

Biofilm formation and genotyping of bovine mastitis isolates: evidence for lack of penicillin- resistance in type II strains

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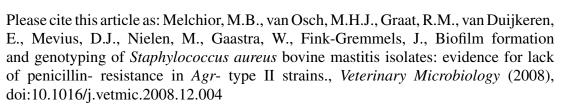
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1	Research Article:					
2	Title:					
3	Biofilm formation and genotyping of Staphylococcus aureus bovine mastitis isolates:					
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1 Abstract

The increasing evidence for a role of biofilm formation in bovine mastitis caused by 2 3 Staphylococcus aureus led to further investigations on biofilm formation by S. aureus 4 isolates from mastitis in two growth media (TSBg and bovine milk serum). The ability of 99 5 S. aureus strains that were recently isolated or obtained from a culture collection (historical 6 strains) to form biofilm, in both growth media as well as the correlation of biofilm formation 7 with the presence of the ica-, bap-, and IS257 genes is described. These genes have been 8 correlated with biofilm formation by human S. aureus isolates. All strains were also 9 genotyped with respect to their Agr- type and - subtype, and for the presence of the antibiotic resistance genes *blaZ* and *smr* by PCR. The prevalence of the *Agr* types and the investigated 10 11 genes and their correlation with biofilm formation were statistically evaluated.

The *Agr*-type of a strain had a marked effect on the biofilm formation, by that strain, however in contrast to human isolates no significant effect of *ica*- and *IS257* genes on biofilm formation was observed. The *bap* gene was not found in any of the investigated strains. The presence of biofilm related genes showed a high correlation with the *Agr*-type of the strains. The data give evidence for a very strong correlation of *Agr*-type I strains and penicillinresistance in the bovine *S. aureus* mastitis strains; none of the *Agr*-type II strains was found to harbor penicillin- resistance genes.

19 These data indicate that the most prevalent *Agr*-types in *S. aureus* bovine mastitis, *Agr*-type I 20 and II, can be regarded as different subspecies, with different abilities for the formation of 21 biofilm in bovine milk serum. The very high correlation between *Agr*- type II and penicillin-22 susceptibility strongly suggests that these strains are not able to accommodate *blaZ* genes.

23

24 Keywords: S. aureus, biofilm, bovine mastitis, genotyping, penicillin resistance, Agr- type.

25

1 Introduction

2 There is increasing evidence that S. aureus can form biofilms in the udder of cows suffering 3 from mastitis. Biofilms impair the action of both the host immune system and antimicrobial 4 agents and allow the persistence of the infection (Melchior et al., 2006b). In a study, with a 5 limited number of strains, it was shown that all strains were able to grow in a biofilm 6 (Melchior et al., 2006a). A standard CLSI susceptibility test and a biofilm susceptibility assay 7 for antimicrobials commonly used in mastitis therapy, showed that the strains are less 8 susceptible for these antimicrobials when growing in biofilm (Melchior et al., 2006a, 2007). 9 Biofilm formation by S. aureus is influenced by environmental factors like sugars (glucose 10 and/or lactose) or proteases present in the growth medium and depends also on the genetic 11 make-up of a particular S. aureus isolate. The Agr-(accessory gene regulator) type, Agr-12 subtype and Trap-(target of RAP) system (Gilot et al., 2002; Gilot and van Leeuwen, 2004), the ica-(inter cellular adhesion), bap-(biofilm associated protein) and IS257 genes, all are 13 examples of 14 15 components of the genetic make-up of a particular strain related to biofilm formation in vitro 16 (Cramton et al., 1999; Cucarella et al., 2004; Kozitskaya et al., 2004). Agr, Trap and ica are 17 loci involved in quorum sensing and have two component regulatory systems. In human 18 medicine a correlation between Agr type and certain diseases caused by S. aureus is 19 demonstrated. (Jarraud et al., 2002). Penicillin resistance encoding *blaZ*- and *smr* loci (De Oliveira et al., 2000; Bjorland et al., 2001; Sidhu et al., 2001; MARAN, 2003 - 2005; Bjorland 20 21 et al., 2005) as well as biofilm formation influence the outcome of clinical therapy and lead to 22 higher risk of persistent intramammary infections and poor antimicrobial therapy (Haveri et 23 al., 2007). A relationship of these loci with Insertional Sequences (IS) was demonstrated 24 (Bjorland et al., 2001; Sidhu et al., 2002; Olsen et al., 2006).

The aim of this study was to determine the relation between biofilm formation with the presence of the *ica-*, *bap-*, *IS257* and *blaZ* genes and *Agr* types in mastitis *S. aureus* isolates. The simultaneous study of biofilm production, genetic profile and resistance allowed the discovery of associations between these traits. To determine the effect of growth medium on biofilm formation (Melchior et al., 2006a), a comparison between an artificial growth medium and serum milk was also made.

7

8 Materials and Methods

9 Collection of *S. aureus* isolates

10 The strains used in this study were selected with respect to date of isolation, since over the 11 years the genetic make-up of *S. aureus* strains from bovine mastitis and their penicillin 12 resistance has evolved (Sol, 2002), and are from three different sources:

13 A: field strains. From December 2005 until September 2006, cows from farms spread over the Netherlands were sampled. Cow selection was based on their 4 - 6 week somatic cell count 14 15 (SCC) pattern. The selection criterion for a *subclinical* infection was a cow SCC > 120.000 16 cell/ ml, without any other signs of infection. Milk samples were send to the Animal Health Service in Deventer (Gezondheidsdienst voor Dieren). During the same period, milk from 17 animals with *clinical* bovine mastitis, send to the Animal Health Service for diagnostic 18 19 reasons, was randomly collected as well. All milk samples were incubated according to 20 standard laboratory procedures of the National Mastitis Council (ISO 17025 certified 21 laboratory) and the isolated S. aureus strains were stored at -70° C. From the S. aureus 22 positive samples all 58 strains from 54 farms were included in this study. Only one strain per cow was selected. These strains are designated the **F** strains (see Table 1). 23

24

B: Penicillin- resistant S. aureus strains: Because of the low number of penicillin- resistant
strains in collection A (F strains, ~10%), which is in accordance with the current prevalence
of penicillin-resistance in the Netherlands (*MARAN*, 2003 - 2005), selected penicillin resistant
strains were added to this collection.

In total, twenty penicillin resistant *S. aureus* strains from bovine mastitis from the Dutch
antimicrobial surveillance program (*MARAN*, 2003 - 2005) collected between 2003 and 2005
were obtained from the Central Veterinary Institute Lelystad (CVI, Lelystad). These strains
are designated the **P** strains (Table 1).

9

C: Historical isolates: Preliminary results in this study revealed remarkable differences 10 11 between our results and those from Gilot et al., (2002; 2004). These strains were collected 12 from 1950 – 2000 and therefore it was decided to analyse a number of strains isolated before 13 the year 2000. Twenty-one S. aureus strains from bovine mastitis collected between 1988 and 1994 were provided by the Veterinary Medical Diagnostic Centre of the Veterinary Faculty 14 15 (VMDC; University of Utrecht). The strains were selected randomly from cases of bovine 16 clinical mastitis and are stored for research purposes. These strains are designated the H 17 strains (see Table 1).

Three strains were used as controls; strain BMA/FR/032/0074 was used as a high slime producing, *bap* locus positive strain, strain BMA/UK/032/0112 was used as a *smr* locus positive strain and strain Newbould 305 (ATCC 29740) was used as control for the *Agr* typing assays (Gilot et al., 2002) (designated 0074, 0112 and N305 respectively, in this study). All three strains have been used previously in biofilm antimicrobial susceptibility studies (Melchior et al., 2006a).

The identity of all used strains as *S. aureus* was confirmed by PCR according to Martineau
 (1998). The growth media for the quantitative biofilm assay were TSB with 1% glucose
 (TSBg) and bovine milk serum prepared according to the procedure below.

4

5 **Production of milk serum**

Fresh milk was taken from a single cow with monthly somatic cell count (SCC) records of <6 7 50.000 for at least four consecutive months. The SCC of this milk sample was measured in 8 duplicate for confirmation of the cell count of the sample (Delaval Cell Counter DCC). The 9 milk was centrifuged twice for 17 min at 6000 x g at 4°C and the supernatant was transferred to sterile bottles. The resulting skimmed milk supernatant was centrifuged at 46.000 x g at 10 11 4°C for one hour (for pelleting of the casein proteins) and the supernatant was transferred into 12 a sterile bottle. Sterility of the milk and the supernatants for all centrifuge steps was tested by 13 taking 100 µl milk or supernatant in duplicate, and incubating it on sheep blood agar plates for overnight growth at 37°C. The milk serum was filter sterilized (0,45 µm filters, Corning, NY) 14 15 and stored at -20° C. From the milk serum prepared in this way, the bulk of lipid and protein contents is removed. The milk serum consists of roughly 5% lactose, milk serum proteins and 16 17 all the unbound enzymes (including proteases) in milk (Fox and Kelly, 2006).

18

19 Gene typing

Agr type, Agr subtype and Trap. Detection of the *Agr* group- specific region and the variable region of the *Agr* operon was performed as described (Gilot et al., 2002; Gilot and van Leeuwen, 2004). In brief, the 1070-bp variable region of the *Agr* operon was amplified by PCR (for primers see Table 2), and the amplicons were electrophoresed to determine the molecular weight. After digestion with *AluI* or *RsaI*, the resulting fragments were separated

by electrophoresis through a 3% agarose gel containing ethidium bromide and visualized by
 transillumination under UV light.

The PCR amplification of the *Trap* gene was also performed according to the method of Gilot et al. . In brief, the 504-bp open reading frame of the *trap* gene was amplified by PCR, and the size of the amplicons was estimated by electrophoresis. The *Trap* amplicons were digested with *MseI* and electrophoresed through a 3% agarose gel yielding three *Trap* types.

7 Classification of *Agr* types and the *Trap* types was based on the study of Gilot and van
8 Leeuwen (Gilot et al., 2002).

9

The *ica*, *bap*, *blaZ*, *smr* locus and *IS257*. The presence of the *icaA* and *icaD* genes of the *ica*locus, the *bap* locus, the *smr* locus, the *blaZ* gene and the *IS257* was determined with primers
described previously (Bjorland et al., 2001; Sidhu et al., 2002; Cucarella et al., 2004;
Melchior et al., 2006a; Olsen et al., 2006)(Table 2).

14

15 Quantitative biofilm assay

16 The biofilm forming capacity of the strains was determined as previously described (Melchior 17 et al., 2006a) with slight modifications. In brief, strains were grown overnight in TSBg at 18 37°C. This overnight culture (37°C) was diluted 1:100 in TSBg or in milk serum, and an 19 aliquot of 150 µl was placed in ten wells of a sterile 96-well U bottomed polystyrene microtitre plates (Costar, Corning, NY, USA). After cultivation for 24 h at 37°C, the plates 20 21 were carefully washed with sterile phosphate-buffered saline, air dried for one hour under a hood, and stained with 0.025% safranin for 10 min. Optical density (OD) at 540 nm was 22 23 measured with a 96-well plate reader (Bio-Rad model 3550 plate reader). Each assay was 24 performed in duplicate on two occasions. Only strains of Agr-type I and- II were included in

the assay, *Agr*-types III- and IV were excluded because they were only present in low
 numbers (see Table 1). Strains N305 and BMA/FR/032/0074 were used as controls.

3

4 Statistics

For calculation of the statistical significance of the differences in the measured gene locus prevalence between the *Agr* typing groups, a Chi-Square test was used (SPSS for Windows, release 1.0.0 Standard Version). Absorbance values from the quantitative biofilm assays were compared between groups based on the *Agr*-type or presence of genes by oneway Anova (SPSS).

10

11 **Results**

12 Agr type, Agr subtype and Trap

All 99 strains were tested by *Agr*-typing and *Agr*-subtyping which resulted in *Agr*-typing- and restriction patterns (*Agr*-subtyping) for 99 and 95 strains respectively; from 4 strains the *Agr*subtype could not be identified. The 58 strains from the F collection showed a high prevalence of the RIV-A7 restriction pattern (81%)(*Agr* subtype II), the second most prevalent pattern was RIII-A1 (9%)(*Agr* subtype I) and the three remaining patterns, RI'A1 (*Agr* subtype I), RIV-A5 (*Agr* subtype II) and RVI-A8 (*Agr* subtype III) had a low prevalence ($\leq 3\%$) (Fig 1).

In contrast, the strains from the P and the H collection had a high prevalence of RIII-A1 patterns (75 and 86%, respectively) and a low prevalence of the patterns RI'-A1, RIII-A2 and RIV-A7 (all below 10%). In other words, a high prevalence of *Agr*-type II was observed in the F strains, and a high prevalence of *Agr*-type I in the P and the H strains.

The results of the Agr-typing, Agr-subtyping and Trap-typing showed a strict correlation
 between Agr-type, Agr-subtype and Trap-type, as strains possessing the same Agr restriction
 type, also contained the same Trap-type(Fig 1).

4

5 Detection of the *ica*, *bap*, *blaZ*, *smr* locus and *IS257*

The *ica* locus was found in 74% of all strains and subdivision of strains based on their Agrtype showed a marked difference in occurrence of the most prevalent Agr-types, I and II
(Table 1). The *IS257* sequence was found in 33% of the strains and the highest prevalence
(50%) was found in Agr-type II strains.

PCR with the two primer pairs for the beta-lactamase locus, *blaZ1* and *blaZ2* (Table 2)
resulted in 39% and 35% *blaZ* positive strains, respectively. The *blaZ* locus was not found in
any of *Agr*-type II strains.

The *bap* locus was not found in any of the tested strains, with exception of the positive
control, and the *smr* locus was only found in 5% of the strains.

Statistic calculations comparing the presence of *ica*, *IS257*, *BlaZ1* and *BlaZ2* in *Agr*-type I
and II strains revealed a significant pair wise difference in prevalence of p=0.000, p=0.001,
p=0.000 and p=0.000 respectively (Table 1).

18

19 Quantitative biofilm assay

Quantification of biofilm production by the *Agr*-type- I and II strains in TSBg and milk serum is shown in Fig. 2. When the results for all strains and for both growth media were compared, it became evident that the variation in biofilm production in milk serum is clearly larger than in TSBg. This larger variation is mainly due to the higher optical density values for quantitative biofilm production in milk serum medium, as the results showed a maximum

biofilm production of 2.3 and 1.5 OD and a minimum biofilm production of 0.3 and 0.4 OD
 for milk serum and TSBg, respectively.

When the correlation between *Agr*-types and quantitative biofilm production was evaluated, clear differences between the two growth media (Fig 2) were observed. In general, biofilm production was higher for *Agr*-I than *Agr*- II stains in TSBg, but lower for *Agr*-I than *Agr*-II strains in milk serum. The *ica* locus and *IS257* have little effect on biofilm production, although the variation in biofilm production is lower for *ica* negative strains, both in TSBg and milk serum (data not shown).

9 Statistic calculations comparing the biofilm production by *Agr*-type- I and II strains in TSBg
10 and milk serum showed a significant difference (p=0.000 and p=0.005, respectively) in
11 optical density between *Agr*-type- I and II strains for these growth media.

12 The outcomes in means and standard deviations for control stains N305 and 13 BMA/FR/032/0074 were 1.007 ± 0.185 , 1.331 ± 0.389 and 0.705 ± 0.165 , 2.438 ± 0.178 14 respectively for TSBg and milk serum medium.

15

16 **Discussion**

17 Biofilm formation is influenced by numerous factors, and one of these is the growth medium. 18 In this study quantitative biofilm assays of S. aureus strains from bovine mastitis were 19 performed in TSBg and bovine milk serum. These growth media differ in various ways, i.e. in 20 their sugar content and concentration (glucose versus lactose) and also in the presence of 21 proteolytic enzymes (Fox and Kelly, 2006; Kelly, 2006). Both proteolytic enzymes and sugars 22 are known to influence biofilm formation (Rohde et al., 2005; Coelho et al., 2008). Milk 23 serum was chosen since it can be considered to closely mimic the *in vivo* situation. The milk 24 serum used for the experiments came from a low cell count cow, and thus mimics the 25 situation in a healthy udder that becomes infected for the first time. Proteolytic enzymes in the

1 milk come from: blood plasma, the cytoplasm of secretory cells, the milk producing 2 mammary cells and somatic cells (leucocytes) which enter the mammary gland in response to 3 bacterial infection (Fox and Kelly, 2006; Kelly, 2006; Larsen, 2006). 4 Significant differences between Agr-type I and Agr-type II strains were noted, both in milk 5 serum and TSBg medium (p=0.005 and p=0.000 respectively). Biofilm production was higher for Agr-I strains compared to Agr-II strains in TSBg, but lower for Agr-I than for Agr-II 6 7 strains in milk serum (Fig.2). The effect of the biofilm related loci *ica* and IS257 on biofilm 8 formation by Agr-type I and II strains, when present in these strains (both have a prevalence 9 of \sim 50% in both Agr-types), did not reveal significant differences. The lower biofilm 10 production by Agr I strains in milk serum is not due to the absence of the *ica* locus, since *ica* 11 positive Agr I strains tend to produce less biofilm in milk serum than ica negative strains (data 12 not shown). IS257 has no effect on the biofilm production in milk serum by Agr II strains, but 13 the variation in biofilm quantity was larger for the IS257 positive group. It can not be excluded that this is caused by the limited number of strains used. Therefore the specific 14 15 effect of IS257 has to be studied in more detail before its effect on biofilm formation will be 16 clear. A similar IS, IS256 modulates staphylococcal biofilm formation (Ziebuhr et al., 1999; 17 Cho et al., 2002; Conlon et al., 2004) by virtue of its is localization in biofilm associated 18 genes.

The *ica* locus is the best understood biofilm mechanism in staphylococci and the majority of clinical isolates, both from human and bovine mastitis contain the *ica* operon (O'Gara, 2007). The existence of *ica* independent biofilm formation mechanisms in *S. aureus* was recently shown (Rohde et al., 2005; 2007). Biofilm formation in an *ica* negative strain depends on the expression of a truncated isoform of the 220 kDa accumulation-associated protein Aap (Rohde et al., 2005). Expression of full-length Aap does not lead to a biofilm positive phenotype. The truncated Aap function is induced by proteolytic processing through

staphylococcal proteases. Added serine proteases like trypsine, elastase and cathepsin G are also able to induce this proteolytic processing and thus can induce biofilm formation. This shows the importance of the presence of proteases in the milk serum medium.

4 Pathogenic bacteria interact with the proteinase dependent cascade systems of their host, 5 including coagulation, fibrinolyis, complement activation and phagocytosis. Bacteria can also induce the release of proteolytic enzymes or their precursors from phagocytic cells 6 7 (Lahteenmaki et al., 2001). During infection with intramammary bacteria the SCC of the milk 8 increases simultaneously with an increase in activity of plasmin and non-plasmin proteinases. 9 Although the pattern is similar for all species, each bacterial species elicits a response in a 10 species specific manner (Leitner, 2006). The effect of these changes of proteolytic enzymes during infection of the mammary gland on biofilm formation need to be addressed in future 11 12 studies.

13 Our data confirm that the division of bovine mastitis S. aureus in penicillin resistant strains, and penicillin sensitive strains is dependent on more than the mere presence or absence of the 14 15 BlaZ gene as suggested by Haveri et al. (2007). We found that almost all penicillin positive 16 strains are from Agr type I, and none of the Agr type II strains contained penicillin resistance 17 genes. We also showed that these Agr types have a significantly different ability for biofilm 18 formation, which are not the only differences between the Agr types of S. aureus. In a recent 19 study Buzzola et al. (2007) showed that Agr I strains can be internalized in MAC-T cells significantly better, than isolates of Agr type II, III and IV. It was concluded that Agr-type I 20 21 strains are not only internalized more efficiently by epithelial cells, but also persist in higher 22 numbers in mammary gland tissue than Agr-type II, III and IV strains in the mouse infection 23 model (Buzzola et al., 2007). These data clearly show the different virulence protperties of 24 different Agr types of S. aureus, which is relevant for our studies.

Genotyping of the strains in our collection revealed large differences in the distribution of *Agr*-types amongst the recently isolated F strains and the strains isolated between the 1950s and 2000s (Gilot et al., 2002; 2004). It was also shown that the strains from the H collection have an *Agr*-type prevalence similar to the strains studied by Gilot and van Leeuwen (2002; 2004). These results indicate a shift in *Agr* type over time, and a concomitant decrease in penicillin resistance. Indeed, data from the Dutch Animal Health service show that penicillin resistance decreased from the 1970's to 2002 (Sol, 2002).

8 The practical and clinical implications of all these are that it be concluded that there is 9 evidence that bovine mastitis strains of the Agr-types I and II are probably equipped with different toolboxes to survive in the mammary gland. Agr I strains seem to be better adapted 10 11 to an intracellular survival and biofilm formation might not be an important trait. Thus 12 effective therapeutic intervention of these infections requires the use of an antimicrobial agent 13 with sufficient intracellular concentrations (the most common antimicrobials in bovine mastitis, except aminoglycosides). Agr II strains seem to prefer an extracellular niche and 14 15 hence biofilm formation is an important survival mechanism for these strains. Thus here 16 therapy requires drugs with good efficacy in biofilms and in vitro results suggest that 17 penicillins are a good choice (Melchior et al., 2007). However, the lack of information on 18 biofilm formation in high SCC milk serum requires that one should be cautious with these 19 conclusions.

In conclusion, the results presented here show a strict separation in *Agr* type between penicillin-susceptible and penicillin resistant strains and that these *Agr* types contain a different subset of genes, which cause significant differences in biofilm formation between *Agr* I and II strains, the two most prevalent *Agr* types in *S. aureus* strains isolated from bovine mastitis.

8	Acknowledgement:
7	mimics the situation in a healthy udder becoming infected for the first time was developed.
6	standardize the biofilm assay with milk serum from low SSC milk. Thereby an assay that
5	the amount of these enzymes (Ballou et al., 1995; Albenzio et al., 2004) made it necessary to
4	and Kelly, 2006) and the positive correlation between the milk somatic cell count (SCC) and
3	The importance of proteolytic enzymes in bovine milk serum (Hayes and Nielsen, 2000; Fox
2	for this awaits further study.
1	Bovine mastitis S. aureus Agr-II strains were not found to be penicillin resistant. The reason

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10 was financially supported by the Dutch Dairy Board.

11

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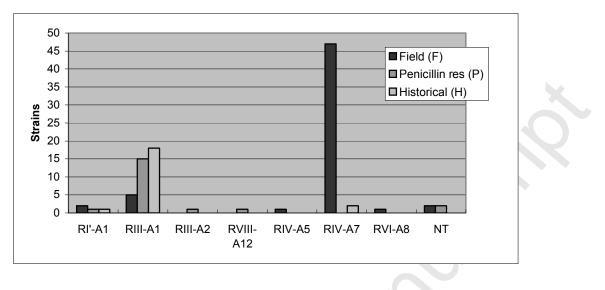
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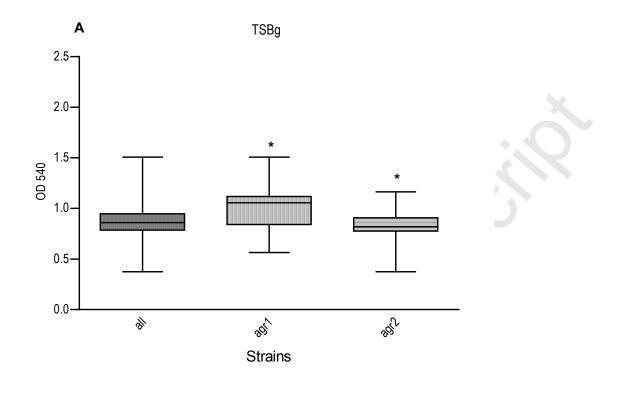
- Table 1. Correlation of *Agr* types and presence of biofilm related genes for strains in all three
 samples. The samples F strains, P strains and H strains are subdivided according to their *Agr* types, and set out against the frequencies of present genes.
- 4
- Fig 2. Quantitative biofilm production in TSBg (A) and milk serum (B) for all tested strains,
 and for *Agr*-type I and- II separately. Box and whisker plots with mean and 25% percentile
 boxes. The oneway Anova statistical analysis revealed a significant difference (A: p= 0.000,
 B: p=0.005) in optical density values between *Agr*-type I and *Agr*-type II (*).

CeR

- 10



Trap								
type	1	1	2	3	3	2	3	1,2, 3
Agr-type								
	Ι	Ι	Ι	Ι	II	II	III	I, II, III, IV





Milk serum

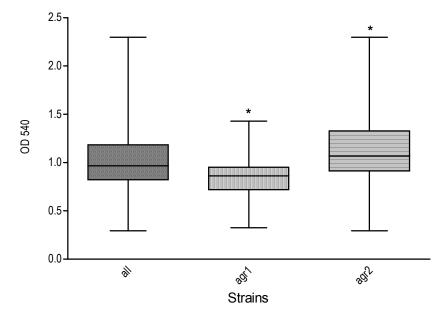




Table 1. Correlation of *Agr* types and presence of biofilm related genes for strains in all three samples. The samples F strains, P strains and H strains are subdivided according to their *Agr* types, and set out against the frequencies of present genes.

		N =	Ica	IS257	BlaZ1	BlaZ2	bap	smr
F strain	15							
2006		58						
	Ι	8	3	2	4	-	-	-
Agr type	II	49	49	23	-	-	-	1
ty A	III	1	1	-	-	-	-	-
P strain	18							
2003-20	005	20						
	Ι	18	16	4	18	18	-	3
Agr type	III	1	1	-	1	1	-	-
Ч Ч	IV	1	1	-	1	1	-	-
H strai	ns							
1988-19	994	21						
	Ι	19	1	2	17	17	-	1
Agr type	II	2	1	2	-		-	-
All stra	ins	99						
e	Ι	45	20 ^a	8 ^b	39 ^c	35 ^d	-	4
Agr type	Π	51	51 ^a	25 ^b	_ ^c	_d	-	1
 	III	2	1	-	1	1	-	-
A	IV	1	1		1	1	-	-
Total			73	33	41	35	-	5

^{a,b,c,d} Significant pair wise difference between Agr I and II according to Pearson Chi-Square tests.

^{a, c, d} p = .000, ^b p = .001

Table 2. Primers

Primer (5'-	3')	reference
Agr B1	TAT GCT CCT GCA GCA ACT AA	Gilot 2002
Agr C2	CTT GCG CAT TTC GTT GTT GA	
ICAAF	CCT AAC TAA CGA AAG GTA G	Cramton 1999
ICAAR	AAG ATA TAG CGA TAA GTG C	
ICADF	AAA CGT AAG AGA GGT GG	
ICADR	GGC AAT ATG ATC AAG ATA C	•
Sasp-6m	CCC TAT ATC GAA GGT GTA GAA	Cucarella 2004
_	TTG CAC	
Sasp-7c	GCT GTT GAA GTT AAT ACT GTA	C ·
	CCT GC	
487*	TAA GAG ATT TGC CTA TGC TT	Olsen 2006
373*	TTA AAG TCT TAC CGA AAG CAG	*(blaZ1 in table1)
486#	GTT GCG AAC TCT TGA ATA GG	
488#	GGA GAA TAA GCA ACT ATA TCA	
	TC	#(blaZ2 in table1)
Smr F	ATA AGT ACT GAA GTT ATT GGA	Bjorland 2001
	AGT	
Smr R	TTC CGA AAA TGT TTA ACG AAA	
	СТА	
IS257F	TTG GGT TCA AGA ATA TGC CC	Sidhu 2002
IS257R	CTT CGT TGA AGG TGC CTG AT	

TIUCE CTT CGT TGA AUG .