentially to the cheese matrix after 5 h and 10 h of growth to mimic the pH decrease in mixed culture.

Chemical analysis of UF cheeses. Determination of sugars, organic acids and free amino-acid content was performed as described previously (Cretenet et al., submitted).

Quantification of enterotoxin C production. Detection and quantification of enterotoxin C were performed by the EU-CRL screening method (Anonymous, 2007) and confirmed by the EU-CRL confirmatory method when positive (Hennekinne et al., 2007).

Construction of the *codY* mutant strain. A *codY* deletion mutant of *S. aureus* MW2 was obtained by double crossing over as previously described by Hiron et al (Hiron et al., 2007), using plasmid pCG29 constructed and described by Pohl et al (Pohl et al., 2009).

RNA extraction and transcriptome analysis. RNA samples were extracted from both pure and mixed cultures at different time points (6 h, 8 h, 10 h, 24 h and 7 days) in order to monitor the dynamic response of *S. aureus* MW2 in cheese matrix, with and without *L. lactis*. Briefly, cells were separated from the cheese matrix as previously described (Ulve et al., 2008). RNA samples from *S. aureus* in pure or mixed cultures were then obtained and quantified, and their qualities were evaluated as described in Even et al (Even et al., 2009). Labelling and hybridization using a dedicated microarray were performed as previously described (Even et al., 2009). The expression profiles of *S. aureus* in pure and mixed cultures were analysed with the R software (R Development Core Team, 2007) following the protocol from Even et al. (Even et al., 2009). Hybridizations were carried out with a constant amount of total RNAs to maintain the efficiency and reproducibility of the labelling and hybridisation steps. In mixed cultures, RNA samples were characterized by a mixture of both lactococcal and staphylococcal cDNA, resulting in lower signals. Total RNA yielded a signal (signal /noise ratio >2) in 90% of the spots retained for statistical analysis in pure cultures, but this figure decreased to 18% at 7 days in mixed culture. The sampling time 7 days was therefore removed from our statistical analysis for insufficient quality. Statistical analyses were performed in pure and mixed cultures only until 24 h of culture. Statistical analysis was performed using the ANOVA test considering a P value and FDR lower than 0.05. Genes showing at least a 2-fold change were considered to be differentially expressed. The microarray data for *S. aureus* in pure and mixed cultures were deposited in the public repository database ArrayExpress under the accession numbers E-MEXP-2617 and XXXX. All genes showing statistically significant variations of expression with time with a minimum

2-fold change in pure or mixed cultures are presented in Table S1. This first analysis was used to reveal trends in gene expression and to establish a list of genes, the expression of which was verified and completed by quantitative RT-qPCR over the complete duration of the experiment (including day 7).

Reverse transcription-quantitative PCR. Reverse transcription-quantitative PCR (RT-qPCR) were performed using the oligonucleotides listed in Table S3 as previously described (Even et al., 2009), with three independent biological replicates for all experimental time points. *gyrB*, was used as an internal standard for normalization as previously described (Beenken et al., 2004; Bore et al., 2007). *gyrB* was not differentially expressed over time in the microarray data in either the pure or the mixed culture. Gene expression was thus reported relative to *gyrB* and calculated using the following formula: (copies of each gene/copies of *gyrB*) X 10 in each cDNA preparation. Statistical analysis was performed using the ANOVA test considering a P value lower than 0.05 to identify genes showing significant change in expression with time. Similarly, statistical analysis was performed using the T-test considering a P value lower than 0.05 to identify, for each time point, genes showing a significant change in expression in pure *versus* mixed cultures.

Acknowledgements

Spotting and hybridization were provided by the transcriptomic platform of Ouest Genopole (Rennes, France) and the transcriptomic platform IFR140 GFAS (Rennes, France), respectively. Authors are grateful to Aurélie Le Cam, Jérôme Monfort, Amandine Etchevery and Régis Bouvet for their help and technical assistance during this work. We thank Christiane Wolz for providing us with plasmid pCG29. Marina Cretenet is a recipient of a CIFRE PhD fellowship from Centre National Interprofessionnel de l'Economie Laitière. This work was financially supported by the French National Research Agency (ANR) project GenoFerment (ANR-05-PNRA-020) and Nabab (ANR-08-ALIA-11).

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Table 1: Expression profiles of selected genes determined by RT-qPCR. The average gene expression of three independent biological replicates is expressed relative to *gyrB* x10. Statistically differentially expressed genes are in bold.

MW2 ORF	Gene name	Description of gene product	Gene expression in pure culture					Gene expression in mixed culture					Ratio of expression Mixed/Pure				
			6 h	8 h	10 h	24 h	7 d	6 h	8 h	10 h	24 h	7 d	6 h	8 h	10 h	24 h	7 d
Cell division																	
MW1069	<i>ftsZ</i>	cell division protein	68.1	60.9	59.8	40.3	74.5	57.3	53.9	28.4	16.9	14.6	0.8	0.9	0.5	0.4	0.2
MW0604	<i>pbp4</i>	Penicillin-binding protein 4	2.9	1.8	1.6	1.0	3.3	4.0	4.7	2.8	1.1	0.3	1.4	2.7	1.8	1.1	0.1
Stress response																	
MW1532	<i>dnaK</i>	DnaK protein	40.9	26.0	26.2	15.8	19.2	55.8	43.5	60.7	132.7	438.6	1.4	1.7	2.3	8.4	22.9
MW0477	<i>ctsR</i>	transcription repressor of stress genes	5.5	6.9	8.8	9.0	6.1	7.7	7.0	9.5	46.1	149.0	1.4	1.0	1.1	5.1	24.3
MW2212	<i>ureD</i>	urease accessory protein	8.5	5.5	3.5	1.2	1.8	9.6	13.9	15.0	13.3	35.1	1.1	2.5	4.3	11.4	19.9
MW2553	<i>arcC</i>	carbamate kinase	1.6	7.7	15.6	0.6	6.5	5.7	15.3	14.5	8.5	27.5	3.5	2.0	0.9	13.4	4.3
MW2552	<i>arcR</i>	deaminase pathway repressor	2.3	9.0	16.6	1.2	8.3	10.0	21.5	21.4	13.0	39.0	4.4	2.4	1.3	10.8	4.7
MW1505	<i>sodA</i>	superoxide dismutase	122.0	189.5	209.6	137.8	68.2	135.8	178.4	157.8	506.3	288.3	1.1	0.9	0.8	3.7	4.2
MW1028	<i>trxA</i>	thioredoxin	75.3	86.6	94.9	57.7	64.0	104.0	108.0	64.5	39.3	25.5	1.4	1.2	0.7	0.7	0.4
MW1221	<i>katA</i>	catalase	14.4	31.2	51.6	37.4	26.2	16.7	27.5	26.3	20.2	5.5	1.2	0.9	0.5	0.5	0.2
MW1988	<i>sigB</i>	sigma factor B	33.2	32.4	33.9	31.0	59.4	26.4	43.4	33.9	31.4	12.8	0.8	1.3	1.0	1.0	0.2
MW2108	<i>asp23</i>	alkaline shock protein 23	428.4	1079	1331	1013	1239	206.8	300.4	423.5	1016	794.0	0.5	0.3	0.3	1.0	0.6
MW2482	<i>crtN</i>	staphyloxanthin synthase	12.7	12.5	13.7	9.6	20.3	6.2	8.0	8.8	4.4	4.7	0.5	0.6	0.6	0.5	0.2
MW2469	<i>clpL</i>	ATPdependent Clp proteinase chain	83.0	165.2	255.2	46.9	103.7	104.7	82.3	182.4	353.2	791.7	1.3	0.5	0.7	7.5	7.6
MW0480	<i>clpC</i>	ATPdependent Clp proteinase chain	13.5	13.4	11.7	14.7	14.0	12.7	12.3	27.2	145.9	422.1	0.9	0.9	2.3	9.9	30.2
MW0730	<i>clpP</i>	ATPdependent Clp protease	40.6	41.7	41.5	32.2	45.4	59.9	57.9	42.5	34.8	21.0	1.5	1.4	1.0	1.1	0.5
MW1290	<i>cspA</i>	cold shock protein A	22.2	16.5	23.3	12.4	9.4	35.7	40.2	19.0	9.4	5.4	1.6	2.4	0.8	0.8	0.6
MW2623	<i>cspB</i>	cold shock protein B	238.0	147.5	130.5	25.9	45.2	248.7	214.1	131.6	64.5	43.1	1.0	1.5	1.0	2.5	1.0
Virulence																	
MW1959	<i>hld (RNAIII)</i>	deltahemolysin	86.8	494.5	1104	4243	3293	94.5	233.8	285.8	164.9	189.5	1.1	0.5	0.3	3.9E-02	0.1
MW2586	<i>icaA</i>	intercellular adhesion protein A	0.2	0.5	0.9	0.1	0.3	0.04	0.04	0.01	ND	ND	0.2	0.1	5.7E-03	NC	NC
MW2559	<i>isaB</i>	immunodominant antigen B	21.4	35.0	56.9	57.7	11.1	23.6	24.4	22.1	83.7	158.7	1.1	0.7	0.4	1.5	14.3

MW2 ORF	Gene name	Description of gene product	Gene expression in pure culture					Gene expression in mixed culture					Ratio of expression Mixed/Pure				
			6 h	8 h	10 h	24 h	7 d	6 h	8 h	10 h	24 h	7 d	6 h	8 h	10 h	24 h	7 d
MW0764	<i>clfA</i>	clumping factor A	74.8	123.6	206.5	147.9	144.8	52.4	74.6	80.5	337.8	409.2	0.7	0.6	0.4	2.3	2.8
MW0516	<i>sdrC</i>	SerAsp rich fibrinogenbinding,	0.1	0.2	0.1	0.1	0.1	0.6	2.2	4.1	2.8	3.1	4.1	14.0	32.9	37.8	30.1
MW0124	<i>cap8A</i>	capsular polysaccharide Cap8A	19.5	46.7	64.6	55.8	26.8	10.8	11.6	20.5	66.2	13.9	0.6	0.2	0.3	1.2	0.5
MW1885	<i>sak</i>	staphylokinase	1.5	1.7	1.4	0.4	0.6	2.9	3.1	0.9	0.5	1.6	1.9	1.9	0.6	1.2	2.6
MW1889	<i>sea</i>	enterotoxin A	5.8	6.7	6.0	2.2	1.1	10.4	14.9	6.5	5.6	3.2	1.8	2.2	1.1	2.5	2.9
MW1937	<i>seg2</i>	enterotoxin G	3.4	4.1	4.9	1.8	2.2	2.9	3.6	1.9	0.6	0.5	0.9	0.9	0.4	0.4	0.2
MW1938	<i>sek2</i>	enterotoxin K	1.5	1.7	1.9	0.8	0.9	1.6	2.0	0.9	0.4	0.7	1.1	1.2	0.5	0.5	0.8
MW0760	<i>sel2</i>	enterotoxin L	2.5	2.8	3.6	1.2	1.5	4.1	5.5	3.0	2.6	3.8	1.7	1.9	0.8	2.1	2.6
MW0051	<i>seh</i>	enterotoxin H	1.6	1.4	2.5	0.1	0.2	2.7	3.3	2.1	1.8	4.2	1.7	2.3	0.8	12.7	17.2
MW0759	<i>sec4</i>	enterotoxin C	3.1	3.4	3.7	1.8	4.6	4.1	7.7	4.6	1.9	2.1	1.3	2.3	1.3	1.1	0.4
Carbohydrate metabolism																	
MW2115	<i>lacG</i>	6phosphobetagalactosidase	2.4	11.5	20.5	17.1	55.0	9.8	30.4	19.4	7.0	23.6	4.0	2.7	0.9	0.4	0.4
MW1641	<i>pykA</i>	pyruvate kinase	25.8	24.5	29.8	15.1	24.7	27.0	24.3	33.9	28.2	77.6	1.0	1.0	1.1	1.9	3.1
MW0217	<i>lctE</i>	Llactate dehydrogenase	93.4	120.2	217.7	4.2	73.9	71.4	73.3	13.4	3.6	8.7	0.8	0.6	0.1	0.8	0.1
MW0568	<i>adh1</i>	alcohol dehydrogenase I	18.3	25.3	41.7	0.5	4.9	15.4	19.8	3.5	1.2	3.6	0.8	0.8	0.1	2.5	0.7
MW0202	<i>pflA</i>	formate acetyltransferase enzyme	65.5	122.7	125.4	3.6	20.0	176.7	269.7	73.1	28.2	86.1	2.7	2.2	0.6	7.9	4.3
MW1237	<i>citb</i>	aconitate hydratase	12.4	34.2	47.1	27.0	18.2	15.2	32.0	28.0	46.0	7.6	1.2	0.9	0.6	1.7	0.4
MW2526	<i>mgo2</i>	malate/quinone oxidoreductase	48.1	36.3	31.8	25.9	25.0	42.1	36.0	28.0	23.5	38.8	0.9	1.0	0.9	0.9	1.6
MW1129	<i>sucD</i>	succinylCoA synthetase	80.9	97.6	84.7	63.5	31.2	87.0	89.7	38.2	25.6	18.1	1.1	0.9	0.5	0.4	0.6
MW2460	<i>cidC</i>	pyruvate oxydase	12.9	20.6	21.4	26.6	33.6	9.5	11.9	22.1	78.9	50.8	0.7	0.6	1.0	3.0	1.5
MW2462	<i>cidA</i>	holin-like protein cidA	0.1	0.1	0.1	0.1	0.3	0.5	1.5	2.3	4.8	3.3	3.9	14.2	19.4	79.0	12.2
MW0238	<i>lrgA</i>	holin-like protein LrgA	0.4	0.5	0.5	0.1	1.0	2.4	1.1	0.5	0.3	0.9	5.3	2.2	1.0	2.0	1.0
MW2132	<i>alsS</i>	alpha-acetolactate synthase	0.8	0.8	1.0	0.5	4.4	2.9	8.5	15.6	48.0	87.9	3.6	11.2	15.2	89.2	20.1
MW0100	<i>butA</i>	acetoin(diacetyl)reductase	9.2	13.5	20.8	24.7	14.5	12.6	15.9	23.9	48.2	193.1	1.4	1.2	1.2	2.0	13.3
Nitrogen metabolism																	
MW0705	<i>pepT</i>	aminotripeptidase	9.7	11.0	9.8	10.2	10.8	9.9	9.9	7.2	4.2	5.1	1.0	0.9	0.7	0.4	0.5
MW1694		XaaHis dipeptidase homolog	2.6	3.1	3.3	2.2	2.7	3.4	4.2	3.8	1.3	0.9	1.3	1.3	1.2	0.6	0.3
MW1584	<i>relA</i>	GTP pyrophosphokinase	6.0	7.5	7.7	4.1	7.6	5.6	5.2	4.5	1.0	1.0	0.9	0.7	0.6	0.2	0.1
MW1977	<i>ilvD</i>	dihydroxy-acid dehydratase	11.2	9.2	4.1	25.2	2.4	46.0	4.7	2.2	0.2	1.1	4.1	0.5	0.5	7.8E-03	0.4

MW2 ORF	Gene name	Description of gene product	Gene expression in pure culture					Gene expression in mixed culture					Ratio of expression Mixed/Pure				
			6 h	8 h	10 h	24 h	7 d	6 h	8 h	10 h	24 h	7 d	6 h	8 h	10 h	24 h	7 d
MW1981	<i>leuA</i>	2-isopropylmalate synthase	16.6	15.0	13.0	34.5	3.8	116.1	13.4	1.8	1.0	2.7	7.0	0.9	0.1	2.8E-02	0.7
MW1138	<i>codY</i>	transcription pleiotropic repressor	24.0	23.8	24.3	13.7	30.1	31.9	35.6	26.8	10.4	11.3	1.3	1.5	1.1	0.8	0.4
Regulators																	
MW1963	<i>agrA (RNAII)</i>	accessory gene regulator A	20.7	38.7	51.8	111.1	200.4	25.1	61.4	93.4	59.7	53.1	1.2	1.6	1.8	0.5	0.3
MW0580	<i>sarA</i>	staphylococcal accessory regulator A	313.0	459.2	544.4	417.4	420.8	257.3	298.7	342.4	418.0	162.0	0.8	0.7	0.6	1.0	0.4
MW1705	<i>rot</i>	transcriptional regulator	36.8	31.1	36.3	12.1	5.6	38.7	37.7	24.9	22.0	19.5	1.1	1.2	0.7	1.8	3.5
MW0667	<i>saeS</i>	histidine protein kinase	20.1	18.5	11.4	5.3	27.3	19.5	28.2	11.7	3.7	1.3	1.0	1.5	1.0	0.7	0.0
MW0648	<i>mgrA</i>	transcriptional regulator	37.1	26.7	27.6	17.3	20.6	48.1	32.0	18.1	12.2	9.4	1.3	1.2	0.7	0.7	0.5
MW2585	<i>icaR</i>	operon ica repressor	8.6	13.0	19.7	10.5	3.9	10.6	13.3	9.3	12.0	3.0	1.2	1.0	0.5	1.1	0.8
MW1446	<i>srrA</i>	staphylococcal respiratory response	27.3	25.5	28.4	11.7	17.9	29.0	31.7	15.6	21.9	9.5	1.1	1.2	0.6	1.9	0.5

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Table 2. Expression ratio of SE genes and *saeS* in *S. aureus* MW2 strain grown in CDM versus cheese matrix, as determined by RT-qPCR, using *gyrB* as an internal standard for normalisation. Data on CDM were adapted from Even et al. (Even et al., 2009). Statistically differentially expressed genes between CDM and cheese matrix are in bold (as determined by T-test considering a P value lower than 0.05).

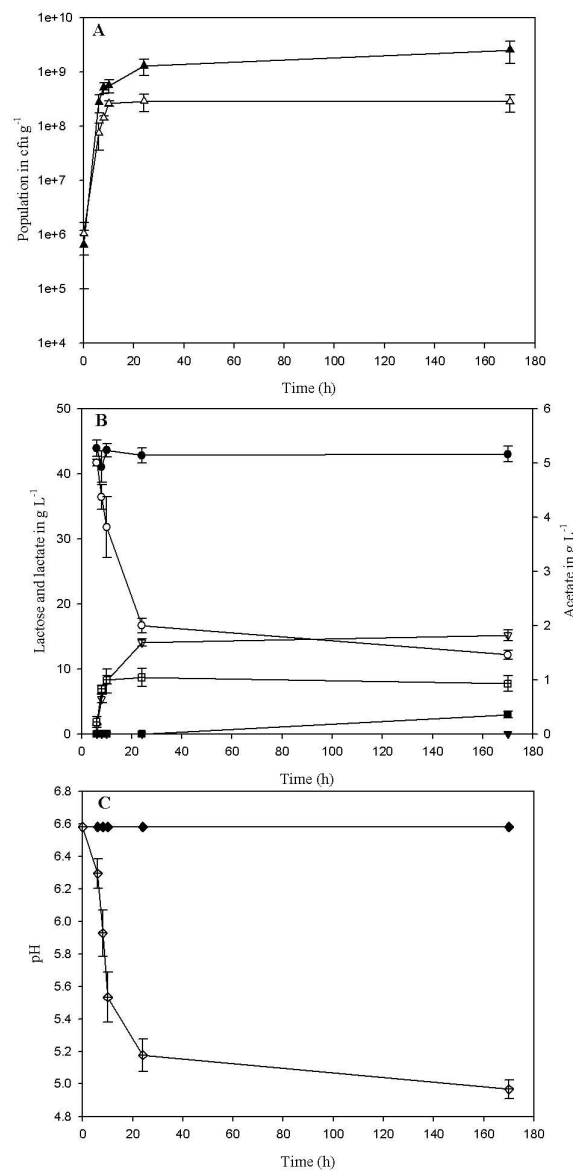
MW2 ORF	Gene name	Description of gene product	Ratio of expression CDM/cheese matrix			
			6 h - exponential phase	8 h - late exponential phase	10 h - entry into stationary phase	24 h - stationary phase
MW1889	<i>sea</i>	enterotoxin A	0.8	1.2	0.8	0.5
MW1937	<i>seg2</i>	enterotoxin G	1.4	2.3	1.2	1.4
MW1938	<i>sek2</i>	enterotoxin K	1.8	2.7	1.4	1.3
MW0760	<i>sel2</i>	enterotoxin L	3.6	7.9	3.8	41.6
MW0051	<i>seh</i>	enterotoxin H	5.8	10.1	4.5	64.0
MW0759	<i>sec4</i>	enterotoxin C	3.3	11.6	15.1	22.8
MW0667	<i>saeS</i>	histidine protein kinase	0.5	3.1	2.0	7.6

Figure legends

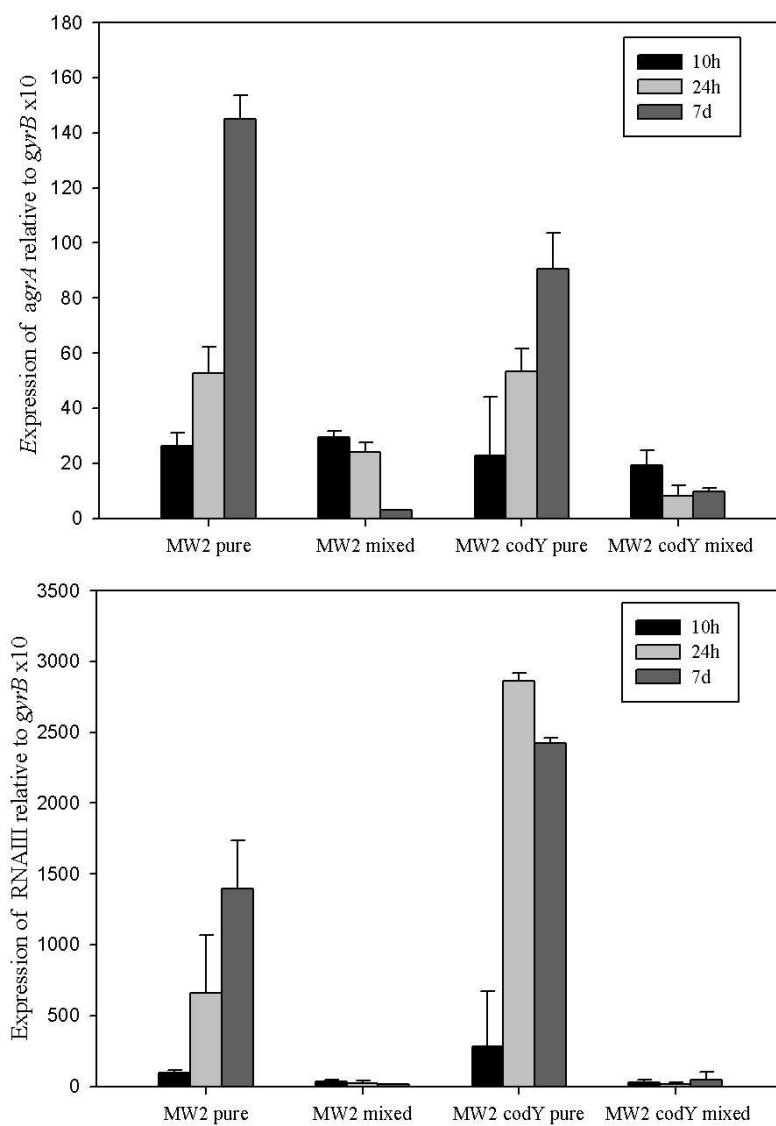
Fig. 1: Kinetics of growth of *S. aureus* MW2 in cheese matrix (▲) (A), lactose consumption (●) lactate production (▼), acetate production (■) (B) and pH (◆) (C). Pure cultures are in black. Mixed cultures are in white.

Fig. 2: Gene expression (relative to *gyrB*) of *agrA* (RNAII) (A) and RNAIII (B) in *S. aureus* MW2 wild-type and a *codY* mutant at 10 h, 24 h and 7 days of culture.

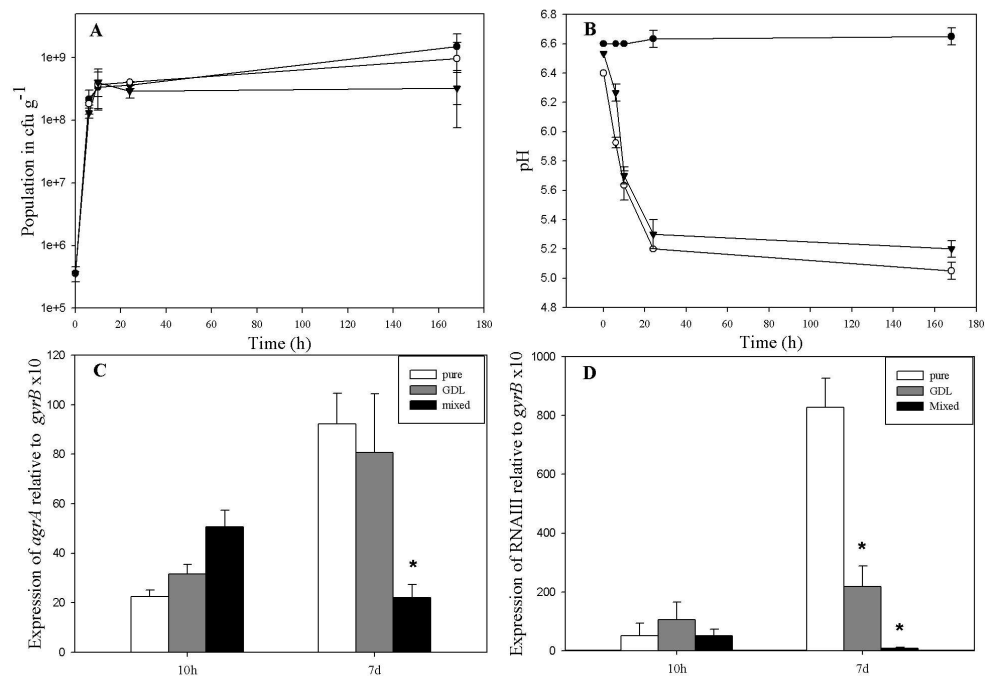
Fig. 3: *S. aureus* population (A), pH (B) and profiles of gene expression (relative to *gyrB*) of *agrA* (RNAII) (C) and RNAIII (D) in pure culture of *S. aureus* (●), pure culture of *S. aureus* with addition of GDL (○) and mixed culture with *L. lactis* (▼). Asterisks: significant change in expression compared to pure culture as determined by T-test considering a P value lower than 0.05.



80x168mm (300 x 300 DPI)



80x115mm (300 x 300 DPI)



168x130mm (300 x 300 DPI)

Table S1. Expression profiles of *S. aureus* MW2 genes that exhibited significant variations in pure and/or mixed cultures with *L. lactis* LD61 in cheese matrix.

Expression levels in pure and mixed cultures at 6, 8, 10 and 24 h, detected with the *S. aureus* microarray and presented as normalized cDNA/gDNA ratios. Only genes that showed significant variations in expression levels in pure and or mixed cultures over time (as determined by the ANOVA test with the criterion of an FDR of 0.05) and a degree of change of 2-fold were defined as differentially expressed. Statistically differentially expressed genes are in bold.

MW2 ORF	Gene Name	Description of gene product	Gene expression in pure culture				Gene expression in mixed culture			
			6 h	8 h	10 h	24 h	6 h	8 h	10 h	24 h
DNA replication, recombination and repair										
MW1362	<i>hu</i>	DNA binding protein II	54.3	86.8	84.3	70.6	53.1	24.2	20.2	10.8
MW1168	<i>recA</i>	RecA protein	9.3	9.5	11.1	9.9	4.4	2.9	2.9	1.9
MW0720	<i>uvrB</i>	exinuclease ABC subunit B	0.7	0.7	0.7	1.4	0.8	0.8	0.7	0.8
MW1029	<i>uvrC</i>	exinuclease ABC subunit C	0.8	0.9	1.1	1.6	1.2	1.4	1.4	1.3
MW1078	<i>tnp</i>	transposase	0.9	1.0	1.1	2.5	1.4	1.9	2.0	2.3
Transcription, translation and cellular division										
MW2045	<i>rho</i>	transcription termination factor Rho	2.0	1.5	1.3	1.3	1.3	1.0	0.9	0.7
MW0498	<i>rpoC</i>	RNA polymerase beta prime chain	6.0	3.1	2.1	6.7	3.2	1.8	1.5	1.2
MW1513	<i>sigA</i>	RNA polymerase sigma factor	2.4	2.4	2.4	5.0	1.6	1.4	1.9	2.0
MW1623	<i>rpmI</i>	50S ribosomal protein L35	9.3	6.0	4.0	3.9	6.0	3.3	3.1	2.3
MW0502	<i>fus</i>	translational elongation factor G	26.9	12.6	5.1	11.1	13.8	5.3	3.8	1.8
MW0503	<i>tufA</i>	translational elongation factor TU	44.1	24.2	11.8	20.0	23.5	11.2	8.4	3.5
IGS2		intergenic sequence 16S-23S	24.3	18.5	11.8	10.6	13.1	7.4	6.5	3.4
MW0466	<i>ftsH</i>	cell division protein	6.1	6.3	5.7	8.2	5.2	3.6	3.7	1.8

MW1063	<i>ftsL</i>	cell division protein	5.1	5.6	3.4	2.0	2.5	1.7	1.4	0.7
MW1069	<i>ftsZ</i>	cell division protein	5.9	4.3	5.0	5.3	3.4	2.2	1.9	1.4
MW2007		rod shape determining protein RodA	4.1	14.3	25.5	106.1	2.6	3.0	4.8	2.3
Cell wall biosynthesis and associated protein										
MW2589	<i>icaC</i>	intercellular adhesion protein C	0.4	1.0	1.4	1.5	0.7	0.6	0.6	0.9
MW1363	<i>gpsA</i>	glycerol3phosphate dehydrogenase	3.8	2.8	2.0	2.4	2.2	1.6	1.3	1.0
MW1064	<i>pbpA</i>	penicillinbinding protein 1	2.2	1.6	1.2	0.9	1.6	1.3	1.3	1.3
MW0604	<i>pbp4</i>	penicillin binding protein 4	4.2	2.4	1.3	2.0	2.3	1.4	1.2	0.9
MW0031	<i>mecA</i>	penicillin binding protein 2 prime	0.5	0.7	1.2	1.3	0.9	1.5	1.2	1.2
MW2013		lipoprotein precursor	4.6	3.6	1.6	2.8	3.2	1.6	1.2	1.0
Carbohydrate metabolism										
MW2115	<i>lacG</i>	6phosphobetagalactosidase	0.6	1.7	3.1	4.6	1.2	1.6	1.7	1.0
MW0217	<i>lctE</i>	Llactate dehydrogenase	5.7	8.6	12.7	0.8	2.7	1.8	0.9	0.8
MW0568	<i>adh1</i>	alcohol dehydrogenase I	1.5	1.7	3.2	1.0	1.1	1.0	0.8	0.9
MW1129	<i>sucD</i>	succinylCoA synthetase	13.7	17.4	16.5	19.7	6.8	4.2	2.9	1.7
MW2459	<i>ptsG</i>	PTS system, glucosespecific	2.4	0.7	0.8	0.5	0.6	0.5	0.5	0.5
MW2084	<i>mtlA</i>	PTS system, mannitol specific	1.5	2.6	2.3	3.6	1.0	0.8	1.0	1.3
MW0163	<i>glcA</i>	PTS enzyme II	1.5	0.4	0.4	0.3	0.5	0.7	0.6	0.8
MW0245	<i>rbsD</i>	ribose permease	0.7	1.8	1.3	0.6	0.8	0.8	0.6	0.6
MW0218		PTS enzyme, maltose and glucose specific	0.8	0.5	0.7	0.3	0.8	0.6	0.5	0.7
MW2538		similar to Mg citrate secondary transporter	3.3	2.1	1.9	1.5	1.8	1.0	0.8	0.7
MW2175		glucose uptake protein homolog	1.1	0.7	0.5	0.7	1.1	1.2	1.1	1.2
Nitrogen metabolism										
MW1980	<i>ilvC</i>	alphaketobetahydroxylacil reductoisomerase	5.6	6.3	1.2	5.7	5.4	0.7	0.6	0.6

MW2304	<i>gltT</i>	proton/sodiumglutamate symport protein	7.0	5.4	4.1	7.0	3.5	2.2	1.6	1.0
MW1694		XaaHis dipeptidase homolog	0.6	0.7	0.9	1.1	1.9	1.5	1.2	0.7
MW0705	<i>pepT</i>	aminotripeptidase	1.9	2.5	2.5	4.6	1.2	1.0	1.0	1.1
MW2522		amino acid transporter	7.1	5.0	4.2	3.2	3.3	1.2	1.0	0.6
MW0875	<i>appF</i>	oligopeptide transport system ATPbinding protein AppF homologue	0.6	1.0	0.6	0.5	3.1	2.3	1.3	1.0
MW0868	<i>oppB</i>	oligopeptide transport system permease protein	6.1	5.9	6.1	4.2	2.7	2.2	1.8	1.0
MW0871	<i>opp3</i>	oligopeptide transport system ATPbinding protein OppF homologue	6.4	5.9	5.3	5.0	2.4	1.8	1.3	1.0
MW2553	<i>arcC</i>	carbamate kinase	0.3	1.2	2.1	0.3	0.7	0.9	1.1	0.8
MW1138	<i>codY</i>	transcription pleiotropic repressor	3.8	4.6	3.2	3.2	2.4	1.7	1.6	0.9
Energetic metabolism										
MW0999	<i>ctaB</i>	cytochrome caa3 oxidase homologue	4.2	4.4	4.9	3.1	2.7	2.1	1.5	1.2
MW0588		MnhD homologue, similar to Na ⁺ /H ⁺ antiporter subunit	15.5	7.9	4.0	6.3	7.3	3.6	2.7	1.6
MW2526	<i>mgo2</i>	malate/quinone oxidoreductase	3.1	1.5	1.7	1.9	1.2	1.0	1.0	0.9
Vitamins, nucleotides and nucleic acid metabolism										
MW2536		anaerobic (class III) ribonucleotide reductase small subunit chain	0.7	0.7	1.1	0.3	0.7	0.8	0.9	0.9
MW2196	<i>modB</i>	probable molybdenum transport permease	1.4	1.6	1.8	3.2	0.5	0.6	0.7	0.7
MW2186	<i>moaA</i>	molybdenum cofactor biosynthesis protein A	0.5	0.5	0.5	0.9	0.5	0.6	0.7	0.8
MW0476	<i>nupC</i>	pyrimidine nucleoside transport protein	2.5	2.3	2.0	1.6	2.0	1.4	1.0	0.8
Iron metabolism										
MW1011	<i>isdB</i>	ironregulated cell wallanchored protein	0.4	0.4	0.6	0.6	0.7	0.9	1.0	1.1
MW1834		ferritin	0.9	4.6	8.6	5.4	0.8	1.8	1.7	3.1
MW0200		similar to periplasmicironbinding protein BitC	0.5	0.9	0.9	1.2	0.6	0.8	0.7	0.9
Stress response										

MW1531	<i>dnaJ</i>	DnaJ protein	3.9	2.2	1.8	2.0	2.6	1.8	2.8	3.0
MW1532	<i>dnaK</i>	DnaK protein	5.5	5.0	4.0	4.6	3.7	2.2	4.7	7.5
MW0477	<i>ctsR</i>	transcription repressor of stress genes	1.2	1.6	2.0	3.3	1.2	1.1	1.3	2.8
MW2469	<i>clpL</i>	ATPdependent Clp proteinase chain	6.5	11.9	15.5	5.3	4.0	1.9	6.5	7.2
MW1136	<i>clpQ</i>	heat shock protein HslV	3.7	3.9	3.2	3.3	2.8	2.0	1.8	1.3
MW1618	<i>clpX</i>	protease	5.5	5.0	4.0	4.6	2.3	1.5	1.5	1.6
MW0726	<i>trxB</i>	thioredoxine reductase	5.7	5.5	6.0	5.8	4.0	3.1	3.2	1.6
MW2535	<i>cudT</i>	choline transporter	0.3	0.4	0.5	1.1	0.7	0.8	0.6	0.6
MW0356	<i>ahpF</i>	alkyl hydroperoxide reductase subunit F	0.6	0.7	0.9	4.5	1.0	0.9	1.0	1.1
MW1221	<i>katA</i>	catalase	10.4	21.7	24.5	36.2	9.9	9.6	13.8	9.1
MW2212	<i>ureD</i>	urease accessory protein	1.2	0.7	0.6	0.4	1.1	1.2	1.6	1.3
MW0453	<i>spoVG</i>	stage V sporulation protein G homologue	1.4	2.3	4.1	6.5	0.9	0.9	1.3	1.5
MW1991	<i>rsbU</i>	sigmaB regulation protein	4.1	3.5	2.8	2.9	1.6	1.1	1.0	0.7
MW2108	<i>asp23</i>	alkaline shock protein 23	28.3	57.4	72.3	78.6	14.7	9.1	26.6	35.7
MW1682		general stress proteinlike protein	13.3	24.2	34.6	41.5	6.6	4.4	8.4	7.8
MW0781		similar to general stress protein	4.2	10.9	17.0	29.1	2.2	1.8	4.6	6.6
Virulence										
MW1963	<i>agrA</i>	accessory gene regulator A	1.4	2.3	3.3	10.8	1.2	1.5	3.0	1.5
sRNA_RNAIII	RNAIII	RNAIII	8.2	39.2	68.5	116.7	6.5	8.3	15.1	6.3
MW0668	<i>saeR</i>	response regulator	4.5	4.3	3.9	2.6	2.4	2.0	1.5	0.7
MW2418	<i>sarH2</i>	staphylococcal accessory regulator A homolog	0.2	0.3	0.5	1.1	0.5	0.7	0.8	1.0
MW2420	<i>fnbB</i>	fibronectinbinding protein homolog	0.5	0.3	0.2	0.2	0.5	0.5	0.5	0.5
MW2421	<i>fnb</i>	fibrinogenbinding protein	0.5	0.3	0.2	0.2	3.4	2.8	5.4	9.5
MW0764	<i>fnb</i>	fibrinogenbinding protein	6.0	12.7	16.2	18.3	3.4	2.8	5.4	9.5
MW1369	<i>ebpS</i>	elastin binding protein	2.1	3.5	5.8	7.0	2.1	1.8	2.8	2.3
MW2559	<i>isaB</i>	immunodominant antigen B	1.3	2.7	3.7	5.8	1.2	1.1	1.1	2.3
MW0517	<i>sdrD</i>	SerAsp rich fibrinogenbinding	0.2	0.2	0.2	0.4	0.4	0.6	0.6	0.9

MW0124	<i>cap8A</i>	capsular polysaccharide synthesis enzyme Cap5A	4.0	10.7	12.2	15.9	1.6	1.3	2.3	4.1
MW0139	<i>cap8P</i>	capsular polysaccharide synthesis enzyme Cap5P	1.0	0.9	1.0	0.4	0.7	0.7	0.8	1.2
MW0627		secretory antigen SsaA homologue	6.9	7.8	10.3	9.1	3.8	3.6	3.4	1.8
MW2589	<i>aur</i>	zinc metalloproteinase aureolysin	3.0	3.0	1.4	0.9	2.2	1.7	0.9	0.9
MW0802		hemolysin	0.6	1.0	1.1	1.4	0.6	0.7	0.8	1.1
MW2096		hemolysin III	0.9	0.9	1.2	2.8	0.9	0.9	0.9	1.0
MW2344	<i>hlgB</i>	gamma-hemolysin component B	0.9	0.5	0.5	0.2	0.7	0.7	0.6	0.6
Signal transduction/secretion										
MW1775	<i>traP</i>	signal transduction protein	3.9	4.2	4.4	2.5	1.9	1.4	1.3	1.0
MW2149	<i>secY</i>	preprotein translocase SecY subunit	45.0	20.5	10.7	26.4	21.6	8.8	6.0	3.2
Transporters										
MW1235	<i>mscL</i>	large-conductance mechanosensitive channel	6.8	7.0	10.2	9.5	3.1	2.3	1.9	1.4
MW0988		Mn ²⁺ -transport protein	3.1	2.8	3.8	4.5	13.3	16.9	11.1	4.5
MW1507		ABC transporter MreB	1.1	0.8	0.7	0.8	1.0	0.9	1.1	1.5
MW1554		probable transmembrane transport protein	0.4	0.5	0.5	0.7	0.4	0.5	0.5	0.7
MW2298		cationic transporter	0.2	0.6	0.6	1.5	0.4	0.5	0.4	0.5
MW0586		Na ⁺ /H ⁺ antiporter	5.8	2.2	1.4	2.7	3.0	1.6	1.6	1.2
MW0605		ATP-binding cassette transporter A	1.2	1.2	1.3	3.3	2.6	2.3	3.6	3.1
MW2478	<i>copA</i>	copper-transporting ATPase	0.5	0.5	0.4	1.0	0.5	0.6	0.9	1.7
MW2334		ABC transporter (ATP binding subunit)	0.5	0.3	0.4	0.4	0.6	0.7	0.7	0.8
MW0213		similar to nickel ABC transporter nickel-binding protein	0.4	0.3	0.4	0.2	0.6	0.6	0.6	0.6
Regulators										
MW1446	<i>srrA</i>	staphylococcal respiratory response protein	3.4	3.3	2.8	2.4	2.2	1.6	1.3	1.2
MW1445	<i>srrB</i>	staphylococcal respiratory response protein	1.1	0.9	0.8	0.6	1.1	1.0	1.1	1.1
MW1790	<i>yhcS</i>	two-component sensor histidine kinase	0.6	0.7	0.9	2.0	0.6	0.6	0.7	0.8
MW1789	<i>yhcR</i>	two-component response regulator homolog	0.6	0.7	0.8	0.9	0.9	1.0	1.3	1.5

MW0018	<i>vicR</i>	response regulator	1.9	3.1	3.5	2.7	1.7	1.5	1.8	2.0
MW1637	<i>phoP</i>	alkaline phosphatase synthesis transcriptional regulatory protein	1.6	3.1	3.4	3.5	1.4	1.3	1.5	1.7
MW1801	<i>perR</i>	transcription regulator Fur family homolog	1.3	1.5	2.1	4.5	1.1	1.0	1.0	1.0
MW0879	<i>spx</i>	conserved hypothetical protein	8.0	10.2	16.2	24.3	4.5	2.9	3.7	3.1
MW1111		transcription factor fapR	3.4	3.0	2.0	1.4	2.0	1.4	1.1	0.9
MW2552		transcriptional regulator	0.4	1.0	2.1	1.0	0.9	1.1	1.4	1.0
Antibiotic related genes										
MW0623	<i>vraF</i>	ABC transporter ATPbinding protein	1.2	1.3	1.3	0.7	0.9	0.9	0.7	0.9
MW1158		similar to metalloβ-lactamase family protein	4.3	3.4	3.2	2.2	2.2	1.4	1.6	1.2
Others										
sRNA_sgrA	sgrA		1.3	2.0	2.9	5.1	2.6	2.6	3.8	4.5
sRNA_sbrD	sbrD		0.2	0.2	0.3	0.6	0.4	0.5	0.7	0.9
sRNA_45S	45S		0.2	0.3	0.5	0.5	1.6	1.6	2.9	2.8
MW1494		exogenous DNA-binding protein comGC	7.6	8.9	9.4	10.1	5.9	3.0	2.3	2.0
MW0906		competence transcription factor	0.1	0.2	0.2	0.2	0.5	0.6	0.7	0.8
MW1619	<i>tig</i>	prolyl isomerase	3.7	2.5	2.0	1.9	3.8	2.3	1.9	1.7

Table S2: Quantification of amino acids and urea in cheese matrix inoculated by *S. aureus* MW2, *L. lactis* LD61 or both. Concentrations are expressed in mmol g⁻¹.

Amino acids	Initial	6 h			8 h			10 h			24 h			7 d		
		<i>L. lactis</i>	Mixed	<i>S. aureus</i>	<i>L. lactis</i>	Mixed	<i>S. aureus</i>	<i>L. lactis</i>	Mixed	<i>S. aureus</i>	<i>L. lactis</i>	Mixed	<i>S. aureus</i>	<i>L. lactis</i>	Mixed	<i>S. aureus</i>
Urea	568.1	658.9	540.5	571.7	575.9	353.9	431.9	604.3	181.8	369.0	523.1		253.1	501.2	-	-
Asp	1.9	8.2	11.4	1.8	17.8	37.6	2.1	30.2	34.3	2.1	55.2	62.9	1.3	65.7	81.7	4.8
Thr	-	-	-	-	-	-	-	2.5	19.3	-	83.9	139.9	-	281.8	383.8	-
Ser	-	-	-	-	-	2.1	0.9	4.5	15.3	-	58.6	73.3	-	196.5	160.1	-
asn	-	-	-	-	-	-	-	-	4.4	-	32.6	61.3	-	141.7	208.6	-
Glu	47.2	64.3	47.4	15.2	61.8	94.9	7.3	119.5	212.2	15.6	496.4	569.2	6.2	849.1	974.0	39.8
Gln				-			-	-	9.6	-	33.1	55.6	-	253.7	242.2	-
Gly	13.9	16.9	3.5	-	5.4	6.4	-	9.4	19.4	-	79.3	106.8	-	126.2	193.4	-
Ala	4.4	6.7	8.0	-	10.7	16.6	-	24.0	43.4	-	131.6	180.3	-	340.7	430.9	3.9
Cit	-	-	-	-	-	7.2	-	13.3	15.2	-	37.0	35.2	-	63.6	57.3	-
Val			13.1	-	-	25.3	13.9	19.6	65.5	11.4	188.1	253.6	15.1	445.4	528.1	6.2
Met	-	-	-	-	-	-	-	-	-	-	2.1	6.5	-	17.8	25.3	-
Ile	-	-	-	-	-	-	-	-	9.1	-	60.1	98.4	-	166.1	235.9	-
Leu	-	-	-	-	-	-	-	-	24.0	-	100.8	135.6	-	276.9	330.7	3.2
Tyr	-	3.1	5.6	-	7.3	13.1	-	11.0	15.6	-	34.8	41.7	-	65.4	74.9	4.2
Phe	-	-	2.5	-	3.8	7.7	-	6.7	14.2	-	39.2	49.8	-	93.0	113.9	8.6
Orn	-	-	-	-	-	2.7	-	1.5	5.8	-	16.6	21.9	-	42.0	57.0	-
Lys	9.2	29.5	41.1	5.7	58.1	74.0	3.5	73.9	97.7	2.7	173.6	195.9	-	279.4	318.7	-
His	-	6.6	8.6	-	13.0	18.2	-	17.3	21.0	-	35.1	40.2	-	61.3	70.1	-
Pro	-	15.5	41.4	-	56.5	224.1	-	100.4	160.5	-	249.5	293.9	-	387.5	464.0	-

“-“ : not detected

Table S3. List of oligonucleotides used in this study

MW2 ORF	Gene name	Description of gene product	Forward primer	Reverse primer
MW0005	<i>gyrB</i>	gyrase	AATCAGCGTTAGATGTAGCAAGC	GTACCGACAGATTTTGTAGACC
MW0051	<i>seh</i>	enterotoxin H	TGGTCAATATAATCACCCATTCA	TCAAAATCATTGCCACTATCACC
MW0100	<i>butA</i>	acetoin(diacetyl)reductase	TTATCAATGCAACATCTCAAGCA	CTAAATCTTGTGCGGCTACTTGT
MW0124	<i>cap8A</i>	capsular polysaccharide Cap8A	GCGCTATTGTACATTTTTCGTC	TCTTGTGCCATAAACTGAGGATT
MW0202	<i>pflA</i>	formate acetyltransferase enzyme	AGGGACACTTACATTTCTGTCGAA	CAAGTATCTGGAATTGTGGCAATA
MW0217	<i>lctE</i>	Lactate dehydrogenase	AAATGAAGATGCCGTATTGACTGT	GATTTCTACGACGTTGCCAATAC
MW0238	<i>lrgA</i>	holin-like protein LrgA	CTGTTAAGTTAGGCGAAGTCGAA	GCTTGGCTAATGACACCTAAAGA
MW0477	<i>ctsR</i>	transcription repressor of stress genes	CAGCTGATTGGACCTTCTATTTTC	GCTTGAATCATTTTAGCTTCACG
MW0480	<i>clpC</i>	ATPdependent Clp proteinase chain	AGTTATTGCAGGATGGACAGGTA	TTTGCCCAATAACTCTCTCATGT
MW0516	<i>sdrC</i>	SerAsp rich fibrinogenbinding,	GGCATGATACCAAAATCGATTAAA	CTTATGACCACTTAACCCAAAAA
MW0568	<i>adhI</i>	alcohol dehydrogenase I	TGCTGATTTTGGTGATGTTACAG	TAGACACACGTCCTCCAATTTTT
MW0580	<i>sarA</i>	staphylococcal accessory regulator A	TTGCTTTGAGTTGTATCAATGG	TTTCTCTTTGTTTTCGCTGATGT
MW0604	<i>pbp4</i>	penicillin binding protein 4	ATCCAGCGTCTATGACCAAATTA	TTCTTTGTTCTGTCATTGTGACAG
MW0648	<i>mgrA</i>	transcriptional regulator	CGAAGTCGATCAACGTGAAGTAT	AGAAGAAGCTGAAGCGCATTTGT
MW0667	<i>saeS</i>	histidine protein kinase	TCAATATTGCAACCATATGAGCA	AGTGGCGTTTCGATATTGATAAAA
MW0705	<i>pepT</i>	aminotripeptidase	GATATTCCAGCAAACACTGAACC	GAAGTTACCGCAACCTGTAAAGA
MW0730	<i>clpP</i>	ATPdependent Clp protease	GCTGGTTTTGCGATTTATGATAC	TTGCAACAGCTGCTAATAAGAAT
MW0759	<i>sec4</i>	enterotoxin C	AAACATGAAGGAAACCACTTTGA	TTTGCACTTCAAAAGAAAATTGTG
MW0760	<i>sel2</i>	enterotoxin L	GGTTACCGCACAAGAAATAGATG	TGCCGTATTCTTTACCTTTACCA
MW0764	<i>clfA</i>	clumping factor A	TTACGAATCAGTTGACGAATGTG	AGGCACTGAAAAACCAATAATTCA
MW1028	<i>trxA</i>	thioredoxin	TAAATGTATCGCTCCGTTATTAG	TTTAGCTGCAGTTGATGGATTTT
MW1069	<i>ftsZ</i>	cell division protein	CTTCAAAATTCATCAAATGCACAA	CGTCTTGTCTCTCTGAAACGCT
MW1129	<i>sucD</i>	succinylCoA synthetase	ATGCCTGGCTATATTCACAAAAA	CCAACAGCTGTAGTTTGACCAAT
MW1138	<i>codY</i>	transcription pleiotropic repressor	ATGGAATCTTACGTGAGAAAGCA	ATGTTCAATCGCTTCTTTTTCAG
MW1221	<i>kata</i>	catalase	ATTTACGTATATGTCATGGGTTTC	TTTTCAATACCTTGTTCGGTTCT
MW1237	<i>ciib</i>	aconitate hydratase	GCGAGGTACCAATTTAAACCTTCT	AGTAAATATCTCCCCCAACGTCAT
MW1290	<i>cspA</i>	cold shock protein A	TCCGAAGTTGAAGGAGAAAAATGAC	ACTTCAAACTCAACAGCTTGACC
MW1446	<i>srrA</i>	staphylococcal respiratory response	ATCTTTTGAATCCATGAAGCAA	TCCATTTTCAGGCAACATTAATC
MW1505	<i>sodA</i>	superoxide dismutase	TTCTGGGAGTTACTTTACCAAAA	CTGCTTTGTTCAGCAAAATCTTTT
MW1532	<i>dnaK</i>	DnaK protein	AAGGTTACGTCACAACCCATCT	GATTGAACAGTGTGTTGGGTTGT
MW1584	<i>relA</i>	GTP pyrophosphokinase	TCCGAAGGCGATATAAATGGTAGA	ATAACACGTATCGCCAACAAATC
MW1641	<i>pykA</i>	pyruvate kinase	GTATTGGACGTGGATCAGTTGTT	ACAAACGTTTCATCGATTGAGTT
MW1694		XaaHis dipeptidase homolog	AAATTATTGAAAAAGGCGACATGA	TCAGTTTAGGATCTGGTTCTCCA
MW1705	<i>rot</i>	transcriptional regulator	ATTGGGAGATGTTTAGCATGAAA	TTCAATCTCGCTGAAAAATTGAGT
MW1885	<i>sak</i>	staphylokinase	CGCAAAGATCGAAGTCACCTTATT	ATGCTCTGATAAATCTGGGACAA
MW1889	<i>sea</i>	enterotoxin A	TAATCGATTGACCGAAGAGAAAA	ATAACGTCTTGCTTGAAGATCCA
MW1937	<i>seg2</i>	enterotoxin G	TACGATTTGTTTTACACCGGAAC	TCCAAATGAAAAATCTCTGCATC
MW1938	<i>sek2</i>	enterotoxin K	CTACACAGGAGATGATGGGCTAC	CATCCAAATGGAAATTTCTCAGAC
MW1959	<i>hld (RNAIII)</i>	deltahemolysin	TAAGGAAGGAGTGATTTCAATGG	GTGAATTTGTCTACTGTGTGCGAT
MW1963	<i>agrA (RNAII)</i>	accessory gene regulator A	CCTCGCAACTGATAATCCTTATG	ACGAATTTCACTGCCTAATTTGA
MW1977	<i>ilvD</i>	dihydroxy-acid dehydratase	GATGAAGAAAGATGGCACGTTAC	GAGGGTGAATGACATCAAAAGTTC
MW1981	<i>leuA</i>	2-isopropylmalate synthase	CGTCTCTTATCAATGCCATAAC	AACCTGTTGGTGTAAGCACGACT
MW1988	<i>sigB</i>	sigma factor B	TTCACCTGAGCAAAATTAACCAAT	ATCTTCGTGATGTGATTGTCCTT
MW2108	<i>asp23</i>	alkaline shock protein 23	AGACATGAAAGGTGGCTTAACCTG	GCTTGTTTTTACCAACTTCAAC
MW2115	<i>lacG</i>	6phosphobetagalactosidase	AGTATTCTCGTGAAACGATGGAA	GCTGCATCTAAAATGGCATAATC
MW2132	<i>alsS</i>	alpha-acetolactate synthase	CCAATTTACCCGTTGTAGAAACA	ATTATCACCAACTTGATTACGG
MW2212	<i>ureD</i>	urease accessory protein	ATTTCGATTGTCGTGTGCTATTT	TCTGCGATATAGCTTTGGATGAT
MW2460	<i>cidC</i>	pyruvate oxydase	ACAATGCAAGGATGCAGATTTACT	TTTTAGGATTTGTGTCGATTTGG
MW2462	<i>cidA</i>	holin-like protein cidA	TGTACCGTAACTTGGGTAGAAG	TTCGGAAGCAACATCCATAAATC
MW2469	<i>clpL</i>	ATPdependent Clp proteinase chain	AAGATGCACTGATTCCGACTTGAT	TGTCATCATAACCGACATAACCA
MW2482	<i>crtN</i>	staphyloxanthin synthase	AAGATGTTTTTACAGCGTGTGGT	AAATCTGTAGGCAACGTTATACGA
MW2526	<i>mgo2</i>	malate/quinone oxidoreductase	CGATGCCAAAGTTTATGGTAAAG	AGCAAAATGGTCCAAATAACAATG
MW2552	<i>arcR</i>	deaminase pathway repressor	TTCTTGATTGCTAGAGAAATTG	TTCATGTGTGTGCTCATTATC
MW2553	<i>arcC</i>	carbamate kinase	AAATCCAAACAAGCTAAAATCGAACA	GATTGATTTCAAGTTTCCAAACCA
MW2559	<i>isaB</i>	immunodominant antigen B	AGGAAGCTGATAGCGGTATTTT	TGTTCAACTGTTACTTCGACAAC
MW2585	<i>icaR</i>	operon ica repressor	AAATCGAACTATTCAATTGATGC	CAGAAAAATTCCTCAGGCGTATTA
MW2586	<i>icaA</i>	intercellular adhesion protein A	AAGAAGCTGACATAAATGTGGA	TCTCGTATTTGAGTGCAAGACA
MW2623	<i>cspB</i>	cold shock protein B	AATGGTTTTAACCGCAGAAAAAGGT	TCTTCTAAAGTTTTGTAGCCATCG