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Genetic characterization of antimicrobial resistance in coagulase-negative Staphylococci from bovine mastitis

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I dedicate this thesis to my parents who unremittingly supported me during my years of study.

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Summary

Coagulase-negative staphylococci (CNS) (n = 417) were isolated from bovine milk and identified by MALDI-TOF MS. Nineteen different species were identified, and *S. xylosus*, *S. chromogenes*, and *S. haemolyticus* were the most abundant species. Resistance to oxacillin (47.0% of the isolates), fusidic acid (33.8%), tiamulin (31.9%), penicillin (23.3%), tetracycline (15.8%), streptomycin (9.6%), erythromycin (7.0%), sulfonamides (5%), trimethoprim (4.3%), clindamycin (3.4%), kanamycin (2.4%) and gentamicin (2.4%) was detected. Resistance to oxacillin was attributed to the *mecA* gene in 9.7% of the oxacillin-resistant isolates. The *mecA* gene was detected in *S. fleurettii*, *S. epidermidis*, *S. haemolyticus*, and *S. xylosus*. Resistance to tetracycline was attributed to the presence of *tet*(K) and *tet*(L), penicillin resistance to *blaZ*, streptomycin resistance to *str* and *ant(6)-Ia*, erythromycin resistance to *erm*(C), *erm*(B), and *msr*. In total, 15.1% of the CNS isolates were multidrug-resistant (i.e., exhibiting resistance to two or more antimicrobials). The remaining CNS isolates were susceptible to antimicrobials commonly used in mastitis treatment. Methicillin-resistant CNS isolates were diverse, as determined by *mecA* gene sequence analysis, SCC*mec* typing, and PFGE. Because this study revealed the presence of multidrug-resistant CNS in a heterogeneous CNS population, we recommend antibiogram analysis of CNS in persistent infections prior to treatment with antimicrobials.

Keywords: methicillin-resistance, CNS, genotyping, antibiotic resistance, SCC*mec*

OVERVIEW AND AIM OF THE THESIS

Mastitis is one of the most important diseases in bovine medicine. It is defined as an infection of the mammary gland and occurs in all mammals. Bovine mastitis has many different causes, and is classified roughly in clinical and subclinical mastitis. Mastitis normally leads to a decrease of the milk yield in cows and therefore to severe economic losses for the farmers.

In modern dairy cow herds, major mastitis pathogens such as *S. agalactiae*, *S. dysgalactiae*, *S. aureus*, and *E. coli* are managed and reduced quite well. However, minor pathogens such as coagulase-negative staphylococci (CNS) or *C. bovis* are increasingly causing mastitis. Many studies showed that CNS are the microorganisms most commonly isolated from bovine milk in many countries, and that they are an important cause of mastitis.

CNS are a group of aerobic living, gram-positive, coagulase-negative bacteria and belong to the cocci genus. Most of the CNS are opportunistic skin commensals, in cows they are often found on udder skin, teat skin and on the teat apices from where they can enter the udder and cause infections.

Antibiotic treatment of the mammary gland is a frequent practice in bovine industry. Not only in cases of acute mastitis but also preventive for dry cow therapy. In Switzerland, β-lactam antimicrobials (including penicillin and cephalosporins), aminoglycosides (gentamicin and neomycin), and macrolides (spiramycin) are commonly used to treat mastitis. Under this selection pressure bacteria such as CNS have the ability to adapt and acquire antibiotic resistance genes.

The aim of our study is to identify the different CNS species in milk from cows with different types of mastitis (clinical and subclinical), to characterize their antimicrobial resistance mechanisms, and to determine whether specific methicillin-resistant and multidrug-resistant CNS clones are common in dairy cows.

Further, this project will allow implementing a new and cheap method for the rapid identification of CNS at species level in the veterinary diagnostic. The results will also give an overview of the prevalence and the phenotypic and genotypic antibiotic resistance profile of CNS isolated from mastitis milk in Switzerland.

THESIS

Genetic characterization of antimicrobial resistance in coagulase-negative Staphylococci from bovine mastitis

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Running title: Antibiotic resistance in CNS from bovine mastitis

Key words: methicillin-resistant, CNS, genotyping, antibiotic resistance, SCC*mec*

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1.) ABSTRACT

Coagulase-negative staphylococci (CNS) (n = 417) were isolated from bovine milk and identified by MALDI-TOF MS. Nineteen different species were identified, and *S. xylosus*, *S. chromogenes*, *S. haemolyticus*, and *S. sciuri* were the most abundant species. Resistance to oxacillin (47.0% of the isolates), fusidic acid (33.8%), tiamulin (31.9%), penicillin (23.3%), tetracycline (15.8%), streptomycin (9.6%), erythromycin (7.0%), sulfonamides (5%), trimethoprim (4.3%), clindamycin (3.4%), kanamycin (2.4%) and gentamicin (2.4%) was detected. Resistance to oxacillin was attributed to the *mecA* gene in 9.7% of the oxacillin-resistant isolates. The remaining oxacillin-resistant CNS did not contain the *mecC* gene or *mecA1* promoter mutations. The *mecA* gene was detected in *S. fleurettii*, *S. epidermidis, S. haemolyticus*, and *S. xylosus*. Resistance to tetracycline was attributed to the presence of *tet*(K) and *tet*(L), penicillin resistance to *blaZ*, streptomycin resistance to *str* and *ant(6)-Ia*, erythromycin resistance to *erm*(C), *erm*(B), and *msr*. Resistance to tiamulin and fusidic acid could not be attributed to an acquired resistance gene. In total, 15.1% of the CNS isolates were multidrug-resistant (i.e., exhibiting resistance to two or more antimicrobials). The remaining CNS isolates were susceptible to antimicrobials commonly used in mastitis treatment. Methicillin-resistant CNS isolates were diverse, as determined by *mecA* gene sequence analysis, staphylococcal cassette chromosome *mec* (SCC*mec*) typing, and pulsed-field gel electrophoresis (PFGE). Arginine catabolic mobile element (ACME) types 1 and 3 were detected in both methicillin-resistant and susceptible *S. epidermidis* and were associated with sequence types ST59 and ST111. Because this study revealed the presence of multidrug-resistant CNS in a heterogeneous CNS population, we recommend antibiogram analysis of CNS in persistent infections prior to treatment with antimicrobials.

2.) INTRODUCTION

Coagulase-negative staphylococci (CNS) are the microorganisms most commonly isolated from bovine milk in many countries, and they are an important cause of mastitis (Rajala-Schultz et al., 2009;Pyörälä and Taponen, 2009;Piessens et al., 2011;De Vliegher et al., 2012). CNS are opportunistic pathogens that are usually diagnosed as a group without species identifications. They cause subclinical intramammary infections that result in an increase in the somatic cell count and reduced milk quality, leading to economic losses (Pyörälä and Taponen, 2009). Because simple subclinical CNS infections can be self-limiting, they are usually not treated with antibiotics. However, CNS often appear with other major pathogens such as *Staphylococcus aureus*, *Streptococcus* species or coliform bacteria. In these cases and in persistent CNS infections, the cows undergo antimicrobial treatment. Currently, β-lactam antimicrobials (including penicillin and cephalosporins), aminoglycosides (gentamicin and neomycin), and macrolides (spiramycin) are commonly used to treat mastitis in Switzerland (Büttner et al., 2011). Resistance to these antibiotics has been increasingly reported in CNS associated with bovine mastitis (Walther and Perreten, 2007;Sawant et al., 2009;Sampimon et al., 2011). CNS may also harbor antimicrobial resistance elements and pathogenicity islands, such as the staphylococcal cassette chromosome (SCC*mec*) element (Wielders et al., 2001;Barbier et al., 2010;Tsubakishita et al., 2010) and the arginine catabolic mobile element (ACME) (Diep et al., 2006;Diep et al., 2008;Miragaia et al., 2009) that can be transferred to *S. aureus*. ACMEs are genomic islands in *S. epidermidis* that have been associated with host colonization, fitness and pathogenicity. ACME mobilitiy is associated with recombinase genes present on the SCC*mec* elements (Goering et al., 2007;Diep et al., 2008). SCC*mec* contains the *mec* genes like *mecA* and *mecC* ($mecA_{LGA251}$), which encode alternative penicillin binding proteins (PBP 2a) and confer resistance to all β-lactam antimicrobials (García-Álvarez et al., 2011;Ito et al., 2012). In *S. sciuri*, the *mecA* gene homologue *mecA1* is a native gene that is not part of the *mec* gene complex (Couto et al., 1996;Wu et al., 1998;Couto et al., 2000;Wu et al., 2001;Tsubakishita et al., 2010). Most *S. sciuri* isolates are susceptible to beta-lactam antimicrobials. However, alterations in the promoter regions of *mecA1* up-regulate *mecA1* expression and methicillin resistance (Wu et al., 2001;Couto et al., 2003;Wu et al., 2005). Methicillin-resistant staphylococci are often also resistant to other classes of drugs such as the aminoglycosides and the macrolides (Woodford 2005). Nevertheless, little is known about the molecular mechanisms of the antimicrobial resistance (Lüthje and Schwarz, 2006) or the genetic backgrounds of multidrug-resistant CNS strains in bovine milk.

We have identified the different CNS species in milk from cows with clinical and subclinical bovine mastitis, characterized their antimicrobial resistance mechanisms, and determined whether specific methicillin-resistant and multidrug-resistant CNS clones are common in dairy cows.

3.) MATERIALS AND METHODS

Origin of the milk samples

CNS (n = 417) were isolated from milk (n = 370) obtained from cows diagnosed with clinical (n = 115) and subclinical (n = 255) mastitis and control samples (n = 47) in Switzerland. Control samples were collected from cows that had suffered from mastitis previously and had been treated; the control milk samples contained < 150,000 cells/ml. The 417 isolates came from 363 different cows and from two different mammary quarters of seven cows. The 363 cows originated from 195 different farms (n_f) in the cantons of Berne (n_f = 91), Jura (n_f = 56), Fribourg (n_f = 26), Vaud (n_f = 8), Lucerne (n_f = 5), Valais (n_f = 4), Solothurn (n_f = 3), Aargau (n_f = 1) and Thurgau (n_f = 1). In 47 cases, two different CNS strains were found in the same milk sample.

Isolation and identification of CNS

Milk samples were centrifuged at 590x*g* for 10 min at room temperature. The milk pellets were cultivated on tryptone soy agar containing 5% defibrinated sheep blood (TSA-SB, Becton, Dickinson and Company, Franklin Lakes, NJ) and incubated at 37°C for 18 to 24 hours. Staphylococci were selected based on colony morphology, gram-positive staining of cocci and catalase production and were subcultured on TSA-SB.

The isolates were identified by Matrix-Assisted-Laser-Desorption/Ionization-Time-Of-Flight-Mass-Spectrometry (MALDI-TOF MS) analysis using the ethanol-formic acid extraction method for better resolution (Application Note, MT-80, Bruker) (Microflex LT, Bruker Daltonics GmbH, Bremen). Species identification was considered valid when the matching score with reference spectra of the MALDI Biotyper v3.0 database (Bruker) was ≥ 2, according to the criteria proposed by the manufacturer. Isolates whose measured spectra had score < 2.0 were further identified by DNA sequencing of the 16S rDNA (Kuhnert et al., 1996). The CNS strains were stored at -80°C in trypticase soy medium containing 30% glycerin (Becton, Dickinson and Company, Franklin Lakes, NJ).

DNA extraction and amplification

To obtain total DNA, cells were incubated in 100 µl TE buffer containing 0.1 mg/ml lysostaphin for 15 min at 37°C, and then, 450 µl lysis buffer (0.1 M Tris-HCl pH 8.5, 0.05% Tween 20, 0.24 mg/ml proteinase K) was added and incubated at 60°C for 45 min. The DNA was then denatured at 95°C for 15-min.

PCRs were performed with HOT FIREPol® DNA Polymerase (Solis BioDyne, Tartu, Estonia), and the primers and conditions are listed in Table 1.

Antimicrobial resistance tests

The CNS isolates were tested for antimicrobial susceptibility with the broth microdilution technique (Clinical and Laboratory Standards Institute 2009) using Sensititre susceptibility plates NLEUST (Trek Diagnostics Systems, East Grinstead, West Sussex; MCS diagnostics BV, JL Swalmen, The Netherlands) that contained the following 19 antimicrobials: chloramphenicol, ciprofloxacin, clindamycin, dalfopristin-quinupristin, erythromycin, fusidic acid, gentamicin, kanamycin, linezolid, mupirocin, oxacillin, penicillin, rifampicin, streptomycin, sulfamethoxazole, tetracycline, tiamulin, trimethoprim, and vancomycin. The resistance breakpoints were those proposed for CNS in the EUCAST guidelines (www.eucast.org) (Table 2). The production of β-lactamase was tested on nitrocefin dry slides (Becton, Dickinson and Company, Franklin Lakes, NJ) using colonies grown on Mueller Hinton agar for 18 h at 37°C with 0.05 µg penicillin per ml to induce β-lactamase production (Schnellmann et al., 2006). The antimicrobial resistance genes were detected by a custom-made microarray (AMR+ve-2 array tubes, Alere technologies GmbH, Jena, Germany) (Perreten et al., 2005). The microarray results were analyzed using the IconoClust program (Alere GmbH), and the data were interpreted visually.

Characterization of the *mec* genes and SCC*mec* elements

All isolates displaying a MIC for oxacillin above the resistance breakpoint (MIC > 0.25 µg/ml), which suggests the presence of an alternative PBP (CLSI, EUCAST), were additionally tested by PCR for the *mecA*, *mecA1* and *mecC* genes (García-Álvarez et al., 2011;Ito et al., 2012) using the primers listed in Table 1. The complete nucleotide sequences of the *mecA* genes were obtained by PCR amplification with the mecA-F7 and mecA-R7 primers (Table 1). Sequencing was performed on an ABI PRISM 3100 genetic analyzer (Applied Biosystems, Foster City, CA). The SCC*mec* types were determined by the Kondo method (Kondo et al., 2007).

Analysis of the *mecA1* promoter region in *S. sciuri*

S. sciuri isolates carrying a *mecA1* homologue (n = 37) were analyzed for a point mutation (Wu et al., 2001) in the promoter region by restriction analysis of PCR products amplified with primers mecAscK1-F and mecAsc-R (Table 1). The 335 bp PCR product was tested for PsiI cleavage using the manufacturer's suggested conditions (New England BioLabs, Beverly, MA). PsiI recognizes the mutated promoter sequences TATAAT but not the wild-type sequence TATATT.

Genotyping of methicillin-resistant CNS

Methicillin-resistant, *mecA*-positive CNS isolates and multiresistant, *mecA*-negative *S. epidermidis* isolates were genotyped by pulsed-field gel electrophoresis (PFGE). Analysis of SmaI-digested chromosomal DNA was performed as described previously (Schnellmann et al., 2006). Digested DNA was separated by gel electrophoresis in a contour-clamped homogenous electric field DRIII device (Bio-Rad Laboratories, Inc., Richmond, CA) with a ramped pulse time of 5 to 40 s at 6 V/cm for 21 h at 12°C. The lambda ladder PFG marker (New England BioLabs) was used as a size reference. The digital PFGE pattern images were analyzed with the BioNumerics software (Applied Maths, Kortrijk, Belgium), and the PFGE profiles were defined by the DNA banding patterns and criteria of Tenover et al. (Tenover et al., 1995).

Multilocus sequence typing (MLST)

All *S. epidermidis* isolates (n=15) were examined by multilocus sequence typing (MLST) which is based on the sequencing of internal fragments of seven housekeeping genes (Thomas et al., 2007). Allele and sequence type (ST) numbers were assigned according to the *S. epidermidis* MLST database (http://sepidermidis.mlst.net/).

Detection of *ica* and ACME

The *S. epidermidis* isolates (n=15) were tested by PCR for the biofilm operon *ica* (Gu et al., 2005) and the arginine catabolic mobile element (ACME). The presence and type of ACME was determined using the primer pairs AIPS.27 and AIPS.28 for *arcA* and AIPS.45 and AIPS.46 for *opp3* gene clusters (Diep et al., 2008).

Statistical analysis

Antimicrobial resistance phenotypes (Table 2) were compared using the Fisher's exact test. This test is useful when the sample size is small (zero in some cells), and the test evaluates the hypothesis that the 2 column percentages in a 2x2 table are equal. Statistical analysis was

performed with the statistical software NCSS 2007 (www.ncss.com). The overall level of statistical significance was set to $P < 0.05$.

4.) RESULTS

Incidence and identification of CNS

In total, 97.8% of the CNS isolates (n = 408) were clearly identified at the species level by MALDI-TOF MS analysis. The most frequent CNS species were *S. xylosus*, *S. chromogenes*, *S. sciuri*, and *S. haemolyticus* (Table 3). The remaining 2.2% were identified by 16S rDNA analysis as *S. chromogenes* (n=1), *S. saprophyticus* (n=1) or new *Staphylococcus* species (n=7) (Table 3). Neither clinical nor subclinical mastitis could be correlated with the presence of individual bacterial species. Similar species were identified in control milk samples with low somatic cell counts. Of the 417 CNS isolated, 268 isolates (64.3%) were the only species present in the milk from which they originated. Eighteen CNS isolates were co-purified with *S. aureus* (4.3%), while 83 isolates were present with *Streptococcus* species (19.9%). Altogether, 48 isolates (11.5%) were coincident in milk with at least one other bacterium (e.g., *A. pyogenes*, *E. coli*, *C. bovis* or a mix of more than 3 different bacteria).

Analysis of antimicrobial resistance phenotypes and genotypes

Oxacillin resistance, which is the indicator of *mec* gene-mediated methicillin resistance, was the most frequent resistance phenotype (47.0% of isolates), followed by resistance to fusidic acid (34.1%), tiamulin (31.9%), penicillin (23.3%), tetracycline (15.8%), streptomycin (9.6%), and erythromycin (7.0%) (Table 2). Resistance to two or more antibiotics was observed in 15.1% of the CNS isolates. Multiresistant isolates were found in milk from clinical (n = 21) and subclinical (n = 34) mastitis cases and control milk (n = 8). Oxacillin resistance was significantly more frequent in clinical mastitis isolates (56.5%) than in subclinical mastitis isolates (43.9%), whereas sulfamethoxazole resistance was significantly more frequent in clinical mastitis isolates (11.3%) than in control milk. No significant difference in resistance between isolates was observed for the other antimicrobials tested (Table 2).

Oxacillin resistance was attributed to the *mecA* gene present in 9.7% (n=19) of the oxacillin resistant isolates (n = 196). The *mecA* gene was detected in *S. fleurettii* (11/12), *S. epidermidis* (6/15), *S. haemolyticus* (1/37), and *S. xylosus* (1/155) isolates. The *mecA* or *mecC* gene was not detected in the other 177 oxacillin-resistant isolates (90.3%) (Table 4). These isolates

exhibited an oxacillin MIC of 0.5 or 1.0 µg/ml, which is just above the clinical resistance breakpoint.

All *S. sciuri* isolates (n = 37) contained the *mecA1* gene, and exhibited low-level resistance to oxacillin (MIC between 0.5 and 1.0 µg/ml). The low oxacillin resistance was due to the absence of the T-A mutation in the -10 promoter sequence (Wu et al., 2001), as demonstrated by PsiI restriction analysis.

Resistance to other antimicrobials was attributed to the beta-lactamase gene *blaZ*, the tetracycline efflux genes *tet*(L) and *tet*(K), the streptomycin adenyltransferase and nucleotidyltransferase genes *ant(6)-Ia* and *str*, the chloramphenicol acetyltransferase genes cat_{pC221} and cat_{pC223}, the gentamicin acetyltransferase gene *aac(6')-Ie*, the kanamycin-neomycin phosphotransferase genes *aph(2')-Ia* and *aph(3')-III*, the macrolide and lincosamide 23S rRNA methylase genes *erm*(B) and *erm*(C), the macrolide efflux gene *msr*, the lincosamide nucleotidyltransferase gene *lnu*(A) and the trimethoprim-resistant dihydrofolate reductase genes *dfr*(A), *dfr*(D), *dfr*(G), and *dfr*(K) (Table 4). In a few strains, resistance to erythromycin, clindamycin, streptomycin, gentamicin, chloramphenicol, and trimethoprim could not be explained by the presence of any of the tested genes, suggesting new antimicrobial resistance mechanisms in CNS (Table 4). Resistance to fusidic acid was not due to the known fusidic acid resistance genes *fus*(B), and *fus*(C) suggesting the appearance of new resistance genes or mutations in the elongation factor G *fus*(A) (Farrell et al., 2011). Similarly, no known tiamulin resistance genes (*vga* or *lsa*) were detected in the tiamulin-resistant strains. Resistance to sulfonamides was not further characterized.

Multiple combinations of these genes were found in 4.8% of the CNS isolates. The most frequent resistance genes detected in combination were those conferring resistance to oxacillin, tetracycline, penicillin, streptomycin, gentamicin, kanamycin, erythromycin and clindamycin (Table 5). The presence of several genes in one isolate was linked to the presence of *mecA* in *S. epidermidis* (n = 6), *S. sciuri* (n = 3), *S. haemolyticus* (n = 1), and *S. fleurettii* (n = 1). The other *mecA* positive isolates (*S. fleurettii* (n = 10), and *S. xylosus* (n = 1)) contained only the *mecA* gene. CNS isolates lacking *mecA*, but containing several other resistance genes were classified as *S. chromogenes* (n = 3), *S. epidermidis* (n = 3), *S. haemolyticus* (n = 1), and *S. warneri* (n = 2) (Table 5). All CNS isolates containing several resistance genes were obtained from cows presenting with subclinical or clinical mastitis (Table 5). Although one *S. xylosus* isolate contained a *mecA* gene, multidrug resistance was never observed in *S. xylosus*, the most frequently detected CNS in our study.

Genotyping of methicillin-resistant CNS

CNS strains containing the *mecA* gene (n = 19) were further analyzed for *mecA* sequences, clonality, SCC*mec* and ACME types. Two different *mecA* genes with slight sequence differences were detected in *S. epidermidis* isolates (Fig.1). Four different *mecA* genes that slightly differed from each other were found in *S. fleurettii* (Fig. 1). The *mecA* genes detected in *S. haemolyticus* and *S. xylosus* also differed slightly from each other and from those in *S. epidermidis* and *S. fleurettii* (Fig.1).

PFGE analysis of methicillin-resistant *S. epidermidis* (n=6) and *S. fleurettii* (n=11) showed that strains of the same species were not clonally related, except for four *S. fleurettii* from four different farms that showed two similar PFGE patterns (Figure 1). Methicillin-resistant *S. epidermidis* belonged to ST59 (n = 2), ST55, ST89, and the new strains ST452 and ST454, while *S. epidermidis* strains lacking the *mecA* gene (MSSE), and displaying a multidrug-resistance profile belonged to ST111 (n = 4), ST184 (n = 1), ST293 (n = 1) and to the new strain ST453 (n = 1). MSSE also showed a different PFGE profile (data not shown).

Several different SCC*mec* elements were detected among the methicillin-resistant CNS isolates (Fig. 1). *S. epidermidis* strains contained SCC*mec* IV (n = 4), SCC*mec* V (n = 1), and one non-typeable SCC*mec* related to types IV and VI. *S. haemolyticus* (n = 1) and *S. xylosus* (n = 1) both contained a non-typeable SCC*mec*. The SCC*mec* elements of *S. fleurettii* strains (n = 11) could not be assigned to a known SCC*mec* element. These SCC*mec* elements contained the known *mec* gene complex A, but lacked a known *ccr* element. The *S. haemolyticus* and the *S. xylosus* strains were not typeable (Fig. 1). Two methicillin-resistant *S. epidermidis* strains, ST59-SCC*mec* IV and ST454-SCC*mec* V, contained a type 2 and type 3 ACME, respectively. ACME type 1 was detected in four MSSE ST111 and in one MSSE ST456. None of the *S. epidermidis* isolates carried the biofilm-formation operon *ica* (Fig. 1).

5.) DISCUSSION

Many diverse CNS species have been identified in bovine milk, and MALDI-TOF MS is a reliable and rapid method to identify CNS species (Loonen et al., 2012). We observed that a short ethanol-formic acid extraction is necessary for accurate identification. CNS in milk were frequently detected as single bacterial species, suggesting that these species were the infectious agents. However, the presence of these CNS species was not correlated with a clinical mastitis diagnosis (Table 3). The most frequently occurring species in this study were *S. xylosus, S. chromogenes, S. sciuri*, and *S. haemolyticus*, as reported in other studies (Waller

et al., 2011;Piessens et al., 2011;Supré et al., 2011). Although *S. xylosus* is not known to cause mastitis, it was detected in 35.9% of the milk samples in our study and, as a single species in 22.8% of those samples, emphasizing the previous conclusions that *S. xylosus* is an underestimated pathogenic CNS in bovine mastitis (Supré et al., 2011). Additionally, two-thirds of the *S. xylosus* isolates were resistant to oxacillin but lacked a known *mec* gene. The absence of a *mecA* gene was also observed in other oxacillin-resistant CNS isolates (Table 4). For these oxacillin-resistant isolates, *mec*-independent mechanisms, which may not be related to an acquired resistance gene, explain the decreased susceptibility to oxacillin with MIC in the range of 0.5 – 2.0 µg/ml. Oxacillin resistance in *S. sciuri* may also depend on *mecA1* gene overexpression. Alterations to the promoter region of *mecA1* are necessary for high level *mecA1* expression and oxacillin resistance in *S. sciuri* (Wu et al., 2001;Couto et al., 2003;Wu et al., 2005). In our study, none of the *S. sciuri* strains contained the -10 promoter mutation that is associated with oxacillin resistance (Wu et al., 2001). However, the MICs for these isolates were between 0.5 and 1.0 µg/ml, which are values above the CLSI and the EUCAST resistance breakpoints. The clinical and therapeutic relevance of decreased susceptibility to oxacillin remains to be clarified. The oxacillin breakpoint may be set to low to properly gauge resistance in CNS from bovine mastitis cases (Fessler et al., 2010), and detection of acquired *mec* genes may be necessary for correct interpretation of the antibiogram.

The *mecA* gene was detected in *S. epidermidis*, *S. fleurettii*, *S. haemolyticus* and *S. xylosus*. Three different *mecA* genes that differ from each other by only a few base pairs were found in the methicillin-resistant *S. fleurettii* and *S. epidermidis* isolates, suggesting the independent acquisition of SCC*mec* elements in these species. This conclusion is supported by the observation that the different SCC*mec* elements were detected in individual *S. epidermidis* isolates. All but one *S. fleurettii* isolate contained a *mecA* gene associated with a non-typeable SCC*mec* element. Genetic diversity was confirmed by PFGE, which showed that with the exception of two pairs of *S. fleurettii* with similar PFGE profiles, all other methicillin-resistant CNS isolates had different PFGE profiles. Despite different PFGE profiles, *S. epidermidis* isolates belonging to the ST111 and ST59 groups were predominant in bovine mastitis cases, suggesting that a specific clonal lineage of *S. epidermidis* has adapted to the udder environment (Piessens et al., 2012). Half of the *S. epidermidis* isolates contained an ACME operon, which may be involved in host adaption in humans (Miragaia et al., 2009). ACMEs were mainly observed in the *S. epidermidis* ST 59 or ST 111 groups, suggesting that it may also play a role in host adaption in cows. Additionally, *S. epidermidis* was the predominant CNS species among those that contained multiple antimicrobial resistance genes. Multiple

resistance genes were also found in *S. sciuri*, *S. chromogenes*, *S. haemolyticus*, and *S. fleurettii*, and these genes were frequently associated with the presence of the *mecA* gene. Genes conferring resistance to clinically relevant antimicrobials such as the penicillins, macrolides, lincosamides, and aminoglycosides were also detected. In total, 15.1% of the isolates studied were resistant to more than two antimicrobials, and some strains were virtually resistant to all antimicrobials authorized for the treatment of mastitis. The remaining CNS isolates were susceptible to antimicrobials commonly used in mastitis treatment.

Our study demonstrated that CNS species in milk from cows experiencing mastitis are generally susceptible to the antimicrobials commonly used for treatment. However, CNS have the potential to acquire resistance genes, leading to therapeutic failures. Some multidrug-resistant isolates, especially *S. epidermidis*, *S. chromogenes* and *S. haemolyticus*, are present in bovine mastitis milk and may resist antimicrobial treatment. An antibiogram is therefore recommended for targeted therapy, and chronically infected cows should be culled from the herd.

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8.) TABLES AND FIGURE

Table 1. Primer list

Target genes	Primer names and oligonucleotides	Size of PCR fragment	Annealing -temp.
mecA, mecA1, mecA2	mecAu-F: 5'-AAAAGATAAATCTTGGGGTG mecAu-R: 5'-CCTTGTTTCATYTTGAGTTC	525 bp	51°C
mecA	mecA-1: 5'-AAAATCGATGGTAAAGGTTGGC mecA-2: 5'-AGTTCTGCAGTACCGGATTTGC	533 bp	54°C
*mecA*1	mecA1-sc-F: 5'-ATTAATCATCGCCATCGTGA mecA1-sc-R: 5'-TTTGTATCTTGATTCATATTTTGAACA	663 bp	52°C
mecC	mecA-LA251-F: 5'-CAGCCAGATTCATTTGTACC mecA-LA251-R: 5'-AACATCGTACGATGGGGTAC	486 bp	54°C
mecA1 Promoter	mecAscK1-F: 5'-CATATATATATTTATACGCTCATC mecAsc-R: 5'-TTCAATGGCATCAATTGTTTC	335 bp	50°C
mecA[a)] (full-length gene)	mecA-F7: 5'-GATAACACCTGCTACAC mecA-R7: 5'-AAGGGAGAAGTAACAGC	2194 bp	51°C

a) Primers annealing external to *mecA* for amplification and sequencing of the full-length gene.

Table 2. Distribution of antimicrobial resistance phenotypes in CNS

Antimicrobial substance	Abr.	Breakpoints (µg/ml)	Resistance phenotypes							
			Total (n_{total} = 417)		clinical mastitis (n_{total} = 115)		subclinical mastitis (n_{total} = 255)		control milk (n_{total} = 47)	
			No.	%	No.	%	No.	%	No.	%
Oxacillin	OXA	R > 0.25	196	47.0	65[a]	56.5	112[a]	43.9	19	40.4
Fusidic acid	FUS	R > 1.0	141	33.8	44	38.3	81	31.8	16	34.0
Tiamulin	TIA	R > 2.0	133	31.9	34	29.6	85	33.3	14	29.8
Penicillin	PEN	R > 0.125	97	23.3	26	22.6	63	24.7	8	17.0
Tetracycline	TET	R > 2.0	66	15.8	18	15.7	37	14.5	11	23.4
Streptomycin	STR	R > 16	40	9.6	9	7.8	29	11.4	2	4.3
Erythromycin	ERY	R > 2.0	29	7.0	7	6.1	18	7.1	4	8.5
Sulfamethoxazole	SMX	R > 128	21	5.0	13[b]	11.3	8	3.1	0[b]	0.0
Trimethoprim	TMP	R > 4.0	18	4.3	6	5.2	11	4.3	1	2.1
Clindamycin	CLI	R > 0.5	14	3.4	3	2.6	10	3.9	1	2.1
Chloramphenicol	CHL	R > 8.0	13	3.1	4	3.5	8	3.1	1	2.1
Gentamicin	GEN	R > 1.0	10	2.4	5	4.4	5	2.0	0	0.0
Kanamycin	KAN	R > 8.0	10	2.4	5	4.4	5	2.0	0	0.0
Quinupristin-Dalfopristin	Q–D	R > 2.0	0	0.0	0	0.0	0	0.0	0	0.0
Rifampicin	RIF	R > 0.5	0	0.0	0	0.0	0	0.0	0	0.0
Ciprofloxacin	CIP	R > 1.0	0	0.0	0	0.0	0	0.0	0	0.0
Mupirocin	MUP	R > 256	0	0.0	0	0.0	0	0.0	0	0.0

a) Denotes a significant difference (P = 0.0324) in the number of oxacillin-resistant isolates from clinical and subclinical mastitis cases, as determined by Fisher's exact test.

b) Denotes a significant difference (P=0.0208) in the number of sulfamethoxazole-resistant isolates from clinical mastitis cases and control milk, as determined by Fisher's exact test.

Table 3. Incidence of coagulase-negative staphylococci (CNS) and distribution of the different CNS strains in clinical and subclinical mastitis milk and control milk[1].

Coagulase-negative staphylococci	Total		clinical mastitis milk		subclinical mastitis milk		control milk[1]	
	No.	%	No.	%	No.	%	No.	%
Total strains	417	100.0	115	100.0	255	100.0	47	100.0
S. xylosus	150	36.0	43	37.4	95	37.2	12	25.5
S. chromogenes	70	16.8	20	17.4	40	15.7	10	21.3
S. sciuri	37	8.9	10	8.7	25	9.8	2	4.3
S. haemolyticus	35	8.4	8	6.9	23	9.0	4	8.5
S. devriesei	18	4.3	7	6.0	11	4.3	0	0.0
S. warneri	17	4.1	4	3.5	6	2.3	7	14.8
S. simulans	16	3.8	1	0.9	13	5.1	2	4.3
S. epidermidis	15	3.6	4	3.5	10	3.9	1	2.1
S. fleurettii	12	2.9	6	5.2	4	1.6	2	4.3
S. succinus	9	2.2	0	0.0	7	2.8	2	4.3
S. vitulinus	9	2.2	5	4.4	4	1.6	0	0.0
S. hyicus	6	1.4	2	1.7	4	1.6	0	0.0
S. equorum	6	1.4	1	0.9	2	0.8	3	6.3
S. saprophyticus	2	0.5	1	0.9	1	0.4	0	0.0
S. auricularis	2	0.5	1	0.9	1	0.4	0	0.0
S. capitis	2	0.5	0	0.0	2	0.8	0	0.0
S. cohnii	2	0.5	0	0.0	0	0.0	2	4.3
S. hominis	1	0.2	0	0.0	1	0.4	0	0.0
S. lentus	1	0.2	0	0.0	1	0.4	0	0.0
Staphylococcus sp.	7	1.6	2	1.7	5	1.9	0	0.0

[1] control milk; milk taken from cows after mastitis treatment.

Table 4. Distribution of antimicrobial resistance and antimicrobial resistance genes in CNS from bovine milk

Antimicrobial substances	Percentage of phenotypical resistance (%)	Resistance genes	Proportion of resistance genes in resistant isolates		Number of strains (n)
			No.	%	
Oxacillin[a]	47.0	*mecA*	19	9.7	*S. fleurettii* (11), *S. epidermidis* (6), *S. haemolyticus* (1), *S. xylosus* (1)
		mecA1	37	18.9	*S. sciuri* (37)
		unknown	140	71.4	*S. xylosus* (102), *S. chromogenes* (11), *S. vitulinus* (8), *S. succinus* (5), *S. warneri* (3), *S. cohnii* (2), *S. saprophyticus* (2), *S. devriesei* (1), *S. equorum* (1), *S. hyicus* (1), *S. lentus* (1), *S. simulans* (1), *Staphylococcus* sp. (2)
Penicillin[b]	23.3	*blaZ*	88	90.7	*S. chromogenes* (37), *S. devriesei* (11), *S. haemolyticus* (11), *S. xylosus* (9), *S. epidermidis* (9), *S. warneri* (3), *S. cohnii* (2), *S. saprophyticus* (2), *S. auricularis* (1), *S. capitis* (1), *S. fleurettii* (1), *S. hominis* (1)
		no β-lactamase[c]	8	8.3	*S. fleurettii* (8)
		unknown	1	1.0	*S. xylosus* (1)[d]
Tetracycline	15.8	*tet*(K)	62	95.4	*S. xylosus* (33), *S. warneri* (7), *S. epidermidis* (6), *S. sciuri* (4), *S. chromogenes* (3), *S. simulans* (3), *S. fleurettii* (2), *S. vitulinus* (2), *S. haemolyticus* (1), *Staphylococcus* sp. (1)
		tet(L)	3	4.6	*S. chromogenes* (3)
Streptomycin	9.6	*str*	36	90.0	*S. chromogenes* (12), *S. epidermidis* (7), *S. sciuri* (5), *S. haemolyticus* (4), *S. devriesei* (3), *S. warneri* (2), *S. simulans* (1), *S. vitulinus* (1), *S. fleurettii* (1)
		ant(6)-Ia	3	7.5	*S. epidermidis* (2), *S. haemolyticus* (1)
		unknown	1	2.5	*S. haemolyticus* (1)
Erythromycin	7.0	*erm*(B)	2	7.4	*S. chromogenes* (1), *S fleurettii* (1)
		erm(C)	11	40.8	*S. epidermidis* (6), *S. haemolyticus* (4), *S. warneri* (1)
		msr	6	22.2	*S. xylosus* (3), *S. epidermidis* (2), *S. hominis* (1)
		unknown	8	29.6	*S. equorum* (3), *S. xylosus* (1), *S. cohnii* (1), *S. fleurettii* (1), *Staphylococcus* sp. (2)
Clindamycin	3.4	*erm*(B)	2	14.3	*S. chromogenes* (1), *S. sciuri* (1)
		erm(C)	8	57.2	*S. haemolyticus* (4), *S. epidermidis* (4)
		lnu(A)	1	7.1	*S. xylosus* (1)
		unknown	3	21.4	*S. xylosus* (1), *S. fleurettii* (1), *S. lentus* (1)
Chloramphenicol	3.1	cat_{pC221}	7	53.8	*S. epidermidis* (3), *S. xylosus* (2), *S. chromogenes* (1), *S. sciuri* (1)
		cat_{pC223}	4	30.8	*S. cohnii* (1), *S. haemolyticus* (1), *S. simulans* (1), *S. xylosus* (1)
		unknown	2	15.4	*S. haemolyticus* (1), *S. simulans* (1)
Kanamycin	2.4	*aac(6')-Ie – aph(2')-Ia*	7	70.0	*S. epidermidis* (4), *S. sciuri* (1), *S. chromogenes* (1), *S. fleurettii* (1)
		aph(3')-III	3	30.0	*S. haemolyticus* (2), *S. epidermidis* (1)
Gentamicin	2.4	*aac(6')-Ie – aph(2')-Ia*	7	70.0	*S. epidermidis* (4), *S. sciuri* (1), *S. chromogenes* (1), *S. fleurettii* (1)
		unknown	3	30.0	*S. haemolyticus* (2), *S. xylosus* (1)
Trimethoprim	1.2	*dfr*(A)	1	20.0	*S. epidermidis* (1)
		dfr(D)	2	40.0	*S. sciuri* (1), *S. fleurettii* (1)
		dfr(G)	1	20.0	*S. vitulinus* (1)
		dfr(K)	1	20.0	*S. chromogenes* (1)

Legend Table 4.

Antimicrobial resistance genes and their functions:
aac(6')-Ie – aph(2')-Ia, gentamicin, kanamycin and neomycin acetyltransferase; *aph(3')-III*, kanamycin and neomycin phosphotransferase; *ant(6)-Ia*, streptomycin adenyltransferase; *blaZ*, β-lactamase; cat_{pC221} and cat_{pC223}, chloramphenicol acetyltransferases; *dfr*(A), *dfr*(D), *dfr*(G),*dfr*(K), trimethoprim-resistant dihydrofolate reductases; *erm*(B) and *erm*(C), macrolide, lincosamide and streptogramin B 23S rRNA methylase; *lnu*(A), lincosamide nucleotidyltransferase; *mecA* and *mecA1*, penicillin-binding proteins; *str*, streptomycin nucleotidyltransferase; and *tet*(K) and *tet*(L), tetracycline efflux proteins.

a) Oxacillin, indicator antimicrobial for the presence of an alternative PBP 2a encoded by *mec* genes.
b) Penicillin used for the prediction of a β-lactamase.
c) Do not produce β-lactamase, but contained *mecA*.
d) β-lactamase-positive.

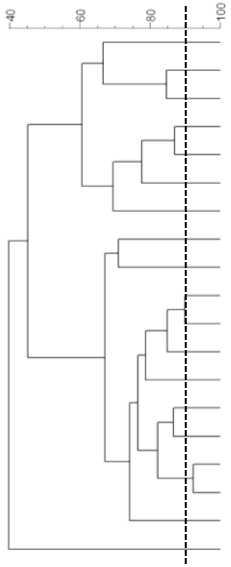
Table 5. Occurrence of multiple antimicrobial resistance genes in CNS isolated from the milk of 20 different cows suffering from bovine mastitis.

Isolate	CNS species	Mastitis	Resistances
mecA positive:			
M1529/10	*S. epidermidis*	subclinical	*erm*(C): CLI, ERY; *tet*(K): TET; *str*: STR; *blaZ*: PEN; *aac(6')-Ie – aph(2')-Ia*: GEN-KAN; *dfr*(A): TMP; *mecA:* OXA
M1186/10	*S. epidermidis*	clinical	*erm*(C): CLI, ERY; *tet*(K): TET; *ant(6)-Ia*: STR; *blaZ:* PEN; *aac(6')-Ie – aph(2')-Ia:* GEN-KAN; *mecA*: OXA
M4460/09	*S. fleurettii*	clinical	*erm*(B): CLI, ERY; *str*: STR; *blaZ*: PEN; *aac(6')-Ie – aph(2')-Ia:* GEN-KAN; *dfr*(D): TMP; *mecA:* OXA
M1570/10	*S. haemolyticus*	clinical	*erm*(C): CLI, ERY; *tet*(K): TET; *blaZ*: PEN; *aph(3')-III*: KAN; *mecA*: OXA
M744/10	*S. epidermidis*	subclinical	*str*: STR; cat_{pC221}*:* CHL; *aac(6')-Ie – aph(2')-Ia*: GEN-KAN; *erm*(C): CLI. ERY; *mecA:* OXA
M1383/10	*S. epidermidis*	subclinical	*erm*(C): CLI, ERY; *blaZ:* PEN; *aac(6')-Ie – aph(2')-Ia:* GEN-KAN; *mecA:* OXA
M1965/10	*S. sciuri*	clinical	*tet*(K): TET; *str*: STR; *aac(6')-Ie – aph(2')-Ia:* GEN-KAN; *dfr*(D): TMP; *mecA1:* OXA
M8/10	*S. epidermidis*	clinical	*ant(6)-Ia*: STR; *blaZ*: PEN; cat_{pC221}: CHL; *aph(3')-III:* KAN; *erm*(C): CLI, ERY; *mecA*: OXA
M1201/10	*S. sciuri*	subclinical	*tet*(K): TET; *str*: STR; cat_{pC221}*:* CHL; *mecA1:* OXA
M703/10	*S. epidermidis*	subclinical	*blaZ:* PEN; *msr:* ERY; *mecA*: OXA
M3901/09	*S. sciuri*	clinical	*tet*(K): TET; *str:* STR; *mecA1*: OXA
mecA negative:			
M425/10	*S. chromogenes*	subclinical	*erm*(B): CLI, ERY; *tet*(L): TET; *blaZ*: PEN; cat_{pC221}*:* CHL; *dfr*(K): TMP
M47/10	*S. chromogenes*	subclinical	*tet*(L): TET; *str*: STR; *blaZ*: PEN; *aac(6')-Ie – aph(2')-Ia:* GEN-KAN
M1256/10	*S. warneri*	subclinical	*str*: STR; *blaZ*: PEN; *erm*(C): CLI, ERY
M4233-1/09	*S. epidermidis*	subclinical	*erm*(C): CLI-ERY; *tet*(K): TET; *str*: STR
M4298-1/09	*S. epidermidis*	subclinical	*tet*(K): TET; *str:* STR; *blaZ:* PEN; cat_{pC221}*:* CHL
M46/10	*S. chromogenes*	subclinical	*tet*(K): TET; *str:* STR; *blaZ:* PEN
M523/10	*S. epidermidis*	clinical	*tet*(K): TET; *str:* STR; *blaZ:* PEN
M619-2/10	*S. haemolyticus*	subclinical	*ant(6)-Ia:* STR; *blaZ*: PEN; *aph(3')-III:* KAN
M1094-1/10	*S. warneri*	subclinical	*tet*(K): TET; *str:* STR; *blaZ*, PEN

Antimicrobial resistance genes and their functions: *aac(6')-Ie – aph(2')-Ia,* gentamicin, kanamycin and neomycin acetyltransferase; *aph(3')-III,* kanamycin phosphotransferase; *ant(6)-Ia*, streptomycin adenyltransferase; *blaZ*, β-lactamase; cat_{pC221} and cat_{pC223}, chloramphenicol acetyltransferases; *dfr*(A), *dfr*(D) and *dfr*(K), trimethoprim-resistant dihydrofolate reductases; *erm*(B) and *erm*(C), macrolide, lincosamide and streptogramin B 23S rRNA methylase; *msr*, macrolide efflux protein; *mecA* and *mecA1*, penicillin-binding proteins; *str*, streptomycin nucleotidyltransferase; and *tet*(K) and *tet*(L), tetracycline efflux proteins.

CLI, clindamycin; TET, tetracycline; STR, streptomycin; PEN, penicillin; KAN, kanamycin; GEN, gentamicin; TMP, trimethoprim; ERY, erythromycin; OXA, oxacillin; CHL, chloramphenicol

Figure 1: PFGE profile, SCCmec, ST and ACME types of 19 methicillin-resistant coagulase-negative staphylococci



Strains	Species	Anamnesis	*mecA*	Identity to *mecA* of *S. aureus* N315	SCC*mec* type	ST type	ACME type
M1570/10	*S. haemolyticus*	clinical	*mecA*[a]	99.85	NT	-	-
M1186/10	*S. epidermidis*	clinical	*mecA*[b]	99.95	IV	89	-
M1383/10	*S. epidermidis*	subclinical	*mecA*[b]	99.95	IV, VI	452	-
M1529/10	*S. epidermidis*	subclinical	*mecA*[b]	99.95	IV	59	2
M744/10	*S. epidermidis*	subclinical	*mecA*[b]	99.95	IV	59	-
M8/10	*S. epidermidis*	clinical	*mecA*[c]	99.90	IV	55	-
M703/10	*S. epidermidis*	subclinical	*mecA*[d]	99.90	V	454	3
M143/10	*S. fleurettii*	clinical	*mecA*[e]	99.80	class A[i]	-	-
M3783/09	*S. fleurettii*	subclinical	*mecA*[f]	99.70	class A[i]	-	-
M1125-2/10	*S. fleurettii*	clinical	*mecA*[e]	99.80	class A[i]	-	-
M404-1/10	*S. fleurettii*	clinical	*mecA*[e]	99.80	class A[i]	-	-
M1191-2/10	*S. fleurettii*	subclinical	*mecA*[e]	99.80	class A[i]	-	-
M1961/10	*S. fleurettii*	subclinical	*mecA*[e]	99.80	class A[i]	-	-
M205/10	*S. fleurettii*	control milk	*mecA*[g]	99.70	class A[i]	-	-
M4276-1/09	*S. fleurettii*	subclinical	*mecA*[e]	99.80	class A[i]	-	-
M277/10	*S. fleurettii*	clinical	*mecA*[e]	99.80	class A[i]	-	-
M545/10	*S. fleurettii*	clinical	*mecA*[c]	99.80	class A[i]	-	-
M4460/09	*S. fleurettii*	clinical	*mecA*[h]	98.95	class A[i]	-	-
M1545/10	*S. xylosus*	clinical	*mecA*[i]	99.85	NT	-	-

Figure 1. Genetic background and properties of methicillin-resistant coagulase-negative staphylococci (CNS) from bovine mastitis milk from Switzerland. The phylogenetic tree was constructed from pulsed-field gel electrophoresis (PFGE) patterns of 19 methicillin-resistant CNS isolates. Cluster analysis was generated by Bionumerics 6.6; Applied Maths, Kortijk, Belgium. Comparison settings: Dice, UPGMA, optimization 1.5%, position tolerance 1.5%. The dotted line indicates the cut-off value of ≥ 90% determining clonality between the isolates, according to the criteria of Tenover et al. 1995.

a) *mecA* of *S. haemolyticus* M1570/10 (EMBL Accession no HE978799)
b) *mecA* identical to *mecA* of *S. epidermidis RP26A* (EMBL Accession no CP000029.1)
c) *mecA* of *S. epidermidis* M8/10 (EMBL Accession no HE978797)
d) *mecA* of *S. epidermidis* M703/10 (EMBL Accession no HE978798)
e) *mecA* identical to *mecA* of *S. fleurettii* M143/10 (EMBL Accession no HE978795)
f) *mecA* of *S. fleurettii* M3783/09 (EMBL Accession no HE978796)
g) *mecA* of *S. fleurettii* M205/10 (EMBL Accession no HE978794)
h) *mecA* of *S. fleurettii* M4460/09 (EMBL Accession no HE861945)
i) *mecA* of *S. xylosus* M1545/10 (EMBL Accession no HE978800)
j) class A; no *ccr* gene detected

NT, not typeable.

Antibiotic resistance in coagulase–negative staphylococci from bovine mastitis

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Antibiotic resistance in coagulase–negative staphylococci from bovine mastitis

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Coagulase–negative staphylococci (CoNS) are regarded as important opportunistic mastitis pathogens in cows which may persist after therapy. The aim of the project is to investigate which CoNS strains are present in bovine mastitis milk and if methicillin-resistant CoNS play a role in bovine mastitis.

448 CoNS were isolated from milk of cows suffering from subclinical or clinical mastitis. The isolates were identified at species level using MALDI-TOF. Species with unclear identification were submitted to Vitek 2 and DNA sequence analysis of 16S rDNA and hsp60 marker. Antibiotic susceptibility was tested by broth dilution method. MICs were interpreted using resistance breakpoints from EUCAST. The antibiotic resistance genes were detected using a microarray.

The 448 CoNS isolates were identified as *S. xylosus* (39.2%), *S. chromogenes* (16.3%), *S. sciuri* (8.9%), *S. haemolyticus* (8.5%), *S. devriesi* (4.5%), *S. warneri* (4.0%), *S. simulans* (3.8%), *S. epidermidis* (3.4%) *S. fleuretti* (2.2%), *S. succinus* (2.2%), *S. vitulinus* (2.0%) and 8 other species (each <1%).The most frequent resistances were those to oxacillin (47.1%), fusidic acid (34.2%), tiamulin (33.3%), penicillin (22.8%), tetracycline (15.4%), streptomycin (9.2%), erythromycin (7.4%), kanamycin (2.5%) and gentamicin (2.5%). Resistance to oxacillin was attributed to the presence of the *mecA* gene in 32.2% of the oxacillin-resistant isolates. The mechanism of resistance for the remaining oxacillin-resistant isolates remained unknown. The *mecA* gene was detected in *S. xylosus*, *S. fleurettii*, *S. epidermidis* and *S. sciuri*. Resistance to tetracycline was attributed to *tet*(K) (96%) and *tet*(L) (4%), penicillin resistance to *blaZ* (90%) and/or *mecA* (32.2%), streptomycin resistance to *str* (90%) and *ant(6)-Ia* (10%), erythromycin resistance to *erm*(C) (36.4%), *erm*(B) (6.0%), *msr* (21.2%), *mph*(C) (18.2%) and unknown genes (12.1%), whereas resistance to tiamulin and fusidic acid could not be attributed to an acquired resistance gene.

Methicillin-resistant CoNS are present in bovine mastitis milk in Switzerland. These isolates are resistant to all beta-lactam antibiotics (including cephalosporins) which are widely used in

the treatment of mastitis. The strains were also resistant, but in a lower proportion, to other classes of drugs (macrolides, aminoglycosides) that are also used for the treatment of mastitis. Exact identification of the staphylococcus species followed by an antibiogram is recommended prior therapy.

Acknowledgements

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Antibiotic resistance in coagulase-negative staphylococci from bovine mastitis

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Introduction

Coagulase–negative staphylococci (CNS) are regarded as important opportunistic mastitis pathogens in cows which cause an increase of the somatic cell count (SCC) and light intramammary infections (IMI). After therapy CNS may persist because of the decreased susceptibility to antibiotics. The aim of the project was to investigate which CNS strains are present in bovine mastitis milk and if methicillin-resistant CNS as well as other multidrug-resistant CNS are associated with bovine mastitis.

Table 1: Antimicrobial resistance profile of CNS from bovine mastitis

Antimicrobial substances	Phenotypical Resistance[1] (%)	Resistance genes	Resistance No.	Resistance %	Number of strains
Oxacillin	47.0	*mecA*	18	9.2	*S. fleurettii* (11), *S. epidermidis* (6), *S. haemolyticus* (1)
		mecA1	37	19.0	*S. sciuri* (37)
		unknown	140	71.8	*S. xylosus* (103), *S. chromogenes* (11), *S. vitulinus* (8), *S. succinus* (5), *S. warneri* (3), *S. cohnii* (2), *S. saprophyticus* (2), *S. devriesei* (1); *S. equorum* (1), *S. hyicus* (1), *S. lentus* (1), *S. sciuri* (1); *S. simulans* (1)
Penicillin	23.3	*blaZ*	81	83.5	*S. chromogenes* (36), *S. devriesei* (11), *S. haemolyticus* (10), *S. xylosus* (9), *S. epidermidis* (4), *S. warneri* (3), *S. cohnii* (2), *S. saprophyticus* (2), *S. fleurettii* (1), *S. auricularis* (1), *S. capitis* (1), *S. hominis* (1)
		blaZ, mecA	5	5.2	*S. epidermidis* (4), *S. haemolyticus* (1)
		mecA	9	9.3	*S. fleurettii* (8), *S. sciuri* (1)
		unknown	2	2.0	*S. epidermidis* (1), *S. xylosus* (1)
Tetracycline	14.9	*tet*(K)	62	95.4	*S. xylosus* (34), *S. warneri* (7), *S. epidermidis* (6), *S. sciuri* (4), *S. chromogenes* (3), *S. simulans* (3), *S. fleurettii* (2), *S. vitulinus* (2), *S. haemolyticus* (1)
		tet(L)	3	4.6	*S. chromogenes* (3)
Streptomycin	9.6	*str*	36	90.0	*S. chromogenes* (12), *S. epidermidis* (7), *S. sciuri* (5), *S. haemolyticus* (4), *S. devriesei* (3), *S. warneri* (2), *S. simulans* (1), *S. vitulinus* (1), *S. fleurettii* (1)
		ant(6)-Ia	3	7.5	*S. epidermidis* (2), *S. haemolyticus* (1)
		unknown	1	2.5	*S. haemolyticus* (1)
Erythromycin	6.7	*erm*(B)	2	7.4	*S. chromogenes* (1), *S fleurettii* (1)
		erm(C)	11	40.8	*S. epidermidis* (6), *S. haemolyticus* (4), *S. warneri* (1)
		msr	6	22.2	*S. xylosus* (3), *S. epidermidis* (2), *S. hominis* (1)
		mph(C)	6	22.2	*S. equorum* (3), *S. xylosus* (3)
		unknown	2	7.4	*S. cohnii* (1), *S. fleurettii* (1)
Clindamycin	3.4	*erm*(B)	2	14.3	*S. chromogenes* (1), *S. sciuri* (1)
		erm(C)	8	57.1	*S. haemolyticus* (4), *S. epidermidis* (4)
		lnu(A)	1	7.1	*S. xylosus* (1)
		unknown	3	21.4	*S. xylosus* (1), *S. fleurettii* (1), *S. lentus* (1)
Chloramphenicol	3.1	cat_{pC221}	7	53.8	*S. epidermidis* (3), *S. xylosus* (2), *S. chromogenes* (1), *S. sciuri* (1)
		cat_{pC223}	4	30.8	*S. cohnii* (1), *S. haemolyticus* (1), *S. simulans* (1), *S. xylosus* (1)
		unknown	2	15.4	*S. haemolyticus* (1), *S. simulans* (1)
Kanamycin	2.4	*aac(6')-Ie–aph(2')-Ia*	7	70.0	*S. epidermidis* (4), *S. sciuri* (1), *S. chromogenes* (1), *S. fleurettii* (1)
		aph(3')-III	3	30.0	*S. haemolyticus* (2), *S. epidermidis* (1)
Gentamicin	2.4	*aac(6')-Ie–aph(2')-Ia*	7	70.0	*S. epidermidis* (4), *S. sciuri* (1), *S. chromogenes* (1), *S. fleurettii* (1)
		unknown	3	30.0	*S. haemolyticus* (2), *S. xylosus* (1)
Trimethoprim	1.4	*dfr*(A)	1	16.7	*S. epidermidis* (1)
		dfr(D)	2	33.3	*S. sciuri* (1), *S. fleurettii* (1)
		dfr(G)	1	16.7	*S. vitulinus* (1)
		dfr(K)	1	16.7	*S. chromogenes* (1)
		unknown	1	16.6	*S. xylosus* (1)

[1] MIC determining the resistance breakpoints were those from EUCAST (www.eucast.org).

Material and Methods

Sample collection: 417 CNS isolates from 363 different dairy cows in Switzerland.
Identification of the CNS: MALDI-TOF MS (Bruker), Vitek 2 (Biomérieux) and DNA sequencing analysis of 16SrDNA and *hsp60* marker.
Antibiotic susceptibility test: broth microdilution method [Sensititre susceptibility plates NLEUST (Trek diagnostics)], 19 different antimicrobial substances.
Antibiotic resistance genes detection: microarray AMR+ve-2 (Identibac, Alere Tech) and PCR.

Results I: Identification of CNS isolates

The 417 CNS isolates from bovine mastitis milk were identified as *S. xylosus* (37.2%), *S. chromogenes* (16.6%), *S. sciuri* (9.6%), *S. haemolyticus* (8.9%), *S. devriesi* (4.3%), *S. warneri* (4.1%), *S. simulans* (3.8%), *S. epidermidis* (3.6%), *S. fleuretti* (2.4%), *S. succinus* (2.2%), *S. vitulinus* (2.2%), and 8 other species (each <1%)

Fig.1: Microarray results of *S. epidermidis* strain M1186/10 from bovine mastitis

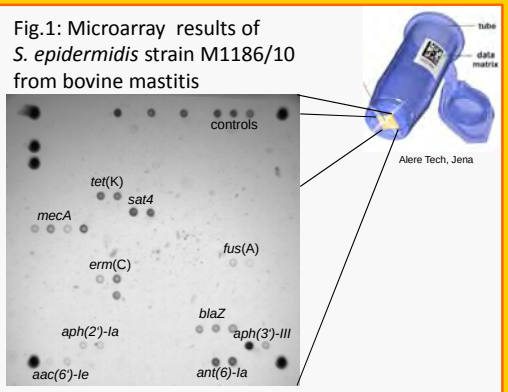

Table 2: Multiresistance profiles of CNS from bovine mastitis

Isolate	CNS species	Anamnesis	Resistances
mecA positive:			
M1529/10	*S. epidermidis*	subclinical	*erm*(C): CLI, ERY; *tet*(K): TET; *str*: STR; *blaZ*: PEN; *aac(6')-Ie–aph(2')-Ia*: GEN-KAN; *dfr*(A): TMP; *mecA*: OXA
M1186/10	*S. epidermidis*	clinical	*erm*(C): CLI, ERY; *tet*(K): TET; *ant(6)-Ia*: STR; *blaZ*: PEN; *aac(6')-Ie–aph(2')-Ia*: GEN-KAN; *mecA*: OXA
M4460/10	*S. fleurettii*	clinical	*erm*(B): CLI, ERY; *str*: STR; *blaZ*: PEN; *aac(6')-Ie–aph(2')-Ia*: GEN-KAN; *dfr*(D): TMP; *mecA*: OXA
M1570/10	*S. haemolyticus*	clinical	*erm*(C): CLI, ERY; *tet*(K): TET; *blaZ*: PEN; *aph(3')-III*: KAN; *mecA*: OXA
M744/10	*S. epidermidis*	subclinical	*str*: STR; cat_{pC221}: CHL; *aac(6')-Ie–aph(2')-Ia*: GEN-KAN; *erm*(C):ERY; *mecA*: OXA
M1383/10	*S. epidermidis*	subclinical	*erm*(C): CLI, ERY; *blaZ*: PEN; *aac(6')-Ie–aph(2')-Ia*: GEN-KAN; *mecA*: OXA
M1965/10	*S. sciuri*	clinical	*tet*(K): TET; *str*: STR; *aac(6')-Ie–aph(2')-Ia*: GEN-KAN; *dfr*(D): TMP; *mecA1*: OXA
M8/10	*S. epidermidis*	clinical	*ant(6)-Ia*: STR; cat_{pC221}: CHL; *aph(3')-III*: KAN; *erm*(C): ERY; *mecA*: OXA
M1201/10	*S. sciuri*	subclinical	*tet*(K): TET; *str*: STR; cat_{pC221}: CHL; *mecA1*: OXA
M703/10	*S. epidermidis*	subclinical	*blaZ*: PEN; *msr*: ERY; *mecA*: OXA
M3901/09	*S. sciuri*	clinical	*tet*(K): TET; *str*: STR; *mecA1*: OXA
M545/10	*S. fleurettii*	clinical	*tet*(K): TET; *mecA*: OXA, PEN
mecA negative:			
M425/10	*S. chromogenes*	subclinical	*erm*(B): CLI, ERY; *tet*(L): TET; *blaZ*: PEN; cat_{pC221}: CHL; *dfr*(K): TMP
M47/10	*S. chromogenes*	subclinical	*tet*(L): TET; *str*: STR; *blaZ*: PEN; *aac(6')-Ie–aph(2')-Ia*: GEN-KAN
M1256/10	*S. warneri*	subclinical	*str*: STR; *blaZ*: PEN; *erm*(C): ERY
M4233-1/09	*S. epidermidis*	subclinical	*erm*(C): CLI, ERY; *tet*(K): TET; *str*: STR
M4298-1/09	*S. epidermidis*	subclinical	*tet*(K): TET; *str*: STR; *blaZ*: PEN; cat_{pC221}: CHL
M46/10	*S. chromogenes*	subclinical	*tet*(K): TET; *str*: STR; *blaZ*: PEN
M523/10	*S. epidermidis*	clinical	*tet*(K): TET; *str*: STR; *blaZ*: PEN
M619-2/10	*S. haemolyticus*	subclinical	*ant(6)-Ia*: STR; *blaZ*: PEN; *aph(3')-III*: KAN
M1094-1/10	*S. warneri*	subclinical	*tet*(K): TET; *str*: STR; *blaZ*: PEN

Results II: Antimicrobial resistance in CNS

The distribution of antimicrobial resistance in CNS is shown in Table 1. 5% of the CNS exhibited resistance to three or more different antibiotics. Multiresistance was most frequently found in *S. epidermidis* strains (Table 2 and Figure 1).

Resistance to oxacillin was attributed to the presence of the *mecA* genes (*mecA*, *mecA1*) in 28.2% of the oxacillin–resistant isolates. The remaining 71.8% displayed resistance to oxacillin and did not contain *mecA*. For these isolates, the MIC of oxacillin was 0.5 µg/ml which is just above the EUCAST resistance breakpoint (> 0.25 µg/ml) (Figure 2).

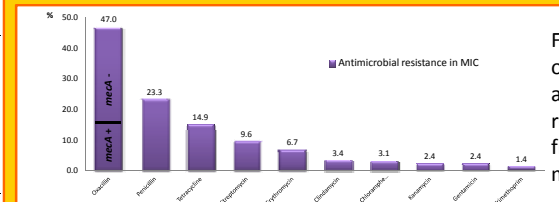

Fig. 2: Distribution of phenotypical antimicrobial resistance in CNS from bovine mastitis

Discussion and Conclusion

The clinical breakpoint of oxacillin may not be appropriate for CNS of bovine mastitis. Confirmation of the presence of *mecA* is necessary. Methicillin-resistant and multiresistant CNS are present in bovine mastitis milk in Switzerland and are resistant to antibiotics which are widely used in the treatment of mastitis. Exact identification of staphylococci and antibiogram is recommended prior therapy.

This study was financed by grant BVET 1.11.21 from the Swiss Veterinary Office.

Genetic properties of multidrug-resistant *Staphylococcus epidermidis* isolates from bovine mastitis

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Keywords: CNS, milk, methicillin-resistance, antibiotic, animal

Coagulase-negative staphylococci (CNS) have become the most commonly isolated microorganisms from bovine milk in many countries and are regarded as important mastitis pathogens. *S. epidermidis* is one of the CNS that frequently persists after antibiotic treatment. In this study, we determined whether specific multidrug-resistant *S. epidermidis* clones are associated with bovine mastitis.

The *S. epidermidis* isolates were identified using MALDI-TOF MS and genotyped by MLST. Antibiotic resistance profile was tested by broth dilution and microarray. The presence of the biofilm-formation operon *ica* and of the arginine catabolic mobile element ACME, a putative pathogenic island conferring growth and survival advantage of the bacteria in the hosts, were determined by PCR. Out of 363 cows suffering from mastitis, 13 were found to be infected with a multidrug-resistant *S. epidermidis*, including 6 methicillin-resistant *S. epidermidis* (MRSE). The MRSE displayed resistance to antibiotics like the beta-lactams (*mecA*; *blaZ*), macrolides and lincosamides [*erm*(C)], tetracycline [*tet*(K)], aminoglycosides streptomycin [*str* or *ant(6)-Ia*], and gentamicin and kanamycin [*aac(6')-Ie – aph(2)-Ia*; *aph(3)-III*], and trimethoprim [*dfr*(A)]. They belonged to CC59 (n=2), CC55, CC57, CC119, and CC291.The remaining multidrug-resistant *S. epidermidis* displayed resistance to penicillin (*blaZ*), macrolides (*msr*), macrolides and lincosamides [*erm*(C)], tetracycline [*tet*(K)], and streptomycin (*str*) and belonged to CC111 (n=4), CC184, CC57, and CC5. None of the isolates contained the *ica* operon. The presence of the ACME operon was mainly associated to CC111 in methicillin-susceptible, but multidrug-resistant *S. epidermidis*, and to CC59 and CC119 in MRSE.

The use of antibiotics in dairy farms has likely selected for multidrug-resistant *S. epidermidis*. The isolates are resistant to antibiotics which are widely used in the treatment of mastitis. They belonged to specific clonal lineages, with CC111 being the most common. The presence of the ACME in *S. epidermidis* may favor colonization of bovine udder and contribute to the spread of multidrug-resistant *S. epidermidis* in dairy cows.

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Introduction

Coagulase-negative staphylococci (CNS) have become the most commonly isolated microorganisms from bovine milk in many countries and are regarded as important mastitis pathogens. *S. epidermidis* is one of the CNS that frequently persists after antimicrobial treatment. In this study, we determined whether specific multidrug-resistant *S. epidermidis* clones are associated with bovine mastitis.

Material and Methods

The *S. epidermidis* isolates were identified using MALDI-TOF MS and genotyped by PFGE and MLST. Antibiotic resistance profile was tested by broth dilution method and microarray. The presence of the biofilm-formation operon *ica* and of the arginine catabolic mobile element (ACME), a putative pathogenic island conferring growth and survival advantage of the bacteria in the hosts, were determined by PCR.

Results

Out of 363 cows suffering from mastitis, 13 were found to be infected with a multidrug-resistant *S. epidermidis* strain, including 6 methicillin-resistant *S. epidermidis* (MRSE) strains.

Antimicrobial resistance genes: The MRSE (n = 6) displayed resistance to antibiotics like the beta-lactams (*mecA*; *blaZ*), the macrolides and the lincosamides [*erm*(C)], tetracycline [*tet*(K)], the aminoglycosides like streptomycin [*str* or *ant(6)-Ia*], gentamicin and kanamycin [*aac(6')-Ie – aph(2)-Ia*; *aph(3)-III*], and trimethoprim [*dfr*(A)]. The remaining multidrug-resistant *S. epidermidis* isolates displayed resistance to penicillin (*blaZ*), macrolides (*msr*), macrolides and lincosamides [*erm*(C)], tetracycline [*tet*(K)], and streptomycin (*str*) (Table 1).

Genotyping of methicillin-resistant isolates: Two different *mecA* genes whose sequences differed slightly from each other were detected in *S. epidermidis* isolates (Fig.1). MRSE contained SCC*mec* type IV (n=4), type V (n=1) and one non-typeable SCC*mec* related to type IV and VI (Fig.1).

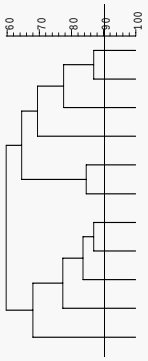
Clonality: MRSE belonged to ST59 (n = 2), ST55, ST89, and to two new ST types (ST452 and ST454), whereas MSSE belonged to ST111 (n=4), ST184, ST293, and a new ST. PFGE analysis of the *S. epidermidis* (n = 11) isolates showed that the strains of were not clonally related. However, MRSE and MSSE clustered in two different PFGE branches (Fig. 1).

ACME and *ica* operons: The presence of the ACME operons was mainly associated to ST111 in methicillin-susceptible, but multidrug-resistant *S. epidermidis* isolates, and to ST59 and ST454 in MRSE. None of the *S. epidermidis* isolates contained the biofilm-formation operon *ica* (Fig.1).

Table 1: Antimicrobial resistance in *S. epidermidis* strains from clinical and subclinical mastitis

Strains	Mastitis	Resistances
M1529/10	subclinical	*erm*(C): CLI, ERY; *tet*(K): TET; *str*: STR; *blaZ*: PEN; *aac(6')-Ie – aph(2')-Ia*: GEN-KAN; *dfr*(A): TMP; *mecA:* OXA
M1186/10	clinical	*erm*(C): CLI, ERY; *tet*(K): TET; *ant(6)-Ia*: STR; *blaZ*: PEN; *aac(6')-Ie – aph(2')-Ia:* GEN-KAN; *mecA*: OXA
M744/10	subclinical	*str*: STR; cat_{pC221}: CHL; *aac(6')-Ie – aph(2')-Ia*: GEN-KAN; *erm*(C): CLI. ERY; *mecA:* OXA
M1383/10	subclinical	*erm*(C): CLI, ERY; *blaZ*: PEN; *aac(6')-Ie – aph(2')-Ia:* GEN-KAN; *mecA:* OXA
M8/10	clinical	*ant(6)-Ia*: STR; *blaZ*: PEN; cat_{pC221}: CHL; *aph(3')-III:* KAN; *erm*(C): CLI, ERY; *mecA*: OXA
M703/10	subclinical	*blaZ:* PEN; *msr:* ERY; *mecA*: OXA
M4298-1/09	subclinical	*tet*(K): TET; *str:* STR; *blaZ:* PEN; cat_{pC221}: CHL
M4233-1/09	subclinical	*erm*(C): CLI-ERY; *tet*(K): TET; *str*: STR
M523/10	clinical	*tet*(K): TET; *str:* STR; *blaZ:* PEN
M864/10	subclinical	*blaZ:* PEN; *tet*(K): TET
M1725/10	clinical	*str*: STR; *msr:* ERY
M1662/10	clinical	*blaZ:* PEN
M1977/10	subclinical	*str*: STR

Figure 1. PFGE, SCC*mec* types, ST types, and ACME types of 13 *S. epidermidis* isolates



Strain	*mecA* PCR	Identity to *mecA* of *S. epidermidis* RP62A: %	Identity to *mecA* of *S. epidermidis* RP62A: variable bp	Identity to *mecA* of *S. aureus* N315: %	Identity to *mecA* of *S. aureus* N315: variable bp	SCC*mec* type	ST type	ACME type	*ica* PCR
M1529/10	*mecA*-positive	100.00	-	99.95	75	Typ IV	ST 59	type 2	-
M744/10	*mecA*-positive	100.00	-	99.95	75	Typ IV	ST 59	-	-
M8/10	*mecA*-positive	99.95	737	99.90	75, 737	Typ IV	ST 55	-	-
M703/10	*mecA*-positive	99.95	675	99.90	75, 675	Typ V	ST 454	type 3	-
M1186/10	*mecA*-positive	100.00	-	99.95	75	Typ IV	ST 89	-	-
M1383/10	*mecA*-positive	100.00	-	99.95	75	Typ IV &VI	ST 452	-	-
M1662/10	*mecA*-negative					NT	ST 111	type 1	-
M523/10	*mecA*-negative					NT	ST 111	type 1	-
M4298-1/09	*mecA*-negative					NT	ST 111	type 1	-
M1977/10	*mecA*-negative					NT	ST 111	type 1	-
M4233-1/09	*mecA*-negative					NT	new ST	type 1	-
No current PFGE result									
M864/10	*mecA*-negative					NT	ST 184	-	-
No current PFGE result									
M1725/10	*mecA*-negative					NT	ST 111	-	-

Discussion & Conclusion

The use of antibiotics in dairy farms has likely selected for multidrug-resistant *S. epidermidis*. The isolates are resistant to antibiotics which are widely used in the treatment of mastitis. They belonged to specific sequence types, with ST111 being the most common. The presence of the ACME in *S. epidermidis* may favor colonization of bovine udder and contribute to the spread of multidrug-resistant *S. epidermidis* in dairy cows.

This study was supported by Grant No.1.11.21 of the Swiss Federal Veterinary Office (BVET).

Antibiotic resistance in coagulase-negative staphylococci from bovine mastitis

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Oral presentation held at the workshop “Bovine mastitis research in Switzerland” of the VPH institute of the Vetsuisse-Faculty Bern, in Bern; 16 March 2012

Antibiotic resistance in coagulase-negative staphylococci from bovine mastitis

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Vetsuisse Faculty, University of Bern

Introduction and origin of the milk samples

- CNS = coagulase-negative staphylococci
  Cocci, Gram – positive; Coagulase – negative
- CNS were isolated from milk which was sent to the IVB for diagnostic in 2009 & 2010
  - dairy milk cows
  - cantons: BE, JU, FR, VD and LU
- CNS were isolated from:
  - clinical mastitis (n=121)
  - subclinical mastitis (n = 276)

Identification of CNS

- Identification of the isolates using MALDI TOF
  - Mass spectrometer (Matrix-Assisted-Laser-Desorption/Ionization–Time-Of-Flight-Mass-Spectrometry)
  - Mass analysis of ribosomal proteins (< 1min for species identification)
- MALDI TOF results were validated with 16S rDNA sequences.

Incidence of CNS…

… in clinical mastitis (n= 121)		… in subclinical mastitis (n=276)	
— *S. xylosus*	42.2 %	— *S. xylosus*	39.9 %
— *S. chromogenes*	15.7 %	— *S. chromogenes*	15.9 %
— *S. sciuri*	9.9 %	— *S. haemolyticus*	9.4 %
— *S. haemolyticus*	6.6 %	— *S. sciuri*	9.1 %
— *S. devriesi*	5.8 %	— *S. simulans*	5.1%
— *S. vitulinus*	4.1%	— *S. devriesi*	4.7%
— *S. warneri*	3.3 %	— *S. epidermidis*	3.6 %
— *S. epidermidis*	3.3 %	— *S. succinus*	2.9 %
— *S. fleuretti*	3.3 %	— *S. warneri*	2.2%
— others	each < 1.0 %	— *S. fleuretti*	1.8 %
		— others	each < 1.5 %

Antimicrobial resistance testing

- Determination of the phenotypical antibiotic resistance
  - Micro dilution in Mueller Hinton Bouillon
  - Sensititre susceptibilitiy plates with 19 different antibiotics
  - Resistance breakpoints → EUCAST guidelines (www.eucast.org)

- Determination of the antibiotic resistance genes
  - Microarray

Phenotypical antimicrobial resistance in CNS

- Resistance in %

	ERY	CLI	TET	STR	GEN	KAN	FUS	SMX	TMP	OXA	PEN
CNS from clinical mastitis (n=121)	5.8	3.3	16.5	9.1	5.8	5.0	39.7	11.6	5.0	58.7	21.5
CNS from subclinical mastitis (n=276)	6.8	4.3	13.3	10.8	1.8	2.2	62.1	2.9	4.3	43.0	24.4

indicator for methicillin-resistance
→ Confirmation by detection of *mecA*

Methicillin-resistant CNS

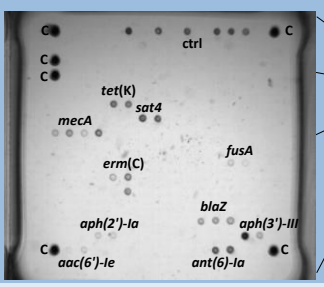
- Confirmation by micro array and PCR:
  → 32.2% (n=64) of the oxacillin-resistant CNS carried a *mecA*.
- In total, 15% of CNS contained the *mecA* gene.

mecA gene → resistance to all β-lactam-antibiotics and combinations of ß-lactam/ß-lactamase inhibitors

Methicillin-resistant staphylococci often are resistant to several other antibiotics.

Detection of AB – resistance genes

- Antibiotic-resistance genes of *S. epidermidis* (M1186/10) from clinical mastitis



Clondiag technologies, Jena

Antibiotic Resistances of the *S. epidermidis* isolate M1186/10

Beta-Lactams:	Resistance genes:
- Amoxicillin/clavulanic acid	*mecA*
- Cephalosporins	*mecA*
- Oxacillin	*mecA*
- Penicillin	*blaZ*
Macrolides (e.g. Spiramycin)	*erm*(C)
Lincosamides (e.g. Clindamycin)	*erm*(C)
Tetracyclines	*tetK*
Aminoglycosides:	
- Gentamicin/Kanamycin	*aac(6')-Ie – aph(2')-Ia*
- Kanamycin/Neomycin	*aph(3')-III*
- Streptomycin	*ant(6)-Ia*

Mulitresistance in methicillin-resistant CNS

- Methicillin-resistant CNS from bovine mastitis showed additional resistances to:

— Tetracycline	19.1%
— Streptomycin	14.7%
— Erythromycin	8.8%
— Clindamycin	8.8%
— Gentamicin/Kanamycin	8.8%
— Penicillin	7.4%
— Kanamycin/Neomycin	5.9%
— Trimethoprim	4.4%

6% of all tested CNS were multiresistant!

The most frequently occurring strains were *S. epidermidis* and *S. sciuri*.

Summary

- The most common CNS – species in mastitis milk were: *S. xylosus*, *S. chromogenes*, *S. sciuri* and *S. haemolyticus* as identified by using rapid identification tool (MALDI TOF).
- 15% of the isolates carried a *mecA* gene, some of them were resistant to other classes of drugs.
- No significant differences were observed between resistances in CNS from subclinical and clinical mastitis.
- Mulitresistant CNS are present in bovine mastitis; some CNS isolates have resistance genes making them resistant to frequently used antibiotic in bovine mastitis treatment.
- Antibiogram is recommended for targeted antimicrobial treatment.

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- Andreas Thomann
- Sybille Schwendener
- Juliette Wipf
- Alexandra Collaud

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APPENDIX

Strains used in this thesis

name, storage number, species, anamnesis, antibiotic resistance profiles and dedected antibiotic resistance genes

115 isolates from clinical mastitis

Name	Storage number	Species	Anamnesis	Break-points µg/ml	MIC = minimal inhibitory concentration in µg/ml																	Resistance genes
					CLI	TET	RIF	STR	FUS	PEN	CHL	KAN	TIA	SYN	VAN	GEN	TMP	ERY	CIP	OXA	LZD	MUP	SMX	
					> 0.5	> 2.0	> 0.5	> 16	> 1.0	> 0.125	> 8.0	> 8.0	> 2.0	> 2.0	> 2.0	> 1.0	> 4.0	> 2.0	> 1.0	> 0.25	> 4.0	> 256	> 128	
M8/10	2|3|35	*S. epidermidis*	clinical		<=0.12	1	<=0.016	>32	<=0.5	>2	64	>64	<=0.5	<=0.5	<=1	<=1	<=2	>8	<=0.25	4	<=1	<=0.5	256	*ant(6)-Ia* ; *cat* $_{pc221}$; *aph(3')-III*; *erm* (C); *mecA*
M36/10	2|3|42	*S. xylosus*	clinical		<=0.12	<=0.5	0.03	<=4	1	<=0.12	8	<=4	<=0.5	1	2	<=1	<=2	<=0.25	0.5	0.5	2	<=0.5	<=64	n.r.
M39-1/10	2|3|43	*S. devriesei*	clinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	0.25	<=4	<=4	<=0.5	<=0.5	<=1	<=1	8	<=0.25	<=0.25	<=0.25	2	1	<=64	*blaZ*
M39-2/10	2|3|44	*S. xylosus*	clinical		<=0.12	<=0.5	0.03	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	2	<=1	<=2	<=0.25	<=0.25	0.5	<=1	<=0.5	<=64	n.r.
M50/10	2|3|47	*S. vitulinus*	clinical		<=0.12	>16	<=0.016	<=4	1	<=0.12	<=4	<=4	2	<=0.5	<=1	<=1	4	<=0.25	0.5	0.5	2	<=0.5	<=64	*mecA1; tet* (K)
M65-2/10	2|3|48	*S. vitulinus*	clinical		0.25	<=0.5	<=0.016	<=4	2	<=0.12	8	<=4	>4	<=0.5	<=1	<=1	8	<=0.25	0.5	0.5	2	<=0.5	<=64	n.r.
M143/10	2|3|69	*S. fleurettii*	clinical		0.5	<=0.5	<=0.016	<=4	1	0.25	<=4	<=4	>4	1	<=1	<=1	<=2	<=0.25	0.5	4	2	2	<=64	*mecA*
M150/10	2|3|71	*S. chromogenes*	clinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	1	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	*blaZ*
M269/10	2|4|25	*S. chromogenes*	clinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	8	<=4	<=0.5	<=0.5	2	<=1	<=2	0.5	<=0.25	<=0.25	2	<=0.5	<=64	n.r.
M277/10	2|4|27	*S. fleurettii*	clinical		<=0.12	<=0.5	<=0.016	<=4	2	0.5	8	<=4	>4	1	<=1	<=1	<=2	<=0.25	0.5	>8	2	<=0.5	<=64	*mecA*
M324/10	2|4|35	*S. xylosus*	clinical		<=0.12	<=0.5	0.03	<=4	2	<=0.12	8	<=4	1	1	2	<=1	<=2	0.5	0.5	0.5	2	<=0.5	<=64	n.r.
M341/10	2|4|36	*S. chromogenes*	clinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	8	<=4	1	<=0.5	2	<=1	<=2	<=0.25	<=0.25	<=0.25	2	<=0.5	<=64	n.r.
M344/10	2|4|37	*S. xylosus*	clinical		0.25	<=0.5	<=0.016	8	4	<=0.12	8	<=4	1	1	<=1	<=1	<=2	0.5	<=0.25	0.5	2	<=0.5	<=64	n.r.
M346/10	2|4|38	*S. devriesei*	clinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	4	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M347/10	2|4|39	*S. xylosus*	clinical		0.25	<=0.5	0.03	<=4	1	<=0.12	8	<=4	1	1	2	<=1	<=2	0.5	<=0.25	0.5	2	<=0.5	<=64	n.r.
M348/10	2|4|40	*S. xylosus*	clinical		0.25	<=0.5	<=0.016	<=4	2	<=0.12	<=4	<=4	>4	2	2	<=1	<=2	<=0.25	0.5	0.5	<=1	<=0.5	<=64	n.r.
M361/10	2|4|44	*S. xylosus*	clinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	>4	1	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M404-1/10	2|4|56	*S. fleurettii*	clinical		<=0.12	<=0.5	<=0.016	<=4	4	<=0.12	<=4	<=4	2	<=0.5	<=1	<=1	<=2	<=0.25	0.5	2	<=1	<=0.5	<=64	*mecA*
M441/10	2|4|67	*S. xylosus*	clinical		<=0.12	<=0.5	0.06	8	1	<=0.12	<=4	<=4	>4	1	<=1	<=1	<=2	0.5	<=0.25	0.5	<=1	<=0.5	<=64	n.r.
M545/10	3|2|8	*S. fleurettii*	clinical		0.25	>16	<=0.016	<=4	4	0.25	<=4	<=4	>4	1	<=1	<=1	<=2	<=0.25	0.5	2	<=1	<=0.5	<=64	*mecA* ; *tet* (K)
M549-1/10	3|2|9	*S. vitulinus*	clinical		<=0.12	>16	<=0.016	>32	<=0.5	<=0.12	<=4	<=4	1	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	0.5	2	<=0.5	<=64	*str* ; *tet* (K)
M549-2/10	3|2|10	*S. chromogenes*	clinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	1	8	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	256	*blaZ*
M573/10	3|2|20	*S. devriesei*	clinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	4	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M645/10	3|2|45	*S. xylosus*	clinical		<=0.12	>16	<=0.016	<=4	2	<=0.12	<=4	<=4	<=0.5	1	2	<=1	<=2	<=0.25	0.5	0.5	<=1	<=0.5	<=64	*tet* (K)
M683/10	3|2|57	*S. equorum*	clinical		0.25	<=0.5	<=0.016	8	<=0.5	<=0.12	8	<=4	2	<=0.5	2	<=1	<=2	1	<=0.25	<=0.25	2	<=0.5	<=64	n.r.
M711-1/10	3|2|61	*S. hyicus*	clinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M711-2/10	3|2|68	*S. chromogenes*	clinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	2	8	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	*blaZ*
M799/10	3|3|6	*S. xylosus*	clinical		0.25	<=0.5	<=0.016	<=4	2	<=0.12	<=4	<=4	>4	2	2	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M800/10	3|3|7	*S. xylosus*	clinical		<=0.12	<=0.5	<=0.016	<=4	1	<=0.12	<=4	<=4	<=0.5	1	2	<=1	4	<=0.25	<=0.25	0.5	<=1	<=0.5	<=64	n.r.
M811/10	3|3|13	*S. xylosus*	clinical		<=0.12	<=0.5	<=0.016	<=4	2	<=0.12	<=4	<=4	<=0.5	1	2	<=1	<=2	0.5	0.5	0.5	<=1	<=0.5	<=64	n.r.
M874/10	3|3|33	*S. haemolyticus*	clinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M886/10	3|3|39	*S. xylosus*	clinical		<=0.12	<=0.5	0.03	16	2	<=0.12	<=4	<=4	<=0.5	<=0.5	2	<=1	<=2	<=0.25	0.5	<=0.25	<=1	<=0.5	<=64	n.r.
M1067/ 10	3|3|78	*S. warneri*	clinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	0.5	<=1	<=0.5	<=64	n.r.
M1082/ 10	3|4|11	*S. xylosus*	clinical		<=0.12	<=0.5	0.03	<=4	2	<=0.12	<=4	<=4	<=0.5	1	2	<=1	<=2	0.5	0.5	0.5	<=1	<=0.5	<=64	n.r.
M1125-1/ 10	3|4|24	*S. haemolyticus*	clinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	4	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M1125-2/10	3|4|25	*S. fleurettii*	clinical		<=0.12	<=0.5	<=0.016	8	4	0.25	<=4	<=4	4	<=0.5	<=1	<=1	<=2	<=0.25	0.5	4	2	<=0.5	<=64	*mecA*
M1186/10	3|4|44	*S. epidermidis*	clinical		>4	>16	<=0.016	>32	<=0.5	>2	<=4	>64	<=0.5	<=0.5	<=1	16	<=2	>8	<=0.25	>8	<=1	<=0.5	>512	*ant(6)-Ia* ; *aac(6')-Ie* ; *aph(2')-Ia* ; *aph(3')-III* ; *blaZ*; *erm* (C); *mecA* ; *tet* (K)
M1215/10	3|4|57	*S. sciuri*	clinical		0.5	<=0.5	<=0.016	<=4	4	<=0.12	<=4	<=4	>4	2	<=1	<=1	4	<=0.25	0.5	1	2	2	<=64	*mecA1*
M1262/10	3|4|67	*S. xylosus*	clinical		<=0.12	>16	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	4	1	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	*tet* (K)
M1296/10	3|4|76	*S. xylosus*	clinical		<=0.12	<=0.5	0.03	<=4	1	<=0.12	<=4	<=4	<=0.5	<=0.5	2	<=1	<=2	<=0.25	<=0.25	1	<=1	<=0.5	<=64	n.r.
M1349/10	4|2|7	*S. warneri*	clinical		<=0.12	>16	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	*tet* (K)
M1365-2/10	4|2|35	*S. chromogenes*	clinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	128	n.r.
M1416-1/10	4|2|61	*S. xylosus*	clinical		<=0.12	<=0.5	<=0.016	<=4	2	<=0.12	64	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	*cat* $_{pC221}$
M1475/10	4|3|14	*S. xylosus*	clinical		0.25	<=0.5	0.03	<=4	2	<=0.12	<=4	<=4	>4	1	2	<=1	<=2	<=0.25	<=0.25	0.5	<=1	<=0.5	<=64	n.r.
M1506/10	4|3|20	*S. sciuri*	clinical		0.5	<=0.5	<=0.016	<=4	4	<=0.12	<=4	<=4	>4	2	<=1	<=1	4	<=0.25	1	1	2	2	<=64	*mecA1*
M1508/10	4|3|21	*S. hyicus*	clinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	8	<=4	1	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	0.5	2	<=0.5	<=64	n.r.
M1541-3/10	4|3|39	*S. xylosus*	clinical		0.25	<=0.5	0.06	<=4	1	<=0.12	<=4	<=4	>4	2	2	<=1	<=2	<=0.25	<=0.25	0.5	<=1	<=0.5	<=64	n.r.
M1542-1/10	4|3|34	*S. chromogenes*	clinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	8	<=4	1	<=0.5	<=1	<=1	<=2	0.5	<=0.25	<=0.25	4	<=0.5	<=64	n.r.
M1542-2/10	4|3|35	*S. sciuri*	clinical		0.5	>16	<=0.016	<=4	4	<=0.12	<=4	<=4	>4	2	<=1	<=1	<=2	<=0.25	0.5	1	2	2	<=64	*mecA1* ; *tet* (K)
M1544/10	4|3|40	*S. haemolyticus*	clinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M1545/10	4|3|41	*S. xylosus*	clinical		0.25	>16	0.03	<=4	<=0.5	<=0.12	8	<=4	>4	2	<=1	<=1	<=2	0.5	<=0.25	0.5	2	<=0.5	<=64	*mecA* ; *tet* (K)
M1547/10	4|3|43	*S. devriesei*	clinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	0.25	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	*blaZ*
M1555/10	4|3|45	*S. warneri*	clinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	1	2	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M1570/10	4|3|46	*S. haemolyticus*	clinical		>4	>16	<=0.016	>32	<=0.5	>2	>64	>64	<=0.5	<=0.5	2	>16	<=2	>8	<=0.25	>8	<=1	<=0.5	>512	*aph(3')-III* ; *blaZ*; *erm* (C); *mph* (C); *mecA* ; *tet* (K)

Name	Storage number	Species	Anamnesis	Break-points µg/ml	MIC = minimal inhibitory concentration in µg/ml																	Resistance genes
					CLI > 0.5	TET > 2.0	RIF > 0.5	STR > 16	FUS > 1.0	PEN > 0.125	CHL > 8.0	KAN > 8.0	TIA > 2.0	SYN > 2.0	VAN > 2.0	GEN > 1.0	TMP > 4.0	ERY > 2.0	CIP > 1.0	OXA > 0.25	LZD > 4.0	MUP > 256	SMX > 128	
M1571/10	4|3|47	*S. xylosus*	clinical		0.25	<=0.5	0.03	<=4	2	<=0.12	8	<=4	1	1	2	<=1	<=2	0.5	<=0.25	0.5	2	<=0.5	<=64	n.r.
M1595-1/10	4|3|58	*S. sciuri*	clinical		<=0.12	<=0.5	<=0.016	<=4	4	<=0.12	<=4	<=4	>4	2	<=1	<=1	<=2	<=0.25	1	1	2	<=0.5	<=64	*mecA1*
M1595-2/10	4|3|59	*S. xylosus*	clinical		<=0.12	<=0.5	<=0.016	<=4	4	<=0.12	<=4	<=4	<=0.5	1	<=1	<=1	<=2	<=0.25	<=0.25	0.5	<=1	<=0.5	<=64	n.r.
M1618/10	4|3|69	*S. xylosus*	clinical		0.5	1	<=0.016	<=4	2	0.25	8	<=4	>4	2	2	<=1	<=2	0.5	0.5	0.5	2	1	<=64	*blaZ*
M1658-1/10	4|3|72	*S. chromogenes*	clinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	1	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	*blaZ*
M1658-2/10	4|3|73	*S. xylosus*	clinical		<=0.12	>16	<=0.016	<=4	1	<=0.12	<=4	<=4	1	1	2	<=1	8	<=0.25	<=0.25	0.5	<=1	<=0.5	<=64	*tet* (K)
M1662/10	4|4|1	*S. epidermidis*	clinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	0.25	<=4	<=4	<=0.5	<=0.5	2	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	*blaZ* ; *dfr* (A)
M1691-1/10	4|4|31	*S. haemolyticus*	clinical		<=0.12	<=0.5	<=0.016	16	<=0.5	0.25	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	*blaZ*
M1725/10	4|4|39	*S. epidermidis*	clinical		<=0.12	2	<=0.016	>32	>4	<=0.12	<=4	<=4	<=0.5	<=0.5	2	<=1	<=2	>8	<=0.25	<=0.25	<=1	<=0.5	512	*msr* ; *str*
M1736/10	4|4|42	*S. auricularis*	clinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	4	<=0.25	<=0.25	<=0.25	<=1	<=0.5	128	n.r.
M1863/10	5|2|9	*S. xylosus*	clinical		0.25	<=0.5	0.06	<=4	1	<=0.12	8	<=4	>4	1	2	<=1	<=2	0.5	0.5	0.5	2	<=0.5	<=64	n.r.
M1905/10	5|2|24	*S. devriesei*	clinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M1915/10	5|2|27	*S. chromogenes*	clinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	1	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	*blaZ*
M1956/10	5|2|41	*S. devriesei*	clinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	4	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M1965/10	5|2|49	*S. sciuri*	clinical		<=0.12	>16	<=0.016	32	4	<=0.12	<=4	>64	>4	2	<=1	16	>32	<=0.25	0.5	0.5	<=1	1	<=64	*aac(6')-Ie* ; *aph(2')-Ia* ; *dfr* (D); *mecA1* ; *str* ; *tet* (K)
M1972/10	5|2|51	*S. chromogenes*	clinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	>2	8	<=4	<=0.5	<=0.5	<=1	<=1	<=2	0.5	<=0.25	0.5	2	<=0.5	<=64	*blaZ*
M1990/10	5|2|57	*S. chromogenes*	clinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M1997-2/10	5|2|59	*S. xylosus*	clinical		<=0.12	<=0.5	<=0.016	<=4	1	<=0.12	64	<=4	<=0.5	<=0.5	2	<=1	4	<=0.25	<=0.25	0.5	<=1	<=0.5	<=64	cat_{pC223}
M2122/10	5|3|26	*S. warneri*	clinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	4	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M2165/10	5|3|45	*S. chromogenes*	clinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	8	<=4	<=0.5	<=0.5	2	<=1	<=2	<=0.25	<=0.25	<=0.25	2	<=0.5	256	n.r.
M2169/10	5|3|49	*S. chromogenes*	clinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M2174/10	5|3|51	*S. xylosus*	clinical		<=0.12	<=0.5	0.03	<=4	2	<=0.12	<=4	<=4	<=0.5	<=0.5	2	<=1	<=2	>8	<=0.25	0.5	<=1	<=0.5	<=64	msr; *mph* (C)
M2200/10	5|3|64	*S. xylosus*	clinical		<=0.12	<=0.5	0.03	<=4	2	<=0.12	<=4	<=4	<=0.5	1	2	<=1	<=2	<=0.25	0.5	0.5	<=1	<=0.5	<=64	n.r.
M2220/10	5|3|70	*S. chromogenes*	clinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	8	<=4	1	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	4	2	<=64	n.r.
M2307/10	5|4|20	*S. chromogenes*	clinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	8	<=4	<=0.5	<=0.5	2	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	256	n.r.
M2395/10	5|4|61	*S. xylosus*	clinical		0.25	>16	0.12	<=4	2	<=0.12	8	<=4	>4	1	2	<=1	<=2	0.5	<=0.25	0.5	2	<=0.5	<=64	*tet* (K)
M3574/09	1|2|11	*S. chromogenes*	clinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	512	n.r.
M3592/09	1|2|18	*S. xylosus*	clinical		<=0.12	<=0.5	<=0.016	<=4	4	<=0.12	8	<=4	1	<=0.5	2	<=1	<=2	1	<=0.25	0.5	2	<=0.5	512	n.r.
M3636/09	1|2|40	*S. xylosus*	clinical		<=0.12	<=0.5	<=0.016	<=4	1	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	0.5	<=1	<=0.5	<=64	n.r.
M3665/09	1|2|51	*S. haemolyticus*	clinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	2	<=1	<=2	<=0.25	0.5	<=0.25	<=1	<=0.5	>512	n.r.
M3668-1/09	1|2|52	*S. haemolyticus*	clinical		<=0.12	<=0.5	<=0.016	>32	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	*str*
M3668-2/09	1|2|53	*Staph. sp.*	clinical		<=0.12	<=0.5	<=0.016	16	2	<0.12	<=4	<=4	1	<=0.5	<=1	<=1	<=2	0.5	<=0.25	0.5	<=1	<=0.5	<=64	n.r.
M3709-2/09	1|2|75	*S. haemolyticus*	clinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	0.5	<=0.25	<=1	<=0.5	>512	n.r.
M3719/09	1|2|78	*S. chromogenes*	clinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	1	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	*blaZ*
M3727/09	1|3|4	*S. saprophyticus*	clinical		<=0.12	<=0.5	<=0.016	8	4	0.25	<=4	<=4	<=0.5	1	<=1	<=1	<=2	<=0.25	0.5	1	<=1	<=0.5	<=64	*blaZ*
M3738/09	1|3|7	*S. simulans*	clinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	8	<=4	<=0.5	<=0.5	<=1	<=1	4	<=0.25	<=0.25	0.5	2	<=0.5	256	n.r.
M3741-1/09	1|3|12	*Staph. sp.*	clinical		<=0.12	<=0.5	<=0.016	<=4	2	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	8	1	<=0.25	2	<=0.5	<=64	*mph* (C)
M3741-2/09	1|3|13	*S. sciuri*	clinical		0.5	<=0.5	<=0.016	<=4	4	<=0.12	<=4	<=4	>4	2	<=1	<=1	4	<=0.25	1	1	2	1	<=64	*mecA1*
M3742-1/09	1|3|14	*S. xylosus*	clinical		0.25	<=0.5	0.06	<=4	2	<=0.12	<=4	<=4	>4	2	2	<=1	<=2	<=0.25	0.5	0.5	2	<=0.5	<=64	n.r.
M3777-1/09	1|3|24	*S. xylosus*	clinical		<=0.12	>16	<=0.016	<=4	2	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	0.5	<=0.25	0.5	2	<=0.5	<=64	*tet* (K)
M3777-2/09	1|3|25	*S. chromogenes*	clinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	2	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	256	n.r.
M3778-2/09	1|3|27	*S. sciuri*	clinical		0.25	<=0.5	<=0.016	<=4	4	<=0.12	<=4	<=4	>4	2	<=1	<=1	<=2	<=0.25	0.5	0.5	4	1	<=64	*mecA1*
M3828/09	1|3|61	*S. xylosus*	clinical		<=0.12	<=0.5	<=0.016	<=4	2	<=0.12	<=4	<=4	2	1	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M3901/09	1|4|15	*S. sciuri*	clinical		0.25	16	<=0.016	32	4	<=0.12	<=4	<=4	>4	2	<=1	<=1	<=2	<=0.25	1	1	<=1	2	<=64	*mecA1* ; *str* ; *tet* (K)
M3966/09	1|4|20	*S. xylosus*	clinical		0.25	>16	0.03	<=4	4	<=0.12	8	<=4	1	1	2	<=1	<=2	0.5	<=0.25	0.5	2	<=0.5	<=64	*tet* (K)
M3970-1/09	1|4|21	*S. chromogenes*	clinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	1	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	*blaZ*
M3970-2/09	1|4|22	*S. xylosus*	clinical		0.25	1	0.12	<=4	2	<=0.12	<=4	<=4	4	1	2	<=1	<=2	<=0.25	<=0.25	0.5	<=1	<=0.5	<=64	n.r.
M3971-1/09	1|4|23	*S. xylosus*	clinical		0.25	<=0.5	<=0.016	<=4	1	<=0.12	<=4	<=4	>4	2	<=1	4	<=2	<=0.25	<=0.25	0.5	<=1	<=0.5	<=64	n.r.
M3975/09	1|4|25	*S. chromogenes*	clinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	>2	8	<=4	<=0.5	<=0.5	<=1	<=1	<=2	0.5	<=0.25	<=0.25	2	<=0.5	<=64	*blaZ*
M4055/09	1|4|43	*S. xylosus*	clinical		0.25	>16	0.03	<=4	2	<=0.12	8	<=4	1	1	2	<=1	<=2	0.5	<=0.25	0.5	2	<=0.5	<=64	*tet* (K)
M4085/09	1|4|55	*S. xylosus*	clinical		0.25	>16	<=0.016	<=4	1	0.25	<=4	<=4	>4	1	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	*blaZ* ; *tet* (K)
M4212-1/09	1|4|77	*S. sciuri*	clinical		0.5	<=0.5	<=0.016	<=4	4	<=0.12	<=4	<=4	>4	2	<=1	<=1	<=2	<=0.25	0.5	0.5	2	2	<=64	*mecA1*
M4212-2/09	1|4|78	*S. xylosus*	clinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	0.25	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	*blaZ*
M4218-1/09	2|2|1	*S. vitulinus*	clinical		<=0.12	<=0.5	<=0.016	8	1	<=0.12	<=4	<=4	2	<=0.5	<=1	<=1	8	<=0.25	<=0.25	0.5	<=1	<=0.5	<=64	*dfr* (G)
M4218-2/09	2|2|2	*S. xylosus*	clinical		<=0.12	<=0.5	0.06	<=4	2	<=0.12	<=4	<=4	4	1	<=1	<=1	<=2	<=0.25	0.5	0.5	<=1	<=0.5	<=64	n.r.
M4294/09	2|2|54	*S. xylosus*	clinical		<=0.12	<=0.5	0.06	<=4	1	0.25	<=4	<=4	>4	1	<=1	<=1	<=2	<=0.25	<=0.25	0.5	<=1	<=0.5	<=64	n.r.
M4343/09	2|2|57	*S. devriesei*	clinical		<=0.12	<=0.5	0.03	<=4	<=0.5	<=0.12	8	<=4	1	1	2	<=1	<=2	0.5	0.5	0.5	<=1	<=0.5	<=64	n.r.
M4358-1/09	2|2|68	*S. vitulinus*	clinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	1	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M4358-2/09	2|2|72	*S. xylosus*	clinical		0.25	<=0.5	0.06	<=4	1	<=0.12	<=4	<=4	>4	1	<=1	<=1	<=2	<=0.25	<=0.25	0.5	<=1	<=0.5	<=64	n.r.
M4460/09	2|3|25	*S. fleurettii*	clinical		>4	<=0.5	<=0.016	32	2	0.5	8	32	>4	1	<=1	4	>32	>8	0.5	>8	2	<=0.5	<=64	*aac(6')-Ie* ; *aph(2')-Ia* ; *dfr* (D); *erm* (B); *mecA* ; *str*
M4488/09	2|3|29	*S. sciuri*	clinical		0.25	<=0.5	<=0.016	<=4	4	<=0.12	<=4	<=4	>4	2	<=1	<=1	4	<=0.25	0.5	1	2	2	<=64	*mecA1*

255 isolates from subclinical mastitis

Name	Storage number	Species	Anamnesis	Break-points µg/ml	MIC = minimal inhibitory concentration in µg/ml																Resistance genes
					CLI > 0.5	TET > 2.0	RIF > 0.5	STR > 16	FUS > 1.0	PEN > 0.125	CHL > 8.0	KAN > 8.0	TIA > 2.0	SYN > 2.0	VAN > 2.0	GEN > 1.0	TMP > 4.0	ERY > 2.0	CIP > 1.0	OXA > 0.25	LZD > 4.0	MUP > 256	SMX > 128	
M13-1/10	2|3|39	*S. xylosus*	subclinical		<=0.12	<=0.5	0.06	<=4	1	<=0.12	<=4	<=4	2	1	2	<=1	<=2	<=0.25	0.5	0.5	<=1	<=0.5	<=64	n.r.
M13-2/10	2|3|36	*S. sciuri*	subclinical		0.25	<=0.5	<=0.016	<=4	4	<=0.12	<=4	<=4	>4	2	<=1	<=1	<=2	<=0.25	0.5	0.5	<=1	<=0.5	<=64	*mecA1*
M17/10	2|3|37	*S. chromogenes*	subclinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M18/10	2|3|38	*S. vitulinus*	subclinical		<=0.12	<=0.5	<=0.016	<=4	1	<=0.12	<=4	<=4	1	<=0.5	<=1	<=1	4	<=0.25	<=0.25	0.5	2	<=0.5	<=64	n.r.
M31/10	2|3|40	*S. chromogenes*	subclinical		<=0.12	<=0.5	<=0.016	32	<=0.5	1	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	0.5	<=1	<=0.5	<=64	*blaZ* ; *str*
M35/10	2|3|41	*S. haemolyticus*	subclinical		<=0.12	<=0.5	<=0.016	32	<=0.5	0.5	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	*blaZ* , *str*
M46/10	2|3|45	*S. chromogenes*	subclinical		<=0.12	>16	<=0.016	32	<=0.5	1	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	*blaZ*; *str* ; *tet* (K)
M47/10	2|3|46	*S. chromogenes*	subclinical		<=0.12	>16	<=0.016	>32	<=0.5	>2	<=4	>64	<=0.5	<=0.5	<=1	16	<=2	0.5	<=0.25	1	2	<=0.5	<=64	*aac(6')-Ie* ; *aph(2')-Ia* ; *blaZ*; *str* ; *tet* (L)
M67/10	2|3|49	*S. xylosus*	subclinical		<=0.12	<=0.5	<=0.016	<=4	2	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	0.5	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M68-1/10	2|3|50	*S. xylosus*	subclinical		0.25	<=0.5	0.03	<=4	1	<=0.12	<=4	<=4	>4	1	<=1	<=1	<=2	<=0.25	<=0.25	0.5	<=1	<=0.5	<=64	n.r.
M124/10	2|3|62	*S. xylosus*	subclinical		0.5	<=0.5	0.06	<=4	1	<=0.12	<=4	<=4	>4	2	<=1	<=1	<=2	<=0.25	<=0.25	0.5	<=1	<=0.5	<=64	n.r.
M130/10	2|3|64	*S. haemolyticus*	subclinical		>4	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	2	<=1	<=2	>8	<=0.25	<=0.25	<=1	<=0.5	<=64	*erm* (C)
M133-2/10	2|3|66	*S. chromogenes*	subclinical		<=0.12	<=0.5	<=0.016	>32	<=0.5	0.5	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	0.5	<=1	<=0.5	<=64	*blaZ* ; *str*
M161/10	2|3|72	*S. hyicus*	subclinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M163/10	2|3|73	*S. haemolyticus*	subclinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	0.25	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	*blaZ*
M173-2/10	2|3|77	*S. xylosus*	subclinical		0.25	>16	<=0.016	<=4	2	<=0.12	<=4	<=4	>4	1	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	*tet* (L)
M192/10	2|4|3	*S. chromogenes*	subclinical		<=0.12	<=0.5	<=0.016	8	<=0.5	<=0.12	8	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	256	n.r.
M232/10	2|4|11	*S. hyicus*	subclinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M243-2/10	2|4|14	*S. chromogenes*	subclinical		<=0.12	<=0.5	<=0.016	16	<=0.5	2	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	*blaZ*
M250/10	2|4|26	*S. xylosus*	subclinical		0.25	>16	0.06	<=4	1	<=0.12	<=4	<=4	>4	1	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	*tet* (K)
M251/10	2|4|16	*S. xylosus*	subclinical		<=0.12	<=0.5	0.06	<=4	2	<=0.12	<=4	<=4	>4	1	<=1	<=1	<=2	<=0.25	<=0.25	0.5	<=1	<=0.5	<=64	n.r.
M292/10	2|4|31	*S. succinus*	subclinical		<=0.12	<=0.5	0.12	<=4	<=0.5	<=0.12	8	<=4	2	1	2	<=1	<=2	<=0.25	<=0.25	<=0.25	2	<=0.5	<=64	n.r.
M349/10	2|4|41	*S. xylosus*	subclinical		0.25	<=0.5	<=0.016	8	1	<=0.12	<=4	<=4	>4	1	2	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M353-1/10	2|4|42	*S. xylosus*	subclinical		0.25	<=0.5	<=0.016	<=4	1	<=0.12	<=4	<=4	>4	1	2	<=1	<=2	<=0.25	<=0.25	0.5	<=1	<=0.5	<=64	n.r.
M353-2/10	2|4|43	*S. sciuri*	subclinical		0.25	<=0.5	<=0.016	<=4	2	<=0.12	<=4	<=4	>4	2	<=1	<=1	<=2	<=0.25	0.5	0.5	<=1	1	<=64	*mecA1*
M372/10	2|4|47	*S. xylosus*	subclinical		<=0.12	<=0.5	<=0.016	<=4	2	<=0.12	<=4	<=4	>4	1	<=1	<=1	<=2	<=0.25	<=0.25	0.5	<=1	<=0.5	<=64	n.r.
M374/10	2|4|48	*S. vitulinus*	subclinical		<=0.12	<=0.5	<=0.016	<=4	1	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	4	<=0.25	<=0.25	0.5	2	<=0.5	<=64	n.r.
M376-1/10	2|4|49	*S. xylosus*	subclinical		<=0.12	<=0.5	<=0.016	<=4	1	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	8	<=0.25	<=0.25	0.5	<=1	<=0.5	<=64	n.r.
M376-2/10	2|4|50	*S. sciuri*	subclinical		0.25	<=0.5	<=0.016	<=4	4	<=0.12	<=4	<=4	>4	2	<=1	<=1	4	<=0.25	0.5	0.5	<=1	1	<=64	*mecA1*
M383/10	2|4|51	*S. simulans*	subclinical		<=0.12	>16	<=0.016	32	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	8	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	*str* ; *tet* (K)
M400/10	2|4|54	*S. auricularis*	subclinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	2	<=4	<=4	<=0.5	<=0.5	<=1	<=1	8	<=0.25	<=0.25	<=0.25	<=1	<=0.5	128	*blaZ*
M409/10	2|4|58	*S. chromogenes*	subclinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	8	<=4	<=0.5	<=0.5	<=1	<=1	<=2	0.5	<=0.25	<=0.25	2	<=0.5	<=64	n.r.
M414/10	2|4|59	*S. chromogenes*	subclinical		<=0.12	<=0.5	<=0.016	32	<=0.5	1	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	*blaZ* ; *str*
M416-1/10	2|4|60	*S. devriesei*	subclinical		<=0.12	<=0.5	<=0.016	32	<=0.5	0.25	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	*blaZ* ; *str*
M416-2/10	2|4|61	*S. equorum*	subclinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	2	1	<=1	<=1	<=2	8	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M425/10	2|4|62	*S. chromogenes*	subclinical		>4	>16	<=0.016	16	<=0.5	0.25	64	<=4	<=0.5	<=0.5	<=1	<=1	>32	>8	<=0.25	<=0.25	<=1	<=0.5	<=64	*erm* (B); *tet* (L); *blaZ*; *cat* $_{pC221}$; *dfr* (K)
M439/10	2|4|66	*S. xylosus*	subclinical		0.25	<=0.5	<=0.016	<=4	1	<=0.12	<=4	<=4	>4	1	2	<=1	<=2	<=0.25	<=0.25	0.5	<=1	<=0.5	<=64	n.r.
M532-1/10	3|2|6	*S. sciuri*	subclinical		0.5	<=0.5	<=0.016	<=4	4	<=0.12	<=4	<=4	>4	2	<=1	<=1	<=2	<=0.25	<=0.25	1	<=1	<=0.5	<=64	*mecA1*
M532-2/10	3|2|7	*S. xylosus*	subclinical		<=0.12	<=0.5	0.06	<=4	1	<=0.12	<=4	<=4	>4	1	2	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M546-2/10	3|2|12	*S. vitulinus*	subclinical		<=0.12	<=0.5	<=0.016	<=4	1	<=0.12	<=4	<=4	1	<=0.5	<=1	<=1	8	<=0.25	0.5	0.5	<=1	<=0.5	<=64	n.r.
M556/10	3|2|13	*S. chromogenes*	subclinical		<=0.12	<=0.5	<=0.016	>32	<=0.5	1	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	*blaZ* ; *str*
M560/10	3|2|14	*S. xylosus*	subclinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	2	<=1	<=2	<=0.25	<=0.25	0.5	<=1	<=0.5	<=64	n.r.
M562-1/10	3|2|19	*S. chromogenes*	subclinical		<=0.12	>16	<=0.016	<=4	<=0.5	0.25	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	*blaZ* ; *tet* (L)
M562-2/10	3|2|15	*S. xylosus*	subclinical		1	<=0.5	<=0.016	<=4	<=0.5	0.25	<=4	<=4	>4	2	<=1	<=1	<=2	<=0.25	0.5	0.5	<=1	<=0.5	<=64	*blaZ*
M563/10	3|2|16	*S. xylosus*	subclinical		<=0.12	<=0.5	<=0.016	16	2	0.25	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	*blaZ*
M578/10	3|2|18	*S. chromogenes*	subclinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M619-2/10	3|2|44	*S. haemolyticus*	subclinical		<=0.12	<=0.5	<=0.016	>32	<=0.5	0.25	<=4	64	<=0.5	<=0.5	<=1	<=1	4	<=0.25	<=0.25	<=0.25	<=1	<=0.5	512	*ant(6)-Ia* ; *aph(3')-III*; *blaZ*
M650/10	3|2|49	*S. xylosus*	subclinical		<=0.12	>16	<=0.016	<=4	1	<=0.12	<=4	<=4	<=0.5	<=0.5	2	<=1	4	<=0.25	<=0.25	0.5	<=1	<=0.5	<=64	*tet* (K)
M703/10	3|2|59	*S. epidermidis*	subclinical		<=0.12	<=0.5	<=0.016	<=4	4	1	<=4	<=4	<=0.5	<=0.5	2	<=1	<=2	>8	<=0.25	1	<=1	<=0.5	256	*blaZ* ; *mecA* ; *msr* ; *mph* (C)
M744/10	3|2|66	*S. epidermidis*	subclinical		<=0.12	1	<=0.016	>32	<=0.5	<=0.12	32	>64	<=0.5	<=0.5	2	8	<=2	>8	8	2	<=1	<=0.5	256	*aac(6')-Ie* ; *aph(2')-Ia* ; *aph(3')-III*; *cat* $_{pC221}$; *erm* (C); *mecA* ; *str*
M762/10	3|2|73	*S. xylosus*	subclinical		0.25	<=0.5	<=0.016	<=4	1	<=0.12	<=4	<=4	>4	2	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M794-1/10	3|3|5	*S. chromogenes*	subclinical		<=0.12	<=0.5	<=0.016	>32	<=0.5	1	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	0.5	<=0.25	<=0.25	<=1	<=0.5	<=64	*blaZ*; *str*
M839/10	3|3|37	*S. haemolyticus*	subclinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	4	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M840/10	3|3|24	*S. xylosus*	subclinical		0.25	<=0.5	<=0.016	<=4	2	<=0.12	<=4	<=4	<=0.5	<=0.5	2	<=1	<=2	<=0.25	<=0.25	0.5	<=1	<=0.5	<=64	n.r.
M847/10	3|3|25	*S. simulans*	subclinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	4	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M857/10	3|3|35	*S. capitis*	subclinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	2	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.

Name	Storage number	Species	Anamnesis	Break-points µg/ml	MIC = minimal inhibitory concentration in µg/ml																	Resistance genes
					CLI > 0.5	TET > 2.0	RIF > 0.5	STR > 16	FUS > 1.0	PEN > 0.125	CHL > 8.0	KAN > 8.0	TIA > 2.0	SYN > 2.0	VAN > 2.0	GEN > 1.0	TMP > 4.0	ERY > 2.0	CIP > 1.0	OXA > 0.25	LZD > 4.0	MUP > 256	SMX > 128	
M860/10	3|3|36	*S. chromogenes*	subclinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	1	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	0.5	<=1	<=0.5	<=64	*blaZ*
M864/10	3|3|29	*S. epidermidis*	subclinical		<=0.12	>16	<=0.016	<=4	<=0.5	0.25	<=4	<=4	<=0.5	<=0.5	2	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	128	*blaZ*; *tet* (K)
M917/10	3|3|49	*S. chromogenes*	subclinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	0.5	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M974/10	3|3|62	*S. chromogenes*	subclinical		<=0.12	<=0.5	<=0.016	16	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M1032/10	3|3|67	*S. xylosus*	subclinical		0.25	<=0.5	<=0.016	<=4	4	<=0.12	8	<=4	1	1	2	<=1	<=2	0.5	0.5	1	2	<=0.5	<=64	n.r.
M1048/10	3|3|73	*S. lentus*	subclinical		1	<=0.5	<=0.016	<=4	2	<=0.12	8	<=4	>4	2	2	<=1	4	0.5	0.5	1	2	1	<=64	n.r.
M1049/10	3|3|74	*Staph. sp.*	subclinical		0.5	<=0.5	<=0.016	<=4	1	<=0.12	<=4	<=4	>4	2	2	<=1	<=2	8	0.5	0.5	<=1	<=0.5	<=64	*mph* (C)
M1051/10	3|3|75	*S. sciuri*	subclinical		0.5	<=0.5	<=0.016	<=4	4	<=0.12	<=4	<=4	>4	2	<=1	<=1	4	<=0.25	0.5	0.5	<=1	1	<=64	*mecA1*
M1058/10	3|3|77	*S. sciuri*	subclinical		0.5	<=0.5	<=0.016	<=4	2	<=0.12	<=4	<=4	>4	2	<=1	<=1	<=2	<=0.25	0.5	0.5	<=1	1	<=64	*mecA1*
M1085-5/10	3|4|12	*S. chromogenes*	subclinical		<=0.12	<=0.5	0.12	<=4	4	<=0.12	<=4	<=4	2	1	<=1	<=1	<=2	>8	<=0.25	0.5	<=1	<=0.5	<=64	n.r.
M1086/10	3|3|81	*S. xylosus*	subclinical		0.25	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	2	<=1	<=2	<=0.25	<=0.25	0.5	<=1	<=0.5	<=64	n.r.
M1093-2/10	3|4|8	*S. sciuri*	subclinical		0.25	<=0.5	<=0.016	<=4	4	<=0.12	<=4	<=4	>4	2	<=1	<=1	<=2	<=0.25	0.5	1	<=1	2	<=64	*mecA1*
M1094-1/10	3|4|14	*S. warneri*	subclinical		<=0.12	>16	<=0.016	>32	<=0.5	0.25	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	*blaZ*; *str*; *tet* (K)
M1101-1/10	3|4|16	*S. haemolyticus*	subclinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	0.5	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	*blaZ*
M1130-1/10	3|4|27	*S. sciuri*	subclinical		0.5	<=0.5	<=0.016	<=4	4	<=0.12	<=4	<=4	>4	2	<=1	<=1	4	<=0.25	0.5	0.5	2	1	<=64	*mecA1*
M1130-2/10	3|4|28	*S. haemolyticus*	subclinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M1143/10	3|4|30	*S. chromogenes*	subclinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M1154-1/10	3|4|31	*S. xylosus*	subclinical		<=0.12	<=0.5	<=0.016	<=4	2	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M1176/10	3|4|36	*S. xylosus*	subclinical		0.25	>16	0.06	<=4	1	<=0.12	8	<=4	>4	1	2	<=1	<=2	0.5	<=0.25	0.5	2	<=0.5	<=64	*tet* (K)
M1191-2/10	3|4|41	*S. fleurettii*	subclinical		<=0.12	<=0.5	<=0.016	<=4	4	<=0.12	<=4	<=4	>4	1	<=1	<=1	<=2	<=0.25	0.5	0.5	2	<=0.5	<=64	*mecA*
M1201/10	3|4|47	*S. sciuri*	subclinical		0.5	>16	<=0.016	32	4	<=0.12	64	<=4	>4	2	<=1	<=1	<=2	<=0.25	1	1	<=1	2	<=64	cat_{pC221}; *str*; *tet* (K); *mecA1*
M1217/10	3|4|48	*S. xylosus*	subclinical		<=0.12	<=0.5	0.06	<=4	2	<=0.12	<=4	<=4	>4	2	2	<=1	<=2	<=0.25	<=0.25	0.5	<=1	<=0.5	<=64	n.r.
M1219-2/10	3|4|52	*S. xylosus*	subclinical		<=0.12	<=0.5	<=0.016	<=4	2	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M1228/10	3|4|51	*S. warneri*	subclinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M1230-1/10	3|4|58	*S. devriesei*	subclinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M1231-1/10	3|4|54	*S. xylosus*	subclinical		<=0.12	<=0.5	<=0.016	<=4	2	<=0.12	8	<=4	1	1	2	<=1	<=2	>8	<=0.25	0.5	<=1	<=0.5	<=64	*msr*; *mph* (C)
M1231-2/10	3|4|55	*S. succinus*	subclinical		<=0.12	<=0.5	0.12	<=4	<=0.5	<=0.12	8	<=4	2	1	2	<=1	<=2	0.5	<=0.25	0.5	2	<=0.5	<=64	n.r.
M1245-1/10	3|4|60	*S. sciuri*	subclinical		0.25	<=0.5	<=0.016	<=4	4	<=0.12	<=4	<=4	>4	2	<=1	<=1	4	<=0.25	<=0.25	1	2	2	<=64	*mecA1*
M1245-2/10	3|4|61	*S. xylosus*	subclinical		<=0.12	>16	<=0.016	<=4	1	<=0.12	<=4	<=4	<=0.5	<=0.5	2	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	*tet* (K)
M1254/10	3|4|63	*S. xylosus*	subclinical		0.25	>16	<=0.016	<=4	<=0.5	<=0.12	8	<=4	>4	1	2	<=1	<=2	0.5	<=0.25	<=0.25	2	<=0.5	<=64	*tet* (K)
M1256/10	3|4|65	*S. warneri*	subclinical		<=0.12	<=0.5	<=0.016	32	<=0.5	1	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	>8	<=0.25	0.5	<=1	<=0.5	<=64	*erm* (C); *blaZ*; *str*
M1263/10	3|4|69	*S. haemolyticus*	subclinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M1292-1/10	3|4|77	*S. simulans*	subclinical		0.25	<=0.5	<=0.016	8	<=0.5	<=0.12	8	<=4	2	<=0.5	<=1	<=1	4	<=0.25	<=0.25	<=0.25	2	<=0.5	<=64	n.r.
M1300/10	3|4|80	*S. devriesei*	subclinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	0.25	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	0.5	<=0.25	<=1	<=0.5	<=64	*blaZ*
M1312/10	4|2|1	*S. devriesei*	subclinical		<=0.12	<=0.5	<=0.016	32	<=0.5	0.5	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	*blaZ*; *str*
M1351/10	4|2|30	*S. xylosus*	subclinical		0.25	<=0.5	<=0.016	<=4	1	<=0.12	<=4	<=4	>4	2	4	<=1	<=2	<=0.25	<=0.25	<=0.25	2	<=0.5	<=64	n.r.
M1370/10	4|2|40	*S. saprophyticus*	subclinical		<=0.12	<=0.5	<=0.016	<=4	4	0.5	<=4	<=4	2	1	<=1	<=1	4	<=0.25	<=0.25	1	<=1	<=0.5	<=64	*blaZ*
M1375-1/10	4|2|36	*S. devriesei*	subclinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M1375-2/10	4|2|37	*S. xylosus*	subclinical		<=0.12	>16	<=0.016	<=4	2	<=0.12	<=4	<=4	<=0.5	<=0.5	2	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	*tet* (K)
M1376/10	4|2|38	*S. xylosus*	subclinical		<=0.12	<=0.5	<=0.016	<=4	1	<=0.12	<=4	<=4	>4	1	2	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M1383/10 4|2|42		*S. epidermidis*	subclinical		>4	1	<=0.016	<=4	<=0.5	1	<=4	64	<=0.5	<=0.5	2	4	<=2	>8	<=0.25	1	<=1	<=0.5	256	*aac(6')-Ie*; *aph(2')-Ia*; *blaZ*; *erm* (C); *mecA*
M1400/10	4|2|48	*S. xylosus*	subclinical		<=0.12	<=0.5	<=0.016	<=4	2	<=0.12	<=4	<=4	1	<=0.5	2	<=1	<=2	<=0.25	<=0.25	0.5	<=1	<=0.5	<=64	n.r.
M1405/10	4|2|53	*S. devriesei*	subclinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	0.25	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	*blaZ*
M1410-1/10	4|2|54	*S. haemolyticus*	subclinical		>4	<=0.5	0.06	16	4	<=0.12	<=4	8	<=0.5	<=0.5	<=1	2	<=2	>8	0.5	<=0.25	<=1	<=0.5	512	*erm* (C)
M1413-2/10	4|2|59	*S. chromogenes*	subclinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	2	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M1446-1/10	4|3|5	*S. xylosus*	subclinical		<=0.12	<=0.5	<=0.016	<=4	2	0.25	<=4	<=4	4	1	2	<=1	<=2	0.5	<=0.25	0.5	<=1	<=0.5	<=64	*blaZ*
M1450-1/10	4|3|7	*S. haemolyticus*	subclinical		<=0.12	<=0.5	<=0.016	>32	<=0.5	<=0.12	<=4	<=4	2	2	4	<=1	<=2	<=0.25	0.5	<=0.25	<=1	<=0.5	<=64	*str*
M1451-2/10	4|2|79	*S. xylosus*	subclinical		0.25	<=0.5	<=0.016	<=4	2	<=0.12	<=4	<=4	>4	2	2	<=1	<=2	<=0.25	<=0.25	0.5	<=1	<=0.5	<=64	n.r.
M1455/10	4|3|4	*S. xylosus*	subclinical		<=0.12	>16	0.03	<=4	1	<=0.12	<=4	<=4	<=0.5	<=0.5	2	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	*tet* (K)
M1457/10	4|2|74	*S. chromogenes*	subclinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	2	<=1	<=2	0.5	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M1469/10	4|3|2	*S. devriesei*	subclinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	0.25	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	*blaZ*
M1470-1/10	4|3|10	*S. devriesei*	subclinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	0.25	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	*blaZ*
M1487/10	4|3|11	*S. sciuri*	subclinical		0.25	<=0.5	<=0.016	<=4	2	<=0.12	<=4	<=4	>4	2	<=1	<=1	<=2	<=0.25	0.5	0.5	<=1	1	<=64	*mecA1*
M1510/10	4|3|25	*S. xylosus*	subclinical		0.25	<=0.5	<=0.016	<=4	2	<=0.12	<=4	<=4	>4	1	2	<=1	<=2	<=0.25	<=0.25	0.5	<=1	<=0.5	<=64	n.r.
M1529/10	4|3|29	*S. epidermidis*	subclinical		>4	>16	<=0.016	>32	<=0.5	>2	<=4	>64	<=0.5	<=0.5	2	>16	>32	>8	<=0.25	>8	<=1	<=0.5	256	*aac(6')-Ie*; *aph(2')-Ia*; *blaZ*; *dfr* (A); *erm* (C); *lnu* (A); *mecA*; *str*; *tet* (K)
M1532/10	4|3|31	*S. simulans*	subclinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	32	<=4	<=0.5	<=0.5	<=1	<=1	4	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	cat_{pC223}
M1540-2/10	4|3|36	*S. vitulinus*	subclinical		<=0.12	<=0.5	<=0.016	16	<=0.5	<=0.12	<=4	<=4	1	<=0.5	<=1	<=1	4	<=0.25	0.5	0.5	2	<=0.5	<=64	n.r.
M1550/10	4|3|44	*S. xylosus*	subclinical		<=0.12	>16	<=0.016	<=4	2	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	*tet* (K)
M1577/10	4|3|49	*S. simulans*	subclinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	4	<=0.25	<=0.25	<=0.25	<=1	<=0.5	128	n.r.
M1594-1/10	4|3|56	*S. devriesei*	subclinical		<=0.12	<=0.5	<=0.016	32	<=0.5	0.25	<=4	<=4	<=0.5	<=0.5	<=1	<=1	4	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	*blaZ*; *str*

Name	Storage number	Species	Anamnesis	Break-points µg/ml	MIC = minimal inhibitory concentration in µg/ml																	Resistance genes
					CLI > 0.5	TET > 2.0	RIF > 0.5	STR > 16	FUS > 1.0	PEN > 0.125	CHL > 8.0	KAN > 8.0	TIA > 2.0	SYN > 2.0	VAN > 2.0	GEN > 1.0	TMP > 4.0	ERY > 2.0	CIP > 1.0	OXA > 0.25	LZD > 4.0	MUP > 256	SMX > 128	
M1599/10	4|3|61	*Staph. sp.*	subclinical		0.25	<=0.5	0.25	<=4	<=0.5	<=0.12	<=4	<=4	>4	2	2	<=1	<=2	0.5	0.5	0.5	<=1	<=0.5	<=64	n.r.
M1605-1/10	4|3|63	*S. haemolyticus*	subclinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	0.5	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	*blaZ*
M1605-2/10	4|3|64	*S. chromogenes*	subclinical		<=0.12	<=0.5	<=0.016	>32	<=0.5	0.5	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	*blaZ* ; *str*
M1606-1/10	4|3|65	*S. warneri*	subclinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	1	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	0.5	<=1	<=0.5	<=64	*blaZ*
M1607/10	4|3|67	*S. simulans*	subclinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	8	<=0.25	<=0.25	<=0.25	<=1	<=0.5	128	n.r.
M1608/10	4|3|68	*S. succinus*	subclinical		<=0.12	<=0.5	0.12	<=4	<=0.5	<=0.12	8	<=4	4	1	2	<=1	<=2	0.5	<=0.25	<=0.25	2	<=0.5	<=64	n.r.
M1622/10	4|3|70	*S. capitis*	subclinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	0.25	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	*blaZ*
M1623/10	4|3|81	*S. devriesei*	subclinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	0.25	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	*blaZ*
M1638-1/10	4|3|71	*S. haemolyticus*	subclinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	2	<=1	<=2	<=0.25	0.5	<=0.25	<=1	<=0.5	<=64	n.r.
M1638-2/10	4|3|74	*S. chromogenes*	subclinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	0.5	<=4	<=4	<=0.5	<=0.5	2	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	*blaZ*
M1641-2/10	4|3|78	*S. xylosus*	subclinical		0.25	<=0.5	<=0.016	<=4	1	<=0.12	<=4	<=4	>4	1	2	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M1642-1/10	4|3|79	*S. xylosus*	subclinical		1	<=0.5	0.12	<=4	4	<=0.12	<=4	<=4	>4	2	<=1	<=1	<=2	<=0.25	0.5	<=0.25	<=1	<=0.5	<=64	*lnu* (A)
M1643/10	4|3|76	*S. xylosus*	subclinical		<=0.12	<=0.5	0.06	<=4	2	<=0.12	<=4	<=4	<=0.5	<=0.5	2	<=1	<=2	<=0.25	<=0.25	0.5	<=1	<=0.5	<=64	n.r.
M1668/10	4|4|4	*S. chromogenes*	subclinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	1	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	*blaZ*
M1677-2/10	4|4|8	*S. xylosus*	subclinical		<=0.12	>16	<=0.016	<=4	1	<=0.12	<=4	<=4	<=0.5	1	2	<=1	4	<=0.25	<=0.25	0.5	<=1	<=0.5	<=64	*tet* (K)
M1679-1/10	4|4|11	*S. sciuri*	subclinical		0.25	<=0.5	<=0.016	<=4	2	<=0.12	<=4	<=4	>4	2	<=1	<=1	<=2	<=0.25	0.5	0.5	<=1	1	<=64	*mecA1*
M1679-2/10	4|4|12	*S. xylosus*	subclinical		0.25	<=0.5	<=0.016	<=4	1	<=0.12	<=4	<=4	>4	1	2	<=1	<=2	<=0.25	<=0.25	0.5	<=1	<=0.5	<=64	n.r.
M1680-1/10	4|4|13	*S. sciuri*	subclinical		0.5	<=0.5	<=0.016	<=4	4	<=0.12	<=4	<=4	>4	2	<=1	<=1	4	<=0.25	0.5	1	2	1	<=64	*mecA1*
M1680-2/10	4|4|14	*S. xylosus*	subclinical		0.5	<=0.5	<=0.016	<=4	4	<=0.12	<=4	<=4	>4	2	<=1	<=1	4	<=0.25	1	1	2	2	<=64	n.r.
M1684-1/10	4|4|20	*S. xylosus*	subclinical		0.25	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	>4	1	2	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M1685/10	4|4|22	*S. sciuri*	subclinical		0.5	<=0.5	<=0.016	<=4	4	<=0.12	<=4	<=4	>4	2	<=1	<=1	<=2	<=0.25	0.5	1	<=1	2	<=64	*mecA1*
M1687-1/10	4|4|23	*S. sciuri*	subclinical		<=0.12	<=0.5	<=0.016	<=4	2	<=0.12	<=4	<=4	>4	2	2	<=1	<=2	<=0.25	<=0.25	0.5	<=1	<=0.5	<=64	*mecA1*
M1687-2/10	4|4|24	*S. xylosus*	subclinical		0.25	<=0.5	<=0.016	<=4	2	<=0.12	64	<=4	4	1	2	<=1	<=2	0.5	<=0.25	<=0.25	2	<=0.5	<=64	cat_{pC221}
M1688-1/10	4|4|25	*S. sciuri*	subclinical		0.25	<=0.5	<=0.016	<=4	2	<=0.12	8	<=4	>4	2	<=1	<=1	4	<=0.25	0.5	0.5	<=1	2	<=64	*mecA1*
M1688-2/10	4|4|26	*S. xylosus*	subclinical		<=0.12	<=0.5	<=0.016	<=4	1	<=0.12	<=4	<=4	<=0.5	<=0.5	2	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M1689-1/10	4|4|27	*S. sciuri*	subclinical		0.25	<=0.5	<=0.016	<=4	4	<=0.12	<=4	<=4	>4	2	<=1	<=1	<=2	<=0.25	0.5	0.5	<=1	1	<=64	*mecA1*
M1695/10	4|4|29	*S. chromogenes*	subclinical		<=0.12	<=0.5	<=0.016	>32	<=0.5	0.5	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	0.5	<=0.25	<=0.25	<=1	<=0.5	128	*blaZ* ; *str*
M1713/10	4|4|37	*S. sciuri*	subclinical		0.5	<=0.5	<=0.016	16	4	<=0.12	<=4	<=4	>4	2	<=1	<=1	4	<=0.25	1	1	2	2	<=64	*mecA1*
M1720/10	4|4|32	*S. xylosus*	subclinical		0.25	<=0.5	<=0.016	<=4	1	<=0.12	<=4	<=4	1	1	2	<=1	8	0.5	<=0.25	0.5	<=1	<=0.5	<=64	n.r.
M1796/10	4|4|55	*S. xylosus*	subclinical		0.25	<=0.5	<=0.016	<=4	1	<=0.12	8	<=4	1	1	2	<=1	<=2	0.5	<=0.25	<=0.25	2	<=0.5	<=64	n.r.
M1811/10	4|4|48	*S. xylosus*	subclinical		<=0.12	<=0.5	0.03	<=4	1	<=0.12	<=4	<=4	<=0.5	<=0.5	2	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M1813/10	4|4|71	*S. haemolyticus*	subclinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M1814-1/10	4|4|72	*S. epidermidis*	subclinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	2	<=1	<=2	<=0.25	0.5	<=0.25	<=1	<=0.5	<=64	n.r.
M1814-2/10	4|4|66	*S. hominis*	subclinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	0.25	<=4	<=4	<=0.5	<=0.5	2	<=1	<=2	>8	<=0.25	<=0.25	<=1	<=0.5	<=64	*blaZ* ; *msr*
M1816/10	4|4|73	*S. xylosus*	subclinical		<=0.12	<=0.5	0.06	<=4	1	<=0.12	<=4	<=4	2	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	0.5	<=1	<=0.5	<=64	n.r.
M1835/10	5|2|1	*S. xylosus*	subclinical		<=0.12	>16	<=0.016	<=4	2	<=0.12	<=4	<=4	<=0.5	<=0.5	2	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	*tet* (K)
M1840/10	5|2|2	*S. haemolyticus*	subclinical		<=0.12	<=0.5	<=0.016	16	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M1853/10	5|2|8	*S. xylosus*	subclinical		<=0.12	<=0.5	<=0.016	<=4	2	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	0.5	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M1869/10	5|2|18	*S. haemolyticus*	subclinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	0.25	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	*blaZ*
M1877/10	5|2|16	*S. chromogenes*	subclinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	0.25	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	*blaZ*
M1895/10	5|2|17	*S. chromogenes*	subclinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M1936/10	5|2|31	*S. chromogenes*	subclinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	2	8	<=4	<=0.5	<=0.5	<=1	<=1	<=2	0.5	<=0.25	0.5	2	<=0.5	128	*blaZ*
M1961/10	5|2|45	*S. fleurettii*	subclinical		0.25	<=0.5	<=0.016	<=4	4	0.5	<=4	<=4	4	1	2	<=1	4	<=0.25	0.5	>8	2	<=0.5	<=64	*mecA*
M1976/10	5|2|53	*S. sciuri*	subclinical		0.5	<=0.5	<=0.016	<=4	2	<=0.12	<=4	<=4	>4	1	<=1	<=1	<=2	<=0.25	0.5	0.5	2	1	<=64	*mecA1*
M1977/10	5|2|55	*S. epidermidis*	subclinical		<=0.12	<=0.5	<=0.016	>32	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	2	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	*str*
M1981/10	5|2|54	*S. chromogenes*	subclinical		<=0.12	<=0.5	<=0.016	<=4	1	0.5	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	*blaZ*
M2014-1/10	5|2|72	*S. haemolyticus*	subclinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M2014-2/10	5|2|73	*S. xylosus*	subclinical		<=0.12	>16	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	4	1	2	<=1	<=2	<=0.25	<=0.25	0.5	<=1	<=0.5	<=64	*tet* (K)
M2019/10	5|2|74	*S. xylosus*	subclinical		<=0.12	<=0.5	<=0.016	<=4	2	<=0.12	<=4	<=4	>4	1	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M2045/10	5|3|11	*S. xylosus*	subclinical		<=0.12	<=0.5	<=0.016	<=4	2	<=0.12	<=4	<=4	1	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M2046/10	5|3|12	*S. haemolyticus*	subclinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M2048/10	5|3|25	*S. simulans*	subclinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	4	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M2064/10	5|3|28	*S. simulans*	subclinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	4	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M2088/10	5|3|29	*S. simulans*	subclinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	4	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M2093/10	5|3|31	*S. simulans*	subclinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	8	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M2168-1/10	5|3|47	*S. xylosus*	subclinical		0.25	<=0.5	0.06	<=4	1	<=0.12	<=4	<=4	>4	2	2	<=1	4	<=0.25	<=0.25	0.5	<=1	<=0.5	<=64	n.r.
M2171/10	5|3|50	*S. xylosus*	subclinical		<=0.12	>16	<=0.016	<=4	1	<=0.12	<=4	<=4	1	<=0.5	2	<=1	4	<=0.25	<=0.25	0.5	<=1	<=0.5	<=64	*tet* (K)
M2188/10	5|3|60	*S. xylosus*	subclinical		0.25	<=0.5	<=0.016	<=4	1	<=0.12	<=4	<=4	>4	2	2	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M2189/10	5|3|35	*S. xylosus*	subclinical		0.25	<=0.5	0.06	<=4	2	0.25	<=4	<=4	>4	1	2	<=1	<=2	<=0.25	0.5	0.5	<=1	<=0.5	<=64	*blaZ*
M2233/10	5|3|75	*S. epidermidis*	subclinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	2	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M2241-3/10	5|4|5	*S. xylosus*	subclinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	2	<=1	<=2	<=0.25	<=0.25	0.5	<=1	<=0.5	<=64	n.r.
M2248-1/10	5|4|6	*S. xylosus*	subclinical		<=0.12	>16	<=0.016	<=4	1	<=0.12	<=4	<=4	4	1	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	*tet* (K)
M2253-1/10	5|4|7	*S. chromogenes*	subclinical		<=0.12	>16	<=0.016	<=4	<=0.5	0.25	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	*blaZ* ; *tet* (K)

Name	Storage number	Species	Anamnesis	Break-points µg/ml	MIC = minimal inhibitory concentration in µg/ml																	Resistance genes
					CLI > 0.5	TET > 2.0	RIF > 0.5	STR > 16	FUS > 1.0	PEN > 0.125	CHL > 8.0	KAN > 8.0	TIA > 2.0	SYN > 2.0	VAN > 2.0	GEN > 1.0	TMP > 4.0	ERY > 2.0	CIP > 1.0	OXA > 0.25	LZD > 4.0	MUP > 256	SMX > 128	
M2255/10	5|4|8	*Staph. sp.*	subclinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	128	n.r.
M2258/10	5|4|9	*S. haemolyticus*	subclinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M2311-1/10	5|4|36	*S. xylosus*	subclinical		0.5	>16	<=0.016	<=4	2	<=0.12	<=4	<=4	>4	2	2	<=1	<=2	>8	<=0.25	0.5	2	<=0.5	<=64	*msr* ; *mph* (C); *tet* (K)
M2313-1/10	5|4|37	*S. haemolyticus*	subclinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	4	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M3074-1/09	1|4|30	*S. xylosus*	subclinical		0.25	>16	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	>4	1	2	<=1	<=2	0.5	<=0.25	0.5	<=1	<=0.5	<=64	*tet* (K)
M3551/09	1|2|1	*S. xylosus*	subclinical		<=0.12	<=0.5	<=0.016	<=4	2	<=0.12	<=4	<=4	<=0.5	<=0.5	2	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M3566/09	1|2|6	*S. simulans*	subclinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	4	<=0.25	<=0.25	<=0.25	<=1	<=0.5	128	n.r.
M3567-1/09	1|2|7	*S. xylosus*	subclinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	2	<=1	<=2	<=0.25	<=0.25	0.5	<=1	<=0.5	<=64	n.r.
M3569-1/09	1|2|2	*S. xylosus*	subclinical		<=0.12	>16	0.06	<=4	2	<=0.12	<=4	<=4	<=0.5	<=0.5	2	<=1	<=2	<=0.25	<=0.25	0.5	<=1	<=0.5	<=64	*tet* (K)
M3579/09	1|2|15	*S. xylosus*	subclinical		0.25	<=0.5	<=0.016	8	2	<=0.12	<=4	<=4	>4	2	2	<=1	<=2	<=0.25	<=0.25	0.5	<=1	<=0.5	<=64	n.r.
M3607/09	1|2|23	*S. succinus*	subclinical		<=0.12	<=0.5	0.06	<=4	<=0.5	<=0.12	<=4	<=4	>4	2	2	<=1	<=2	<=0.25	<=0.25	0.5	<=1	1	<=64	n.r.
M3608-1/09	1|2|24	*S. sciuri*	subclinical		0.25	<=0.5	<=0.016	<=4	2	<=0.12	<=4	<=4	>4	2	<=1	<=1	4	<=0.25	0.5	0.5	<=1	2	<=64	*mecA1*
M3608-2/09	1|2|25	*S. xylosus*	subclinical		<=0.12	<=0.5	<=0.016	<=4	2	<=0.12	<=4	<=4	<=0.5	<=0.5	2	<=1	<=2	<=0.25	<=0.25	0.5	<=1	<=0.5	<=64	n.r.
M3617-1/09	1|2|27	*S. xylosus*	subclinical		<=0.12	>16	<=0.016	<=4	2	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	*tet* (K)
M3619/09	1|2|29	*S. xylosus*	subclinical		0.25	<=0.5	<=0.016	<=4	4	<=0.12	8	<=4	1	<=0.5	2	<=1	<=2	0.5	<=0.25	0.5	2	<=0.5	<=64	n.r.
M3628/09	1|2|34	*S. xylosus*	subclinical		0.25	<=0.5	0.06	<=4	1	<=0.12	<=4	<=4	>4	2	2	<=1	<=2	<=0.25	<=0.25	0.5	<=1	<=0.5	<=64	n.r.
M3629/09	1|2|35	*S. chromogenes*	subclinical		<=0.12	<=0.5	<=0.016	>32	<=0.5	>2	8	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	0.5	2	<=0.5	<=64	*blaZ* ; *str*
M3631/09	1|2|37	*S. chromogenes*	subclinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	>2	8	<=4	<=0.5	<=0.5	<=1	<=1	<=2	0.5	<=0.25	<=0.25	<=1	<=0.5	128	*blaZ*
M3642/09	1|2|38	*S. chromogenes*	subclinical		<=0.12	>16	<=0.016	<=4	<=0.5	>2	8	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	0.5	<=1	<=0.5	<=64	*blaZ* ; *tet* (K)
M3658-2/09	1|2|48	*S. xylosus*	subclinical		0.25	<=0.5	<=0.016	<=4	2	<=0.12	<=4	<=4	>4	2	2	<=1	<=2	<=0.25	0.5	0.5	<=1	<=0.5	<=64	n.r.
M3660/09	1|2|49	*S. xylosus*	subclinical		0.25	<=0.5	<=0.016	<=4	2	<=0.12	<=4	<=4	>4	1	2	<=1	<=2	<=0.25	<=0.25	0.5	2	<=0.5	<=64	n.r.
M3662/09	1|2|50	*S. xylosus*	subclinical		<=0.12	<=0.5	<=0.016	<=4	2	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	0.5	<=1	<=0.5	<=64	n.r.
M3678-2/09	1|2|58	*S. sciuri*	subclinical		0.5	<=0.5	<=0.016	32	4	<=0.12	<=4	<=4	>4	2	<=1	<=1	4	<=0.25	0.5	0.5	<=1	2	<=64	*mecA1* ; *str*
M3679-2/09	1|2|56	*S. xylosus*	subclinical		0.25	<=0.5	0.03	<=4	1	<=0.12	<=4	<=4	2	<=0.5	2	<=1	<=2	<=0.25	<=0.25	0.5	<=1	<=0.5	<=64	n.r.
M3689/09	1|2|62	*S. haemolyticus*	subclinical		>4	<=0.5	0.03	8	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	>8	<=0.25	<=0.25	<=1	<=0.5	<=64	*erm* (C)
M3698-1/09	1|2|69	*S. xylosus*	subclinical		0.25	<=0.5	<=0.016	<=4	2	0.25	8	<=4	>4	1	2	<=1	<=2	<=0.25	<=0.25	0.5	<=1	<=0.5	<=64	*blaZ*
M3729-2/09	1|3|1	*S. xylosus*	subclinical		0.25	<=0.5	<=0.016	<=4	2	<=0.12	<=4	<=4	>4	1	2	<=1	<=2	<=0.25	<=0.25	0.5	2	<=0.5	<=64	n.r.
M3729-3/09	1|3|2	*S. chromogenes*	subclinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	>2	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	*blaZ*
M3752/09	1|3|20	*S. xylosus*	subclinical		0.25	<=0.5	0.03	<=4	1	<=0.12	<=4	<=4	>4	2	2	<=1	<=2	<=0.25	<=0.25	0.5	<=1	<=0.5	<=64	n.r.
M3761/09	1|3|21	*S. xylosus*	subclinical		<=0.12	<=0.5	<=0.016	<=4	1	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	8	<=0.25	<=0.25	0.5	<=1	<=0.5	<=64	n.r.
M3783/09	1|3|29	*S. fleurettii*	subclinical		<=0.12	<=0.5	0.03	<=4	4	0.25	<=4	<=4	2	<=0.5	<=1	<=1	<=2	2	0.5	8	<=1	<=0.5	512	*mecA*
M3786/09	1|3|35	*S. haemolyticus*	subclinical		<=0.12	<=0.5	<=0.016	32	<=0.5	0.5	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	*blaZ* ; *str*
M3817/09	1|3|44	*S. warneri*	subclinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M3818-1/09	1|3|45	*S. chromogenes*	subclinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	0.25	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	128	*blaZ*
M3818-2/09	1|3|46	*S. hyicus*	subclinical		<=0.12	<=0.5	<=0.016	<=4	1	<=0.12	8	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	2	<=0.5	<=64	n.r.
M3876/09	1|3|68	*S. xylosus*	subclinical		0.25	<=0.5	<=0.016	<=4	2	<=0.12	<=4	<=4	>4	1	2	<=1	<=2	<=0.25	<=0.25	0.5	<=1	<=0.5	<=64	n.r.
M3877/09	1|3|69	*S. sciuri*	subclinical		0.25	<=0.5	<=0.016	<=4	2	<=0.12	<=4	<=4	>4	2	<=1	<=1	<=2	<=0.25	0.5	0.5	<=1	<=0.5	<=64	*mecA1*
M3884-1/09	1|3|71	*S. xylosus*	subclinical		0.25	>16	<=0.016	<=4	2	<=0.12	<=4	<=4	>4	2	2	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	*tet* (K)
M3895-2/09	1|3|73	*S. succinus*	subclinical		<=0.12	<=0.5	0.12	<=4	<=0.5	<=0.12	8	<=4	>4	2	2	<=1	<=2	0.5	<=0.25	0.5	2	<=0.5	<=64	n.r.
M3907-2/09	1|4|18	*S. simulans*	subclinical		<=0.12	>16	<=0.016	<=4	<=0.5	<=0.12	64	<=4	<=0.5	<=0.5	<=1	<=1	4	<=0.25	<=0.25	<=0.25	2	<=0.5	128	*tet* (K)
M3961/09	1|4|19	*Staph. sp.*	subclinical		<=0.12	>16	<=0.016	<=4	1	<=0.12	<=4	<=4	>4	1	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	*tet* (K)
M4023/09	1|4|32	*S. xylosus*	subclinical		<=0.12	<=0.5	0.06	<=4	1	<=0.12	<=4	<=4	>4	1	<=1	<=1	<=2	<=0.25	<=0.25	0.5	<=1	<=0.5	<=64	n.r.
M4029/09	1|4|36	*S. hyicus*	subclinical		<=0.12	<=0.5	<=0.016	<=4	2	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M4031/09	1|4|37	*S. haemolyticus*	subclinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M4074-2/09	1|4|47	*S. sciuri*	subclinical		0.25	<=0.5	<=0.016	<=4	2	<=0.12	<=4	<=4	>4	2	<=1	<=1	4	<=0.25	0.5	0.5	<=1	2	<=64	*mecA1*
M4187-3/09	1|4|62	*S. xylosus*	subclinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	8	<=4	<=0.5	<=0.5	<=1	<=1	<=2	0.5	<=0.25	<=0.25	2	<=0.5	<=64	n.r.
M4195/09	1|4|63	*S. xylosus*	subclinical		<=0.12	<=0.5	<=0.016	<=4	1	<=0.12	<=4	<=4	4	1	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M4204/09	1|4|75	*S. xylosus*	subclinical		<=0.12	<=0.5	<=0.016	<=4	1	<=0.12	<=4	<=4	>4	1	2	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M4207-1/09	1|4|69	*S. xylosus*	subclinical		<=0.12	<=0.5	0.12	<=4	4	<=0.12	<=4	<=4	2	1	2	<=1	<=2	<=0.25	<=0.25	0.5	2	<=0.5	<=64	n.r.
M4207-2/09	1|4|70	*S. succinus*	subclinical		<=0.12	<=0.5	0.06	<=4	<=0.5	<=0.12	8	<=4	1	1	2	<=1	<=2	0.5	<=0.25	<=0.25	2	<=0.5	<=64	n.r.
M4208/09	1|4|76	*S. xylosus*	subclinical		<=0.12	<=0.5	<=0.016	<=4	2	<=0.12	8	<=4	1	<=0.5	2	<=1	<=2	0.5	<=0.25	<=0.25	2	<=0.5	<=64	n.r.
M4210/09	1|4|68	*S. chromogenes*	subclinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M4217/09	1|4|81	*S. sciuri*	subclinical		0.5	<=0.5	<=0.016	32	4	<=0.12	<=4	<=4	>4	2	<=1	<=1	4	<=0.25	0.5	1	2	1	<=64	*mecA1* ; *str*
M4229-1/09	2|2|3	*S. chromogenes*	subclinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	2	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M4229-2/09	2|2|4	*S. xylosus*	subclinical		0.25	>16	<=0.016	<=4	1	<=0.12	8	<=4	1	1	2	<=1	4	0.5	0.5	0.5	2	<=0.5	<=64	*tet* (K)
M4230/09	2|2|5	*S. xylosus*	subclinical		0.25	<=0.5	<=0.016	<=4	4	<=0.12	8	<=4	1	1	2	<=1	<=2	0.5	<=0.25	0.5	2	<=0.5	<=64	n.r.
M4233-1/09	2|2|8	*S. epidermidis*	subclinical		>4	>16	<=0.016	32	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	2	<=1	<=2	>8	<=0.25	<=0.25	<=1	<=0.5	<=64	*erm* (C); *str* ; *tet* (K)
M4259/09	2|2|35	*S. chromogenes*	subclinical		<=0.12	<=0.5	<=0.016	8	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M4276-1/09	2|2|16	*S. fleurettii*	subclinical		0.25	<=0.5	<=0.016	<=4	4	0.5	<=4	<=4	4	<=0.5	<=1	<=1	<=2	<=0.25	0.5	>8	<=1	<=0.5	<=64	*mecA*
M4276-2/09	2|2|17	*S. xylosus*	subclinical		<=0.12	<=0.5	0.06	<=4	1	<=0.12	<=4	<=4	>4	1	2	<=1	<=2	<=0.25	<=0.25	0.5	<=1	<=0.5	<=64	n.r.
M4298-1/09	2|2|36	*S. epidermidis*	subclinical		<=0.12	>16	<=0.016	>32	<=0.5	0.25	32	<=4	<=0.5	<=0.5	2	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	*blaZ* ; cat_{pc221} ; *str* ; *tet* (K)
M4298-2/09	2|2|37	*S. haemolyticus*	subclinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	0.25	32	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	*blaZ* ; cat_{pc223}
M4304-1/09	2|2|39	*S. xylosus*	subclinical		0.25	>16	<=0.016	<=4	1	<=0.12	<=4	<=4	>4	2	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	*tet* (K)

Name	Storage number	Species	Anamnesis	Break-points µg/ml	MIC = minimal inhibitory concentration in µg/ml																	Resistance genes
					CLI	TET	RIF	STR	FUS	PEN	CHL	KAN	TIA	SYN	VAN	GEN	TMP	ERY	CIP	OXA	LZD	MUP	SMX	
					> 0.5	> 2.0	> 0.5	> 16	> 1.0	> 0.125	> 8.0	> 8.0	> 2.0	> 2.0	> 2.0	> 1.0	> 4.0	> 2.0	> 1.0	> 0.25	> 4.0	> 256	> 128	
M4331/09	2|2|66	*Staph. sp.*	subclinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	8	<=0.5	<=0.5	<=1	<=1	8	<=0.25	<=0.25	<=0.25	<=1	<=0.5	128	n.r.
M4341-2/09	2|2|56	*S. xylosus*	subclinical		0.5	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	>4	2	<=1	<=1	<=2	8	<=0.25	0.5	<=1	<=0.5	<=64	*mph* (C)
M4347-1/09	2|2|58	*S. devriesei*	subclinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	0.25	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	0.5	<=0.25	<=1	<=0.5	<=64	*blaZ*
M4347-2/09	2|2|59	*S. xylosus*	subclinical		<=0.12	<=0.5	0.03	<=4	1	<=0.12	<=4	<=4	2	<=0.5	2	<=1	<=2	<=0.25	<=0.25	0.5	<=1	<=0.5	<=64	n.r.
M4347-3/09	2|2|60	*S. succinus*	subclinical		<=0.12	<=0.5	0.12	<=4	<=0.5	<=0.12	8	<=4	4	1	2	<=1	<=2	0.5	<=0.25	0.5	2	<=0.5	<=64	n.r.
M4349-2/09	2|2|62	*S. xylosus*	subclinical		0.25	<=0.5	<=0.016	<=4	2	<=0.12	<=4	<=4	>4	1	<=1	<=1	<=2	0.5	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M4383-1/09	2|2|76	*S. warneri*	subclinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M4385-1/09	2|2|77	*S. chromogenes*	subclinical		<=0.12	<=0.5	<=0.016	<=4	<=0.5	>2	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	*blaZ*
M4397/09	2|3|2	*S. chromogenes*	subclinical		<=0.12	<=0.5	<=0.016	>32	<=0.5	1	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	*blaZ* ; *str*
M4425/09	2|3|11	*S. simulans*	subclinical		0.25	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	2	<=0.5	<=1	<=1	4	<=0.25	<=0.25	<=0.25	2	<=0.5	<=64	n.r.
M4445/09	2|3|24	*S. equorum*	subclinical		0.25	<=0.5	<=0.016	<=4	<=0.5	<=0.12	8	<=4	2	1	2	<=1	<=2	8	<=0.25	<=0.25	2	<=0.5	<=64	*mph* (C)
M4478/09	2|3|26	*S. sciuri*	subclinical		0.25	<=0.5	<=0.016	<=4	4	<=0.12	<=4	<=4	>4	2	<=1	<=1	4	<=0.25	0.5	0.5	<=1	2	<=64	*mecA1*
M4506/09	2|3|33	*S. xylosus*	subclinical		<=0.12	<=0.5	<=0.016	<=4	4	<=0.12	<=4	<=4	<=0.5	<=0.5	2	<=1	<=2	<=0.25	<=0.25	0.5	<=1	<=0.5	<=64	n.r.

47 isolates from control milk

Name	Storage number	Species	Anamnesis	Break-points µg/ml	MIC = minimal inhibitory concentration in µg/ml																	Resistance genes
					CLI	TET	RIF	STR	FUS	PEN	CHL	KAN	TIA	SYN	VAN	GEN	TMP	ERY	CIP	OXA	LZD	MUP	SMX	
					> 0.5	> 2.0	> 0.5	> 16	> 1.0	> 0.125	> 8.0	> 8.0	> 2.0	> 2.0	> 2.0	> 1.0	> 4.0	> 2.0	> 1.0	> 0.25	> 4.0	> 256	> 128	
M107-1/10	2|3|54	*S. sciuri*	control		0.5	<=0.5	0.03	<=4	4	<=0.12	<=4	<=4	>4	2	<=1	<=1	4	<=0.25	0.5	1	<=1	1	<=64	*mecA1*
M107-2/10	2|3|55	*S. xylosus*	control		0.25	<=0.5	<=0.016	<=4	2	<=0.12	<=4	<=4	>4	2	2	<=1	<=2	<=0.25	<=0.25	0.5	<=1	<=0.5	<=64	n.r.
M108-1/10	2|3|56	*S. simulans*	control		<=0.12	4	<=0.016	<=4	<=0.5	<=0.12	8	<=4	1	<=0.5	<=1	<=1	8	<=0.25	<=0.25	<=0.25	2	<=0.5	128	*tet* (K)
M108-2/10	2|3|57	*S. chromogenes*	control		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M115-1/10	2|3|59	*S. xylosus*	control		<=0.12	>16	<=0.016	<=4	2	<=0.12	<=4	<=4	<=0.5	<=0.5	2	<=1	<=2	<=0.25	<=0.25	0.5	<=1	<=0.5	<=64	*tet* (K)
M119/10	2|3|61	*S. simulans*	control		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M132/10	2|3|65	*S. sciuri*	control		<=0.12	<=0.5	<=0.016	<=4	4	<=0.12	<=4	<=4	>4	2	<=1	<=1	<=2	<=0.25	0.5	0.5	<=1	2	<=64	*mecA1*
M205/10	2|4|6	*S. fleurettii*	control		1	>16	<=0.016	<=4	4	0.25	<=4	<=4	>4	1	<=1	<=1	<=2	8	0.5	8	<=1	<=0.5	<=64	*mecA* ; *tet* (K)
M286/10	2|4|29	*S. warneri*	control		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M432/10	2|4|63	*S. xylosus*	control		<=0.12	<=0.5	<=0.016	<=4	2	<=0.12	<=4	<=4	<=0.5	<=0.5	2	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M523/10	2|4|80	*S. epidermidis*	control		<=0.12	>16	<=0.016	>32	<=0.5	0.25	<=4	<=4	<=0.5	<=0.5	2	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	*blaZ* ; *str* ; *tet* (K)
M588/10	3|2|23	*S. equorum*	control		<=0.12	<=0.5	0.03	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	8	<=0.25	<=0.25	<=1	<=0.5	<=64	*mph* (C)
M589-1/10	3|2|24	*S. cohnii*	control		<=0.12	<=0.5	<=0.016	<=4	>4	>2	8	<=4	4	2	<=1	<=1	<=2	<=0.25	<=0.25	2	2	<=0.5	<=64	*blaZ*
M590-1/10	3|2|26	*S. chromogenes*	control		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	0.5	<=1	<=0.5	<=64	n.r.
M1326/10	4|2|9	*S. warneri*	control		<=0.12	>16	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	*tet* (K)
M1327-1/10	4|2|10	*S. haemolyticus*	control		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M1332/10	4|2|14	*S. warneri*	control		<=0.12	>16	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	*tet* (K)
M1334/10	4|2|28	*S. haemolyticus*	control		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M1335/10	4|2|15	*S. warneri*	control		<=0.12	>16	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	*tet* (K)
M1336/10	4|2|16	*S. warneri*	control		<=0.12	>16	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	*tet* (K)
M1343/10	4|2|21	*S. warneri*	control		<=0.12	>16	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	*tet* (K)
M1914/10	5|2|26	*S. haemolyticus*	control		<=0.12	<=0.5	<=0.016	<=4	<=0.5	0.25	<=4	<=4	<=0.5	<=0.5	<=1	<=1	4	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	*blaZ*
M1975-1/10	5|2|52	*S. xylosus*	control		<=0.12	<=0.5	0.06	<=4	2	<=0.12	<=4	<=4	4	1	2	<=1	<=2	<=0.25	<=0.25	0.5	<=1	<=0.5	<=64	n.r.
M2006/10	5|2|66	*S. xylosus*	control		<=0.12	<=0.5	<=0.016	<=4	2	<=0.12	<=4	<=4	>4	2	4	<=1	<=2	<=0.25	<=0.25	0.5	<=1	<=0.5	<=64	n.r.
M2026/10	5|2|77	*S. haemolyticus*	control		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	2	<=1	4	<=0.25	0.5	<=0.25	<=1	<=0.5	<=64	n.r.
M2181-2/10	5|3|56	*S. xylosus*	control		<=0.12	<=0.5	<=0.016	<=4	2	<=0.12	<=4	<=4	2	1	2	<=1	<=2	<=0.25	<=0.25	0.5	<=1	<=0.5	<=64	n.r.
M2206/10	5|3|71	*S. xylosus*	control		0.25	<=0.5	0.06	<=4	1	<=0.12	<=4	<=4	>4	2	2	<=1	<=2	<=0.25	<=0.25	0.5	<=1	<=0.5	<=64	n.r.
M3693-2/09	1|2|67	*S. warneri*	control		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M3724/09	1|2|79	*S. xylosus*	control		<=0.12	<=0.5	<=0.016	<=4	1	<=0.12	<=4	<=4	2	1	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M3747-1/09	1|3|16	*S. fleurettii*	control		<=0.12	<=0.5	<=0.016	<=4	4	<=0.12	<=4	<=4	>4	1	<=1	<=1	<=2	<=0.25	<=0.25	0.5	<=1	<=0.5	<=64	n.r.
M3747-2/09	1|3|17	*S. equorum*	control		0.25	<=0.5	<=0.016	<=4	<=0.5	<=0.12	8	<=4	4	1	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	2	<=0.5	<=64	n.r.
M3794/09	1|3|36	*S. chromogenes*	control		<=0.12	<=0.5	<=0.016	<=4	<=0.5	1	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	*blaZ*
M3827/09	1|3|47	*S. succinus*	control		<=0.12	<=0.5	0.03	<=4	<=0.5	<=0.12	8	<=4	1	1	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M3873-1/09	1|3|66	*S. xylosus*	control		0.25	>16	0.06	<=4	2	<=0.12	<=4	<=4	4	1	2	<=1	<=2	<=0.25	<=0.25	0.5	<=1	<=0.5	<=64	*tet* (K)
M4091/09	1|4|56	*S. cohnii*	control		<=0.12	1	0.25	<=4	4	0.25	64	<=4	2	2	<=1	<=1	<=2	>8	<=0.25	1	2	<=0.5	<=64	*blaZ* ; *cat* $_{pC223}$
M4093/09	1|4|57	*S. equorum*	control		0.25	<=0.5	<=0.016	8	<=0.5	<=0.12	8	<=4	4	1	2	<=1	<=2	8	<=0.25	0.5	2	<=0.5	<=64	*mph* (C)
M4203-2/09	1|4|74	*S. xylosus*	control		<=0.12	>16	0.03	<=4	2	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	0.5	<=1	<=0.5	<=64	*tet* (K)
M4283/09	2|2|20	*S. xylosus*	control		<=0.12	<=0.5	<=0.016	<=4	2	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	0.5	<=0.25	0.5	2	<=0.5	<=64	n.r.
M4406/09	2|3|3	*S. chromogenes*	control		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	2	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M4408-2/09	2|3|8	*S. chromogenes*	control		<=0.12	<=0.5	<=0.016	<=4	<=0.5	0.25	8	<=4	1	<=0.5	2	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	*blaZ*
M4411/09	2|3|4	*S. chromogenes*	control		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M4412/09	2|3|9	*S. chromogenes*	control		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	2	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M4414/09	2|3|5	*S. chromogenes*	control		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M4416/09	2|3|6	*S. chromogenes*	control		<=0.12	<=0.5	<=0.016	<=4	<=0.5	<=0.12	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M4422/09	2|3|10	*S. chromogenes*	control		<=0.12	<=0.5	<=0.016	32	<=0.5	0.5	<=4	<=4	<=0.5	<=0.5	<=1	<=1	<=2	<=0.25	<=0.25	0.5	<=1	<=0.5	<=64	*blaZ* ; *str*
M4438-1/09	2|3|17	*S. xylosus*	control		0.25	<=0.5	<=0.016	<=4	2	<=0.12	<=4	<=4	>4	2	2	<=1	<=2	<=0.25	<=0.25	<=0.25	<=1	<=0.5	<=64	n.r.
M4438-2/09	2|3|20	*S. succinus*	control		0.25	<=0.5	<=0.016	<=4	<=0.5	<=0.12	8	<=4	>4	2	2	<=1	<=2	0.5	0.5	0.5	2	1	<=64	n.r.

Labelling of genomic DNA (DeRisi method, University of California, San Francisco)

Round A

- 2,0 µl of genomic DNA from lysate
- add 0,5µl **5X Sequenase buffer** + 0,5µl **De RisiA primer** (40pmol/ µl) x No. of samples (→ 1µl mix per sample)
- denature for 2min at 94°C and cool down to 10°C for 5min in thermocycler with "DeRisiA" program
- pipet 1,25 µl of the following mix into the denatured DNA:

Mix for labelling:

for **4** reactions:	for **8** react.:	for **16** react.	for **32** react.:
1 µl **5X Sequenase buffer**	2 µl	4 µl	8 µl
1,5 µl **3mM dNTP**	3 µl	6 µl	12 µl
0,75 µl **0,1M DTT**	1,5 µl	3 µl	6 µl
1,5 µl **500 µg/ml BSA**	3 µl	6 µl	12 µl
0,4 µl **Sequenase**	0,8 µl	1,6 µl	3,2 µl

Caution: add sequenase just before pipeting the mix; directly from the fridge!

- **Program A:**
  - 8 min at 37°C (ramping from 10°C-37°C within 8 min)
  - 8 min at 37°C (constant)
  - 2 min at 94°C
  - 5 min at 10°C while adding 0,3 µl of the following mix to each sample:
    - **for 4** reactions: 0,3 µl **Sequenase** +0,9 µl **Sequenase Dil buffer**
    - **for 8** reactions: 0,6 µl **Sequenase** + 1,8 µl **Sequenase Dil buffer**
    - **for 16** reactions: 1,2 µl **Sequenase** + 3,6 µl **Sequenase Dil buffer**
  - 8 min at 37°C (ramping from 10°C-37°C within 8 min)
  - 8 min at 37°C (constant)
  - remove the samples before temperature starts to rise up to 94°C
    → 1 ¾ cycles; duration: ca. 15min
  - **add 11,0 µl water to the sample**

Round B

Preparation of premix for **8** reactions:	for **12** react.:	for **16** react.	for **32** react.
20 µl **10X PCR buffer von Roche**	30 µl	40 µl	80 µl
2 µl **100mM dNTP**	3,0 µl	4 µl	8 µl
1,6 µl **DeRisiB primer** (100pmol/ µl)	2,4 µl	3,2 µl	6,4 µl
146 µl **water**	219 µl	292 µl	584 µl
2 µl **Taq polymerase**	3,0 µl	4,0 µl	8,0 µl

- Caution: add polymerase just before pipeting the mix; directly from the fridge!
- fill 21,25 µl from this mix in each PCR tube
- add **3,75µl template** from Round A per reaction
- put in thermocycler and run the "DeRisiB" program (choose „standard 54" and store the following program)

- **Program B:**
  - 30 sec. at 94°C
  - 30 sec. at 40°C → 35 cycles; duration: ca. 2h
  - 2 min at 72 °C

Round C

	for **12** react.	for **16** react.	for **32** react.:
- Preparation of premix for **8** reactions:			
- **20** µl **10X PCR buffer von Roche**	30 µl	40 µl	80 µl
21 µl **dNTP** (1mM dACGTP & 0,65mM dTTP)	31,5 µl	42 µl	84 µl
3,2 µl **DeRisi Bbiot**	4,8 µl	6,4 µl	12,8 µl
6,2 µl **Biotin**	9,3 µl	12,4 µl	24,8 µl
2 µl **Taq Polymerase**	3,0 µl	4 µl	8 µl
119,6 µl **water**	179,4 µl	239,2 µl	478,4 µl

- Caution: add polymerase just before pipeting the mix; directly from the fridge!
- fill **21 µl** of this mix in each PCR tube
- add **4 µl template** from Round B per reaction
- put in thermocycler an run the "DeRisiC" program

- **Program C:**
  - 30 sec. at 94°C
  - 30 sec. at 40°C
  - 30 sec. at 50°C
  - 2 min. at 72°C

    → 40 cycles; duration: ca. 2h

Micro Array – Hybridization ArrayTubes – peroxidase method

Materials:

- Array tubes (5 pieces in one package)
- Biotin labeled probe (from Round C of the DeRisi PCR)
- Plastic pipettes
- **3XDNA buffer** (hybridization solution)
- **2xSSC/0,2% SDS (1A)**
- **2xSSC/0,01 % Triton (1B)**
- **2xSSC (2)**
- **0,2xSSC (3)**
- 6xSSPE/ 0,005% Triton
- **Blocking powder**
- **Streptavidin – Peroxidase**
- **Peroxidase substrate**

Protocol:

1.) Probe denaturation:

- **10 µl probe** (aus round C) + **90 µl 3DNA buffer** 95°C; 5'
- cool on ice for 2', after that centrifuge shortly

2.) Array washing (tube chips):

- wash the array with **500µl bidest H2O** 25°C; 5', 550rpm
  & take off the liquid with a plastic pipette
- wash the array with **500µl 3DNA buffer** 25°C; 5', 550rpm
  & take off the liquid with a plastic pipette
  Caution: Do not touch the fond of the tube!

3.) Hybridization:

- add **denatured probe (100 µl)** to **denatured array**
- hybridize at least 60 min (better 3h) in the "older" thermocycler at 57°C; slightliy shaking (550rpm); put the tubes in the thermocycler directly after adding the DNA – samples

After Hybridization:

1.) Washing

- 1 wash with **1A (2xSSC/0,2% SDS)** 500µl; 25°C; 5'; 550 rpm
- 2 wash with **2 (2xSSC)** 500µl; 25°C; 5'; 550 rpm
- 3 wash with **3 (0,2xSSC)** 500µl; 25°C; 5'; 550 rpm
  Take off the liquid with a plastic pipette, caution: Do not touch the fond of the tube!

2.) Blocking 100 µl; 30°C; 15'; 550 rpm

- 2% blocking powder in 6xSSPE/0,005% Triton
  - for 4 array tubes: **0,01g blocking powder** in 500 µl 6xSSPE/0,005% Triton
  - for 24 array tubes: **0,06 g blocking powder** in 3000 µl 6xSSPE/0,005% Triton

3.) Conjugation 100 µl; 30°C; 15'; 550 rpm

- dilute **Streptavidin – Peroxidase** 1: 2000 in 6xSSPE/0,005% Triton
    - for 10 array tubes: 999 µl 6xSSPE/0,005% Triton and 1 µl Streptavidin – Peroxidase
    - Streptavidin is in the fridge of alexandra's office; drawer Nr. 6; box named „DeRisi"; add it just before pipeting the mix!

4.) Washing after conjugation

- 1 wash with **1B (2xSSC/0,01 % Triton)** 500µl; 25°C; 5'; 550 rpm
- 2 wash with **2 (2xSSC)** 500µl; 25°C; 5'; 550 rpm
- 3 wash with **3 (0,2xSSC)** 500µl; 25°C; 5'; 550 rpm

5.) Precipitation

- add **100 µl Peroxidase-Substrat** and wait for about 10 min
- open the AlereTech program, Icono-clust and Icono-scan; then place the array tube into the ready (25°C) READER and click on the "eye-symbol" in the program
- save the pictures if they're good, otherwise you can wash again with the **Peroxidase-Substrat**

Microarray protocols

Raster

List with >100 antibiotic resistance genes spotted on microarray chip

Five examples for multiresistant CNS strains analyzed by microarray

Software: Iconoclust program, Alere Tech GmbH, Jena, Germany

16x16 o. MM, 150 µm Spotabstand (ID 6854)

Referenzsystem atref_auto11_gerd

16	246	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246
15		218	219	220	221	222	223	224	225	226	227	228	229	230	231	
14	246	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217
13	246	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202
12		173	174	175	176	177	178	179	180	181	182	183	184	185	186	187
11	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172
10	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156
9	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140
8	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124
7	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108
6	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92
5	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76
4	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
3	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44
2		15	16	17	18	19	20	21	22	23	24	25	26	27	28	
1	246	1	2	3	4	5	6	7	8	9	10	11	12	13	14	246
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16

leer

Biotin

Entwurf Layout 16x16 ohne MM, 150 µm Spotabstand

Spot-ID	Sondenname	Phenotype
1	be_AAC6-Ie_144	aminoglycoside resistance
2	be_AAC6-Ie_475	aminoglycoside resistance
3	be_AAC6-Ii_396	aminoglycoside resistance
4	be_AAC6-Ii_71	aminoglycoside resistance
5	be_AAC6-Im_15	aminoglycoside resistance
6	be_AAC6-Im_286	aminoglycoside resistance
7	VPAB3_ant3-Ia	aminoglycoside resistance
8	VPAB4_ant3-Ia	aminoglycoside resistance
9	be_ANT4-Ia_118	aminoglycoside resistance
10	be_ANT4-Ia_197	aminoglycoside resistance
11	be_ANT6-Ia_433	aminoglycoside resistance
12	be_ANT6-Ia_576	aminoglycoside resistance
13	be_ant(6')-Ib_179	aminoglycoside resistance
14	be_ant(6')-Ib_435	aminoglycoside resistance
15	be_ANT9-Ia_278	aminoglycoside resistance
16	be_ANT9-Ia_560	aminoglycoside resistance
17	be_APH2-Ia_149	aminoglycoside resistance
18	be_APH2-Ia_292	aminoglycoside resistance
19	be_APH2-Ib_317	aminoglycoside resistance
20	be_APH2-Ib_737	aminoglycoside resistance
21	be_APH2-Ic_346	aminoglycoside resistance
22	be_APH2-Ic_58	aminoglycoside resistance
23	be_APH2-Id_249	aminoglycoside resistance
24	be_APH2-Id_354	aminoglycoside resistance
25	VPAB1_aph2-Ie	aminoglycoside resistance
26	VPAB2_aph2-Ie	aminoglycoside resistance
27	be_APH3-III_136	aminoglycoside resistance
28	be_APH3-III_332	aminoglycoside resistance
29	be_APH3-IVa_20	aminoglycoside resistance
30	be_APH3-IVa_474	aminoglycoside resistance
31	be_aadK_175	aminoglycoside resistance
32	be_aadK_61	aminoglycoside resistance
33	VPAB5_aad9	beta-lactam resistance
34	VPAB6_aad9	beta-lactam resistance
35	be_bla1_201	beta-lactam resistance
36	be_bla1_366	beta-lactam resistance
37	be_bla2_192	beta-lactam resistance
38	be_bla2_246	beta-lactam resistance
39	be_blaZ_718	beta-lactam resistance
40	be_blaZ_811	beta-lactam resistance
41	VPAB55_blaZ_663	beta-lactam resistance
42	be_bleO_18	Bleomycin resistance
43	be_bleO_321	Bleomycin resistance
44	be_cat-86_367	chloramphenicol resistance
45	be_cat-86_605	chloramphenicol resistance
46	be_cat-Bant_402	chloramphenicol resistance
47	be_cat-Bant_613	chloramphenicol resistance

48	VP_cat-pC223_135	chloramphenicol resistance
49	VP_cat-pC223_413	chloramphenicol resistance
50	VP_cat-pC223_561	chloramphenicol resistance
51	be_cat-TC_set_170	chloramphenicol resistance
52	be_cat-TC_set_370	chloramphenicol resistance
53	be_catB_233	chloramphenicol resistance
54	be_catB_27	chloramphenicol resistance
55	be_catDP_set_267	chloramphenicol resistance
56	be_catDP_set_281	chloramphenicol resistance
57	be_catQ_186	chloramphenicol resistance
58	be_catQ_66	chloramphenicol resistance
59	be_catS_224	chloramphenicol resistance
60	be_catS_265	chloramphenicol resistance
61	VP_catpC221_411	chloramphenicol resistance
62	be_catpC221_561	chloramphenicol resistance
63	be_cfr_466	chloramphenicol, florfenicol, clindamycin, linezolid resistance
64	be_cfr_908	chloramphenicol, florfenicol, clindamycin, linezolid resistance
65	be_dfrA_172	trimethoprim resistance
66	be_dfrA_20	trimethoprim resistance
67	VP_dfrG_140	trimethoprim resistance
68	VP_dfrG_26	trimethoprim resistance
69	be_dfrD-Lmon_140	trimethoprim resistance
70	be_dfrD-Lmon_27	trimethoprim resistance
71	be_dfrK_19	trimethoprim resistance
72	be_dfrK_241	trimethoprim resistance
73	be_ereA_108	macrolide,lincosamide resistance
74	be_ereA_791	macrolide,lincosamide resistance
75	be_ereB_639	macrolide,lincosamide resistance
76	be_ereB_1209	macrolide,lincosamide resistance
77	be_ermA_193	macrolide,lincosamide resistance
78	be_ermA_590	macrolide,lincosamide resistance
79	be_ermB_112	macrolide,lincosamide resistance
80	be_ermB_520	macrolide,lincosamide resistance
81	be_ermC_149	macrolide,lincosamide resistance
82	be_ermC_372	macrolide,lincosamide resistance
83	be_ermDJK_289	macrolide,lincosamide resistance
84	be_ermDJK_841	macrolide,lincosamide resistance
85	be_ermF_231	macrolide,lincosamide resistance
86	be_ermF_494	macrolide,lincosamide resistance
87	be_ermG_296	macrolide,lincosamide resistance
88	be_ermG_98	macrolide,lincosamide resistance
89	be_ermQ_398	macrolide,lincosamide resistance
90	be_ermQ_521	macrolide,lincosamide resistance
91	be_ermT_104	macrolide,lincosamide resistance
92	be_ermT_149	macrolide,lincosamide resistance
93	be_ermX_231	macrolide,lincosamide resistance
94	be_ermX_282	macrolide,lincosamide resistance
95	be_ermY_122	macrolide,lincosamide resistance
96	be_ermY_258	macrolide,lincosamide resistance
97	be_erm33_368	macrolide,lincosamide resistance

98	be_erm33_419	macrolide,lincosamide resistance
99	be_erm34_166	macrolide,lincosamide resistance
100	be_erm34_582	macrolide,lincosamide resistance
101	be_erm36_245	macrolide,lincosamide resistance
102	be_erm36_644	macrolide,lincosamide resistance
103	be_fexA_541	macrolide,lincosamide resistance
104	be_fexA_1022	macrolide,lincosamide resistance
105	be_fusA_100	fusidic acid resistance
106	be_fusA_1359	fusidic acid resistance
107	be_fusB_337	fusidic acid resistance
108	be_fusB_453	fusidic acid resistance
109	be_fusC_247	fusidic acid resistance
110	be_fusC_406	fusidic acid resistance
111	be_fusD_329	fusidic acid resistance
112	be_fusD_510	fusidic acid resistance
113	be_lnuA_115	lincosamide resistance
114	be_lnuA_218	lincosamide resistance
115	be_lnuB_169	lincosamide resistance
116	be_lnuB_646	lincosamide resistance
117	VPAB11_lnuC	lincosamide resistance
118	VPAB12_lnuC	lincosamide resistance
119	be_lnuD_98	lincosamide resistance
120	be_lnuD_304	lincosamide resistance
121	be_lsaB_375	lincosamide resistance
122	be_lsaB_1003	lincosamide resistance
123	be_mdtA_355	macrolide, tetracycline resistance
124	be_mdtA_571	macrolide, tetracycline resistance
125	be_mecA_1042	beta-lactam resistance
126	be_mecA_871	beta-lactam resistance
127	VPAB53_mecA_1535	beta-lactam resistance
128	VPAB54_mecA_1583	beta-lactam resistance
129	be_mef_set_193	macrolide resistance
130	be_mef_set_39	macrolide resistance
131	VPAB9_mel	macrolide resistance
132	VPAB10_mel	macrolide resistance
133	VPAB31_merB	macrolide resistance
134	VPAB32_merB	macrolide resistance
135	VPAB51_mphC_281	macrolide resistance
136	VPAB52_mphC_527	macrolide resistance
137	be_mreA_420	macrolide resistance
138	be_mreA_78	macrolide resistance
139	be_msrC_1279	macrolide resistance
140	be_msrC_591	macrolide resistance
141	be_msr_set_289	macrolide resistance
142	be_msr_set_655	macrolide resistance
143	VPAB7_mupR	mupirocin resistance
144	VPAB8_mupR	mupirocin resistance
145	be_norA_1027	norfloxacin resistance
146	be_norA_427	norfloxacin resistance
147	be_sat4_161	streptothricin resistance

148	be_sat4_338	streptothricin resistance
149	be_str_334	streptomycin resistance
150	be_str_480	streptomycin resistance
151	be_tet36_116	tetracycline resistance
152	be_tet36_221	tetracycline resistance
153	VPAB29_tet38	tetracycline resistance
154	VPAB30_tet38	tetracycline resistance
155	be_tet44_171	tetracycline resistance
156	be_tet44_1433	tetracycline resistance
157	be_tetAP_244	tetracycline resistance
158	be_tetAP_290	tetracycline resistance
159	be_tetBP_1211	tetracycline resistance
160	be_tetBP_1538	tetracycline resistance
161	be_tetK_259	tetracycline resistance
162	be_tetK_351	tetracycline resistance
163	be_tetL_1_151	tetracycline resistance
164	be_tetL_1_676	tetracycline resistance
165	be_tetL_2_269	tetracycline resistance
166	be_tetL_2_504	tetracycline resistance
167	be_tetM_1378	tetracycline resistance
168	be_tetM_81	tetracycline resistance
169	be_tetO_571	tetracycline resistance
170	be_tetO_915	tetracycline resistance
171	VPAB13_tetO32O	tetracycline resistance
172	VPAB14_tetO32O	tetracycline resistance
173	VPAB15_tetWO32WO	tetracycline resistance
174	VPAB16_tetWO32WO	tetracycline resistance
175	be_tetS_18	tetracycline resistance
176	be_tetS_776	tetracycline resistance
177	be_tetT_1326	tetracycline resistance
178	be_tetT_232	tetracycline resistance
179	be_tetU_133	tetracycline resistance
180	be_tetU_191	tetracycline resistance
181	be_tetW_455	tetracycline resistance
182	be_tetW_66	tetracycline resistance
183	be_tetZ_43	tetracycline resistance
184	be_tetZ_93	tetracycline resistance
185	be_vanA_192	vancomycin resistance
186	be_vanA_884	vancomycin resistance
187	be_vanB_set_151	vancomycin resistance
188	be_vanB_set_65	vancomycin resistance
189	be_vanC-1_497	vancomycin resistance
190	be_vanC-1_77	vancomycin resistance
191	be_vanC_set_184	vancomycin resistance
192	be_vanC_set_37	vancomycin resistance
193	be_vanD1-2-3_388	vancomycin resistance
194	be_vanD1-2-3_532	vancomycin resistance
195	be_vanD4-5_183	vancomycin resistance
196	be_vanD4-5_267	vancomycin resistance
197	VPAB17_vanE	vancomycin resistance

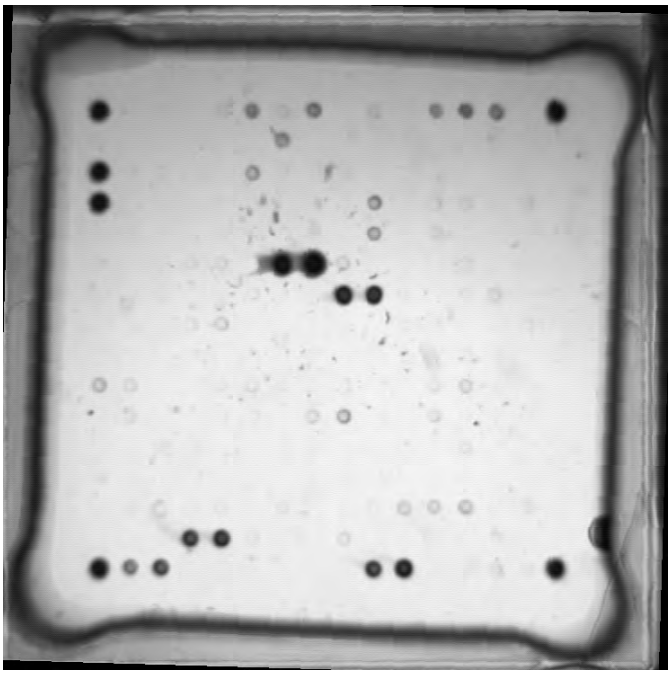
VPAB18_vanE	vancomycin resistance
be_vanG_362	vancomycin resistance
be_vanG_549	vancomycin resistance
be_vanZ_328	vancomycin resistance
be_vanZ_455	vancomycin resistance
be_vatA_288	streptogramin A resistance
be_vatA_429	streptogramin A resistance
be_vatB_109	streptogramin A resistance
be_vatB_9	streptogramin A resistance
be_vatC_474	streptogramin A resistance
be_vatC_552	streptogramin A resistance
be_vatD_234	streptogramin A resistance
be_vatD_282	streptogramin A resistance
VPAB19_vatE	streptogramin A resistance
VPAB20_vatE	streptogramin A resistance
be_vatG_19	streptogramin A resistance
be_vatG_301	streptogramin A resistance
be_vgaA_1389	streptogramin B resistance
be_vgaA_195	streptogramin B resistance
be_vgaAv_1401	streptogramin B resistance
be_vgaAv_174	streptogramin B resistance
be_vgaB_569	streptogramin B resistance
be_vgaB_649	streptogramin B resistance
be_vgaC_160	streptogramin B resistance
be_vgaC_860	streptogramin B resistance
be_vgaD_92	streptogramin B resistance
be_vgaD_800	streptogramin B resistance
be_vgaE_169	streptogramin B resistance
be_vgaE_834	streptogramin B resistance
be_vgbA_142	streptogramin B resistance
be_vgbA_281	streptogramin B resistance
be_vgbB_273	streptogramin B resistance
be_vgbB_444	streptogramin B resistance
be_lukPV_156	Penton-Valentine virulence gene
be_lukPV_1691	Penton-Valentine virulence gene
VPAB27_lukS-Si	leukocidin virulence gene
VPAB28_lukS-Si	leukocidin virulence gene
VPAB41_16S_Sther	positive control
VPAB42_16S_Sther	positive control
VPAB43_16S_Llactis	positive control
VPAB44_16S_Llactis	positive control
VPAB45_16S_Ljohn	positive control
VPAB46_16S_Ljohn	positive control
VPAB47_16S_Blactis	positive control
VPAB48_16S_Blactis	positive control
VPAB49_16S_ctrl1	positive control
VPAB50_16S_ctrl2	positive control

Biotin-Marke_2,5µM

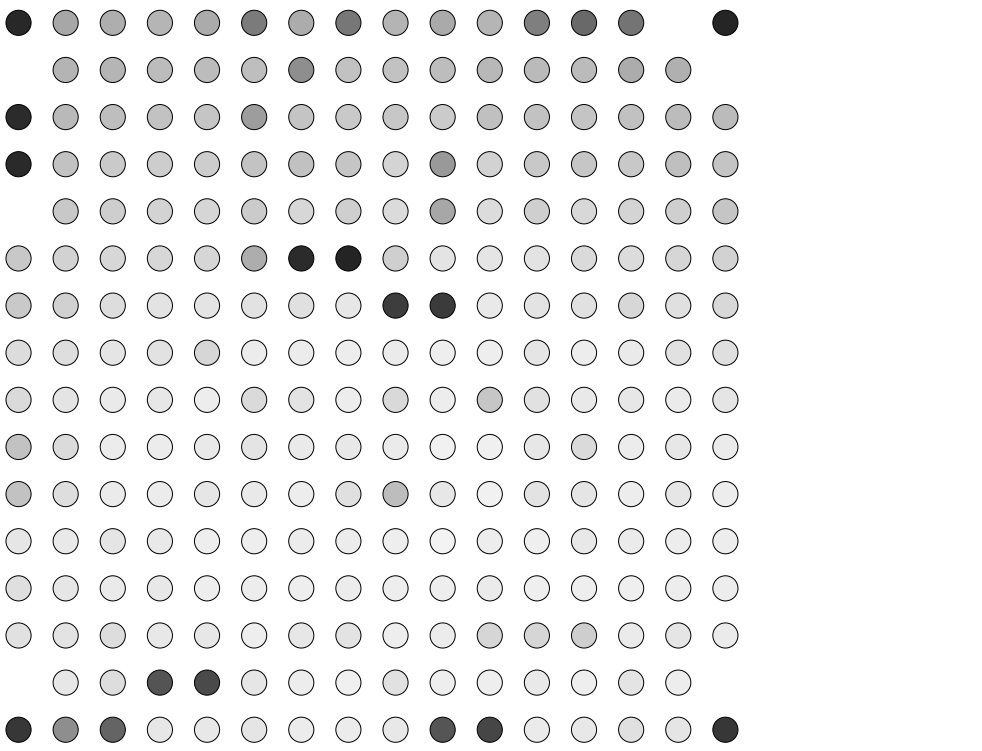
Protocol

Thu Oct 27 10:10:27 2011
Experimentator: Yvonne
M47-10
Labelling 25.10.2011

Image M47-10.bmp:



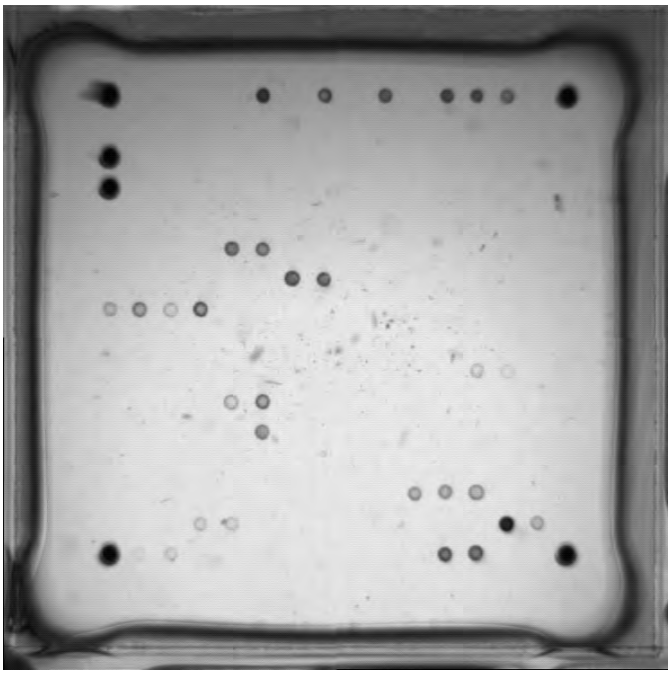
Results Mean:



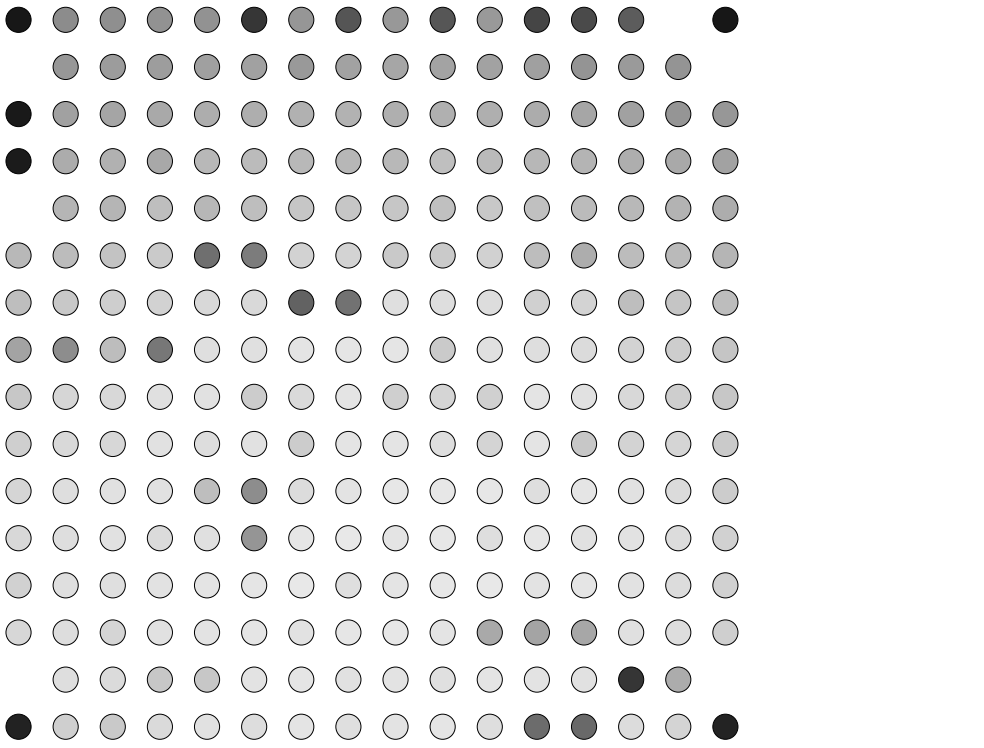
Protocol

Fri Oct 07 10:09:56 2011
Experimentator: Yvonne
M1186-10
Labelling 05.10.2011

Image M1186-10.bmp:



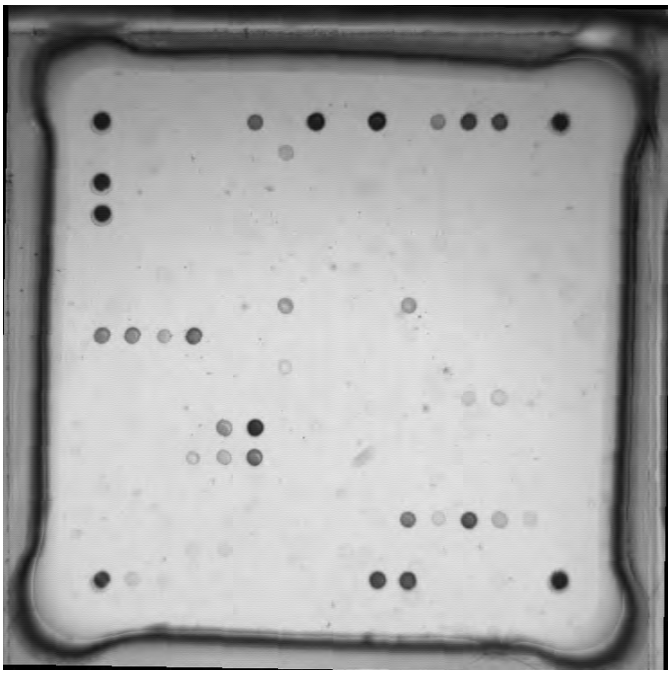
Results Mean:



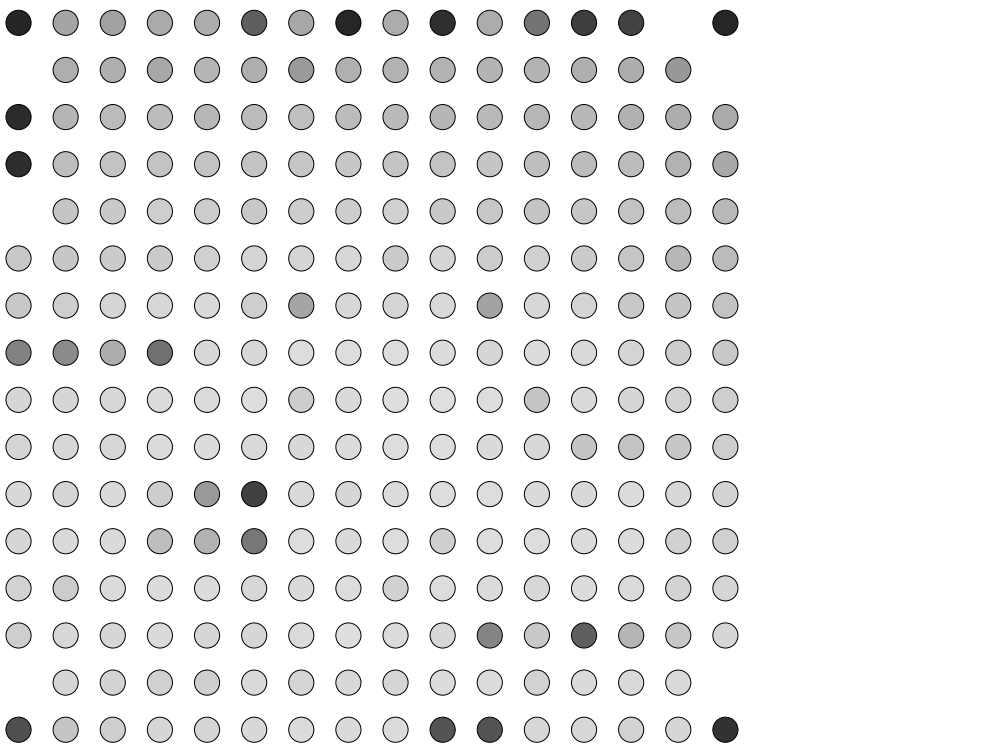
Protocol

Tue Jan 17 16:56:00 2012
Experimentator: Yvonne Frey
M1383-10n
2ter Versuch
Labelling 10.01.2012

Image M1383-10n.bmp:



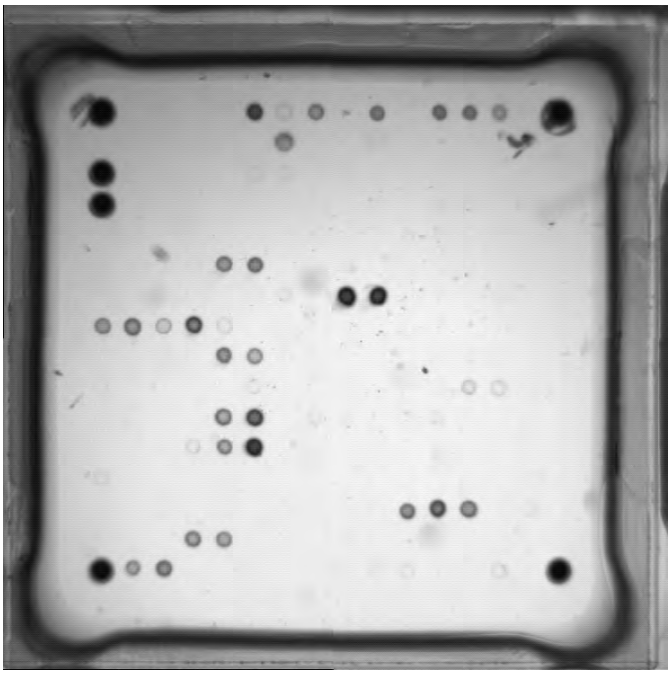
Results Mean:



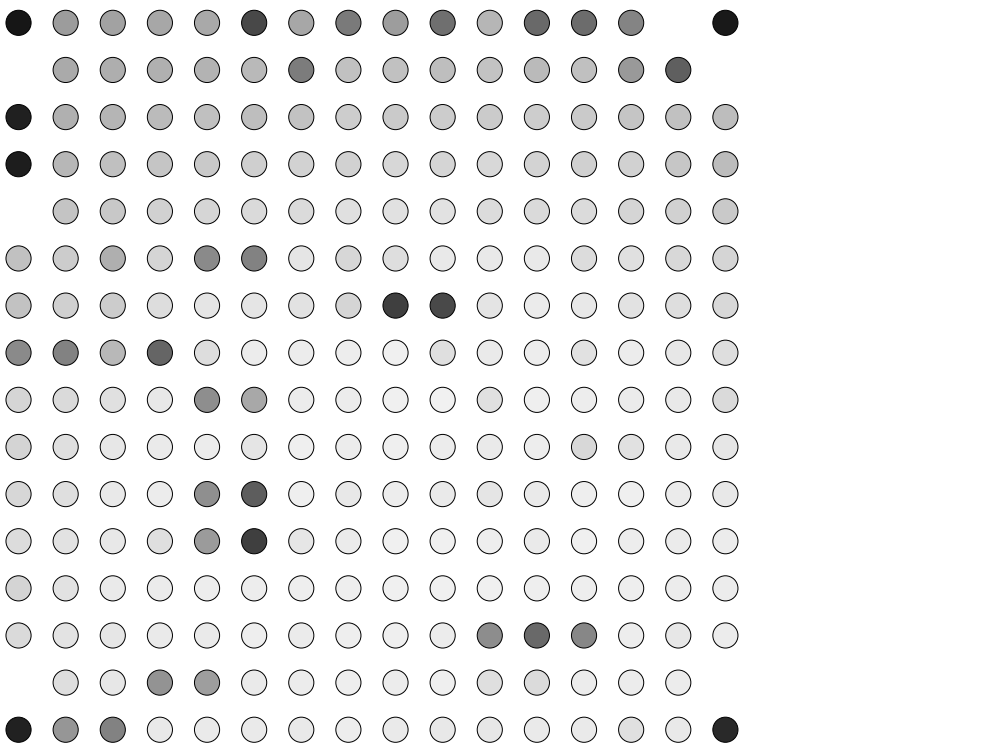
Protocol

Fri Oct 21 16:51:55 2011
Experimentator: YVONNE
M1529.10
LABLING 19.10.2011

Image M1529.10.bmp:



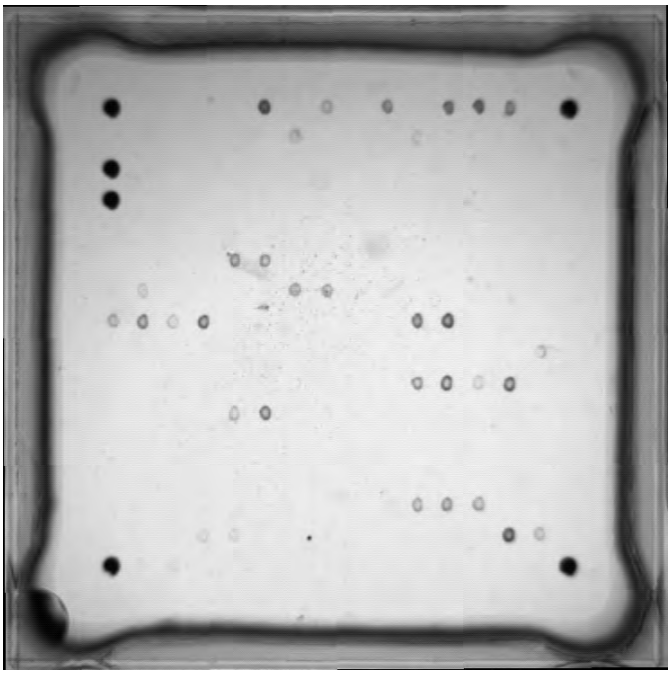
Results Mean:



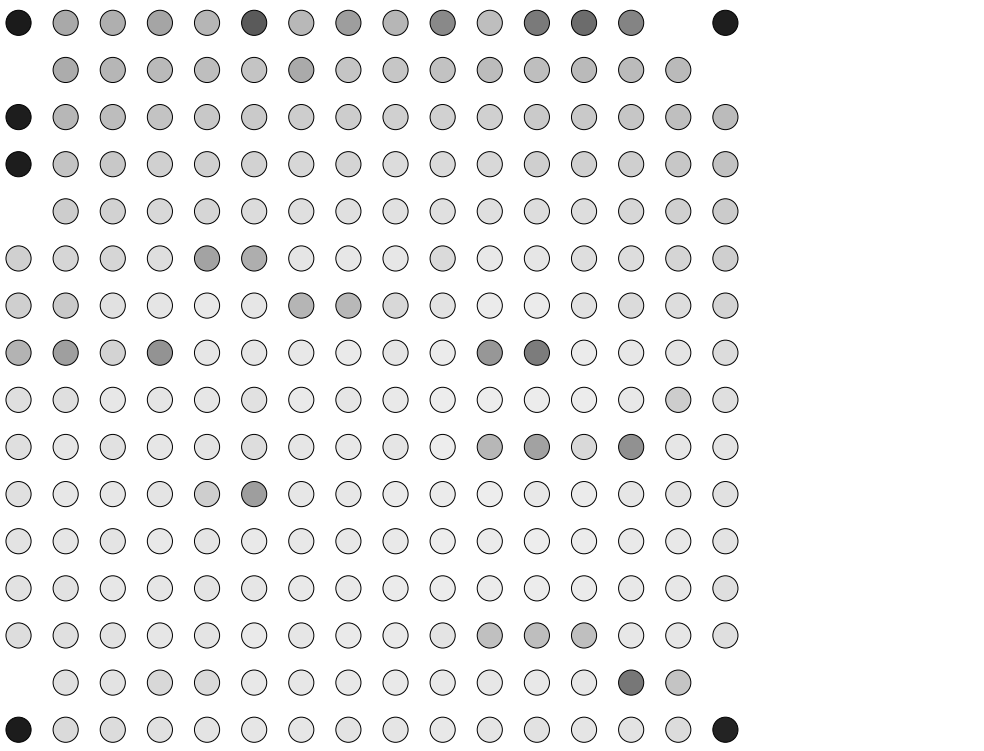
Protocol

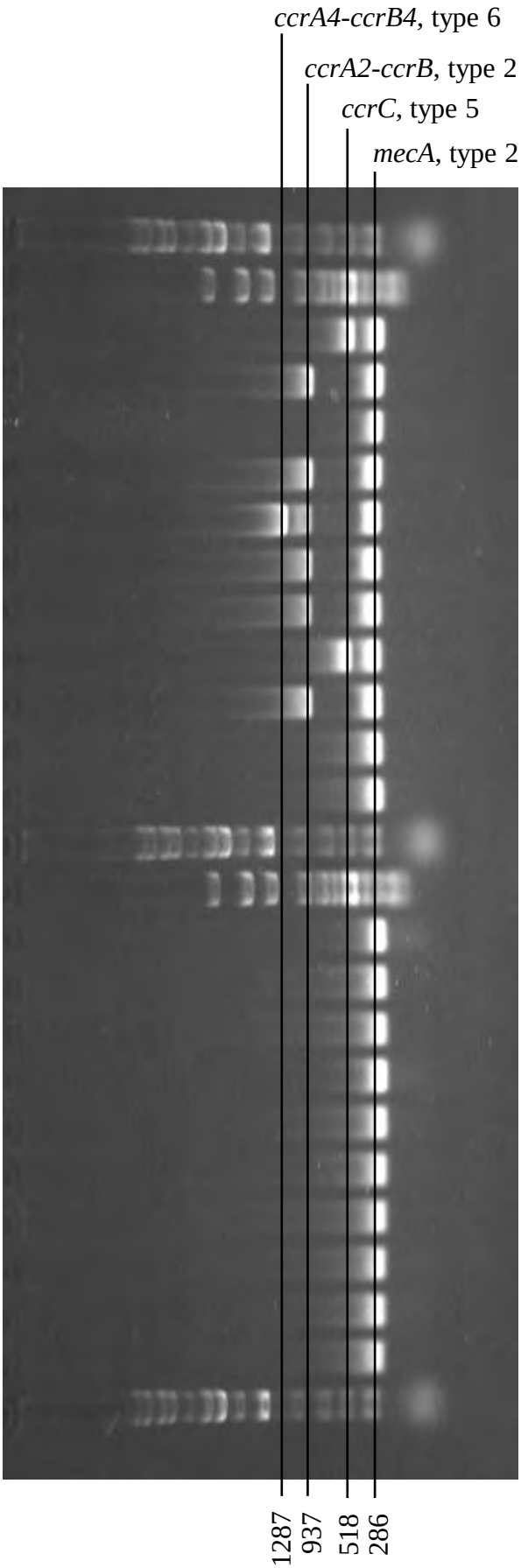
Fri Oct 07 10:26:15 2011
Experimentator: Yvonne
M1570-10
Labelling 05.10.2011

Image M1570-10.bmp:



Results Mean:





DNA Ladder 1kb
DNA Ladder 10b

control 3: IMD 1532/11
control 2: IMD 1530/11
control 1: IMD 1528/11

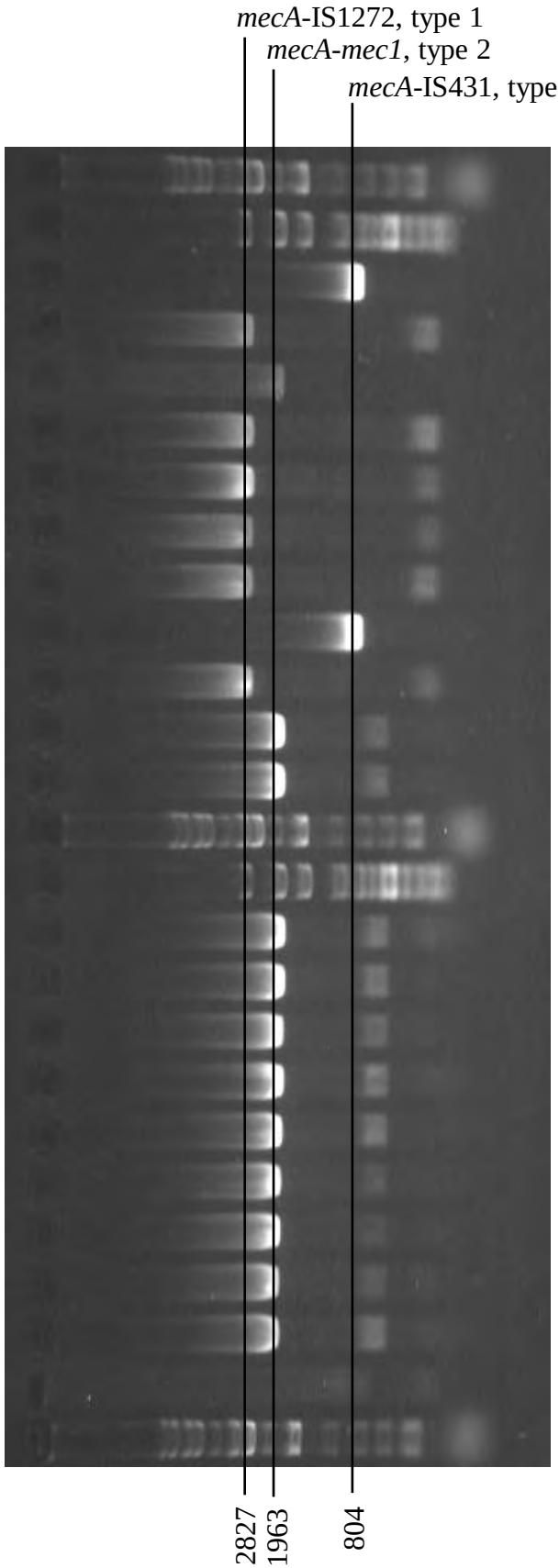
M1529/10 *S. epidermidis*
M1383/10 *S. epidermidis*
M1186/10 *S. epidermidis*
M744/10 *S. epidermidis*
M703/10 *S. epidermidis*
M8/10 *S. epidermidis*
M4276-1/09 *S. fleurettii*
M3783/09 *S. fleurettii*

DNA Ladder 1kb
DNA Ladder 10b

M1961/10 *S. fleurettii*
M1191-2/10 *S. fleurettii*
M1125-2/10 *S. fleurettii*
M545/10 *S. fleurettii*
M404-1/10 *S. fleurettii*
M277/10 *S. fleurettii*
M205/10 *S. fleurettii*
M143/10 *S. fleurettii*
M4460/90 *S. fleurettii*
M1570/10 *S. haemolyticus*

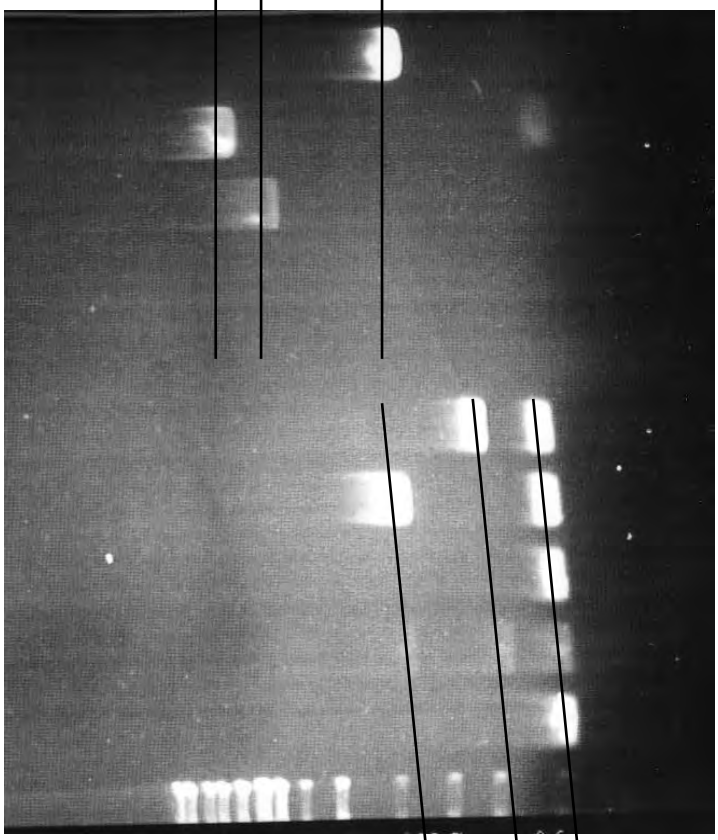
DNA Ladder 1kb

SCC*mec* typing of CNS as determined by PCR using method of Kondo et al., 2007. AAC 51(1): 264-74
Kondo – PCR 1, 18.05.2012



DNA Ladder 1kb
DNA Ladder 10b
control 3: IMD 1532/11
control 2: IMD 1530/11
control 1: IMD 1528/11
M1529/10 *S. epidermidis*
M1383/10 *S. epidermidis*
M1186/10 *S. epidermidis*
M744/10 *S. epidermidis*
M703/10 *S. epidermidis*
M8/10 *S. epidermidis*
M4276-1/09 *S. fleurettii*
M3783/09 *S. fleurettii*
DNA Ladder 1kb
DNA Ladder 10b
M1961/10 *S. fleurettii*
M1191-2/10 *S. fleurettii*
M1125-2/10 *S. fleurettii*
M545/10 *S. fleurettii*
M404-1/10 *S. fleurettii*
M277/10 *S. fleurettii*
M205/10 *S. fleurettii*
M143/10 *S. fleurettii*
M4460/09 *S. fleurettii*
M1570/10 *S. haemolyticus*
DNA Ladder 1kb

Kondo – PCR 2, 18.05.2012



Kondo – PCR 1 and 2, 15.06.2012

Table. MLST results of 13 (multi-)resistant *S. epidermidis* strains

isolates	species	arcC	aroE	gtr	mutS	pyr	tpiA	yqiL	ST (= sequence type)
M8/10	*S. epidermidis*	1	2	1	1	2	1	10	ST55
M523/10	*S. epidermidis*	1	13	2	2	2	1	7	ST111
M703/10	*S. epidermidis*	1	1	2	1	2	1	8	ST454
M744/10	*S. epidermidis*	2	1	1	1	2	1	1	ST59
M864/10	*S. epidermidis*	16	1	2	1	2	1	1	ST184
M1186/10	*S. epidermidis*	1	1	2	1	2	1	1	ST89
M1383/10	*S. epidermidis*	2	1	1	2	2	16	1	ST452
M1529/10	*S. epidermidis*	2	1	1	1	2	1	1	ST59
M1662/10	*S. epidermidis*	1	13	2	2	2	1	7	ST111
M1725/10	*S. epidermidis*	1	1	39	36	2	1	1	ST453
M1977/10	*S. epidermidis*	1	13	2	2	2	1	7	ST111
M4233-1/09	*S. epidermidis*	1	1	2	2	2*	1	1	New type
M4298-1/09	*S. epidermidis*	1	13	2	2	2	1	7	ST111

Pulsed Field Gel Electrophoresis (PFGE) for Staphylococci

Part 1: **Plugs Preparation**

- make an overnight culture of the strain on a blood agar plate
- weight an empty 1.5ml Ependorff tube
- suspend the culture in ≈ 500µl **TE-Buffer** (Tris 10mM, EDTA 100mM, pH 8.0) in this 1.5ml Eppendorff tube
- centrifuge the suspension at 14'000 rpm, 4min, through away the supernatant and dry the cell pellet
- weight the dried cell pellet and resuspend them according to the following formula in x µl **TE-Buffer**:

$$\textbf{x µl} = \frac{\textbf{weight of the cell pellet [mg] x 300 [µl]}}{\textbf{10 [mg]}}$$

- prepare an 1.5% agarose gel (**Seakem Gold agarose**): 0.3 g agarose + 20ml **0,5x TBE** and put it in a waterbath at 50°C
- pipette 200-300µl gel + 200-300µl cell suspension, mix well and mould in the plug (BioRad)
- leave in ice to solidify
- create several plugs (3-4) of each sample
- incubate the plugs in 1.2ml **TE Buffer**, pH 8.0 + 5U (= 3 µl) **Lysostaphine** at 37°C for 5-6 hours
- transfer the plugs in 2ml Eppendorff tubes, incubate overnight with **EDTA 0.5M**, 1% **N-Lauroylsarcosin**, 2mg/ml **Proteinase K**, pH 8.0 at 50°C
- transfer the plugs in a little petri dish and wash 5x 30min. with **TE Buffer** at room temperature
- store at 4°C in **EDTA 0.5M**, pH 8.0 for many months or in **TE Buffer** for many days

Part 2: **Digestion**

- (if the plugs were conserved in **EDTA 0.5M**, equilibrate in **TE Buffer**)
- equilibrate the plugs in **restriction buffer A** for 30 min at 4°C
  (360 µl H_2O+ 40 µl restriction buffer A)
- digest the DNA for 5 hours with 50U **restriction enzyme** (smaI) in 300 µl at 25°C
  (265 µl H_2O + 30 µl restriction buffer A + 5 µl enzyme (smaI))

Part 3: **Electrophoresis**

- make an 1% gel (1g **Bio Red agarose** in 100ml **0,5x TBE**)
- place plugs in slots and seal the gel (1/4 of a plug) with **low melting agarose**
- equilibrate the buffer (≈ 2L **TBE 0.5x** + 9mg/l **Thioruea**) in the machine at 12°C
- after migration, stain gel 45min. with 1U/µl **EtBr** (≈20 µl EtBr in 100ml H_2O)
- rinse 2x 20min with **H_2O**
- Electrophoresis conditions for *S. intermedius*, *S. aureus*:
  SmaI: 6V/cm, Temperature: 12°C, running time:21h; Start: 5sec., End: 40sec.

Primers used for this thesis about Antimicrobial resistance in CNS from bovine milk

Primer name	Sequence (5' –3')	Primer design, reference or source
aac(6')-aph(2')-F	CAGAGCCTTGGGAAGATGAAG	Vakulenko et al., 2003. AAC 47:1423-1426
aac(6')-aph(2')-R	CCTCGTGTAATTCATGTTCTGGC	
AIPS 27	CTAACACTGAACCCCAATG	ACME-arcA ; Diep et al. 2008. JID, 197 : 1523-1530
AIPS 28	GAGCCAGAAGTACGCGAG	
AIPS 45	GCAAATCTGTAAATGGTCTGTTC	ACME-opp3AB; Diep et al. 2008. JID, 197 : 1523-1530
AIPS 46	GAAGATTGGCAGCACAAAGTG	
ant6-I-F2	CAAGCGCAAGGGAGTATG	
ant6-I-R1	CTCTTCTATATCAGCGGC	
aph3-III-F	CCGCTGCGTAAAAGATAC	Perreten et al. 2005. J. Clin. Microbiol. 43: 2291-2302
aph3-III-R	GTCATACCACTTGTCCGC	
arcA-F	GAGCCAGAAGTACGCGAG	Barbier et al. 2011. JAC 66 :29-36
arcA-R	CACGTAACTTGCTAGAACGAG	
blaZ-F	CAGTTCACATGCCAAAGAG	Perreten et al. 2005. J. Clin.
blaZ-R1	CAGCAGGTGTTGAAGTATC	Riesen et al. 2010. Int. J. Syst. Evol. Microbiol.
catpC221-F1	CTGAATCTGATAACAACTTCACT	Institute of Veterinary Bacteriology, Bern, redesigned by VP & ChS
catpC221-R	TGAAGCATGGTAACCATCAC	Schnellmann et al. 2006. J. Clin Microbiol 44:4444-4454
catpC223-F2	AATAGTGAGGGGAATTTG	Institute of Veterinary Bacteriology, Bern, redesigned by VP & ChS
catpC223-R	ACATGGTAACCATCACATAC	Schnellmann et al. 2006. J. Clin Microbiol 44:4444-4454
dfrA-F	CCTTGGCACTTACCAAATG	Perreten et al. 2005. J. Clin. Microbiol. 43: 2291-2302
dfrA-R	CTGAAGATTCGACTTCCC	
dfrA-IS431	CCATGCCACGAAATTAGCAT	for aqcuired *dfr*(A) in *S. epidermidis*, use with dfrA-F
dfrD-F	TTCTTTAATTGTTGCGATGG	
dfrD-R	TTAACGAATTCTCTCATATATATG	
dfrG-F	ATGAAAGTTTCTTTGATTGCTGC	
dfrG-R	CCCTTTTTGGGCAAATACC	
dfrK-F	ATGAAAGTTTCTTTAATTGCTGCG	
dfrK-R	TCAAGAAGCTTTTCGCTCATAA	
erm(33)-F	GAAATYGGCTCAGGAAAAGG	
erm(A)-R	TTAGTGAAACAATTTGTAACTATTG	Institute of Veterinary Bacteriology, Bern
erm(F)-F	CGGGTCAGCACTTTACTATTG	Institute of Veterinary Bacteriology, Bern
erm(F)-R	GGACCTACCTCATAGACAAG	Institute of Veterinary Bacteriology, Bern
erm(G)-F	CATTTCCTAGCCACAATCCAT	Institute of Veterinary Bacteriology, Bern

erm(G)-R	TTAAATAGCGATACAAATTGTTCG	Institute of Veterinary Bacteriology, Bern
erm(Q)F	GAGGAAAAGTTGATATTAGTG	
erm(Q)R	GACGCAATCTACACTAGG	
ermX-F	ACCACAAGATCATCAACTC	
ermX-R	GGAAGAGATCGATCCAGT	
icA-P5	AAGATGTTGGCTGTGATTAC	Gu et al. 2005. J. Hosp. Infection: 61: 342-348
icA-P3	CAACAAGTTGAAGGCATATC	
lnuA-1	GGTGGCTGGGGGGTAGATGTATTAACTGG	
lnuA-2	GCTTCTTTTGAAATACATGGTATTTTTCGATC	
mecA-1	AAAATCGATGGTAAAGGTTGGC	Louie et al. 2002. J. Clin. Microbiol. 40: 2786-2790
mecA-2	AGTTCTGCAGTACCGGATTTGC	
mecA-F	ATGAAAAAGATAAAAATTGTTCCAC	Schnellmann et al. 2006. J. Clin. Microbiol 44:4444-4454
mecA-R	TTATTCATCTATATCGTATTTTTTATTAC	
mecA-F1	GATGATACMTTCGTTCCAC	
mecA-R1	CGAGTGCTACTCTAGCAA	
mecA-R2	TCCTGTATTGGCCAATTC	
mecA-F4	TACTGATTAACCCAGTAC	
mecA-P4	TCCAGATTACAACTTCACCAGG	Oliveira and Milheirico 2007 mecA
mecA-F5	CATTGATCGCAACGTTCAATTT	Francois et al. 2005. J Clin
mecA-F6	ATGGCAAAGATATTCAACTAAC	This study
mecA-R6	ATTGTATTGCTATTATCGTCAAC	This study
mecA-F7	GATAACACCTGCTACAC	This study
mecA-R7	AAGGGAGAAGTAACAGC	This study
mecAv-F	AAAAGATAAATCTTGGGGTG	Anneals in mecA variants of CNS
mecAv-R	CCTTGTTTCATYTTGAGTTC	
mecA LA251-F	CAGCCAGATTCATTTGTACC	
mecA LA251-R	AACATCGTACGATGGGGTAC	
mecA1-sc-F	ATTAATCATCGCCATCGTGA	This study
mecA1-sc-R	TTTGTATCTTGATTCATATTTTGAACA	This study
mecAscK1-F	CATATATATATTTATACGCTCATC	This study
mecAscK3-F	GATTTAATCAAGACTTGCATTC	This study
mecAsc-R	TTCAATGGCATCAATTGTTTC	This study
mphC-F	CATTGAATGAATCGGGAC	Perreten et al. 2005. J. Clin. Microbiol. 43: 2291-2302
mphC-R	TTCATACGCCGATTCTCC	
strpS194-F	TATTGCTCTCGAGGGTTC	Schnellmann et al. 2006. J. Clin Microbiol 44:4444-4454

strpS194-R	CTTTCTATATCCATTCATCTC	
tet(K)-1	TTAGGTGAAGGGTTAGGTCC	Perreten et al. 2005. J. Clin. Microbiol. 43: 2291-2302
tet(K)-2	GCAAACTCATTCCAGAAGCA	
Kondo multiplex PCR 1:		
mA1	TGCTATCCACCCTCAAACAGG	Type II.1 *mecA* (mA1-mA2) Kondo et al. 2007
mA2	AACGTTGTAACCACCCCAAGA	Type II.1 Kondo et al. 2007
α1	AACCTATATCATCAATCAGTACGT	Type I.1 *ccrA1-ccrB* Kondo et al. 2007
α2	TAAAGGCATCAATGCACAAACACT	Type II.1 *ccrA2-ccrB* Kondo et al. 2007
α3	AGCTCAAAAGCAAGCAATAGAAT	III.1 *ccrA3-ccrB* Kondo et al. 2007
βc	ATTGCCTTGATAATAGCCITCT	*ccrB1*, *ccrB2*,*ccrB3* Type I.1,II.1, III.1 Kondo et al. 2007
α4.2	GTATCAATGCACCAGAACTT	Type VI *ccrA4-ccrB4* Kondo et al. 2007
β4.2	TTGCGACTCTCTTGGCGTTT	Type VI Kondo et al. 2007
γR	CCTTTATAGACTGGATTATTCAAAATAT	type V *ccrC* Kondo et al. 2007
γF	CGTCTATTACAAGATGTTAAGGATAAT	type V Kondo et al. 2007
Kondo multiplex PCR 2:		
ml6	CATAACTTCCCATTCTGCAGATG	Type II.1 *mecA-mecI* Kondo et al. 2007
IS7	ATGCTTAATGATAGCATCCGAATG	Type I.1 *mecA*-IS*1272* upstream of *mecA* Kondo et al. 2007
IS2 (iS-2)	TGAGGTTATTCAGATATTTCGATGT	Type V *mecA*-IS*431* upstream of *mecA* Kondo et al. 2007
mA7	ATATACCAAACCCGACAACTACA	Type I.1, II.1 mecA Kondo et al. 2007
MLST – Primer:		
arcC-F	TGTGATGAGCACGCTACCGTTAG	Thomas et al. 2007 JMC.01934-06: 616-619
arcC-R	TCCAAGTAAACCCATCGGTCTG	
aroE-F	CATTGGATTACCTCTTTGTTCAGC	Thomas et al. 2007 JMC.01934-06: 616-619
aroE-R	CAAGCGAAATCTGTTGGGG	
gtr-F	CAGCCAATTCTTTTATGACTTTT	Thomas et al. 2007 JMC.01934-06: 616-619
gtr-R	GTGATTAAAGGTATTGATTTGAAT	
gtr-R1	GAAACTGAAGTGATTAAAGG	This study
mutS-F3	GATATAAGAATAAGGGTTGTGAA	Thomas et al. 2007 JMC.01934-06: 616-619
mutS-R3	GTAATCGTCTCAGTTATCATGTT	
pyr-F2	GTTACTAATACTTTTGCTGTGTTT	Thomas et al. 2007 JMC.01934-06: 616-619
pyr-R4	GTAGAATGTAAAGAGACTAAAATGAA	
tpi-F2	ATCCAATTAGACGCTTTAGTAAC	Thomas et al. 2007 JMC.01934-06: 616-619
tpi-R2	TTAATGATGCGCCACCTACA	
yqil-F2	CACGCATAGTATTAGCTGAAG	Thomas et al. 2007 JMC.01934-06: 616-619
yqil-R2	CTAATGCCTTCATCTTGAGAAATAA	

Sequence alignment of methicillin resistance gene *mecA* in *S. epidermidis* isolates

using MultAlign Program http://multalin.toulouse.inra.fr/multalin/

Reference strains:

- *S.aureus* N315
- *S.epidermidis* RPA62A

```
             1                                                                                                                          130
 S.aurN315  ATGAAAAAGA TAAAAATTGT TCCACTTATT TTAATAGTTG TAGTTGTCGG GTTTGGTATA TATTTTTATG CTTCCAAAGA TAAAGAAATT AATAATACTA TTGATGCAAT TGAAGATAAA AATTTCAAAC
S.epiRP62A  ATGAAAAAGA TAAAAATTGT TCCACTTATT TTAATAGTTG TAGTTGTCGG GTTTGGTATA TATTTTTATG CTTCAAAAGA TAAAGAAATT AATAATACTA TTGATGCAAT TGAAGATAAA AATTTCAAAC
   M744/10  ATGAAAAAGA TAAAAATTGT TCCACTTATT TTAATAGTTG TAGTTGTCGG GTTTGGTATA TATTTTTATG CTTCAAAAGA TAAAGAAATT AATAATACTA TTGATGCAAT TGAAGATAAA AATTTCAAAC
  M1529/10  ATGAAAAAGA TAAAAATTGT TCCACTTATT TTAATAGTTG TAGTTGTCGG GTTTGGTATA TATTTTTATG CTTCAAAAGA TAAAGAAATT AATAATACTA TTGATGCAAT TGAAGATAAA AATTTCAAAC
  M1383/10  ATGAAAAAGA TAAAAATTGT TCCACTTATT TTAATAGTTG TAGTTGTCGG GTTTGGTATA TATTTTTATG CTTCAAAAGA TAAAGAAATT AATAATACTA TTGATGCAAT TGAAGATAAA AATTTCAAAC
  M1186/10  ATGAAAAAGA TAAAAATTGT TCCACTTATT TTAATAGTTG TAGTTGTCGG GTTTGGTATA TATTTTTATG CTTCAAAAGA TAAAGAAATT AATAATACTA TTGATGCAAT TGAAGATAAA AATTTCAAAC
   M703/10  ATGAAAAAGA TAAAAATTGT TCCACTTATT TTAATAGTTG TAGTTGTCGG GTTTGGTATA TATTTTTATG CTTCAAAAGA TAAAGAAATT AATAATACTA TTGATGCAAT TGAAGATAAA AATTTCAAAC
     M8/10  ATGAAAAAGA TAAAAATTGT TCCACTTATT TTAATAGTTG TAGTTGTCGG GTTTGGTATA TATTTTTATG CTTCAAAAGA TAAAGAAATT AATAATACTA TTGATGCAAT TGAAGATAAA AATTTCAAAC
 Consensus  ATGAAAAAGA TAAAAATTGT TCCACTTATT TTAATAGTTG TAGTTGTCGG GTTTGGTATA TATTTTTATG CTTCaAAAGA TAAAGAAATT AATAATACTA TTGATGCAAT TGAAGATAAA AATTTCAAAC

             131                                                                                                                        260
 S.aurN315  AAGTTTATAA AGATAGCAGT TATATTTCTA AAAGCGATAA TGGTGAAGTA GAAATGACTG AACGTCCGAT AAAAATATAT AATAGTTTAG GCGTTAAAGA TATAAACATT CAGGATCGTA AAATAAAAAA
S.epiRP62A  AAGTTTATAA AGATAGCAGT TATATTTCTA AAAGCGATAA TGGTGAAGTA GAAATGACTG AACGTCCGAT AAAAATATAT AATAGTTTAG GCGTTAAAGA TATAAACATT CAGGATCGTA AAATAAAAAA
   M744/10  AAGTTTATAA AGATAGCAGT TATATTTCTA AAAGCGATAA TGGTGAAGTA GAAATGACTG AACGTCCGAT AAAAATATAT AATAGTTTAG GCGTTAAAGA TATAAACATT CAGGATCGTA AAATAAAAAA
  M1529/10  AAGTTTATAA AGATAGCAGT TATATTTCTA AAAGCGATAA TGGTGAAGTA GAAATGACTG AACGTCCGAT AAAAATATAT AATAGTTTAG GCGTTAAAGA TATAAACATT CAGGATCGTA AAATAAAAAA
  M1383/10  AAGTTTATAA AGATAGCAGT TATATTTCTA AAAGCGATAA TGGTGAAGTA GAAATGACTG AACGTCCGAT AAAAATATAT AATAGTTTAG GCGTTAAAGA TATAAACATT CAGGATCGTA AAATAAAAAA
  M1186/10  AAGTTTATAA AGATAGCAGT TATATTTCTA AAAGCGATAA TGGTGAAGTA GAAATGACTG AACGTCCGAT AAAAATATAT AATAGTTTAG GCGTTAAAGA TATAAACATT CAGGATCGTA AAATAAAAAA
   M703/10  AAGTTTATAA AGATAGCAGT TATATTTCTA AAAGCGATAA TGGTGAAGTA GAAATGACTG AACGTCCGAT AAAAATATAT AATAGTTTAG GCGTTAAAGA TATAAACATT CAGGATCGTA AAATAAAAAA
     M8/10  AAGTTTATAA AGATAGCAGT TATATTTCTA AAAGCGATAA TGGTGAAGTA GAAATGACTG AACGTCCGAT AAAAATATAT AATAGTTTAG GCGTTAAAGA TATAAACATT CAGGATCGTA AAATAAAAAA
 Consensus  AAGTTTATAA AGATAGCAGT TATATTTCTA AAAGCGATAA TGGTGAAGTA GAAATGACTG AACGTCCGAT AAAAATATAT AATAGTTTAG GCGTTAAAGA TATAAACATT CAGGATCGTA AAATAAAAAA

             261                                                                                                                        390
 S.aurN315  AGTATCTAAA AATAAAAAAC GAGTAGATGC TCAATATAAA ATTAAAACAA ACTACGGTAA CATTGATCGC AACGTTCAAT TTAATTTTGT TAAAGAAGAT GGTATGTGGA AGTTAGATTG GGATCATAGC
S.epiRP62A  AGTATCTAAA AATAAAAAAC GAGTAGATGC TCAATATAAA ATTAAAACAA ACTACGGTAA CATTGATCGC AACGTTCAAT TTAATTTTGT TAAAGAAGAT GGTATGTGGA AGTTAGATTG GGATCATAGC
   M744/10  AGTATCTAAA AATAAAAAAC GAGTAGATGC TCAATATAAA ATTAAAACAA ACTACGGTAA CATTGATCGC AACGTTCAAT TTAATTTTGT TAAAGAAGAT GGTATGTGGA AGTTAGATTG GGATCATAGC
  M1529/10  AGTATCTAAA AATAAAAAAC GAGTAGATGC TCAATATAAA ATTAAAACAA ACTACGGTAA CATTGATCGC AACGTTCAAT TTAATTTTGT TAAAGAAGAT GGTATGTGGA AGTTAGATTG GGATCATAGC
  M1383/10  AGTATCTAAA AATAAAAAAC GAGTAGATGC TCAATATAAA ATTAAAACAA ACTACGGTAA CATTGATCGC AACGTTCAAT TTAATTTTGT TAAAGAAGAT GGTATGTGGA AGTTAGATTG GGATCATAGC
  M1186/10  AGTATCTAAA AATAAAAAAC GAGTAGATGC TCAATATAAA ATTAAAACAA ACTACGGTAA CATTGATCGC AACGTTCAAT TTAATTTTGT TAAAGAAGAT GGTATGTGGA AGTTAGATTG GGATCATAGC
   M703/10  AGTATCTAAA AATAAAAAAC GAGTAGATGC TCAATATAAA ATTAAAACAA ACTACGGTAA CATTGATCGC AACGTTCAAT TTAATTTTGT TAAAGAAGAT GGTATGTGGA AGTTAGATTG GGATCATAGC
     M8/10  AGTATCTAAA AATAAAAAAC GAGTAGATGC TCAATATAAA ATTAAAACAA ACTACGGTAA CATTGATCGC AACGTTCAAT TTAATTTTGT TAAAGAAGAT GGTATGTGGA AGTTAGATTG GGATCATAGC
 Consensus  AGTATCTAAA AATAAAAAAC GAGTAGATGC TCAATATAAA ATTAAAACAA ACTACGGTAA CATTGATCGC AACGTTCAAT TTAATTTTGT TAAAGAAGAT GGTATGTGGA AGTTAGATTG GGATCATAGC

             391                                                                                                                        520
 S.aurN315  GTCATTATTC CAGGAATGCA GAAAGACCAA AGCATACATA TTGAAAATTT AAAATCAGAA CGTGGTAAAA TTTTAGACCG AAACAATGTG GAATTGGCCA ATACAGGAAC AGCATATGAG ATAGGCATCG
S.epiRP62A  GTCATTATTC CAGGAATGCA GAAAGACCAA AGCATACATA TTGAAAATTT AAAATCAGAA CGTGGTAAAA TTTTAGACCG AAACAATGTG GAATTGGCCA ATACAGGAAC AGCATATGAG ATAGGCATCG
   M744/10  GTCATTATTC CAGGAATGCA GAAAGACCAA AGCATACATA TTGAAAATTT AAAATCAGAA CGTGGTAAAA TTTTAGACCG AAACAATGTG GAATTGGCCA ATACAGGAAC AGCATATGAG ATAGGCATCG
  M1529/10  GTCATTATTC CAGGAATGCA GAAAGACCAA AGCATACATA TTGAAAATTT AAAATCAGAA CGTGGTAAAA TTTTAGACCG AAACAATGTG GAATTGGCCA ATACAGGAAC AGCATATGAG ATAGGCATCG
  M1383/10  GTCATTATTC CAGGAATGCA GAAAGACCAA AGCATACATA TTGAAAATTT AAAATCAGAA CGTGGTAAAA TTTTAGACCG AAACAATGTG GAATTGGCCA ATACAGGAAC AGCATATGAG ATAGGCATCG
  M1186/10  GTCATTATTC CAGGAATGCA GAAAGACCAA AGCATACATA TTGAAAATTT AAAATCAGAA CGTGGTAAAA TTTTAGACCG AAACAATGTG GAATTGGCCA ATACAGGAAC AGCATATGAG ATAGGCATCG
   M703/10  GTCATTATTC CAGGAATGCA GAAAGACCAA AGCATACATA TTGAAAATTT AAAATCAGAA CGTGGTAAAA TTTTAGACCG AAACAATGTG GAATTGGCCA ATACAGGAAC AGCATATGAG ATAGGCATCG
     M8/10  GTCATTATTC CAGGAATGCA GAAAGACCAA AGCATACATA TTGAAAATTT AAAATCAGAA CGTGGTAAAA TTTTAGACCG AAACAATGTG GAATTGGCCA ATACAGGAAC AGCATATGAG ATAGGCATCG
 Consensus  GTCATTATTC CAGGAATGCA GAAAGACCAA AGCATACATA TTGAAAATTT AAAATCAGAA CGTGGTAAAA TTTTAGACCG AAACAATGTG GAATTGGCCA ATACAGGAAC AGCATATGAG ATAGGCATCG
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            521                                                                                                                    650
S.aurN315   TTCCAAAGAA TGTATCTAAA AAAGATTATA AAGCAATCGC TAAAGAACTA AGTATTTCTG AAGACTATAT CAAACAACAA ATGGATCAAA ATTGGGTACA AGATGATACC TTCGTTCCAC TTAAAACCGT
S.epiRP62A  TTCCAAAGAA TGTATCTAAA AAAGATTATA AAGCAATCGC TAAAGAACTA AGTATTTCTG AAGACTATAT CAAACAACAA ATGGATCAAA ATTGGGTACA AGATGATACC TTCGTTCCAC TTAAAACCGT
M744/10     TTCCAAAGAA TGTATCTAAA AAAGATTATA AAGCAATCGC TAAAGAACTA AGTATTTCTG AAGACTATAT CAAACAACAA ATGGATCAAA ATTGGGTACA AGATGATACC TTCGTTCCAC TTAAAACCGT
M1529/10    TTCCAAAGAA TGTATCTAAA AAAGATTATA AAGCAATCGC TAAAGAACTA AGTATTTCTG AAGACTATAT CAAACAACAA ATGGATCAAA ATTGGGTACA AGATGATACC TTCGTTCCAC TTAAAACCGT
M1383/10    TTCCAAAGAA TGTATCTAAA AAAGATTATA AAGCAATCGC TAAAGAACTA AGTATTTCTG AAGACTATAT CAAACAACAA ATGGATCAAA ATTGGGTACA AGATGATACC TTCGTTCCAC TTAAAACCGT
M1186/10    TTCCAAAGAA TGTATCTAAA AAAGATTATA AAGCAATCGC TAAAGAACTA AGTATTTCTG AAGACTATAT CAAACAACAA ATGGATCAAA ATTGGGTACA AGATGATACC TTCGTTCCAC TTAAAACCGT
M703/10     TTCCAAAGAA TGTATCTAAA AAAGATTATA AAGCAATCGC TAAAGAACTA AGTATTTCTG AAGACTATAT CAAACAACAA ATGGATCAAA ATTGGGTACA AGATGATACC TTCGTTCCAC TTAAAACCGT
M8/10       TTCCAAAGAA TGTATCTAAA AAAGATTATA AAGCAATCGC TAAAGAACTA AGTATTTCTG AAGACTATAT CAAACAACAA ATGGATCAAA ATTGGGTACA AGATGATACC TTCGTTCCAC TTAAAACCGT
Consensus   TTCCAAAGAA TGTATCTAAA AAAGATTATA AAGCAATCGC TAAAGAACTA AGTATTTCTG AAGACTATAT CAAACAACAA ATGGATCAAA ATTGGGTACA AGATGATACC TTCGTTCCAC TTAAAACCGT

            651                                                                                                                    780
S.aurN315   TAAAAAAATG GATGAATATT TAAGTGATTT CGCAAAAAAA TTTCATCTTA CAACTAATGA AACAGAAAGT CGTAACTATC CTCTAGGAAA AGCGACTTCA CATCTATTAG GTTATGTTGG TCCCATTAAC
S.epiRP62A  TAAAAAAATG GATGAATATT TAAGTGATTT CGCAAAAAAA TTTCATCTTA CAACTAATGA AACAGAAAGT CGTAACTATC CTCTAGGAAA AGCGACTTCA CATCTATTAG GTTATGTTGG TCCCATTAAC
M744/10     TAAAAAAATG GATGAATATT TAAGTGATTT CGCAAAAAAA TTTCATCTTA CAACTAATGA AACAGAAAGT CGTAACTATC CTCTAGGAAA AGCGACTTCA CATCTATTAG GTTATGTTGG TCCCATTAAC
M1529/10    TAAAAAAATG GATGAATATT TAAGTGATTT CGCAAAAAAA TTTCATCTTA CAACTAATGA AACAGAAAGT CGTAACTATC CTCTAGGAAA AGCGACTTCA CATCTATTAG GTTATGTTGG TCCCATTAAC
M1383/10    TAAAAAAATG GATGAATATT TAAGTGATTT CGCAAAAAAA TTTCATCTTA CAACTAATGA AACAGAAAGT CGTAACTATC CTCTAGGAAA AGCGACTTCA CATCTATTAG GTTATGTTGG TCCCATTAAC
M1186/10    TAAAAAAATG GATGAATATT TAAGTGATTT CGCAAAAAAA TTTCATCTTA CAACTAATGA AACAGAAAGT CGTAACTATC CTCTAGGAAA AGCGACTTCA CATCTATTAG GTTATGTTGG TCCCATTAAC
M703/10     TAAAAAAATG GATGAATATT TAAGAGATTT CGCAAAAAAA TTTCATCTTA CAACTAATGA AACAGAAAGT CGTAACTATC CTCTAGGAAA AGCGACTTCA CATCTATTAG GTTATGTTGG TCCCATTAAC
M8/10       TAAAAAAATG GATGAATATT TAAGTGATTT CGCAAAAAAA TTTCATCTTA CAACTAATGA AACAGAAAGT CGTAACTATC CTCTAGAAAA AGCGACTTCA CATCTATTAG GTTATGTTGG TCCCATTAAC
Consensus   TAAAAAAATG GATGAATATT TAAGtGATTT CGCAAAAAAA TTTCATCTTA CAACTAATGA AACAGAAAGT CGTAACTATC CTCTAGgAAA AGCGACTTCA CATCTATTAG GTTATGTTGG TCCCATTAAC

            781                                                                                                                    910
S.aurN315   TCTGAAGAAT TAAAACAAAA AGAATATAAA GGCTATAAAG ATGATGCAGT TATTGGTAAA AAGGGACTCG AAAAACTTTA CGATAAAAAG CTCCAACATG AAGATGGCTA TCGTGTCACA ATCGTTGACG
S.epiRP62A  TCTGAAGAAT TAAAACAAAA AGAATATAAA GGCTATAAAG ATGATGCAGT TATTGGTAAA AAGGGACTCG AAAAACTTTA CGATAAAAAG CTCCAACATG AAGATGGCTA TCGTGTCACA ATCGTTGACG
M744/10     TCTGAAGAAT TAAAACAAAA AGAATATAAA GGCTATAAAG ATGATGCAGT TATTGGTAAA AAGGGACTCG AAAAACTTTA CGATAAAAAG CTCCAACATG AAGATGGCTA TCGTGTCACA ATCGTTGACG
M1529/10    TCTGAAGAAT TAAAACAAAA AGAATATAAA GGCTATAAAG ATGATGCAGT TATTGGTAAA AAGGGACTCG AAAAACTTTA CGATAAAAAG CTCCAACATG AAGATGGCTA TCGTGTCACA ATCGTTGACG
M1383/10    TCTGAAGAAT TAAAACAAAA AGAATATAAA GGCTATAAAG ATGATGCAGT TATTGGTAAA AAGGGACTCG AAAAACTTTA CGATAAAAAG CTCCAACATG AAGATGGCTA TCGTGTCACA ATCGTTGACG
M1186/10    TCTGAAGAAT TAAAACAAAA AGAATATAAA GGCTATAAAG ATGATGCAGT TATTGGTAAA AAGGGACTCG AAAAACTTTA CGATAAAAAG CTCCAACATG AAGATGGCTA TCGTGTCACA ATCGTTGACG
M703/10     TCTGAAGAAT TAAAACAAAA AGAATATAAA GGCTATAAAG ATGATGCAGT TATTGGTAAA AAGGGACTCG AAAAACTTTA CGATAAAAAG CTCCAACATG AAGATGGCTA TCGTGTCACA ATCGTTGACG
M8/10       TCTGAAGAAT TAAAACAAAA AGAATATAAA GGCTATAAAG ATGATGCAGT TATTGGTAAA AAGGGACTCG AAAAACTTTA CGATAAAAAG CTCCAACATG AAGATGGCTA TCGTGTCACA ATCGTTGACG
Consensus   TCTGAAGAAT TAAAACAAAA AGAATATAAA GGCTATAAAG ATGATGCAGT TATTGGTAAA AAGGGACTCG AAAAACTTTA CGATAAAAAG CTCCAACATG AAGATGGCTA TCGTGTCACA ATCGTTGACG

            911                                                                                                                   1040
S.aurN315   ATAATAGCAA TACAATCGCA CATACATTAA TAGAGAAAAA GAAAAAAGAT GGCAAAGATA TTCAACTAAC TATTGATGCT AAAGTTCAAA AGAGTATTTA TAACAACATG AAAAATGATT ATGGCTCAGG
S.epiRP62A  ATAATAGCAA TACAATCGCA CATACATTAA TAGAGAAAAA GAAAAAAGAT GGCAAAGATA TTCAACTAAC TATTGATGCT AAAGTTCAAA AGAGTATTTA TAACAACATG AAAAATGATT ATGGCTCAGG
M744/10     ATAATAGCAA TACAATCGCA CATACATTAA TAGAGAAAAA GAAAAAAGAT GGCAAAGATA TTCAACTAAC TATTGATGCT AAAGTTCAAA AGAGTATTTA TAACAACATG AAAAATGATT ATGGCTCAGG
M1529/10    ATAATAGCAA TACAATCGCA CATACATTAA TAGAGAAAAA GAAAAAAGAT GGCAAAGATA TTCAACTAAC TATTGATGCT AAAGTTCAAA AGAGTATTTA TAACAACATG AAAAATGATT ATGGCTCAGG
M1383/10    ATAATAGCAA TACAATCGCA CATACATTAA TAGAGAAAAA GAAAAAAGAT GGCAAAGATA TTCAACTAAC TATTGATGCT AAAGTTCAAA AGAGTATTTA TAACAACATG AAAAATGATT ATGGCTCAGG
M1186/10    ATAATAGCAA TACAATCGCA CATACATTAA TAGAGAAAAA GAAAAAAGAT GGCAAAGATA TTCAACTAAC TATTGATGCT AAAGTTCAAA AGAGTATTTA TAACAACATG AAAAATGATT ATGGCTCAGG
M703/10     ATAATAGCAA TACAATCGCA CATACATTAA TAGAGAAAAA GAAAAAAGAT GGCAAAGATA TTCAACTAAC TATTGATGCT AAAGTTCAAA AGAGTATTTA TAACAACATG AAAAATGATT ATGGCTCAGG
M8/10       ATAATAGCAA TACAATCGCA CATACATTAA TAGAGAAAAA GAAAAAAGAT GGCAAAGATA TTCAACTAAC TATTGATGCT AAAGTTCAAA AGAGTATTTA TAACAACATG AAAAATGATT ATGGCTCAGG
Consensus   ATAATAGCAA TACAATCGCA CATACATTAA TAGAGAAAAA GAAAAAAGAT GGCAAAGATA TTCAACTAAC TATTGATGCT AAAGTTCAAA AGAGTATTTA TAACAACATG AAAAATGATT ATGGCTCAGG

            1041                                                                                                                  1170
S.aurN315   TACTGCTATC CACCCTCAAA CAGGTGAATT ATTAGCACTT GTAAGCACAC CTTCATATGA CGTCTATCCA TTTATGTATG GCATGAGTAA CGAAGAATAT AATAAATTAA CCGAAGATAA AAAAGAACCT
S.epiRP62A  TACTGCTATC CACCCTCAAA CAGGTGAATT ATTAGCACTT GTAAGCACAC CTTCATATGA CGTCTATCCA TTTATGTATG GCATGAGTAA CGAAGAATAT AATAAATTAA CCGAAGATAA AAAAGAACCT
M744/10     TACTGCTATC CACCCTCAAA CAGGTGAATT ATTAGCACTT GTAAGCACAC CTTCATATGA CGTCTATCCA TTTATGTATG GCATGAGTAA CGAAGAATAT AATAAATTAA CCGAAGATAA AAAAGAACCT
M1529/10    TACTGCTATC CACCCTCAAA CAGGTGAATT ATTAGCACTT GTAAGCACAC CTTCATATGA CGTCTATCCA TTTATGTATG GCATGAGTAA CGAAGAATAT AATAAATTAA CCGAAGATAA AAAAGAACCT
M1383/10    TACTGCTATC CACCCTCAAA CAGGTGAATT ATTAGCACTT GTAAGCACAC CTTCATATGA CGTCTATCCA TTTATGTATG GCATGAGTAA CGAAGAATAT AATAAATTAA CCGAAGATAA AAAAGAACCT
M1186/10    TACTGCTATC CACCCTCAAA CAGGTGAATT ATTAGCACTT GTAAGCACAC CTTCATATGA CGTCTATCCA TTTATGTATG GCATGAGTAA CGAAGAATAT AATAAATTAA CCGAAGATAA AAAAGAACCT
M703/10     TACTGCTATC CACCCTCAAA CAGGTGAATT ATTAGCACTT GTAAGCACAC CTTCATATGA CGTCTATCCA TTTATGTATG GCATGAGTAA CGAAGAATAT AATAAATTAA CCGAAGATAA AAAAGAACCT
M8/10       TACTGCTATC CACCCTCAAA CAGGTGAATT ATTAGCACTT GTAAGCACAC CTTCATATGA CGTCTATCCA TTTATGTATG GCATGAGTAA CGAAGAATAT AATAAATTAA CCGAAGATAA AAAAGAACCT
Consensus   TACTGCTATC CACCCTCAAA CAGGTGAATT ATTAGCACTT GTAAGCACAC CTTCATATGA CGTCTATCCA TTTATGTATG GCATGAGTAA CGAAGAATAT AATAAATTAA CCGAAGATAA AAAAGAACCT
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            1171                                                                                                1300
S.aurN315   CTGCTCAACA AGTTCCAGAT TACAACTTCA CCAGGTTCAA CTCAAAAAAT ATTAACAGCA ATGATTGGGT TAAATAACAA AACATTAGAC GATAAAACAA GTTATAAAAT CGATGGTAAA GGTTGGCAAA
S.epiRP62A  CTGCTCAACA AGTTCCAGAT TACAACTTCA CCAGGTTCAA CTCAAAAAAT ATTAACAGCA ATGATTGGGT TAAATAACAA AACATTAGAC GATAAAACAA GTTATAAAAT CGATGGTAAA GGTTGGCAAA
M744/10     CTGCTCAACA AGTTCCAGAT TACAACTTCA CCAGGTTCAA CTCAAAAAAT ATTAACAGCA ATGATTGGGT TAAATAACAA AACATTAGAC GATAAAACAA GTTATAAAAT CGATGGTAAA GGTTGGCAAA
M1529/10    CTGCTCAACA AGTTCCAGAT TACAACTTCA CCAGGTTCAA CTCAAAAAAT ATTAACAGCA ATGATTGGGT TAAATAACAA AACATTAGAC GATAAAACAA GTTATAAAAT CGATGGTAAA GGTTGGCAAA
M1383/10    CTGCTCAACA AGTTCCAGAT TACAACTTCA CCAGGTTCAA CTCAAAAAAT ATTAACAGCA ATGATTGGGT TAAATAACAA AACATTAGAC GATAAAACAA GTTATAAAAT CGATGGTAAA GGTTGGCAAA
M1186/10    CTGCTCAACA AGTTCCAGAT TACAACTTCA CCAGGTTCAA CTCAAAAAAT ATTAACAGCA ATGATTGGGT TAAATAACAA AACATTAGAC GATAAAACAA GTTATAAAAT CGATGGTAAA GGTTGGCAAA
M703/10     CTGCTCAACA AGTTCCAGAT TACAACTTCA CCAGGTTCAA CTCAAAAAAT ATTAACAGCA ATGATTGGGT TAAATAACAA AACATTAGAC GATAAAACAA GTTATAAAAT CGATGGTAAA GGTTGGCAAA
M8/10       CTGCTCAACA AGTTCCAGAT TACAACTTCA CCAGGTTCAA CTCAAAAAAT ATTAACAGCA ATGATTGGGT TAAATAACAA AACATTAGAC GATAAAACAA GTTATAAAAT CGATGGTAAA GGTTGGCAAA
Consensus   CTGCTCAACA AGTTCCAGAT TACAACTTCA CCAGGTTCAA CTCAAAAAAT ATTAACAGCA ATGATTGGGT TAAATAACAA AACATTAGAC GATAAAACAA GTTATAAAAT CGATGGTAAA GGTTGGCAAA

            1301                                                                                                1430
S.aurN315   AAGATAAATC TTGGGGTGGT TACAACGTTA CAAGATATGA AGTGGTAAAT GGTAATATCG ACTTAAAACA AGCAATAGAA TCATCAGATA ACATTTTCTT TGCTAGAGTA GCACTCGAAT TAGGCAGTAA
S.epiRP62A  AAGATAAATC TTGGGGTGGT TACAACGTTA CAAGATATGA AGTGGTAAAT GGTAATATCG ACTTAAAACA AGCAATAGAA TCATCAGATA ACATTTTCTT TGCTAGAGTA GCACTCGAAT TAGGCAGTAA
M744/10     AAGATAAATC TTGGGGTGGT TACAACGTTA CAAGATATGA AGTGGTAAAT GGTAATATCG ACTTAAAACA AGCAATAGAA TCATCAGATA ACATTTTCTT TGCTAGAGTA GCACTCGAAT TAGGCAGTAA
M1529/10    AAGATAAATC TTGGGGTGGT TACAACGTTA CAAGATATGA AGTGGTAAAT GGTAATATCG ACTTAAAACA AGCAATAGAA TCATCAGATA ACATTTTCTT TGCTAGAGTA GCACTCGAAT TAGGCAGTAA
M1383/10    AAGATAAATC TTGGGGTGGT TACAACGTTA CAAGATATGA AGTGGTAAAT GGTAATATCG ACTTAAAACA AGCAATAGAA TCATCAGATA ACATTTTCTT TGCTAGAGTA GCACTCGAAT TAGGCAGTAA
M1186/10    AAGATAAATC TTGGGGTGGT TACAACGTTA CAAGATATGA AGTGGTAAAT GGTAATATCG ACTTAAAACA AGCAATAGAA TCATCAGATA ACATTTTCTT TGCTAGAGTA GCACTCGAAT TAGGCAGTAA
M703/10     AAGATAAATC TTGGGGTGGT TACAACGTTA CAAGATATGA AGTGGTAAAT GGTAATATCG ACTTAAAACA AGCAATAGAA TCATCAGATA ACATTTTCTT TGCTAGAGTA GCACTCGAAT TAGGCAGTAA
M8/10       AAGATAAATC TTGGGGTGGT TACAACGTTA CAAGATATGA AGTGGTAAAT GGTAATATCG ACTTAAAACA AGCAATAGAA TCATCAGATA ACATTTTCTT TGCTAGAGTA GCACTCGAAT TAGGCAGTAA
Consensus   AAGATAAATC TTGGGGTGGT TACAACGTTA CAAGATATGA AGTGGTAAAT GGTAATATCG ACTTAAAACA AGCAATAGAA TCATCAGATA ACATTTTCTT TGCTAGAGTA GCACTCGAAT TAGGCAGTAA

            1431                                                                                                1560
S.aurN315   GAAATTTGAA AAAGGCATGA AAAAACTAGG TGTTGGTGAA GATATACCAA GTGATTATCC ATTTTATAAT GCTCAAATTT CAAACAAAAA TTTAGATAAT GAAATATTAT TAGCTGATTC AGGTTACGGA
S.epiRP62A  GAAATTTGAA AAAGGCATGA AAAAACTAGG TGTTGGTGAA GATATACCAA GTGATTATCC ATTTTATAAT GCTCAAATTT CAAACAAAAA TTTAGATAAT GAAATATTAT TAGCTGATTC AGGTTACGGA
M744/10     GAAATTTGAA AAAGGCATGA AAAAACTAGG TGTTGGTGAA GATATACCAA GTGATTATCC ATTTTATAAT GCTCAAATTT CAAACAAAAA TTTAGATAAT GAAATATTAT TAGCTGATTC AGGTTACGGA
M1529/10    GAAATTTGAA AAAGGCATGA AAAAACTAGG TGTTGGTGAA GATATACCAA GTGATTATCC ATTTTATAAT GCTCAAATTT CAAACAAAAA TTTAGATAAT GAAATATTAT TAGCTGATTC AGGTTACGGA
M1383/10    GAAATTTGAA AAAGGCATGA AAAAACTAGG TGTTGGTGAA GATATACCAA GTGATTATCC ATTTTATAAT GCTCAAATTT CAAACAAAAA TTTAGATAAT GAAATATTAT TAGCTGATTC AGGTTACGGA
M1186/10    GAAATTTGAA AAAGGCATGA AAAAACTAGG TGTTGGTGAA GATATACCAA GTGATTATCC ATTTTATAAT GCTCAAATTT CAAACAAAAA TTTAGATAAT GAAATATTAT TAGCTGATTC AGGTTACGGA
M703/10     GAAATTTGAA AAAGGCATGA AAAAACTAGG TGTTGGTGAA GATATACCAA GTGATTATCC ATTTTATAAT GCTCAAATTT CAAACAAAAA TTTAGATAAT GAAATATTAT TAGCTGATTC AGGTTACGGA
M8/10       GAAATTTGAA AAAGGCATGA AAAAACTAGG TGTTGGTGAA GATATACCAA GTGATTATCC ATTTTATAAT GCTCAAATTT CAAACAAAAA TTTAGATAAT GAAATATTAT TAGCTGATTC AGGTTACGGA
Consensus   GAAATTTGAA AAAGGCATGA AAAAACTAGG TGTTGGTGAA GATATACCAA GTGATTATCC ATTTTATAAT GCTCAAATTT CAAACAAAAA TTTAGATAAT GAAATATTAT TAGCTGATTC AGGTTACGGA

            1561                                                                                                1690
S.aurN315   CAAGGTGAAA TACTGATTAA CCCAGTACAG ATCCTTTCAA TCTATAGCGC ATTAGAAAAT AATGGCAATA TTAACGCACC TCACTTATTA AAAGACACGA AAAACAAAGT TTGGAAGAAA AATATTATTT
S.epiRP62A  CAAGGTGAAA TACTGATTAA CCCAGTACAG ATCCTTTCAA TCTATAGCGC ATTAGAAAAT AATGGCAATA TTAACGCACC TCACTTATTA AAAGACACGA AAAACAAAGT TTGGAAGAAA AATATTATTT
M744/10     CAAGGTGAAA TACTGATTAA CCCAGTACAG ATCCTTTCAA TCTATAGCGC ATTAGAAAAT AATGGCAATA TTAACGCACC TCACTTATTA AAAGACACGA AAAACAAAGT TTGGAAGAAA AATATTATTT
M1529/10    CAAGGTGAAA TACTGATTAA CCCAGTACAG ATCCTTTCAA TCTATAGCGC ATTAGAAAAT AATGGCAATA TTAACGCACC TCACTTATTA AAAGACACGA AAAACAAAGT TTGGAAGAAA AATATTATTT
M1383/10    CAAGGTGAAA TACTGATTAA CCCAGTACAG ATCCTTTCAA TCTATAGCGC ATTAGAAAAT AATGGCAATA TTAACGCACC TCACTTATTA AAAGACACGA AAAACAAAGT TTGGAAGAAA AATATTATTT
M1186/10    CAAGGTGAAA TACTGATTAA CCCAGTACAG ATCCTTTCAA TCTATAGCGC ATTAGAAAAT AATGGCAATA TTAACGCACC TCACTTATTA AAAGACACGA AAAACAAAGT TTGGAAGAAA AATATTATTT
M703/10     CAAGGTGAAA TACTGATTAA CCCAGTACAG ATCCTTTCAA TCTATAGCGC ATTAGAAAAT AATGGCAATA TTAACGCACC TCACTTATTA AAAGACACGA AAAACAAAGT TTGGAAGAAA AATATTATTT
M8/10       CAAGGTGAAA TACTGATTAA CCCAGTACAG ATCCTTTCAA TCTATAGCGC ATTAGAAAAT AATGGCAATA TTAACGCACC TCACTTATTA AAAGACACGA AAAACAAAGT TTGGAAGAAA AATATTATTT
Consensus   CAAGGTGAAA TACTGATTAA CCCAGTACAG ATCCTTTCAA TCTATAGCGC ATTAGAAAAT AATGGCAATA TTAACGCACC TCACTTATTA AAAGACACGA AAAACAAAGT TTGGAAGAAA AATATTATTT

            1691                                                                                                1820
S.aurN315   CCAAAGAAAA TATCAATCTA TTAACTGATG GTATGCAACA AGTCGTAAAT AAAACACATA AAGAAGATAT TTATAGATCT TATGCAAACT TAATTGGCAA ATCCGGTACT GCAGAACTCA AAATGAAACA
S.epiRP62A  CCAAAGAAAA TATCAATCTA TTAACTGATG GTATGCAACA AGTCGTAAAT AAAACACATA AAGAAGATAT TTATAGATCT TATGCAAACT TAATTGGCAA ATCCGGTACT GCAGAACTCA AAATGAAACA
M744/10     CCAAAGAAAA TATCAATCTA TTAACTGATG GTATGCAACA AGTCGTAAAT AAAACACATA AAGAAGATAT TTATAGATCT TATGCAAACT TAATTGGCAA ATCCGGTACT GCAGAACTCA AAATGAAACA
M1529/10    CCAAAGAAAA TATCAATCTA TTAACTGATG GTATGCAACA AGTCGTAAAT AAAACACATA AAGAAGATAT TTATAGATCT TATGCAAACT TAATTGGCAA ATCCGGTACT GCAGAACTCA AAATGAAACA
M1383/10    CCAAAGAAAA TATCAATCTA TTAACTGATG GTATGCAACA AGTCGTAAAT AAAACACATA AAGAAGATAT TTATAGATCT TATGCAAACT TAATTGGCAA ATCCGGTACT GCAGAACTCA AAATGAAACA
M1186/10    CCAAAGAAAA TATCAATCTA TTAACTGATG GTATGCAACA AGTCGTAAAT AAAACACATA AAGAAGATAT TTATAGATCT TATGCAAACT TAATTGGCAA ATCCGGTACT GCAGAACTCA AAATGAAACA
M703/10     CCAAAGAAAA TATCAATCTA TTAACTGATG GTATGCAACA AGTCGTAAAT AAAACACATA AAGAAGATAT TTATAGATCT TATGCAAACT TAATTGGCAA ATCCGGTACT GCAGAACTCA AAATGAAACA
M8/10       CCAAAGAAAA TATCAATCTA TTAACTGATG GTATGCAACA AGTCGTAAAT AAAACACATA AAGAAGATAT TTATAGATCT TATGCAAACT TAATTGGCAA ATCCGGTACT GCAGAACTCA AAATGAAACA
Consensus   CCAAAGAAAA TATCAATCTA TTAACTGATG GTATGCAACA AGTCGTAAAT AAAACACATA AAGAAGATAT TTATAGATCT TATGCAAACT TAATTGGCAA ATCCGGTACT GCAGAACTCA AAATGAAACA
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            1821                                                                                                                          1950
 S.aurN315  AGGAGAAACT GGCAGACAAA TTGGGTGGTT TATATCATAT GATAAAGATA ATCCAAACAT GATGATGGCT ATTAATGTTA AAGATGTACA AGATAAAGGA ATGGCTAGCT ACAATGCCAA AATCTCAGGT
S.epiRP62A  AGGAGAAACT GGCAGACAAA TTGGGTGGTT TATATCATAT GATAAAGATA ATCCAAACAT GATGATGGCT ATTAATGTTA AAGATGTACA AGATAAAGGA ATGGCTAGCT ACAATGCCAA AATCTCAGGT
   M744/10  AGGAGAAACT GGCAGACAAA TTGGGTGGTT TATATCATAT GATAAAGATA ATCCAAACAT GATGATGGCT ATTAATGTTA AAGATGTACA AGATAAAGGA ATGGCTAGCT ACAATGCCAA AATCTCAGGT
  M1529/10  AGGAGAAACT GGCAGACAAA TTGGGTGGTT TATATCATAT GATAAAGATA ATCCAAACAT GATGATGGCT ATTAATGTTA AAGATGTACA AGATAAAGGA ATGGCTAGCT ACAATGCCAA AATCTCAGGT
  M1383/10  AGGAGAAACT GGCAGACAAA TTGGGTGGTT TATATCATAT GATAAAGATA ATCCAAACAT GATGATGGCT ATTAATGTTA AAGATGTACA AGATAAAGGA ATGGCTAGCT ACAATGCCAA AATCTCAGGT
  M1186/10  AGGAGAAACT GGCAGACAAA TTGGGTGGTT TATATCATAT GATAAAGATA ATCCAAACAT GATGATGGCT ATTAATGTTA AAGATGTACA AGATAAAGGA ATGGCTAGCT ACAATGCCAA AATCTCAGGT
   M703/10  AGGAGAAACT GGCAGACAAA TTGGGTGGTT TATATCATAT GATAAAGATA ATCCAAACAT GATGATGGCT ATTAATGTTA AAGATGTACA AGATAAAGGA ATGGCTAGCT ACAATGCCAA AATCTCAGGT
     M8/10  AGGAGAAACT GGCAGACAAA TTGGGTGGTT TATATCATAT GATAAAGATA ATCCAAACAT GATGATGGCT ATTAATGTTA AAGATGTACA AGATAAAGGA ATGGCTAGCT ACAATGCCAA AATCTCAGGT
 Consensus  AGGAGAAACT GGCAGACAAA TTGGGTGGTT TATATCATAT GATAAAGATA ATCCAAACAT GATGATGGCT ATTAATGTTA AAGATGTACA AGATAAAGGA ATGGCTAGCT ACAATGCCAA AATCTCAGGT

            1951                                                     2007
 S.aurN315  AAAGTGTATG ATGAGCTATA TGAGAACGGT AATAAAAAAT ACGATATAGA TGAATAA
S.epiRP62A  AAAGTGTATG ATGAGCTATA TGAGAACGGT AATAAAAAAT ACGATATAGA TGAATAA
   M744/10  AAAGTGTATG ATGAGCTATA TGAGAACGGT AATAAAAAAT ACGATATAGA TGAATAA
  M1529/10  AAAGTGTATG ATGAGCTATA TGAGAACGGT AATAAAAAAT ACGATATAGA TGAATAA
  M1383/10  AAAGTGTATG ATGAGCTATA TGAGAACGGT AATAAAAAAT ACGATATAGA TGAATAA
  M1186/10  AAAGTGTATG ATGAGCTATA TGAGAACGGT AATAAAAAAT ACGATATAGA TGAATAA
   M703/10  AAAGTGTATG ATGAGCTATA TGAGAACGGT AATAAAAAAT ACGATATAGA TGAATAA
     M8/10  AAAGTGTATG ATGAGCTATA TGAGAACGGT AATAAAAAAT ACGATATAGA TGAATAA
 Consensus  AAAGTGTATG ATGAGCTATA TGAGAACGGT AATAAAAAAT ACGATATAGA TGAATAA
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Sequence alignment of methicillin resistance gene *mecA* in *S. fleurettii* isolates

using MultAlign Program http://multalin.toulouse.inra.fr/multalin/

S. fleurettii reference strains:

- *S. fleurettii* SMFP08
- *S. fleurettii* CCUG43834

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             1                                                                                                                               130
S.fleurSMF   ATGAAGAAGA TAAAAATTGT TCCACTTATT TTAATAGTTG TAGTTGTCGG GTTTGGTATA TATTTGTATG CTTCAAAAGA TAAAGAAATT AATAAAACTA TTGATGCAAT TGAAGATAAA AATTTCAAAC
S.fleurCCU   ATGAAAAAGA TAAAAATTGT TCCACTTATT TTAATAGTTG TAGTTGTCGG GTTTGGTATA TATTTTTATG CTTCAAAAGA TAAAGAAATT AATAATACTA TTGATGCAAT TGAAGATAAA AATTTCAAAC
   M143/10   ATGAAAAAGA TAAAAATTGT TCCACTTATT TTAATAGTTG TAGTTGTCGG GTTTGGTATA TATTTTTATG CTTCAAAAGA TAAAGAAATT AATAATACTA TTGATGCAAT TGAAGATAAA AATTTCAAAC
   M277/10   ATGAAAAAGA TAAAAATTGT TCCACTTATT TTAATAGTTG TAGTTGTCGG GTTTGGTATA TATTTTTATG CTTCAAAAGA TAAAGAAATT AATAATACTA TTGATGCAAT TGAAGATAAA AATTTCAAAC
 M404-1/10   ATGAAAAAGA TAAAAATTGT TCCACTTATT TTAATAGTTG TAGTTGTCGG GTTTGGTATA TATTTTTATG CTTCAAAAGA TAAAGAAATT AATAATACTA TTGATGCAAT TGAAGATAAA AATTTCAAAC
   M545/10   ATGAAAAAGA TAAAAATTGT TCCACTTATT TTAATAGTTG TAGTTGTCGG GTTTGGTATA TATTTTTATG CTTCAAAAGA TAAAGAAATT AATAATACTA TTGATGCAAT TGAAGATAAA AATTTCAAAC
M4276-1/09   ATGAAAAAGA TAAAAATTGT TCCACTTATT TTAATAGTTG TAGTTGTCGG GTTTGGTATA TATTTTTATG CTTCAAAAGA TAAAGAAATT AATAATACTA TTGATGCAAT TGAAGATAAA AATTTCAAAC
M1125-2/10   ATGAAAAAGA TAAAAATTGT TCCACTTATT TTAATAGTTG TAGTTGTCGG GTTTGGTATA TATTTTTATG CTTCAAAAGA TAAAGAAATT AATAATACTA TTGATGCAAT TGAAGATAAA AATTTCAAAC
  M1961/10   ATGAAAAAGA TAAAAATTGT TCCACTTATT TTAATAGTTG TAGTTGTCGG GTTTGGTATA TATTTTTATG CTTCAAAAGA TAAAGAAATT AATAATACTA TTGATGCAAT TGAAGATAAA AATTTCAAAC
M1191-2/10   ATGAAAAAGA TAAAAATTGT TCCACTTATT TTAATAGTTG TAGTTGTCGG GTTTGGTATA TATTTTTATG CTTCAAAAGA TAAAGAAATT AATAATACTA TTGATGCAAT TGAAGATAAA AATTTCAAAC
  M3783/10   ATGAAAAAGA TAAAAATTGT TCCACTTATT TTAATAGTTG TAGTTGTCGG GTTTGGTATA TATTTTTATG CTTCAAAAGA TAAAGAAATT AATAATACTA TTGATGCAAT TGAAGATAAA AATTTCAAAC
   M205/10   ATGAAAAAGA TAAAAATTGT TCCACTTATT TTAATAGTTG TAGTTGTCGG GTTTGGTATA TATTTTTATG ATTCAAAAGA TAAAGAAATT AATAATACTA TTGATGCAAT TGAAGATAAA AATTTCAAAC
  M4460/09   ATGAAAAAGA TAAAAATTGT TCCACTTATT TTAATAGTTG TAGTTGTCGG GTTTGGTATA TATTTTTATG CTTCAAAAGA TAAAGAAATT AATAAAACTA TTGATGCAAT TGAAGATAAA AATTTCAAAC
 Consensus   ATGAAaAAGA TAAAAATTGT TCCACTTATT TTAATAGTTG TAGTTGTCGG GTTTGGTATA TATTTtTATG cTTCAAAAGA TAAAGAAATT AATAAtACTA TTGATGCAAT TGAAGATAAA AATTTCAAAC

             131                                                                                                                             260
S.fleurSMF   AAGTTTATAA AGATAGCAGT TATATTTCTA AAAGCGATAA TGGCGAAGTA GAAATGACTG AACGTCCGAT AAAAATATAT AAAAGTTTAG GCGTTAAAGA TATAAACATT CAGGACCGCA AAATAAAAAA
S.fleurCCU   AAGTTTATAA AGATAGCAGT TATATTTCTA AAAGCGATAA TGGTGAAGTA GAAATGACTG AACGTCCGAT AAAAATATAT AAAAGTTTAG GCGTTAAAGA TATAAACATT CAGGATCGTA AAATAAAAAA
   M143/10   AAGTTTATAA AGATAGCAGT TATATTTCTA AAAGCGATAA TGGTGAAGTA GAAATGACTG AACGTCCGAT AAAAATATAT AAAAGTTTAG GCGTTAAAGA TATAAACATT CAGGATCGTA AAATAAAAAA
   M277/10   AAGTTTATAA AGATAGCAGT TATATTTCTA AAAGCGATAA TGGTGAAGTA GAAATGACTG AACGTCCGAT AAAAATATAT AAAAGTTTAG GCGTTAAAGA TATAAACATT CAGGATCGTA AAATAAAAAA
 M404-1/10   AAGTTTATAA AGATAGCAGT TATATTTCTA AAAGCGATAA TGGTGAAGTA GAAATGACTG AACGTCCGAT AAAAATATAT AAAAGTTTAG GCGTTAAAGA TATAAACATT CAGGATCGTA AAATAAAAAA
   M545/10   AAGTTTATAA AGATAGCAGT TATATTTCTA AAAGCGATAA TGGTGAAGTA GAAATGACTG AACGTCCGAT AAAAATATAT AAAAGTTTAG GCGTTAAAGA TATAAACATT CAGGATCGTA AAATAAAAAA
M4276-1/09   AAGTTTATAA AGATAGCAGT TATATTTCTA AAAGCGATAA TGGTGAAGTA GAAATGACTG AACGTCCGAT AAAAATATAT AAAAGTTTAG GCGTTAAAGA TATAAACATT CAGGATCGTA AAATAAAAAA
M1125-2/10   AAGTTTATAA AGATAGCAGT TATATTTCTA AAAGCGATAA TGGTGAAGTA GAAATGACTG AACGTCCGAT AAAAATATAT AAAAGTTTAG GCGTTAAAGA TATAAACATT CAGGATCGTA AAATAAAAAA
  M1961/10   AAGTTTATAA AGATAGCAGT TATATTTCTA AAAGCGATAA TGGTGAAGTA GAAATGACTG AACGTCCGAT AAAAATATAT AAAAGTTTAG GCGTTAAAGA TATAAACATT CAGGATCGTA AAATAAAAAA
M1191-2/10   AAGTTTATAA AGATAGCAGT TATATTTCTA AAAGCGATAA TGGTGAAGTA GAAATGACTG AACGTCCGAT AAAAATATAT AAAAGTTTAG GCGTTAAAGA TATAAACATT CAGGATCGTA AAATAAAAAA
  M3783/10   AAGTTTATAA AGATAGCAGT TATATTTCTA AAAGCGATAA TGGTGAAGTA GAAATGACTG AACGTCCGAT AAAAATATAT AAAAGTTTAG GCGTTAAAGA TATAAACATT CAGGATCGTA AAATAAAAAA
   M205/10   AAGTTTATAA AGATAGCAGT TATATTTCTA AAAGCGATAA TGGTGAAGTA GAAATGACTG AACGTCCGAT AAAAATATAT AAAAGTTTAG GCGTTAAAGA TATAAACATT CAGGATCGTA AAATAAAAAA
  M4460/09   AAGTTTATAA AGATAGCAGT TATATTTCCA AAAGCGATAA TGGTGAAGTA GAAATGACTG AACGTCCGAT AAAAATATAT AAAAGTTTAG GCGTTAAAGA TATAAACATT CAAGAACGCA AAATAAAAAA
 Consensus   AAGTTTATAA AGATAGCAGT TATATTTCtA AAAGCGATAA TGGtGAAGTA GAAATGACTG AACGTCCGAT AAAAATATAT AAAAGTTTAG GCGTTAAAGA TATAAACATT CAgGAtCGtA AAATAAAAAA

             261                                                                                                                             390
S.fleurSMF   AATATCTAAA AATAAAAAAA GAGTAGATGC TCAATATAAA ATTAAAACAA ACTACGGTAA CATTGATCGC AACGTTCAAT TTAATTTTGT TAAAGAAGAT GGCATGTGGA AATTAGATTG GGATCATAGC
S.fleurCCU   AGTATCTAAA AATAAAAAAC GAGTAGATGC TCAATATAAA ATTAAAACAA ACTACGGTAA CATTGATCGC AACGTTCAAT TTAATTTTGT TAAAGAAGAT GGTATGTGGA AGTTAGATTG GGATCATAGC
   M143/10   AGTATCTAAA AATAAAAAAC GAGTAGATGC TCAATATAAA ATTAAAACAA ACTACGGTAA CATTGATCGC AACGTTCAAT TTAATTTTGT TAAAGAAGAT GGTATGTGGA AGTTAGATTG GGATCATAGC
   M277/10   AGTATCTAAA AATAAAAAAC GAGTAGATGC TCAATATAAA ATTAAAACAA ACTACGGTAA CATTGATCGC AACGTTCAAT TTAATTTTGT TAAAGAAGAT GGTATGTGGA AGTTAGATTG GGATCATAGC
 M404-1/10   AGTATCTAAA AATAAAAAAC GAGTAGATGC TCAATATAAA ATTAAAACAA ACTACGGTAA CATTGATCGC AACGTTCAAT TTAATTTTGT TAAAGAAGAT GGTATGTGGA AGTTAGATTG GGATCATAGC
   M545/10   AGTATCTAAA AATAAAAAAC GAGTAGATGC TCAATATAAA ATTAAAACAA ACTACGGTAA CATTGATCGC AACGTTCAAT TTAATTTTGT TAAAGAAGAT GGTATGTGGA AGTTAGATTG GGATCATAGC
M4276-1/09   AGTATCTAAA AATAAAAAAC GAGTAGATGC TCAATATAAA ATTAAAACAA ACTACGGTAA CATTGATCGC AACGTTCAAT TTAATTTTGT TAAAGAAGAT GGTATGTGGA AGTTAGATTG GGATCATAGC
M1125-2/10   AGTATCTAAA AATAAAAAAC GAGTAGATGC TCAATATAAA ATTAAAACAA ACTACGGTAA CATTGATCGC AACGTTCAAT TTAATTTTGT TAAAGAAGAT GGTATGTGGA AGTTAGATTG GGATCATAGC
  M1961/10   AGTATCTAAA AATAAAAAAC GAGTAGATGC TCAATATAAA ATTAAAACAA ACTACGGTAA CATTGATCGC AACGTTCAAT TTAATTTTGT TAAAGAAGAT GGTATGTGGA AGTTAGATTG GGATCATAGC
M1191-2/10   AGTATCTAAA AATAAAAAAC GAGTAGATGC TCAATATAAA ATTAAAACAA ACTACGGTAA CATTGATCGC AACGTTCAAT TTAATTTTGT TAAAGAAGAT GGTATGTGGA AGTTAGATTG GGATCATAGC
  M3783/10   AGTATCTAAA AATAAAAAAC GAGTAGATGC TCAATATAAA ATTAAAACAA ACTACGGTAA CATTGATCGC AACGTTCAAT TTAATTTTGT TAAAGAAGAT GGTATGTGGA AGTTAGATTG GGATCATAGC
   M205/10   AGTATCTAAA AATAAAAAAC GAGTAGATGC TCAATATAAA ATTAAAACAA ACTACGGTAA CATTGATCGC AACGTTCAAT TTAATTTTGT TAAAGAAGAT GGTATGTGGA AGTTAGATTG GGATCATAGC
  M4460/09   AATATCTAAA AATAAAAAAC GAGTAGATGC TCAATATAAA ATTAAAACAA ACTACGGTAA CATTGATCGC AACGTTCAAT TTAATTTTGT TAAAGAAGAT GGCATGTGGA AGTTAGATTG GGATCATAGC
 Consensus   AgTATCTAAA AATAAAAAAc GAGTAGATGC TCAATATAAA ATTAAAACAA ACTACGGTAA CATTGATCGC AACGTTCAAT TTAATTTTGT TAAAGAAGAT GGtATGTGGA AgTTAGATTG GGATCATAGC
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            391                                                                                                                           520
S.fleurSMF  GTCATTATTC CAGGAATGCA GAAAGACCAA AGCATACATA TTGAAAATTT AAAATCAGAA CGTGGTAAAA TTTTAGACCG AAACAATGTG GAATTGGCCA ATACAGGAAC AGCATATGAG ATAGGCATCG
S.fleurCCU  GTCATTATTC CAGGAATGCA GAAAGACCAA AGCATACATA TTGAAAATTT AAAATCAGAA CGTGGTAAAA TTTTAGACCG AAACAATGTG GAATTGGCCA ATACAGGAAC AGCATATGAG ATAGGCATCG
   M143/10  GTCATTATTC CAGGAATGCA GAAAGACCAA AGCATACATA TTGAAAATTT AAAATCAGAA CGTGGTAAAA TTTTAGACCG AAACAATGTG GAATTGGCCA ATACAGGAAC AGCATATGAG ATAGGCATCG
   M277/10  GTCATTATTC CAGGAATGCA GAAAGACCAA AGCATACATA TTGAAAATTT AAAATCAGAA CGTGGTAAAA TTTTAGACCG AAACAATGTG GAATTGGCCA ATACAGGAAC AGCATATGAG ATAGGCATCG
 M404-1/10  GTCATTATTC CAGGAATGCA GAAAGACCAA AGCATACATA TTGAAAATTT AAAATCAGAA CGTGGTAAAA TTTTAGACCG AAACAATGTG GAATTGGCCA ATACAGGAAC AGCATATGAG ATAGGCATCG
   M545/10  GTCATTATTC CAGGAATGCA GAAAGACCAA AGCATACATA TTGAAAATTT AAAATCAGAA CGTGGTAAAA TTTTAGACCG AAACAATGTG GAATTGGCCA ATACAGGAAC AGCATATGAG ATAGGCATCG
M4276-1/09  GTCATTATTC CAGGAATGCA GAAAGACCAA AGCATACATA TTGAAAATTT AAAATCAGAA CGTGGTAAAA TTTTAGACCG AAACAATGTG GAATTGGCCA ATACAGGAAC AGCATATGAG ATAGGCATCG
M1125-2/10  GTCATTATTC CAGGAATGCA GAAAGACCAA AGCATACATA TTGAAAATTT AAAATCAGAA CGTGGTAAAA TTTTAGACCG AAACAATGTG GAATTGGCCA ATACAGGAAC AGCATATGAG ATAGGCATCG
  M1961/10  GTCATTATTC CAGGAATGCA GAAAGACCAA AGCATACATA TTGAAAATTT AAAATCAGAA CGTGGTAAAA TTTTAGACCG AAACAATGTG GAATTGGCCA ATACAGGAAC AGCATATGAG ATAGGCATCG
M1191-2/10  GTCATTATTC CAGGAATGCA GAAAGACCAA AGCATACATA TTGAAAATTT AAAATCAGAA CGTGGTAAAA TTTTAGACCG AAACAATGTG GAATTGGCCA ATACAGGAAC AGCATATGAG ATAGGCATCG
  M3783/10  GTCATTATTC CAGGAATGCA GAAAGACCAA AGCATACATA TTGAAAATTT AAAATCAGAA CGTGGTAAAA TTTTAGACCG AAACAATGTG GAATTGGCCA ATACAGGAAC AGCATATGAG ATAGGCATCG
   M205/10  GTCATTATTC CAGGAATGCA GAAAGACCAA AGTATACATA TTGAAAATTT AAAATCAGAA CGTGGTAAAA TTTTAGACCG AAACAATGTG GAATTGGCCA ATACAGGAAC AGCATATGAG ATAGGCATCG
  M4460/09  GTCATTATTC CAGGAATGCA GAAAGACCAA AGCATACATA TTGAAAATTT AAAATCAGAA CGTGGTAAAA TTTTAGACCG AAACAATGTG GAATTGGCCA ATACAGGAAC AGCATATGAG ATAGGCATCG
 Consensus  GTCATTATTC CAGGAATGCA GAAAGACCAA AGcATACATA TTGAAAATTT AAAATCAGAA CGTGGTAAAA TTTTAGACCG AAACAATGTG GAATTGGCCA ATACAGGAAC AGCATATGAG ATAGGCATCG

            521                                                                                                                           650
S.fleurSMF  TTCCAAAGAG TGTATTTAAA AAAGATTATA AAGCAATCGC TAAAGAACTA AGTATTTCTG AAGACTATAT CAAACAACAA ATGGATCAAA ATTGGGTACA AGATGATACC TTCGTTCCAC TTAAAACCGT
S.fleurCCU  TTCCAAAGAA TGTATCTAAA AAAGATTATA AAGCAATCGC TAAAGAACTA AGTATTTCTG AAGACTATAT CAAACAACAA ATGGATCAAA ATTGGGTACA AGATGATACC TTCGTTCCAC TTAAAACCGT
   M143/10  TTCCAAAGAA TGTATCTAAA AAAGATTATA AAGCAATCGC TAAAGAACTA AGTATTTCTG AAGACTATAT CAAACAACAA ATGGATCAAA ATTGGGTACA AGATGATACC TTCGTTCCAC TTAAAACCGT
   M277/10  TTCCAAAGAA TGTATCTAAA AAAGATTATA AAGCAATCGC TAAAGAACTA AGTATTTCTG AAGACTATAT CAAACAACAA ATGGATCAAA ATTGGGTACA AGATGATACC TTCGTTCCAC TTAAAACCGT
 M404-1/10  TTCCAAAGAA TGTATCTAAA AAAGATTATA AAGCAATCGC TAAAGAACTA AGTATTTCTG AAGACTATAT CAAACAACAA ATGGATCAAA ATTGGGTACA AGATGATACC TTCGTTCCAC TTAAAACCGT
   M545/10  TTCCAAAGAA TGTATCTAAA AAAGATTATA AAGCAATCGC TAAAGAACTA AGTATTTCTG AAGACTATAT CAAACAACAA ATGGATCAAA ATTGGGTACA AGATGATACC TTCGTTCCAC TTAAAACCGT
M4276-1/09  TTCCAAAGAA TGTATCTAAA AAAGATTATA AAGCAATCGC TAAAGAACTA AGTATTTCTG AAGACTATAT CAAACAACAA ATGGATCAAA ATTGGGTACA AGATGATACC TTCGTTCCAC TTAAAACCGT
M1125-2/10  TTCCAAAGAA TGTATCTAAA AAAGATTATA AAGCAATCGC TAAAGAACTA AGTATTTCTG AAGACTATAT CAAACAACAA ATGGATCAAA ATTGGGTACA AGATGATACC TTCGTTCCAC TTAAAACCGT
  M1961/10  TTCCAAAGAA TGTATCTAAA AAAGATTATA AAGCAATCGC TAAAGAACTA AGTATTTCTG AAGACTATAT CAAACAACAA ATGGATCAAA ATTGGGTACA AGATGATACC TTCGTTCCAC TTAAAACCGT
M1191-2/10  TTCCAAAGAA TGTATCTAAA AAAGATTATA AAGCAATCGC TAAAGAACTA AGTATTTCTG AAGACTATAT CAAACAACAA ATGGATCAAA ATTGGGTACA AGATGATACC TTCGTTCCAC TTAAAACCGT
  M3783/10  TTCCAAAGAA TGTATCTAAA AAAGATTATA AAGCAATCGC TAAAGAACTA AGTATTTCTG AAGACTATAT CAAACAACAA ATGGATCAAA ATTGGGTACA AGATGATACC TTCGTTCCAC TTAAAACCGT
   M205/10  TTCCAAAGAA TGTATCTAAA AAAGATTATA AAGCAATCGC TAAAGAACTA AGTATTTCTG AAGACTATAT CAAACAACAA ATGGATCAAA ATTGGGTACA AGATGATACC TTCGTTCCAC TTAAAACCGT
  M4460/09  TTCCAAAGAA TGTATCTAAA AAAGATTATA AAGCAATCGC TAAAGAACTA AGTATTTCTG AAGACTATAT TAAACAACAA ATGGATCAAA ATTGGGTACA AGATGATACC TTCGTTCCAC TTAAAACCGT
 Consensus  TTCCAAAGAa TGTATcTAAA AAAGATTATA AAGCAATCGC TAAAGAACTA AGTATTTCTG AAGACTATAT cAAACAACAA ATGGATCAAA ATTGGGTACA AGATGATACC TTCGTTCCAC TTAAAACCGT

            651                                                                                                                           780
S.fleurSMF  TAAAAAAATG GATGAAGATT TAAGTGATTT CGCAAAAAAA TTTCATCTTA CAACTAACGA AACAGAAAGT CGTAACTATC CTCTAGAAGA AGCGACTTCA CATCTATTAG GTTATGTTGG TCCCATTAAC
S.fleurCCU  TAAAAAAATG GATGAAGATT TAAGTGATTT CGCAAAAAAA TTTCATCTTA CAACTAATGA AACAGAAAGT CGTAACTATC CTCTAGAAAA AGCGACTTCA CATCTATTAG GTTATGTTGG TCCCATTAAC
   M143/10  TAAAAAAATG GATGAAGATT TAAGTGATTT CGCAAAAAAA TTTCATCTTA CAACTAATGA AACAGAAAGT CGTAACTATC CTCTAGAAAA AGCGACTTCA CATCTATTAG GTTATGTTGG TCCCATTAAC
   M277/10  TAAAAAAATG GATGAAGATT TAAGTGATTT CGCAAAAAAA TTTCATCTTA CAACTAATGA AACAGAAAGT CGTAACTATC CTCTAGAAAA AGCGACTTCA CATCTATTAG GTTATGTTGG TCCCATTAAC
 M404-1/10  TAAAAAAATG GATGAAGATT TAAGTGATTT CGCAAAAAAA TTTCATCTTA CAACTAATGA AACAGAAAGT CGTAACTATC CTCTAGAAAA AGCGACTTCA CATCTATTAG GTTATGTTGG TCCCATTAAC
   M545/10  TAAAAAAATG GATGAAGATT TAAGTGATTT CGCAAAAAAA TTTCATCTTA CAACTAATGA AACAGAAAGT CGTAACTATC CTCTAGAAAA AGCGACTTCA CATCTATTAG GTTATGTTGG TCCCATTAAC
M4276-1/09  TAAAAAAATG GATGAAGATT TAAGTGATTT CGCAAAAAAA TTTCATCTTA CAACTAATGA AACAGAAAGT CGTAACTATC CTCTAGAAAA AGCGACTTCA CATCTATTAG GTTATGTTGG TCCCATTAAC
M1125-2/10  TAAAAAAATG GATGAAGATT TAAGTGATTT CGCAAAAAAA TTTCATCTTA CAACTAATGA AACAGAAAGT CGTAACTATC CTCTAGAAAA AGCGACTTCA CATCTATTAG GTTATGTTGG TCCCATTAAC
  M1961/10  TAAAAAAATG GATGAAGATT TAAGTGATTT CGCAAAAAAA TTTCATCTTA CAACTAATGA AACAGAAAGT CGTAACTATC CTCTAGAAAA AGCGACTTCA CATCTATTAG GTTATGTTGG TCCCATTAAC
M1191-2/10  TAAAAAAATG GATGAAGATT TAAGTGATTT CGCAAAAAAA TTTCATCTTA CAACTAATGA AACAGAAAGT CGTAACTATC CTCTAGAAAA AGCGACTTCA CATCTATTAG GTTATGTTGG TCCCATTAAC
  M3783/10  TAAAAAAATG GATGAAGATT TAAGTGATTT CGCAAAAAAA TTTCATCTTA CAACTAATGA AACAGAAAGT CGTAACTATC CTCTAGAAAA AGCGACTTCA CATCTATTAG GTTATGTTGG TCCCATTAAC
   M205/10  TAAAAAAATG GATGAAGATT TAAGTGATTT CGCAAAAAAA TTTCATCTTA CAACTAATGA AACAGAAAGT CGTAACTATC CTCTAGAAAA AGCGACTTCA CATCTATTAG GTTATGTTGG TCCCATTAAC
  M4460/09  TAAAAAAATG GATGAAGATT TAAGTGATTT CGCAAAAAAA TTTCATCTTA CAACTAATGA AACAGAAAGT CGTAACTATC CTCTAGAAGA AGCGACTTCA CATCTATTAG GTTATGTTGG TCCCATTAAC
 Consensus  TAAAAAAATG GATGAAGATT TAAGTGATTT CGCAAAAAAA TTTCATCTTA CAACTAAtGA AACAGAAAGT CGTAACTATC CTCTAGAAaA AGCGACTTCA CATCTATTAG GTTATGTTGG TCCCATTAAC
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            781                                                                                                                   910
S.fleurSMF  TCTGAAGAAT TAAAACAAAA AGAATATAAA GGTTATAAAG ATGATGCAGT TGTTGGTAAA AAGGGACTCG AAAAACTTTA CGATAAAAAG CTCCAACATG AAGATGGCTA TCGTGTCACA ATCTTTGACG
S.fleurCCU  TCTGAAGAAT TAAAACAAAA AGAATATAAA GGCTATAAAG ATGATGCAGT TATTGGTAAA AAGGGACTCG AAAAACTTTA CGATAAAAAG CTCCAACATG AAGATGGCTA TCGTGTCACA ATCGTTGACG
M143/10     TCTGAAGAAT TAAAACAAAA AGAATATAAA GGCTATAAAG ATGATGCAGT TATTGGTAAA AAGGGACTCG AAAAACTTTA CGATAAAAAG CTCCAACATG AAGATGGCTA TCGTGTCACA ATCGTTGACG
M277/10     TCTGAAGAAT TAAAACAAAA AGAATATAAA GGCTATAAAG ATGATGCAGT TATTGGTAAA AAGGGACTCG AAAAACTTTA CGATAAAAAG CTCCAACATG AAGATGGCTA TCGTGTCACA ATCGTTGACG
M404-1/10   TCTGAAGAAT TAAAACAAAA AGAATATAAA GGCTATAAAG ATGATGCAGT TATTGGTAAA AAGGGACTCG AAAAACTTTA CGATAAAAAG CTCCAACATG AAGATGGCTA TCGTGTCACA ATCGTTGACG
M545/10     TCTGAAGAAT TAAAACAAAA AGAATATAAA GGCTATAAAG ATGATGCAGT TATTGGTAAA AAGGGACTCG AAAAACTTTA CGATAAAAAG CTCCAACATG AAGATGGCTA TCGTGTCACA ATCGTTGACG
M4276-1/09  TCTGAAGAAT TAAAACAAAA AGAATATAAA GGCTATAAAG ATGATGCAGT TATTGGTAAA AAGGGACTCG AAAAACTTTA CGATAAAAAG CTCCAACATG AAGATGGCTA TCGTGTCACA ATCGTTGACG
M1125-2/10  TCTGAAGAAT TAAAACAAAA AGAATATAAA GGCTATAAAG ATGATGCAGT TATTGGTAAA AAGGGACTCG AAAAACTTTA CGATAAAAAG CTCCAACATG AAGATGGCTA TCGTGTCACA ATCGTTGACG
M1961/10    TCTGAAGAAT TAAAACAAAA AGAATATAAA GGCTATAAAG ATGATGCAGT TATTGGTAAA AAGGGACTCG AAAAACTTTA CGATAAAAAG CTCCAACATG AAGATGGCTA TCGTGTCACA ATCGTTGACG
M1191-2/10  TCTGAAGAAT TAAAACAAAA AGAATATAAA GGCTATAAAG ATGATGCAGT TATTGGTAAA AAGGGACTCG AAAAACTTTA CGATAAAAAG CTCCAACATG AAGATGGCTA TCGTGTCACA ATCGTTGACG
M3783/10    TCTGAAGAAT TAAAACAAAA AGAATATAAA GGCTATAAAG ATGATGCAGT TATTGGTAAA AAGGGACTCG AAAAACTTTA CGATAAAAAG CTCCAACATG AAGATGGCTA TCGTGTCACA ATCGTTGACG
M205/10     TCTGAAGAAT TAAAACAAAA AGAATATAAA GGCTATAAAG ATGATGCAGT TATTGGTAAA AAGGGACTCG AAAAACTTTA CGATAAAAAG CTCCAACATG AAGATGGCTA TCGTGTCACA ATCGTTGACG
M4460/09    TCTGAAGAAT TAAAACAAAA AGAATATAAA GGTTATAAAG ATGATGCAGT TGTTGGTAAA AAGGGACTCG AAAAACTTTA CGATAAAAAG CTCCAACATG AAGATGGCTA TCGTGTCACA ATCGTTGACG
Consensus   TCTGAAGAAT TAAAACAAAA AGAATATAAA GGcTATAAAG ATGATGCAGT TaTTGGTAAA AAGGGACTCG AAAAACTTTA CGATAAAAAG CTCCAACATG AAGATGGCTA TCGTGTCACA ATCgTTGACG

            911                                                                                                                  1040
S.fleurSMF  ATAATAGCAA TACAATCGCA CATACATTAA TAGAGAAAAA GAAAAAAGAT GGCAAAGATA TTCAACTAAC TATTGATGCT AAAGTTCAAA AGAGTATTTA TAACAACATG AAAAATGATT ATGGCTCAGG
S.fleurCCU  ATAATAGCAA TACAATCGCA CATACATTAA TAGAGAAAAA GAAAAAAGAT GGCAAAGATA TTCAACTAAC TATTGATGCT AAAGTTCAAA AGAGTATTTA TAACAACATG AAAAATGATT ATGGCTCAGG
M143/10     ATAATAGCAA TACAATCGCA CATACATTAA TAGAGAAAAA GAAAAAAGAT GGCAAAGATA TTCAACTAAC TATTGATGCT AAAGTTCAAA AGAGTATTTA TAACAACATG AAAAATGATT ATGGCTCAGG
M277/10     ATAATAGCAA TACAATCGCA CATACATTAA TAGAGAAAAA GAAAAAAGAT GGCAAAGATA TTCAACTAAC TATTGATGCT AAAGTTCAAA AGAGTATTTA TAACAACATG AAAAATGATT ATGGCTCAGG
M404-1/10   ATAATAGCAA TACAATCGCA CATACATTAA TAGAGAAAAA GAAAAAAGAT GGCAAAGATA TTCAACTAAC TATTGATGCT AAAGTTCAAA AGAGTATTTA TAACAACATG AAAAATGATT ATGGCTCAGG
M545/10     ATAATAGCAA TACAATCGCA CATACATTAA TAGAGAAAAA GAAAAAAGAT GGCAAAGATA TTCAACTAAC TATTGATGCT AAAGTTCAAA AGAGTATTTA TAACAACATG AAAAATGATT ATGGCTCAGG
M4276-1/09  ATAATAGCAA TACAATCGCA CATACATTAA TAGAGAAAAA GAAAAAAGAT GGCAAAGATA TTCAACTAAC TATTGATGCT AAAGTTCAAA AGAGTATTTA TAACAACATG AAAAATGATT ATGGCTCAGG
M1125-2/10  ATAATAGCAA TACAATCGCA CATACATTAA TAGAGAAAAA GAAAAAAGAT GGCAAAGATA TTCAACTAAC TATTGATGCT AAAGTTCAAA AGAGTATTTA TAACAACATG AAAAATGATT ATGGCTCAGG
M1961/10    ATAATAGCAA TACAATCGCA CATACATTAA TAGAGAAAAA GAAAAAAGAT GGCAAAGATA TTCAACTAAC TATTGATGCT AAAGTTCAAA AGAGTATTTA TAACAACATG AAAAATGATT ATGGCTCAGG
M1191-2/10  ATAATAGCAA TACAATCGCA CATACATTAA TAGAGAAAAA GAAAAAAGAT GGCAAAGATA TTCAACTAAC TATTGATGCT AAAGTTCAAA AGAGTATTTA TAACAACATG AAAAATGATT ATGGCTCAGG
M3783/10    ATAATAGCAA TACAATCGCA CATACATTAA TAGAGAAAAA GAAAAAAGAT GGCAAAGATA TTCAACTAAC TATTGATGCT AAAGTTCAAA AGAGTATTTA TAACAACATG AAAAATGATT ATGGCTCAGG
M205/10     ATAATAGCAA TACAATCGCA CATACATTAA TAGAGAAAAA GAAAAAAGAT GGCAAAGATA TTCAACTAAC TATTGATGCT AAAGTTCAAA AGAGTATTTA TAACAACATG AAAAATGATT ATGGCTCAGG
M4460/09    ATAATAGCAA TACAATCGCA CATACATTAA TAGAGAAAAA GAAAAAAGAT GGCAAAGATA TTCAACTAAC TATTGATGCT AAAGTTCAAA AGAGTATTTA TAACAACATG AAAAATGATT ATGGCTCAGG
Consensus   ATAATAGCAA TACAATCGCA CATACATTAA TAGAGAAAAA GAAAAAAGAT GGCAAAGATA TTCAACTAAC TATTGATGCT AAAGTTCAAA AGAGTATTTA TAACAACATG AAAAATGATT ATGGCTCAGG

            1041                                                                                                                 1170
S.fleurSMF  TACTGCTATT CACCCTCAAA CAGGTGAATT GTTAGCACTT GTAAGCACAC CTTCATATGA CGTGTACCCA TTTATGTATG GCATGAGTAA CGAAGAATAT AATAAATTAA CCGAAGATAA AAAAGAACCA
S.fleurCCU  TACTGCTATC CACCCTCAAA CAGGTGAATT ATTAGCACTT GTAAGCACAC CTTCATATGA CGTCTATCCA TTTATGTATG GCATGAGTAA CGAAGAATAT AATAAATTAA CCGAAGATAA AAAAGAACCT
M143/10     TACTGCTATC CACCCTCAAA CAGGTGAATT ATTAGCACTT GTAAGCACAC CTTCATATGA CGTCTATCCA TTTATGTATG GCATGAGTAA CGAAGAATAT AATAAATTAA CCGAAGATAA AAAAGAACCT
M277/10     TACTGCTATC CACCCTCAAA CAGGTGAATT ATTAGCACTT GTAAGCACAC CTTCATATGA CGTCTATCCA TTTATGTATG GCATGAGTAA CGAAGAATAT AATAAATTAA CCGAAGATAA AAAAGAACCT
M404-1/10   TACTGCTATC CACCCTCAAA CAGGTGAATT ATTAGCACTT GTAAGCACAC CTTCATATGA CGTCTATCCA TTTATGTATG GCATGAGTAA CGAAGAATAT AATAAATTAA CCGAAGATAA AAAAGAACCT
M545/10     TACTGCTATC CACCCTCAAA CAGGTGAATT ATTAGCACTT GTAAGCACAC CTTCATATGA CGTCTATCCA TTTATGTATG GCATGAGTAA CGAAGAATAT AATAAATTAA CCGAAGATAA AAAAGAACCT
M4276-1/09  TACTGCTATC CACCCTCAAA CAGGTGAATT ATTAGCACTT GTAAGCACAC CTTCATATGA CGTCTATCCA TTTATGTATG GCATGAGTAA CGAAGAATAT AATAAATTAA CCGAAGATAA AAAAGAACCT
M1125-2/10  TACTGCTATC CACCCTCAAA CAGGTGAATT ATTAGCACTT GTAAGCACAC CTTCATATGA CGTCTATCCA TTTATGTATG GCATGAGTAA CGAAGAATAT AATAAATTAA CCGAAGATAA AAAAGAACCT
M1961/10    TACTGCTATC CACCCTCAAA CAGGTGAATT ATTAGCACTT GTAAGCACAC CTTCATATGA CGTCTATCCA TTTATGTATG GCATGAGTAA CGAAGAATAT AATAAATTAA CCGAAGATAA AAAAGAACCT
M1191-2/10  TACTGCTATC CACCCTCAAA CAGGTGAATT ATTAGCACTT GTAAGCACAC CTTCATATGA CGTCTATCCA TTTATGTATG GCATGAGTAA CGAAGAATAT AATAAATTAA CCGAAGATAA AAAAGAACCT
M3783/10    TACTGCTATC CACCCTCAAA CAGGTGAATT ATTAGCACTT GTAAGCACAC CTTCATATGA CGTCTATCCA TTTATGTATG GCATGAGTAA CGAAGAATAT AATAAATTAA CCGAAGATAA AAAAGAACCT
M205/10     TACTGCTATC CACCCTCAAA CAGGTGAATT ATTAGCACTT GTAAGCACAC CTTCATATGA CGTCTATCCA TTTATGTATG GCATGAGTAA CGAAGAATAT AATAAATTAA CCGAAGATAA AAAAGAACCT
M4460/09    TACTGCTATC CACCCTCAAA CAGGTGAATT GTTAGCACTT GTAAGCACAC CTTCATATGA CGTGTATCCA TTTATGTATG GTATGAGTAA CGAAGAATAT AATAAATTAA CCGAAGATAA AAAAGAACCT
Consensus   TACTGCTATc CACCCTCAAA CAGGTGAATT aTTAGCACTT GTAAGCACAC CTTCATATGA CGTcTAtCCA TTTATGTATG GcATGAGTAA CGAAGAATAT AATAAATTAA CCGAAGATAA AAAAGAACCt
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             1171                                                                                                                 1300
S.fleurSMF   CTGCTCAACA AGTTCCAGAT TACAACTTCA CCAGGTTCAA CTCAAAAAAT ATTAACAGCA ATGATTGGGT TAAATAACAA AACATTAGAC GATAAAACAA GTTATAAAAT CGATGGTAAA GGTTGGCAAA
S.fleurCCU   CTGCTCAACA AGTTCCAGAT TACAACTTCA CCAGGTTCAA CTCAAAAAAT ATTAACAGCA ATGATTGGGT TAAATAACAA AACATTAGAC GATAAAACAA GTTATAAAAT CGATGGTAAA GGTTGGCAAA
   M143/10   CTGCTCAACA AGTTCCAGAT TACAACTTCA CCAGGTTCAA CTCAAAAAAT ATTAACAGCA ATGATTGGGT TAAATAACAA AACATTAGAC GATAAAACAA GTTATAAAAT CGATGGTAAA GGTTGGCAAA
   M277/10   CTGCTCAACA AGTTCCAGAT TACAACTTCA CCAGGTTCAA CTCAAAAAAT ATTAACAGCA ATGATTGGGT TAAATAACAA AACATTAGAC GATAAAACAA GTTATAAAAT CGATGGTAAA GGTTGGCAAA
 M404-1/10   CTGCTCAACA AGTTCCAGAT TACAACTTCA CCAGGTTCAA CTCAAAAAAT ATTAACAGCA ATGATTGGGT TAAATAACAA AACATTAGAC GATAAAACAA GTTATAAAAT CGATGGTAAA GGTTGGCAAA
   M545/10   CTGCTCAACA AGTTCCAGAT TACAACTTCA CCAGGTTCAA CTCAAAAAAT ATTAACAGCA ATGATTGGGT TAAATAACAA AACATTAGAC GATAAAACAA GTTATAAAAT CGATGGTAAA GGTTGGCAAA
M4276-1/09   CTGCTCAACA AGTTCCAGAT TACAACTTCA CCAGGTTCAA CTCAAAAAAT ATTAACAGCA ATGATTGGGT TAAATAACAA AACATTAGAC GATAAAACAA GTTATAAAAT CGATGGTAAA GGTTGGCAAA
M1125-2/10   CTGCTCAACA AGTTCCAGAT TACAACTTCA CCAGGTTCAA CTCAAAAAAT ATTAACAGCA ATGATTGGGT TAAATAACAA AACATTAGAC GATAAAACAA GTTATAAAAT CGATGGTAAA GGTTGGCAAA
  M1961/10   CTGCTCAACA AGTTCCAGAT TACAACTTCA CCAGGTTCAA CTCAAAAAAT ATTAACAGCA ATGATTGGGT TAAATAACAA AACATTAGAC GATAAAACAA GTTATAAAAT CGATGGTAAA GGTTGGCAAA
M1191-2/10   CTGCTCAACA AGTTCCAGAT TACAACTTCA CCAGGTTCAA CTCAAAAAAT ATTAACAGCA ATGATTGGGT TAAATAACAA AACATTAGAC GATAAAACAA GTTATAAAAT CGATGGTAAA GGTTGGCAAA
  M3783/10   CTGCTCAACA AGTTCCAGAT TACAACTTCA CCAGGTTCAA CTCAAAAAAT ATTAACAGCA ATGATTGGGT TAAATAACAA AACATTAGAC GATAAAACAA GTTATAAAAT CGATGGTAAA GGTTGGCAAA
   M205/10   CTGCTCAACA AGTTCCAGAT TACAACTTCA CCAGGTTCAA CTCAAAAAAT ATTAACAGCA ATGATTGGGT TAAATAACAA AACATTAGAC GATAAAACAA GTTATAAAAT CGATGGTAAA GGTTGGCAAA
  M4460/09   CTGCTCAACA AGTTCCAGAT TACAACTTCA CCAGGTTCAA CTCAAAAAAT ATTAACAGCA ATGATTGGGT TAAATAACAA AACATTAGAC GATAAAACAA GTTATAAAAT CGATGGTAAA GGTTGGCAAA
 Consensus   CTGCTCAACA AGTTCCAGAT TACAACTTCA CCAGGTTCAA CTCAAAAAAT ATTAACAGCA ATGATTGGGT TAAATAACAA AACATTAGAC GATAAAACAA GTTATAAAAT CGATGGTAAA GGTTGGCAAA

             1301                                                                                                                 1430
S.fleurSMF   AAGATAAATC TTGGGGTGGT TACAACGTTA CAAGATATGA AGTGGTAAAT GGTAATATCG ACTTAAAACA AGCAATAGAA TCATCAGATA ACATTTTCTT TGCTAGAGTA GCACTCGAAT TAGGCAGTAA
S.fleurCCU   AAGATAAATC TTGGGGTGGT TACAACGTTA CAAGATATGA AGTGGTAAAT GGTAATATCG ACTTAAAACA AGCAATAGAA TCATCAGATA ACATTTTCTT TGCTAGAGTA GCACTCGAAT TAGGCAGTAA
   M143/10   AAGATAAATC TTGGGGTGGT TACAACGTTA CAAGATATGA AGTGGTAAAT GGTAATATCG ACTTAAAACA AGCAATAGAA TCATCAGATA ACATTTTCTT TGCTAGAGTA GCACTCGAAT TAGGCAGTAA
   M277/10   AAGATAAATC TTGGGGTGGT TACAACGTTA CAAGATATGA AGTGGTAAAT GGTAATATCG ACTTAAAACA AGCAATAGAA TCATCAGATA ACATTTTCTT TGCTAGAGTA GCACTCGAAT TAGGCAGTAA
 M404-1/10   AAGATAAATC TTGGGGTGGT TACAACGTTA CAAGATATGA AGTGGTAAAT GGTAATATCG ACTTAAAACA AGCAATAGAA TCATCAGATA ACATTTTCTT TGCTAGAGTA GCACTCGAAT TAGGCAGTAA
   M545/10   AAGATAAATC TTGGGGTGGT TACAACGTTA CAAGATATGA AGTGGTAAAT GGTAATATCG ACTTAAAACA AGCAATAGAA TCATCAGATA ACATTTTCTT TGCTAGAGTA GCACTCGAAT TAGGCAGTAA
M4276-1/09   AAGATAAATC TTGGGGTGGT TACAACGTTA CAAGATATGA AGTGGTAAAT GGTAATATCG ACTTAAAACA AGCAATAGAA TCATCAGATA ACATTTTCTT TGCTAGAGTA GCACTCGAAT TAGGCAGTAA
M1125-2/10   AAGATAAATC TTGGGGTGGT TACAACGTTA CAAGATATGA AGTGGTAAAT GGTAATATCG ACTTAAAACA AGCAATAGAA TCATCAGATA ACATTTTCTT TGCTAGAGTA GCACTCGAAT TAGGCAGTAA
  M1961/10   AAGATAAATC TTGGGGTGGT TACAACGTTA CAAGATATGA AGTGGTAAAT GGTAATATCG ACTTAAAACA AGCAATAGAA TCATCAGATA ACATTTTCTT TGCTAGAGTA GCACTCGAAT TAGGCAGTAA
M1191-2/10   AAGATAAATC TTGGGGTGGT TACAACGTTA CAAGATATGA AGTGGTAAAT GGTAATATCG ACTTAAAACA AGCAATAGAA TCATCAGATA ACATTTTCTT TGCTAGAGTA GCACTCGAAT TAGGCAGTAA
  M3783/10   AAGATAAATC TTGGGGTGGT TACAACGTTA CAAGATATGA AGTGGTAAAT GGTAATATCG ACTTAAAACA AGCAATAGAA TCATCAGATA ACATTTTCTT TGCTAGAGTA GCACTCGAAT TAGGCAGTAA
   M205/10   AAGATAAATC TTGGGGTGGT TACAACGTTA CAAGATATGA AGTGGTAAAT GGTAATATCG ACTTAAAACA AGCAATAGAA TCATCAGATA ACATTTTCTT TGCTAGAGTA GCACTCGAAT TAGGCAGTAA
  M4460/09   AAGATAAATC TTGGGGTGGT TACAACGTTA CAAGATATGA AGTGGTAAAT GGTAATATCG ACTTAAAACA AGCAATAGAA TCATCAGATA ACATTTTCTT TGCTAGAGTA GCACTCGAAT TAGGCAGTAA
 Consensus   AAGATAAATC TTGGGGTGGT TACAACGTTA CAAGATATGA AGTGGTAAAT GGTAATATCG ACTTAAAACA AGCAATAGAA TCATCAGATA ACATTTTCTT TGCTAGAGTA GCACTCGAAT TAGGCAGTAA

             1431                                                                                                                 1560
S.fleurSMF   GAAGTTTGAA AAAGCCATGA AAAAACTAGG TGTTGGTGAA GATATACCAA GTGATTATCC ATTTTATAAT GCTCAAATTT CAAACAAAAA TTTAGATAAT GAAATATTAT TAGCTGATTC AGGTTACGGA
S.fleurCCU   GAAATTTGAA AAAGGCATGA AAAAACTAGG TGTTGGTGAA GATATACCAA GTGATTATCC ATTTTATAAT GCTCAAATTT CAAACAAAAA TTTAGATAAT GAAATATTAT TAGCTGATTC AGGTTACGGA
   M143/10   GAAATTTGAA AAAGGCATGA AAAAACTAGG TGTTGGTGAA GATATACCAA GTGATTATCC ATTTTATAAT GCTCAAATTT CAAACAAAAA TTTAGATAAT GAAATATTAT TAGCTGATTC AGGTTACGGA
   M277/10   GAAATTTGAA AAAGGCATGA AAAAACTAGG TGTTGGTGAA GATATACCAA GTGATTATCC ATTTTATAAT GCTCAAATTT CAAACAAAAA TTTAGATAAT GAAATATTAT TAGCTGATTC AGGTTACGGA
 M404-1/10   GAAATTTGAA AAAGGCATGA AAAAACTAGG TGTTGGTGAA GATATACCAA GTGATTATCC ATTTTATAAT GCTCAAATTT CAAACAAAAA TTTAGATAAT GAAATATTAT TAGCTGATTC AGGTTACGGA
   M545/10   GAAATTTGAA AAAGGCATGA AAAAACTAGG TGTTGGTGAA GATATACCAA GTGATTATCC ATTTTATAAT GCTCAAATTT CAAACAAAAA TTTAGATAAT GAAATATTAT TAGCTGATTC AGGTTACGGA
M4276-1/09   GAAATTTGAA AAAGGCATGA AAAAACTAGG TGTTGGTGAA GATATACCAA GTGATTATCC ATTTTATAAT GCTCAAATTT CAAACAAAAA TTTAGATAAT GAAATATTAT TAGCTGATTC AGGTTACGGA
M1125-2/10   GAAATTTGAA AAAGGCATGA AAAAACTAGG TGTTGGTGAA GATATACCAA GTGATTATCC ATTTTATAAT GCTCAAATTT CAAACAAAAA TTTAGATAAT GAAATATTAT TAGCTGATTC AGGTTACGGA
  M1961/10   GAAATTTGAA AAAGGCATGA AAAAACTAGG TGTTGGTGAA GATATACCAA GTGATTATCC ATTTTATAAT GCTCAAATTT CAAACAAAAA TTTAGATAAT GAAATATTAT TAGCTGATTC AGGTTACGGA
M1191-2/10   GAAATTTGAA AAAGGCATGA AAAAACTAGG TGTTGGTGAA GATATACCAA GTGATTATCC ATTTTATAAT GCTCAAATTT CAAACAAAAA TTTAGATAAT GAAATATTAT TAGCTGATTC AGGTTACGGA
  M3783/10   GAAATTTGAA AAAGGCATGA AAAAACTAGG TGTTGGTGAA GATATACCAA GTGATTATCC ATTTTATAAT GCTCAAATTT CAAACAAAAA TTTAGATAAT GAAATATTAT TAGCTGATTC AGGTTACGGA
   M205/10   GAAATTTGAA AAAGGCATGA AAAAACTAGG TGTTGGTGAA GATATACCAA GTGATTATCC ATTTTATAAT GCTCAAATTT CAAACAAAAA TTTAGATAAT GAAATATTAT TAGCTGATTC AGGTTACGGA
  M4460/09   GAAATTTGAA AAAGGCATGA AAAAACTAGG TGTTGGTGAA GATATACCAA GTGATTATCC ATTTTATAAT GCTCAAATTT CAAACAAAAA TTTAGATAAT GAAATATTAT TAGCTGATTC AGGTTACGGA
 Consensus   GAAaTTTGAA AAAGgCATGA AAAAACTAGG TGTTGGTGAA GATATACCAA GTGATTATCC ATTTTATAAT GCTCAAATTT CAAACAAAAA TTTAGATAAT GAAATATTAT TAGCTGATTC AGGTTACGGA
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            1561                                                                                                                              1690
S.fleurSMF  CAAGGTGAAA TACTGATTAA CCCAGTACAG ATCCTTTCAA TCTATAGCGC ATTAGAAAAC AATGGCAATA TCAATGCACC TCACTTATTA AAAGACACGA AAAACAAAGT TTGGAAGAAA AATATTATTT
S.fleurCCU  CAAGGTGAAA TACTGATTAA CCCAGTACAG ATCCTTTCAA TCTATAGCGC ATTAGAAAAT AATGGCAATA TTAACGCACC TCACTTATTA AAAGACACGA AAAACAAAGT TTGGAAGAAA AATATTATTT
   M143/10  CAAGGTGAAA TACTGATTAA CCCAGTACAG ATCCTTTCAA TCTATAGCGC ATTAGAAAAT AATGGCAATA TTAACGCACC TCACTTATTA AAAGACACGA AAAACAAAGT TTGGAAGAAA AATATTATTT
   M277/10  CAAGGTGAAA TACTGATTAA CCCAGTACAG ATCCTTTCAA TCTATAGCGC ATTAGAAAAT AATGGCAATA TTAACGCACC TCACTTATTA AAAGACACGA AAAACAAAGT TTGGAAGAAA AATATTATTT
 M404-1/10  CAAGGTGAAA TACTGATTAA CCCAGTACAG ATCCTTTCAA TCTATAGCGC ATTAGAAAAT AATGGCAATA TTAACGCACC TCACTTATTA AAAGACACGA AAAACAAAGT TTGGAAGAAA AATATTATTT
   M545/10  CAAGGTGAAA TACTGATTAA CCCAGTACAG ATCCTTTCAA TCTATAGCGC ATTAGAAAAT AATGGCAATA TTAACGCACC TCACTTATTA AAAGACACGA AAAACAAAGT TTGGAAGAAA AATATTATTT
M4276-1/09  CAAGGTGAAA TACTGATTAA CCCAGTACAG ATCCTTTCAA TCTATAGCGC ATTAGAAAAT AATGGCAATA TTAACGCACC TCACTTATTA AAAGACACGA AAAACAAAGT TTGGAAGAAA AATATTATTT
M1125-2/10  CAAGGTGAAA TACTGATTAA CCCAGTACAG ATCCTTTCAA TCTATAGCGC ATTAGAAAAT AATGGCAATA TTAACGCACC TCACTTATTA AAAGACACGA AAAACAAAGT TTGGAAGAAA AATATTATTT
  M1961/10  CAAGGTGAAA TACTGATTAA CCCAGTACAG ATCCTTTCAA TCTATAGCGC ATTAGAAAAT AATGGCAATA TTAACGCACC TCACTTATTA AAAGACACGA AAAACAAAGT TTGGAAGAAA AATATTATTT
M1191-2/10  CAAGGTGAAA TACTGATTAA CCCAGTACAG ATCCTTTCAA TCTATAGCGC ATTAGAAAAT AATGGCAATA TTAACGCACC TCACTTATTA AAAGACACGA AAAACAAAGT TTGGAAGAAA AATATTATTT
  M3783/10  CAAGGTGAAA TACTGATTAA CCCAGTACAG ATCCTTTCAA TCTATAGCGC ATTAGAAAAT AATGGCAATA TTAACGCACC TCACTTATTA AAAGACACGA AAAACAAAGT TTGGAAGAAA AATATTATTT
   M205/10  CAAGGTGAAA TACTGATTAA CCCAGTACAG ATCCTTTCAA TCTATAGCGC ATTAGAAAAT AATGGCAATA TTAACGCACC TCACTTATTA AAAGACACGA AAAACAAAGT TTGGAAGAAA AATATTATTT
  M4460/09  CAAGGTGAAA TACTGATTAA CCCAGTACAG ATCCTTTCAA TCTATAGCGC ATTAGAAAAT AATGGCAATA TTAACGCACC TCACTTATTA AAAGACACGA AAAACAAAGT TTGGAAGAAA AATATTATTT
 Consensus  CAAGGTGAAA TACTGATTAA CCCAGTACAG ATCCTTTCAA TCTATAGCGC ATTAGAAAAt AATGGCAATA TtAAcGCACC TCACTTATTA AAAGACACGA AAAACAAAGT TTGGAAGAAA AATATTATTT

            1691                                                                                                                              1820
S.fleurSMF  CCAAAGAAAA TATCAATCTA TTAACTGATG GTATGCAACA AGTCGTAAAT AAAACACATA AAGAAGATAT TTATAGACCT TACGCAAACT TAATTGGCAA ATCCGGTACT GCAGAACTCA AAATGAAACA
S.fleurCCU  CCAAAGAAAA TATCAATCTA TTAACTGATG GTATGCAACA AGTCGTAAAT AAAACACATA AAGAAGATAT TTATAGATCT TATGCAAACT TAATTGGCAA ATCCGGTACT GCAGAACTCA AAATGAAACA
   M143/10  CCAAAGAAAA TATAAATCTA TTAACTGATG GTATGCAACA AGTCGTAAAT AAAACACATA AAGAAGATAT TTATAGATCT TATGCAAACT TAATTGGCAA ATCCGGTACT GCAGAACTCA AAATGAAACA
   M277/10  CCAAAGAAAA TATAAATCTA TTAACTGATG GTATGCAACA AGTCGTAAAT AAAACACATA AAGAAGATAT TTATAGATCT TATGCAAACT TAATTGGCAA ATCCGGTACT GCAGAACTCA AAATGAAACA
 M404-1/10  CCAAAGAAAA TATAAATCTA TTAACTGATG GTATGCAACA AGTCGTAAAT AAAACACATA AAGAAGATAT TTATAGATCT TATGCAAACT TAATTGGCAA ATCCGGTACT GCAGAACTCA AAATGAAACA
   M545/10  CCAAAGAAAA TATAAATCTA TTAACTGATG GTATGCAACA AGTCGTAAAT AAAACACATA AAGAAGATAT TTATAGATCT TATGCAAACT TAATTGGCAA ATCCGGTACT GCAGAACTCA AAATGAAACA
M4276-1/09  CCAAAGAAAA TATAAATCTA TTAACTGATG GTATGCAACA AGTCGTAAAT AAAACACATA AAGAAGATAT TTATAGATCT TATGCAAACT TAATTGGCAA ATCCGGTACT GCAGAACTCA AAATGAAACA
M1125-2/10  CCAAAGAAAA TATAAATCTA TTAACTGATG GTATGCAACA AGTCGTAAAT AAAACACATA AAGAAGATAT TTATAGATCT TATGCAAACT TAATTGGCAA ATCCGGTACT GCAGAACTCA AAATGAAACA
  M1961/10  CCAAAGAAAA TATAAATCTA TTAACTGATG GTATGCAACA AGTCGTAAAT AAAACACATA AAGAAGATAT TTATAGATCT TATGCAAACT TAATTGGCAA ATCCGGTACT GCAGAACTCA AAATGAAACA
M1191-2/10  CCAAAGAAAA TATAAATCTA TTAACTGATG GTATGCAACA AGTCGTAAAT AAAACACATA AAGAAGATAT TTATAGATCT TATGCAAACT TAATTGGCAA ATCCGGTACT GCAGAACTCA AAATGAAACA
  M3783/10  CCAAAGAAAA TATAAATCTA TTAACTGATG GTATGCAACA AGTCGTAAAT AAAACACATA AAGAAGATAT TTATAGATCT TATGCAAACT TAATTGGCAA ATCCGGTACT GCAGAACTCA AAATGAAACA
   M205/10  CCAAAGAAAA TATCAATCTA TTAACTGATG GTATGCAACA AGTCGTAAAT AAAACACATA AAGAAGATAT TTATAGATCT TATGCAAACT TAATTGGCAA ATCCGGTACT GCAGAACTCA AAATGAAACA
  M4460/09  CCAAAGAAAA TATCAATCTA TTAACTGATG GCATGCAACA AGTCGTAAAT AAAACACATA AAAAAGATAT TTATAGACCT TACGCAAACT TAATTGGCAA ATCCGGTACT GCAGAACTCA AAATGAAACA
 Consensus  CCAAAGAAAA TATcAATCTA TTAACTGATG GtATGCAACA AGTCGTAAAT AAAACACATA AAgAAGATAT TTATAGAtCT TAtGCAAACT TAATTGGCAA ATCCGGTACT GCAGAACTCA AAATGAAACA

            1821                                                                                                                              1950
S.fleurSMF  AGGAGAAACT GGGAGACAAA TTGGGTGGTT TATATCATAT GATAAAGATA ATCCAAACAT GATGATGGCT ATTAATGTTA AAGATGTACA AGATAAAGGA ATGGCTAGCT ACAATGCCAA AATCTCAGGT
S.fleurCCU  AGGAGAAACT GGCAGACAAA TTGGGTGGTT TATATCATAT GATAAAGATA ATCCAAACAT GATGATGGCT ATTAATGTTA AAGATGTACA AGATAAAGGA ATGGCTAGCT ACAATGCCAA AATCTCAGGT
   M143/10  AGGAGAAACT GGCAGACAAA TTGGGTGGTT TATATCATAT GATAAAGATA ATCCAAACAT GATGATGGCT ATTAATGTTA AAGATGTACA AGATAAAGGA ATGGCTAGCT ACAATGCCAA AATCTCAGGT
   M277/10  AGGAGAAACT GGCAGACAAA TTGGGTGGTT TATATCATAT GATAAAGATA ATCCAAACAT GATGATGGCT ATTAATGTTA AAGATGTACA AGATAAAGGA ATGGCTAGCT ACAATGCCAA AATCTCAGGT
 M404-1/10  AGGAGAAACT GGCAGACAAA TTGGGTGGTT TATATCATAT GATAAAGATA ATCCAAACAT GATGATGGCT ATTAATGTTA AAGATGTACA AGATAAAGGA ATGGCTAGCT ACAATGCCAA AATCTCAGGT
   M545/10  AGGAGAAACT GGCAGACAAA TTGGGTGGTT TATATCATAT GATAAAGATA ATCCAAACAT GATGATGGCT ATTAATGTTA AAGATGTACA AGATAAAGGA ATGGCTAGCT ACAATGCCAA AATCTCAGGT
M4276-1/09  AGGAGAAACT GGCAGACAAA TTGGGTGGTT TATATCATAT GATAAAGATA ATCCAAACAT GATGATGGCT ATTAATGTTA AAGATGTACA AGATAAAGGA ATGGCTAGCT ACAATGCCAA AATCTCAGGT
M1125-2/10  AGGAGAAACT GGCAGACAAA TTGGGTGGTT TATATCATAT GATAAAGATA ATCCAAACAT GATGATGGCT ATTAATGTTA AAGATGTACA AGATAAAGGA ATGGCTAGCT ACAATGCCAA AATCTCAGGT
  M1961/10  AGGAGAAACT GGCAGACAAA TTGGGTGGTT TATATCATAT GATAAAGATA ATCCAAACAT GATGATGGCT ATTAATGTTA AAGATGTACA AGATAAAGGA ATGGCTAGCT ACAATGCCAA AATCTCAGGT
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  M3783/10  AGGAGAAACT GGCAGACAAA TTGGGTGGTT TATATCATAT GATAAAGATA ATCCAAACAT GATGATGGCT ATTAATGTTA AAGATGTACA AGATAAAGGA ATGGCTAGCT ACAATGCCAA AATCTCAGGT
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  M4460/09  AGGAGAAACT GGCAGACAAA TTGGGTGGTT TATATCATAT GATAAAGATA ATCCAAACAT GATGATGGCT ATTAATGTTA AAGATGTACA AGATAAAGGA ATGGCTAGCT ACAATGCCAA AATCTCAGGT
 Consensus  AGGAGAAACT GGcAGACAAA TTGGGTGGTT TATATCATAT GATAAAGATA ATCCAAACAT GATGATGGCT ATTAATGTTA AAGATGTACA AGATAAAGGA ATGGCTAGCT ACAATGCCAA AATCTCAGGT
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```
                1951                                                2007
S.fleurSMF      AAAGTGTATG ATGAGCTATA TGAGAACGGT AATAAAAAAT ACGATATAGA TAAATAA
S.fleurCCU      AAAGTGTATG ATGAGCTATA TGAGAACGGT AATAAAAAAT ACGATATAGA TGAATAA
    M143/10     AAAGTGTATG ATGAGCTATA TGAGAACGGT AATAAAAAAT ACGATATAGA TGAATAA
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    M1961/10    AAAGTGTATG ATGAGCTATA TGAGAACGGT AATAAAAAAT ACGATATAGA TGAATAA
  M1191-2/10    AAAGTGTATG ATGAGCTATA TGAGAACGGT AATAAAAAAT ACGATATAGA TGAATAA
    M3783/10    GAAGTGTATG ATGAGCTATA TGAGAACGGT AATAAAAAAT ACGATATAGA TGAATAA
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mecA gene sequence of *S. fleurettii* strain M4460/09 deposited into EMBL/Genbank/ DDBJ databases

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ID   HE861945; SV 1; linear; genomic DNA; STD; PRO; 2164 BP.
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ST * private 15-JUL-2012
XX
AC   HE861945;
XX
DT   19-JUN-2012 (Rel. 113, Created)
DT   19-JUN-2012 (Rel. 113, Last updated, Version 0)
XX
DE   Staphylococcus fleurettii mecA gene for penicillin binding protein 2',
DE   strain M4460-09
XX
KW   .
XX
OS   Staphylococcus fleurettii
OC   Bacteria; Firmicutes; Bacillales; Staphylococcus.
XX
RN   [1]
RP   1-2164
RA   Perreten V.;
RT   ;
RL   Submitted (15-JUN-2012) to the INSDC.
RL   University of Berne, Institute of Veterinary Bacteriology, Laenggassstrasse
RL   122, CH - 3001 Berne, SWITZERLAND.
XX
RN   [2]
RA   Frey Y., Schwendener S., Perreten V.;
RT   "Methicillin resistance in Staphylococcus fleurettii from bovine mastitis";
RL   Unpublished.
XX

FH   Key             Location/Qualifiers
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FT                   /strain="M4460-09"
FT                   /mol_type="genomic DNA"
FT                   /country="Switzerland:VD"
FT                   /isolation_source="bovine milk"
FT                   /collection_date="23-Dec-2009"
FT                   /db_xref="taxon:150056"
FT   CDS             91..2097
FT                   /codon_start=1
FT                   /transl_table=11
FT                   /gene="mecA"
FT                   /product="penicillin binding protein 2'"
FT                   /protein_id="CCI72001.1"
FT                   /translation="MKKIKIVPLILIVVVVGFGIYFYASKDKEINKTIDAIEDKNFKQV
FT                   YKDSSYISKSDNGEVEMTERPIKIYKSLGVKDINIQERKIKKISKNKKRVDAQYKIKTN
FT                   YGNIDRNVQFNFVKEDGMWKLDWDHSVIIPGMQKDQSIHIENLKSERGKILDRNNVELA
FT                   NTGTAYEIGIVPKNVSKKDYKAIAKELSISEDYIKQQMDQNWVQDDTFVPLKTVKKMDE
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FT                   GYGQGEILINPVQILSIYSALENNGNINAPHLLKDTKNKVWKKNIISKENINLLTDGMQ
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XX
SQ Sequence 2164 BP; 916 A; 296 C; 366 G; 586 T; 0 other;

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     tatatttcca aaagcgataa tggtgaagta gaaatgactg aacgtccgat aaaaatatat       300
     aaaagtttag gcgttaaaga tataaacatt caagaacgca aaataaaaaa aatatctaaa       360
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     caccctcaaa caggtgaatt gttagcactt gtaagcacac cttcatatga cgtgtatcca      1200
     tttatgtatg gtatgagtaa cgaagaatat aataaattaa ccgaagataa aaaagaacct      1260
     ctgctcaaca agttccagat tacaacttca ccaggttcaa ctcaaaaaat attaacagca      1320
     atgattgggt taaataacaa aacattagac gataaaacaa gttataaaat cgatggtaaa      1380
     ggttggcaaa aagataaatc ttggggtggt tacaacgtta caagatatga agtggtaaat      1440
     ggtaatatcg acttaaaaca agcaatagaa tcatcagata acattttctt tgctagagta      1500
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mecA gene sequence of *S. fleurettii* strain M143/10 deposited into EMBL/Genbank/ DDBJ databases

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ID   HE978795; SV 1; linear; genomic DNA; STD; PRO; 2007 BP.
XX
ST * private 25-AUG-2012
XX
AC   HE978795;
XX
DT   16-AUG-2012 (Rel. 113, Created)
DT   16-AUG-2012 (Rel. 113, Last updated, Version 0)
XX
DE   Staphylococcus fleurettii mecA gene for penicillin binding protein 2',
DE   strain M143-10
XX
KW   .
XX
OS   Staphylococcus fleurettii
OC   Bacteria; Firmicutes; Bacillales; Staphylococcus.
XX
RN   [1]
RP   1-2007
RA   Perreten V.;
RT   ;
RL   Submitted (14-AUG-2012) to the INSDC.
RL   University of Berne, Institute of Veterinary Bacteriology, Laenggassstrasse
RL   122, CH - 3001 Berne, SWITZERLAND.
XX
RN   [2]
RA   Frey Y., Schwendener S., Perreten V.;
RT   "Methicillin resistance in Staphylococcus fleurettii from bovine mastitis";
RL   Unpublished.
XX
FH   Key             Location/Qualifiers
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FT   source          1..2007
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FT                   /strain="M143-10"
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FT                   /country="Switzerland"
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FT                   /db_xref="taxon:150056"
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FT                   /protein_id="CCK73176.1"
FT                   /translation="MKKIKIVPLILIVVVVGFGIYFYASKDKEINNTIDAIEDKNFKQV
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FT                   KNDYGSGTAIHPQTGELLALVSTPSYDVYPFMYGMSNEEYNKLTEDKKEPLLNKFQITT
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XX
SQ Sequence 2007 BP; 857 A; 271 C; 342 G; 537 T; 0 other;

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mecA gene sequence of *S. fleurettii* strain M205/10 deposited into EMBL/Genbank/ DDBJ databases

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ID   HE978794; SV 1; linear; genomic DNA; STD; PRO; 2007 BP.
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XX
AC   HE978794;
XX
DT   16-AUG-2012 (Rel. 113, Created)
DT   16-AUG-2012 (Rel. 113, Last updated, Version 0)
XX
DE   Staphylococcus fleurettii mecA gene for penicillin binding protein 2',
DE   strain M205-10
XX
KW   .
XX
OS   Staphylococcus fleurettii
OC   Bacteria; Firmicutes; Bacillales; Staphylococcus.
XX
RN   [1]
RP   1-2007
RA   Perreten V.;
RT   ;
RL   Submitted (14-AUG-2012) to the INSDC.
RL   University of Berne, Institute of Veterinary Bacteriology, Laenggassstrasse
RL   122, CH - 3001 Berne, SWITZERLAND.
XX
RN   [2]
RA   Frey Y., Schwendener S., Perreten V.;
RT   "Methicillin resistance in Staphylococcus fleurettii from bovine mastitis";
RL   Unpublished.
XX
FH   Key             Location/Qualifiers
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FT                   KNDYGSGTAIHPQTGELLALVSTPSYDVYPFMYGMSNEEYNKLTEDKKEPLLNKFQITT
FT                   SPGSTQKILTAMIGLNNKTLDDKTSYKIDGKGWQKDKSWGGYNVTRYEVVNGNIDLKQA
FT                   IESSDNIFFARVALELGSKKFEKGMKKLGVGEDIPSDYPFYNAQISNKNLDNEILLADS
FT                   GYGQGEILINPVQILSIYSALENNGNINAPHLLKDTKNKVWKKNIISKENINLLTDGMQ
FT                   QVVNKTHKEDIYRSYANLIGKSGTAELKMKQGETGRQIGWFISYDKDNPNMMMAINVKD
FT                   VQDKGMASYNAKISGKVYDELYENGNKKYDIDE"
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XX
SQ Sequence 2007 BP; 857 A; 270 C; 342 G; 538 T; 0 other;

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     atggctagct acaatgccaa aatctcaggt aaagtgtatg atgagctata tgagaacggt      1980
     aataaaaaat acgatataga tgaataa                                          2007
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mecA gene sequence of *S. fleurettii* strain M3783/09 deposited into EMBL/Genbank/ DDBJ databases

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ID   HE978796; SV 1; linear; genomic DNA; STD; PRO; 2007 BP.
XX
ST * private 25-AUG-2012
XX
AC   HE978796;
XX
DT   16-AUG-2012 (Rel. 113, Created)
DT   16-AUG-2012 (Rel. 113, Last updated, Version 0)
XX
DE   Staphylococcus fleurettii mecA gene for penicillin binding protein 2',
DE   strain M3783-09
XX
KW   .
XX
OS   Staphylococcus fleurettii
OC   Bacteria; Firmicutes; Bacillales; Staphylococcus.
XX
RN   [1]
RP   1-2007
RA   Perreten V.;
RT   ;
RL   Submitted (14-AUG-2012) to the INSDC.
RL   University of Berne, Institute of Veterinary Bacteriology, Laenggassstrasse
RL   122, CH - 3001 Berne, SWITZERLAND.
XX
RN   [2]
RA   Frey Y., Schwendener S., Perreten V.;
RT   "Methicillin resistance in Staphylococcus fleurettii from bovine mastitis";
RL   Unpublished.
XX
FH   Key             Location/Qualifiers
FH
FT   source          1..2007
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XX
SQ Sequence 2007 BP; 856 A; 271 C; 343 G; 537 T; 0 other;

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mecA gene sequence of *S. epidermidis* strain M8/10 deposited into EMBL/Genbank/ DDBJ databases

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DT   16-AUG-2012 (Rel. 113, Last updated, Version 0)
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DE   strain M8-10
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KW   .
XX
OS   Staphylococcus epidermidis
OC   Bacteria; Firmicutes; Bacillales; Staphylococcus.
XX
RN   [1]
RP   1-2007
RA   Perreten V.;
RT   ;
RL   Submitted (14-AUG-2012) to the INSDC.
RL   University of Berne, Institute of Veterinary Bacteriology, Laenggassstrasse
RL   122, CH - 3001 Berne, SWITZERLAND.
XX
RN   [2]
RA   Frey Y., Schwendener S., Perreten V.;
RT   "Methicillin resistance in Staphylococcus epidermidis from bovine
RT   mastitis";
RL   Unpublished.
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FH   Key             Location/Qualifiers
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XX
SQ Sequence 2007 BP; 855 A; 272 C; 341 G; 539 T; 0 other;

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mecA gene sequence of *S. epidermidis* strain M703/10 deposited into EMBL/Genbank/ DDBJ databases

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AC   HE978798;
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DT   16-AUG-2012 (Rel. 113, Last updated, Version 0)
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DE   strain M703-10
XX
KW   .
XX
OS   Staphylococcus epidermidis
OC   Bacteria; Firmicutes; Bacillales; Staphylococcus.
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RN   [1]
RP   1-2007
RA   Perreten V.;
RT   ;
RL   Submitted (14-AUG-2012) to the INSDC.
RL   University of Berne, Institute of Veterinary Bacteriology, Laenggassstrasse
RL   122, CH - 3001 Berne, SWITZERLAND.
XX
RN   [2]
RA   Frey Y., Schwendener S., Perreten V.;
RT   "Methicillin resistance in Staphylococcus epidermidis from bovine
RT   mastitis";
RL   Unpublished.
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FH   Key             Location/Qualifiers
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SQ Sequence 2007 BP; 855 A; 272 C; 342 G; 538 T; 0 other;

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mecA gene sequence of *S. haemolyticus* strain M1570/10 deposited into EMBL/Genbank/ DDBJ databases

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AC   HE978799;
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DT   16-AUG-2012 (Rel. 113, Created)
DT   16-AUG-2012 (Rel. 113, Last updated, Version 0)
XX
DE   Staphylococcus haemolyticus mecA gene for penicillin binding protein 2',
DE   strain M1570-10
XX
KW   .
XX
OS   Staphylococcus haemolyticus
OC   Bacteria; Firmicutes; Bacillales; Staphylococcus.
XX
RN   [1]
RP   1-2007
RA   Perreten V.;
RT   ;
RL   Submitted (14-AUG-2012) to the INSDC.
RL   University of Berne, Institute of Veterinary Bacteriology, Laenggassstrasse
RL   122, CH - 3001 Berne, SWITZERLAND.
XX
RN   [2]
RA   Frey Y., Schwendener S., Perreten V.;
RT   "Methicillin resistance in Staphylococcus haemolyticus and Staphylococcus
RT   xylosus from bovine mastitis";
RL   Unpublished.
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SQ Sequence 2007 BP; 856 A; 272 C; 341 G; 538 T; 0 other;

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mecA gene sequence of *S. xylosus* strain M1545/10 deposited into EMBL/Genbank/ DDBJ databases

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ID   HE978800; SV 1; linear; genomic DNA; STD; PRO; 2007 BP.
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ST * private 25-AUG-2012
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AC   HE978800;
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DT   16-AUG-2012 (Rel. 113, Created)
DT   16-AUG-2012 (Rel. 113, Last updated, Version 0)
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DE   M1545-10
XX
KW   .
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OS   Staphylococcus xylosus
OC   Bacteria; Firmicutes; Bacillales; Staphylococcus.
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RN   [1]
RP   1-2007
RA   Perreten V.;
RT   ;
RL   Submitted (14-AUG-2012) to the INSDC.
RL   University of Berne, Institute of Veterinary Bacteriology, Laenggassstrasse
RL   122, CH - 3001 Berne, SWITZERLAND.
XX
RN   [2]
RA   Frey Y., Schwendener S., Perreten V.;
RT   "Methicillin resistance in Staphylococcus haemolyticus and Staphylococcus
RT   xylosus from bovine mastitis";
RL   Unpublished.
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FH   Key             Location/Qualifiers
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FT                   YGNIDRNVQFNFVKEDGMWKLDWDHSVIIPGMQKDQSIHIENLKSERGKILDRNNVELA
FT                   NTGTAYEIGIVPKNVSKKDYKAIAKELSISEDYIKQQMDQNWVQDDTFVPLKTVKKMDE
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SQ Sequence 2007 BP; 856 A; 272 C; 341 G; 538 T; 0 other;

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Geburtsdatum	17.11.1985
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Aug. 2001 – Jun. 2005	Gymnasium an der alten Kantonsschule Aarau in Aarau, Schweiz
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