Evaluation of a simplified key for the identification of coagulase-positive Staphylococcus isolated from bovine mastitis

Geraldo Márcio da Costa1*, Luciano Vilela Paiva2, Roberta Hilsdorf Piccoli3, Demétrio Junqueira Figueiredo1, Ulisses de Pádua Pereira1 and Nivaldo da Silva4

1Departamento de Medicina Veterinária, Universidade Federal de Lavras, 37200-000, Centro, Lavras, Minas Gerais, Brazil. 2Departamento de Química, Universidade Federal de Lavras, Lavras, Minas Gerais, Brazil. 3Departamento de Ciências dos Alimentos, Universidade Federal de Lavras, Lavras, Minas Gerais, Brazil. 4Departamento de Medicina Veterinária Preventiva, Escola de Veterinária, Universidade Federal de Minas Gerais, Belo Horizonte, Minas Gerais, Brazil. *Author for correspondence. Email: gmcosta@ufla.br

ABSTRACT. Evaluation of a simplified key for the identification of coagulase-positive Staphylococcus (CPS), isolated from mastitis cases, underwent phenotypic and genotypic tests to evaluate the efficiency of a simplified key, based on phenotypic tests for the discrimination of these microorganisms. The tests consisted of amplification of the femA gene and hemolysis in blood agar, production of acetoin and fermentation of maltose, mannitol and trehalose. Strains that showed negative results in the amplification test of the femA gene or that were not identified as Staphylococcus aureus (S. aureus) by phenotypic tests were tested with the APISTAPH kit (Biomériux-France), for precise identification of species. Phenotypic tests revealed 338 strains (98.25%) as S. aureus, three strains (0.86%) as Staphylococcus hyicus, and three microorganisms (0.86%) as Staphylococcus intermedius. PCR demonstrated that 338 (98.25%) strains belonged to the S. aureus species, confirming the results for 336 strains from 338 identified, through a simplified phenotypic key. A high rate of correlation (98.83%) was verified between the results of genotypic and phenotypic tests for the identification of S. aureus, demonstrating the applicability of the proposed key, for the discrimination of this microorganism in CPS isolated from bovine mastitis.

Key words: mastitis pathogens, characterization, coagulase test, PCR, biochemical tests.

RESUMO. Avaliação de uma chave de identificação simplificada para Staphylococcus coagulase-positivos isolados de mastite bovina. Visando testar a eficiência de uma chave simplificada baseada em testes fenotípicos para a discriminação de Staphylococcus coagulase-positivos (SCP) isolados de infecções intramamárias de bovinos, 344 amostras destes micromagnos foram submetidas a testes fenotípicos e genotípicos. Estes consistiram na amplificação do gene femA, na observação de hemólise em ágar sangue, produção de acetoina e fermentação de maltose, manitol e trehalose. Amostras que apresentaram resultado negativo na amplificação do gene femA ou que foram identificadas com não Staphylococcus aureus (S. aureus) por meio dos testes fenotípicos foram submetidas ao kit APISTAPH (Biomériux-França) para identificação mais precisa. Os testes fenotípicos utilizados na chave simplificada permitiram identificar 338 amostras (98,25%) como S. aureus, três amostras (0,86%) como Staphylococcus hyicus e três (0,86%) como Staphylococcus intermedius. Por meio da reação em cadeia da polimerase (PCR) 338 (98,25%) amostras foram identificadas como S. aureus, ratificando os resultados para 336 das 338 amostras identificadas por meio da chave fenotípica simplificada. Observou-se elevada concordância (98,83%) entre os resultados dos testes genotípicos e fenotípicos para a identificação de S. aureus, demonstrando a aplicabilidade da chave de identificação proposta para a discriminação deste microrganismo entre SCP isolados de casos de mastite bovina.

Palavras-chave: patógenos da mastite, caracterização, teste de coagulase, PCR, testes bioquímicos.

Introduction

The Staphylococcus genus is vastly diversified, containing 39 species (HOLT et al., 1994), and it usually requires the use of laborious and expensive procedures for its correct discrimination. Among the species of the genus, S. aureus is prominent as one of the species most frequently associated with bovine intramammary infections (IMI) in all continents, and it is known as the isolate species that causes the greatest losses in dairy farming worldwide (ANNEMÜLLER et al., 1999; VASUDEVAN et al., 2003).

Despite the fact that S. aureus is more relevant in the etiology of bovine mastitis in comparison to
other species of the genus (ROBERSON et al., 1996) and that its control requires the adoption of specific measures, the precise identification of this microorganism is not carried out by the majority of laboratories. This is due to the high costs of commercial kits used for the identification and the limitations associated to the use of molecular techniques, such as the high cost of equipment and supplies and the necessity of specialized labour. Therefore, the laboratories are only able to classify isolates into coagulase-positive (CPS) or coagulase-negative Staphylococcus, according to the results yielded by the tube coagulase test. In most veterinary laboratories, CPS isolates are empirically discriminated as S. aureus.

The CPS group includes S. aureus, S. hyicus, S. intermedius, S. schleiferi subsp. schleiferi and S. delphini (BES et al., 2000; KONEMAN et al., 2001), Staphylococcus lutrae (FOSTER et al., 1997) and Staphylococcus pseudointermedius (DEVRIESE et al., 2005). S. hyicus and S. intermedius have been associated to IMI in bovines (BOTHA; BRAND, 1987; CAPURRO et al., 1999; ROBERSON et al., 1996); however, according to Roberson et al. (1996), about 95% of CPS samples that are isolated from IMI in bovines are represented by S. aureus.

Though S. aureus is the most frequently involved species in the etiology of bovine mastitis in comparison to other CPS, the non-discrimination of other species makes it difficult to measure the importance of each of them in the etiology of IMIs. In determined herds, such procedure may cause an over-dimensioning of the importance of S. aureus, or a sub-dimensioning of the importance of other CPS species. Therefore, the objective of this study is to test a simplified phenotypic identification key for the discrimination of CPS isolates in bovine mastitis cases.

Material and methods

For this study, 1,693 milk samples from bovines affected by mastitis were microbiologically analyzed. These samples came from 38 herds from the Minas Gerais State. The samples were aseptically collected into sterilised tubes, and then transported to the laboratory under refrigeration, being then incubated at 37°C/6-12 hours for enrichment. After this procedure, they were cultured on blood agar (Blood Agar Base, containing 10% of ovine blood) and incubated at 37°C/24-48 hours, after which they were evaluated for the presence of bacterial growth.

The sorting of microorganisms from the Staphylococcaceae family, belonging to the CPS group was performed through assumptive tests, according to Quinn et al. (1994). They were based on the macroscopic observation of colonies, verifying the presence of hemolysis, size and pigmentation; observation of microscopic morphology through Gram-stained smears, catalase test and tube coagulase test, employing leporine plasma.

Among the microorganisms identified as CPS, 344 were randomly and proportionally selected for the study within the herds. They were submitted to the simplified identification key, which consisted of hemolysis detection in ovine blood agar, trehalose, manitol and maltose fermentation, as well as acetoin production (VP), selected on the basis of the identification keys proposed by Holt et al. (1994). The interpretation of results was made according to Table 1.

### Table 1. Simplified key for identification of coagulase positive Staphylococcus, adapted from Holt et al. (1994).

<table>
<thead>
<tr>
<th>S. aureus</th>
<th>S. intermedius</th>
<th>S. hyicus</th>
<th>S. delphini</th>
<th>S. schleiferi subsp. schleiferi</th>
</tr>
</thead>
<tbody>
<tr>
<td>Hemolysis</td>
<td>+</td>
<td>d</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>VP Test</td>
<td>+</td>
<td>-</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>Fermentation</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Mannitol</td>
<td>+ (d)</td>
<td>-</td>
<td>+</td>
<td>D</td>
</tr>
<tr>
<td>Maltose</td>
<td>+ (w)</td>
<td>nd</td>
<td>-</td>
<td></td>
</tr>
<tr>
<td>Trehalose</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>-</td>
</tr>
</tbody>
</table>

All the 344 samples selected for the study underwent PCR for the amplification of femA, aiming to identify S. aureus through its genotype. Samples with a negative result in this test or which were identified as non-S. aureus through the simplified identification key were tested by the APISTAPH kit (Biomérieux-France), aiming a more precise identification.

The methodology described by Silva and Silva (2005) was used for the extraction of bacterial DNA, execution of the PCR reaction and electrophoresis. Primers obtained from specific S. aureus sequences and reported by Berger-Bachi et al. (1989) were used in the PCR. Fem1: AAA AAA GCA CAT AAC AAG CG and Fem2: GAT AAA GAA GAA ACC AGC AG. The amplification product of the femA gene must contain 132 base pairs.

The results of phenotypic and genotypic identifications were compared by the Kappa (K) test, according to Siegel and Castellan (1988).

Results and discussion

Seven-hundred and ninety-six bacteria belonging to the Staphylococcaceae family were isolated, out of which 580 were identified as CPS. Among these, 344 samples were randomly and proportionally
chosen among the analyzed herds, and then submitted to phenotypic and genotypic tests, as previously described.

From the analyzed samples, the simplified phenotypic identification key allowed the identification of 338 samples (98.25%) as being S. aureus, three isolates (0.87%) as S. hyicus, and another three (0.87%) isolates as S. intermedius. As regards to the PCR, for the amplification of the femA gene (Figure 1), 338 samples (98.25%) showed a positive result, and the remaining six samples (1.75%), negative results.

Among the 338 samples identified as S. aureus through the simplified key, 336 were identified through the PCR, resulting in a high correlation (k = 0.98; p < 0.01) between the results of phenotypic and genotypic tests for this species.

Included among the isolates with a negative PCR result (femA-negative), there were six samples that were previously identified by the simplified key as being S. hyicus (three isolates), S. intermedius (one strain) and S. aureus (two isolates). These six PCR negative strains underwent identification using the APISTAPH kit, evidencing that the two isolates, previously and phenotypically, identified as S. aureus were indeed S. aureus, and the remaining ones were S. hyicus. From the three samples identified as S. intermedius by the phenotypic identification key, one was identified by PCR and by the APISTAPH kit as S. hyicus (PCR-negative for femA and APISTAPH-positive for S. hyicus), and the remaining ones as S. aureus (PCR-positive for femA and APISTAPH-positive for S. aureus). The three samples identified as S. hyicus by the simplified key showed a PCR-negative result, thus being confirmed as S. hyicus by the APISTAPH kit. Table 2 lists the relation of isolates whose identifications were discordants by use of phenotypic and genotypic tests and correct identification.

Table 2. Relation of Staphylococcus strains whose identifications were discordants by use of phenotypic and genotypic tests and correct identification by APISTAPH test.

<table>
<thead>
<tr>
<th>Strains</th>
<th>Identification by Simplified key</th>
<th>Identification by Specific PCR (femA)</th>
<th>Identification by APISTAPH</th>
</tr>
</thead>
<tbody>
<tr>
<td>88</td>
<td>S. intermedius</td>
<td>S. aureus</td>
<td>S. aureus</td>
</tr>
<tr>
<td>118</td>
<td>S. aureus</td>
<td>non S. aureus</td>
<td>S. aureus</td>
</tr>
<tr>
<td>302</td>
<td>S. intermedius</td>
<td>S. aureus</td>
<td>S. aureus</td>
</tr>
<tr>
<td>325</td>
<td>S. hyicus</td>
<td>non S. aureus</td>
<td>S. hyicus</td>
</tr>
<tr>
<td>329</td>
<td>S. hyicus</td>
<td>non S. aureus</td>
<td>S. hyicus</td>
</tr>
<tr>
<td>345</td>
<td>S. hyicus</td>
<td>non S. aureus</td>
<td>S. hyicus</td>
</tr>
<tr>
<td>1195</td>
<td>S. intermedius</td>
<td>non S. aureus</td>
<td>S. hyicus</td>
</tr>
<tr>
<td>1340</td>
<td>S. aureus</td>
<td>non S. aureus</td>
<td>S. aureus</td>
</tr>
</tbody>
</table>

Though the three isolates identified as S. hyicus by the simplified key had their identification confirmed by the APISTAPH kit, the reduced number of isolates of this agent, and of S. intermedius in the studied sample did not allow a safe evaluation of the efficiency of the identification key proposed for the discrimination of these microorganisms.

We observed that S. aureus was the predominant species in the population studied; however, the epidemiological importance of different CPS species may vary among herds and different areas (BOTHÁ; BRAND, 1987; CAPURRO et al., 1999; ROBERSON et al., 1996, consequently requiring the judicious discrimination of them. Considering the importance of S. aureus in the etiology of bovine mastitis, and the potential risk represented to human health (ALTEKRUSE et al., 1998; BUYSER et al., 2001), its correct identification is indispensable to allow quantifying the relative importance in the epidemiology of IMIs in bovine herds, thus allowing, whenever necessary, the adoption or re-adaptation of specific control measures.

Conclusion

The results obtained evidenced the applicability of the identification key, proposed for the fast and accurate discrimination of S. aureus originated from bovine mastitis cases.

References


Received on February 4, 2009.
Accepted on August 4, 2009.

License information: This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.