



Universidade de Évora - Instituto de Investigação e Formação Avançada

Programa de Doutoramento em Ciências Veterinárias

Tese de Doutoramento

**Staphylococci isolated from caprine and ovine mastitic milk:
Virulence Factors and Antimicrobial and Antibiofilm
effectiveness of Propolis Extracts**

Nara Patrícia Cavalcanti Andrade

Orientador(es) | Maria Cristina Queiroga
Marta Sofia Serrano Valente Casimiro Ferreira Laranjo
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Dedication

To my son Gabriel Cavalcanti Alves and my grandparents
who taught me how to live, Maria Alzira and João Domiciano Cavalcanti.

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List of Abbreviations and Symbols

16S – 16S ribosomal RNA	CPS – coagulase positive <i>Staphylococcus</i>
3D – three dimensional	df – degrees of freedom
A – absorbance	dNTP – deoxyribonucleotide triphosphate
AFM – atomic force microscopy	ECC – epicatechin content
AMP – aromatic and medicinal plants	eDNA – environmental DNA
AMR – antimicrobial resistance	EDTA – ethylenediaminetetraacetic acid
ANOVA –analysis of variance	EO – essentials oils
AST – antimicrobial susceptibility testing	ESI – electrospray ionization interface
ATCC – American Type Culture Collection	ϵ – molar absorbance
BA – blood agar	FAO – Agriculture Organization of the United Nations
Bap – biofilm associated protein	FD – dilution factor
BEH – bridged ethylene hybrid	GAE – gallic acid equivalent
BHIb – Brain Heart Infusion broth	GTFs – glycosyltransferases
bp – base pair	HSD – honest significant difference
BR – Brazil	IMI – Intramammary Infection
CAPE – caffeic acid phenolic ester	kV – Kilovolts
CE – Ceará	Lh – litre per hour
CFU – colony forming unit	MBC – minimum bactericidal concentration
CLSI – Clinical and Laboratory Standards Institute	MCA – MacConkey agar
CM – clinical mastitis	MCA – multiple correspondence analysis
CMT – California mastitis test	MDR – multi drug resistant
CNS – coagulase negative <i>Staphylococcus</i>	MG – Minas Gerais

MHA – Muller-Hinton agar	PS/A – polysaccharide capsular adhesin
MHB - Mueller-Hinton broth	PT – Portugal
MIC – minimal inhibitory concentration	QE – quercetin equivalents
MR-CNS –methicillin resistant coagulase-negative staphylococci	QS – quorum sensing
MRSA – methicillin resistant <i>Staphylococcus aureus</i>	r^2 – R-squared
MSCRAMM – microbial surface components recognizing adhesive matrix molecules	S – South
MSSA methicillin sensitive <i>Staphylococcus aureus</i>	SCC – somatic cell count
MW – molecular weight	SCCmec – staphylococcal cassette chromosome mec
N – North	SCM – subclinical mastitis
n.d. – not detectable	SE – Southeast
NE – Northeast	SE – staphylococcal enterotoxin
neg - negative	SEM – standard error of the mean
NET – neutrophil extracellular trap	SPE – solid phase extraction
NMC – National Mastitis Council	SSR – short sequence repeats
NUTs – nomenclature of territorial units	Staph. – <i>Staphylococcus</i>
OD – optical density	TBE – tris/borate/EDTA buffer
OIE – World Organisation for Animal Health	TSBg – tryptone soya broth glucose
PBP – penicillin-binding protein	TSST – toxic shock syndrome toxin
PCR – Polymerase Chain Reaction	UPLC-QTOF-MS/MS – ultra-high-pressure liquid chromatography coupled with a hybrid quadrupole orthogonal time-of-flight mass spectrometer
PDA – photo diode array	WHO – World Health Organization
PIA – polysaccharid intercellular adhesin	Σ – sigma
	χ^2 –chi-square

Staphylococci isolated from caprine and ovine mastitic milk: Virulence Factors and Antimicrobial and Antibiofilm effectiveness of Propolis Extracts

Abstract

Small ruminant mastitis is a major problem for milk producers and consumers causing economic losses and public health threats. This disease is mainly caused by *Staphylococcus*. The aim of this work was to study propolis for the control of small ruminant mastitis as an alternative to conventional antimicrobials. A total of 137 *Staphylococcus* belonging to 13 species, recovered from the milk of goats and sheep, were studied. Phenotypic biofilm production and antimicrobial susceptibility were examined. Genes coding for virulence factors were studied: *coa*, *nuc*, *bap*, *icaA*, *icaD*, *blaZ*, *mecA*, *mecC*, *tetK* and *tetM*. Propolis is a resinous substance produced by honeybees which has been used as a natural medicine for its antiseptic, antimicrobial, antioxidant, anti-inflammatory, and other immunomodulatory properties. Propolis ethanol extracts (PEE) were prepared using different propolis from both Brazil and Portugal. These PEE were chemically characterised and their antimicrobial and antibiofilm activities were assessed. Results showed an association between biofilm production and mastitis inflammatory response. Beta-lactam resistance was mainly detected and an association between animal species and resistance to some antibiotics was found. All isolates were susceptible to gentamicin and cefazolin. The *nuc* gene was detected in several coagulase negative staphylococci, highlighting its inadequacy for *S. aureus* identification. Regarding the use of propolis for mastitis control, most PEE showed inhibitory activity against all staphylococci isolates. Furthermore, PEE are bactericidal, which is a very important feature of propolis. Moreover, PEE are effective in inhibiting biofilm formation and in destroying the formed biofilm. The presence of individual phenolics enhanced bactericidal activity, whereas triterpenes negatively influenced both antimicrobial and antibiofilm activity. The results of the present study suggest that propolis should be considered for the control of small ruminant mastitis caused by staphylococci. Nevertheless, future studies are needed to identify the individual propolis compounds exhibiting both antimicrobial and antibiofilm activity.

Keywords: mastitis, staphylococci, virulence factors, propolis, antimicrobial, antibiofilm.

Estafilococos isolados de leite mastítico caprino e ovino: Factores de Virulência e eficácia Antimicrobiana e Antibiofilme de Extratos de Própolis

Resumo

A mastite dos pequenos ruminantes é um problema para os produtores e consumidores de leite, causando perdas económicas e ameaças à saúde pública. Esta doença é principalmente causada por *Staphylococcus*. O objetivo deste trabalho foi estudar a própolis para o controlo da mastite dos pequenos ruminantes como alternativa aos antimicrobianos. Estudaram-se 137 *Staphylococcus* de 13 espécies, isolados do leite de cabras e ovelhas. Avaliou-se a produção de biofilme e a suscetibilidade aos antimicrobianos. Analisaram-se alguns genes de virulência: *coa*, *nuc*, *bap*, *icaA*, *icaD*, *blaZ*, *mecA*, *mecC*, *tetK* e *tetM*. A própolis é uma substância resinosa, produzida por abelhas, utilizada como medicamento natural pelas suas propriedades antissépticas, antimicrobianas, antioxidantes, anti-inflamatórias, entre outras. Os extratos etanólicos de própolis (PEE) foram preparados com diferentes própolis do Brasil e de Portugal. Estes PEE foram caracterizados quimicamente e as suas atividades antimicrobiana e antibiofilme avaliadas. Existe uma associação entre a produção de biofilme e a resposta inflamatória à mastite. A resistência aos beta-lactâmicos foi a mais frequente e encontrou-se uma associação entre espécie animal e resistência a alguns antimicrobianos. Todos os isolados foram suscetíveis à gentamicina e à cefazolina. O gene *nuc* foi detetado em estafilococos coagulase-negativos, mostrando-se inadequado para a identificação de *S. aureus*. Quanto ao uso de própolis no controlo da mastite, a maioria dos PEE mostrou atividade inibitória contra todos os estafilococos. Além disso, os PEE são bactericidas, uma importante característica do própolis. Adicionalmente, os PEE inibem eficazmente a formação e destroem o biofilme formado. A presença de determinados fenóis aumenta a atividade bactericida, enquanto que os triterpenos influenciam negativamente as atividades antimicrobiana e antibiofilme. Os resultados obtidos sugerem que a própolis seja usada no controlo da mastite de pequenos ruminantes causada por estafilococos. No entanto, são necessários mais estudos para identificar individualmente os compostos do própolis com atividade antimicrobiana e antibiofilme.

Palavras chave: mastites, estafilococos, fatores de virulência, própolis, antimicrobiano, antibiofilme.

Chapter 1

1. Introduction

Small ruminants breeding is sustainably advantageous for its rusticity, adaptation to the environment, easy husbandry, and reproductive capacity. Goat and sheep milk production is a common activity in several countries, especially in developing countries (Viana et al., 2008; Rahmatalla et al., 2017). This activity is highly related to family farming, with a strong commitment to regional development, whose production is intended for home milk consumption and for manufacturing traditional cheeses (Peixoto et al., 2010a; Schröder et al., 2011). Small ruminants' milk is known for its beneficial and therapeutic effects, suitable for individuals who are allergic to cow's milk and is beneficial for the nutrition and health of young and old people (Ribeiro and Ribeiro, 2010).

In 2016, small ruminant milk production showed a global decline of 4.4% compared to the previous year, following the bovine sector, with a reduction of 4,5% (INE, 2017). The main drawback affecting the milk production is the mammary gland inflammatory process, a disease denominated mastitis, which is common in dairy farms. Besides the reduction in

milk yield and on animal performance, this affection increases mortality rate and consequently economic losses to the dairy producer (Blagitz et al., 2008; Peixoto et al., 2010b). Mastitis negatively affects the composition and physical-chemical milk characteristics, leading to fat and lactose loss and a slightly higher milk-protein content (Gelasakis et al., 2018), impairing cheese manufacturing (Seegers et al., 2003; Halasa et al., 2009). Moreover, mastitis pathogens may produce toxins responsible for food poisoning (Argudín et al., 2010; Vasconcellos and Ito, 2011). Therefore, this disease reflects both in animal health and welfare and in milk and dairy products production, as well as in consumers' safety (Keefe, 2012).

1.1 – Motivation

Mastitis control, both prophylaxis and treatment, is currently mostly dependent on antimicrobial and antiseptics use. However, these exert selection pressure on resistant and multi-resistant bacterial strains (Contreras et al., 2007; Viridis et al., 2010; Martins et al., 2017). Antibiotic resistant bacteria, other than impairing mastitis control, may transfer resistance genes to the indigenous microbiota in the consumer's gut (Lee, 2003), consisting in a big threat to public health.

Some antimicrobials that are critically important for human medicine are currently being used for mastitis control. Several antimicrobial resistance genes were already detected in milk isolates causing sheep (Jamali et al., 2015; Martins et al., 2017) and goats mastitis (Viridis et al., 2010).

Resistant bacteria exist in humans, animals, food and the environment. Antimicrobials use, both in animal and human medicine, was responsible for the increase in resistance, leading to a threat to public health systems in the last 20 years (Queenan et al., 2016; Ferri et al., 2017). Antimicrobial resistance (AMR) is a global problem of complex epidemiology and should be considered in a broad and integrated "One Health" approach (Weese et al., 2013).

Measures to avoid the dissemination of resistance genes and the selection pressure for resistant and multiresistant bacteria, must be implemented. To develop new alternatives to the use of antimicrobials and antiseptics for use in mastitis control is urgent,

to improve milk yield and milk quality without risk to public health. Some natural compounds derived from plants, which have already inhibited bacteria without causing microbial resistance, even after prolonged exposure (Ohno et al., 2003), may be addressed as alternatives.

Propolis is a resinous mass produced by bees *Apis mellifera*. Honeybees collect selectively bioactive resin compounds from different plant parts that they manipulate with their salivary gland secretions forming this glue type mass which they use to close the small openings in the hive to protect it from invaders and providing a favourable environment (Drescher et al., 2019).

Propolis biological properties are related to its chemical composition, which differs in its structure and concentration depending on sources availability for resin harvesting (Toreti et al., 2013). Propolis has been used to treat different pathologies, among others, due to its antibacterial activity (Wojtyczka et al., 2013). Its activity against bacterial biofilms has been reported lately (Wojtyczka et al., 2013; Veloz et al., 2015; Doganli, 2016; De Marco et al., 2017).

1.2 – Objectives and thesis outline

Considering propolis antimicrobial and antibiofilm activities, this work was designed to evaluate the use of propolis for small ruminant mastitis control. With that propose, ten propolis samples (seven from Brazil and three from Portugal) were used to produce propolis ethanol extracts (PEE), which were than analysed for their chemical composition and assayed for their antibacterial and antibiofilm performance against staphylococci isolated from milk samples from small ruminants with mastitis.

Therefore, the specific objectives were:

1 - To identify *Staphylococcus* species isolated from small ruminants' milk samples and investigate the ability to produce biofilm and the antimicrobial susceptibility patterns, both phenotypically and genotypically.

2 – To study propolis composition in order to evaluate the use of propolis ethanol extracts (PEE) for mastitis control purposes.

3 – To evaluate the *in vitro* activity of PEE against staphylococci isolated from the milk of sheep and goats with mastitis.

4 – To investigate the *in vitro* antibiofilm activity of PEE against biofilm produced by staphylococci isolated from mastitis milk from sheep and goats, considering both inhibition of biofilm formation and the ability to disrupt established biofilm.

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Chapter 2

2. Literature review

2.1 – Mastitis

The word Mastitis (Greek “mastos”, breast; + “itis”, inflammation) was defined in the mid-19th century as the inflammation reaction of the mammary gland. Mastitis occurs worldwide, being influenced by factors related to the animal and its environmental conditions (Menzies and Ramanoon, 2001; Bergonier et al., 2003; Mendonça et al., 2012).

Mastitis cause may be of physical, chemical, or infectious origin, the latter being the most frequent (Markey et al., 2013). Intramammary infection (IMI) caused by bacteria is the most prevalent in dairy herds (Hussein et al 2020; Puggioni et al 2020), and staphylococci are the main pathogens found in small ruminants mastitis (Peixoto et al., 2010; Queiroga, 2017a).

Mastitis may be clinical (CM), when it involves visible changes in the milk and/or clinical signs, or subclinical if no changes may be observed. For the diagnosis of subclinical mastitis (SCM), it is necessary to assess milk features such as elevated somatic cell count

(SCC), chemical changes and/or bacteriological condition. For SCC in small ruminants, much caution is required not to lead to the wrong diagnosis, due to differences among species, age, breed, parity by number, lactation stage and number, prolificacy, seasonality, farming system and facilities (Jimenez-Granado et al., 2014; Kumar et al., 2016; Mishra et al., 2018).

Milk yield and quality are decreased due to mastitis (Cuccuru et al., 2011). This condition was associated with a loss of 4.1 to 12% milk in sheep and 0.8 to 2.3% in goats (Leitner et al., 2008). Furthermore, milk fat, protein, casein and curd yield levels are also reduced (Silanikove et al., 2014).

2.1.1 – Aetiology

Bacteria of the genus *Staphylococcus* are the most isolated pathogens from mastitic milk samples from small ruminants (Contreras et al., 1999; Queiroga, 2017). Research has suggested that coagulase-negative staphylococci (CNS) are most commonly accountable for sheep (Queiroga et al., 2019) and goats mastitis (Peixoto et al., 2010). Coagulase negative staphylococci are also the most prevalent microorganisms found in goats and sheep udder skin and teat sphincter microbiota (Moroni et al., 2005).

Coagulase negative *Staphylococcus epidermidis* is a pathogen that causes persistent infections in sheep mammary gland (Bergonier et al., 2003) and has been reported as the main SCM etiological agent in small ruminants (Contreras et al., 1999; Queiroga, 2017). *Staphylococcus aureus* has also been isolated from the milk of animals with SCM. However, it is one of the main pathogens found in milk samples from small ruminants with CM, where they cause severe symptoms in them (Constable et al., 2016).

A wide variety of bacteria have been reported as mastitis pathogens in ewes as *Escherichia coli*, *Streptococcus* spp. and *Mannheimia haemolytica*, the latter being a peracute and gangrenous mastitis cause. In addition, mastitis in sheep may be associated with *Clostridium perfringens* A, *Pseudomonas* spp. or *Corynebacterium pseudotuberculosis* in a low percentage (Queiroga et al., 2019). In the inflammation of the goats mammary gland, bacteria such as *Trueperella pyogenes*, *Bacillus coagulans*, *Bacillus licheniformis*, *Klebsiella pneumoniae* and *Actinobacillus equuli* are found in a small percentage (Constable et al., 2016).

2.1.2 – Mastitis control

Mammary gland health depends on careful management and on adequate facilities (Mota, 2008). Hygienic milking, for both hand and machine milking, is an extremely valuable issue since it can prevent or minimize the dissemination of microorganisms from one animal to another (Bergonier et al., 2003). The lack of hygiene in manual milking can lead to bacteria spread from infected animals to the healthy ones through the hand of the milker (Langoni et al., 2017). Failure to periodically review milking equipment can cause vacuum fluctuation and backflow in addition to bacterial contamination. Before milking, routine inspection of the udder and careful milk secretion observation must be performed to prevent milking equipment contamination and further infection dissemination (Mota, 2008).

Primiparous and/or young healthy animals should be milked first, followed by subclinical infections animals, and lastly, the ones showing udder changes and the ones under treatment, whose milk cannot be marketed (Bergonier et al., 2003; Mota, 2008).

Post milking teat dipping procedure has been considered as an effective method to prevent further IMI cases (Contreras et al., 2007; Kamal and Bayoumi, 2015). The main dipping purpose is to eliminate pathogens of the external opening of the teat canal (Rainard, 2017). However, it should be used with caution because mastitis sporadic outbreaks have been related to disinfectants (Contreras and Rodríguez, 2011; Kelly and Wilson, 2016). Some solutions for teat dipping are not suitable for organic agriculture, such as iodine or chlorine-based (Contreras et al., 2007). However, new broad-spectrum antiseptic agents are being tested (Pedrini and Margatho, 2003; Reyes-Jara et al., 2016; Martins et al., 2017b).

In many farms, small ruminants are raised to produce different products such as milk, meat, skin, and wool. Antimicrobials are administered to control different diseases. Antimicrobial use is also the main strategy for mastitis control, both for therapeutic and prophylactic purposes (Queiroga, 2007; Constable et al., 2016). However, licensed antibiotic preparations for intramammary application for sheep and goats are scarce and, occasionally, the estimated dosage and withdrawal time has not been established (Saad and Ahmed, 2018). These must be strictly followed because the incorrect use can lead to residues in the milk (Beltrán et al., 2015) and exert a selection pressure for resistant

bacteria that can cause problems in milk and dairy products consumers (Lee, 2003; Gomes and Henriques, 2016). Antimicrobial residues in milk, water, food and the environment, due to lack of good agriculture practices, lead to antimicrobial entry in the food chain (Lee, 2003; Beltrán et al., 2015; Berruga et al., 2016). Adequate mastitis control at the dairy farm is considered a crucial process to ensure animal health and milk quality (Kamal and Bayoumi, 2015). Information on antimicrobial susceptibility of the most prevalent pathogens in a herd is essential to determine which drug can achieve the best clinical outcome and limit the resistant strain selection.

To reduce the antimicrobial use for mastitis control is a goal for many researchers. Gomes and Henriques (2016) reviewed alternatives to antimicrobials for bovine mastitis control such as bacteriophage therapy, nanoparticles, vaccines, and natural compounds, among others. Regarding bacteriophages therapy, Mishra et al. (2014) provided information for lytic bacteriophages uses against multiresistant *S. aureus* isolated from goat mastitis. Silver nanoparticles were tested by Yuan et al. (2017) in *S. aureus* and *Pseudomonas aeruginosa*, isolated from goats milk samples, and their results showed antibacterial effects, depending on the dose and inhibition time.

Studies on the natural substances used in veterinary medicine include essential oils and vegetables, such as *Punica granatum*, *Hymenaea martiana* and *Ocimum sanctum*, which showed effective results against intramammary inflammation in small ruminants, both *in vitro* and *in vivo* (Jassim and Abdullah, 2014; Peixoto et al., 2016; Kelly and Wilson, 2016; Dash et al., 2016; Abdalhamed et al., 2018); *Schinus terebinthifolius* (Muhs et al., 2017) and *Mimosa tenuiflora*, *Stryphnodendron adstringens* and *Eugenia uniflora* that inhibited the *S. aureus* development, CNS and *Escherichia coli*, among other species (Gonçalves et al., 2005).

Honey and propolis have also been studied. Natural components such as terpenes and phenolic compounds, as tannins, flavonoids, and their pigments like anthocyanins, may potentiate the antimicrobial action of these products (Cisowska et al., 2011; Peixoto et al., 2016; Abdalhamed et al., 2018). Propolis nanoparticles have also been tested against *S. aureus* showing a promising nanocarrier for propolis extract high concentrations in a stable aqueous medium, showing antimicrobial activity with moderate cytotoxicity for mammary alveolar cells *in vitro* (Pinheiro Machado et al., 2019).

The use of vaccines for mastitis prevention depends on their efficacy to the specific etiologic agents (Contreras and Rodríguez, 2011; Constable et al., 2016). For goats and sheep, autovaccines can be produced for the pathogens causing the intramammary infection (IMI) in the flock (Bergonier et al., 2003). Experiments showed that, after vaccination, the infection rate was lower, and the spontaneous cure rate was higher in comparison to the control groups in goats (Kautz et al., 2014) and dairy sheep (Tollersrud et al., 2002; Amorena et al., 1994). Although, vaccines for IMI prevention by *S. aureus* have existed for decades, their efficacy has been limited (Bannerman and Wall, 2005). Considering that there are different strains present in the herd, or even within a single animal, it is difficult to find a vaccine that is effective for the eradication of this disease (Bergonier et al., 2003; Bannerman and Wall, 2005).

2.1.2.1 – Antimicrobial therapy

As previously mentioned, mastitis control is highly dependent on antimicrobial therapy. Different classes of antimicrobials have been used for mastitis treatment and prevention. β -lactams and tetracyclines are the most suitable antimicrobials for the treatment of *Staphylococcus* mastitis and should be chosen over more modern molecules that should only be used in case of resistance, since they must be kept for use in human medicine.

Penicillin and their derivatives are β -lactam antimicrobial acting on cell wall synthesis inhibition. Penicillin-binding proteins (PBPs) are an enzyme group required for bacterial cell wall biosynthesis, which catalyses transpeptidation for the peptidoglycan chain formation. β -lactams bind to PBPs and inhibit peptidoglycan crosslink formation, thus lysing the bacteria (Paterson et al., 2014). Penicillin G, produced by the *Penicillium chrysogenum* fermentation show bactericidal action and is available in drugs for intramammary application.

Tetracyclines are broad-spectrum antibiotics and are also found as synthetic or semi-synthetic form. These molecules inhibit the bacterial cells protein synthesis by preventing the association of aminoacyl-tRNA with the 30S subunit of the ribosome. This association is reversible, explaining its bacteriostatic effect. Most bacteria actively uptake tetracyclines,

so their intracellular concentration gets 50 times higher than the outside concentration ensuring its specific activity (Chopra and Roberts, 2001).

2.2 – *Staphylococcus*

2.2.1 – Identification

Staphylococci belong to the family *Staphylococcaceae*, which comes from the Greek *staphyle*, which means cluster, and *coccus*, meaning grain. These are Gram-positive bacteria that grow in a characteristic pattern that resembles the grapes cluster. Most of these cocci have diameters of 0.5 to 1.5 μm . They are capable of growing under high osmotic pressure conditions and low humidity, under aerobic and anaerobic atmospheric conditions, even in the presence of 10% sodium chloride concentration, and temperature ranging between 18 °C and 40 °C (Murray et al., 2017; Tortora et al., 2017).

Conventional methods are used for the phenotypic characters determination for staphylococci initial identification, through morphological, dyeing, and biochemical characteristics (Quinn et al., 2005). However, it may require days before the result and depend on several factors to be reliable. Other methods such as quick identification kits or automated systems require only a few hours to conclusion demonstrating between 70% and 90% accuracy (Schleifer and Bell, 2009; Fetsch et al., 2018).

Nowadays, staphylococci may be identified through genotypic analysis, which show higher accuracy, comparing with conventional and automated methods (Schleifer and Bell, 2009; Fetsch et al., 2018).

According to the List of Prokaryotic names with Standing in Nomenclature (LPSN), the *Staphylococcus* genus currently includes 55 species (Parte et al., 2020). Some *Staphylococcus* produce the enzyme coagulase, and are called coagulase-positive *Staphylococcus* (CPS), while those that do not exhibit this feature are collectively referred to as coagulase-negative *Staphylococcus* (Murray et al., 2017; Tortora et al., 2017).

2.2.2 – *Staphylococcus* in small ruminant mastitis

As stated above, bacteria of the genus *Staphylococcus* are the most frequently found as small ruminant mastitis aetiology. Coagulase negative staphylococci are more abundant and less virulent, causing mainly SCM (Murray et al., 2017; Tortora et al., 2017), than *S. aureus*, which causes most cases of CM and shows to be more virulent (Queiroga, 2007; Bergonier et al., 2014; Tortora et al., 2017).

Staphylococcus aureus produces coagulase, thus being a CPS. Its name stands for its yellow-gold colonies, because of the carotenoid pigments expression (Liu and Nizet, 2009). This species can cause gangrenous mastitis in goats together with *Clostridium perfringens* and *Escherichia coli* (Ribeiro et al., 2007). Subclinical mastitis caused by *S. aureus* can also result in a 20% to 30% reduction in milk production. In addition, the sheep mortality rate with *S. aureus* CM varies between 25% and 50%, and the affected mammary glands of survivors generally become non-productive (Constable et al., 2016).

Among CNS species, *S. epidermidis* is commonly cited in the literature, usually associated with the high SCC values in dairy ewes (Contreras and Rodríguez, 2011; Queiroga, 2017). This species together with *S. simulans* and *S. warneri* showed major occurrence in sheep, before and after antimicrobial treatment at drying-off for two consecutive milking seasons (Zafalon et al., 2017).

In goat's milk samples, *S. caprae* species is commonly isolated (Bergonier and Berthelot, 2003; Peixoto et al., 2010), besides *S. epidermidis*, *S. xylosus*, *S. chromogenes*, *S. simulans* and *S. haemolyticus* species (Deinhofer and Pernthaner, 1995; Moroni et al., 2005; Vasil', 2007). However, *S. caprae* is also rarely isolated from sheep and cow milk (Vanderhaeghen et al., 2014; Condas et al., 2017).

2.2.3 – Virulence factors

Staphylococcus species hold several virulence factors conferring them the ability to damage the host tissues and to resist defence mechanisms, thus impairing mastitis control (Vasil', 2007; Contreras and Rodríguez, 2011; Ferreira et al., 2014a; Ferreira et al., 2014b; Bertelloni et al., 2015; Martins et al., 2017a).

Toxin production are considered the main virulence factors. Staphylococci produce thermostable enterotoxins through metabolic activity that can remain in milk, even after being pasteurized at 100 °C for 30 minutes. When produced by staphylococci causing mastitis in small ruminants, these may be responsible for food poisoning in contaminated milk and dairy products (Argudín et al., 2010; Vasconcellos and Ito, 2011). Moreover, staphylococcal enterotoxin genes have been detected in *S. aureus* isolated from cheeses and raw milk from goats and sheep (Carfora et al., 2015), as well as in *S. aureus* isolated from a human after consuming goat cheese (Johler et al., 2015). In milk and dairy products from small ruminants, the staphylococcal enterotoxins and toxic shock syndrome toxins are often commonly found in *S. aureus* strains and more seldom in CNS isolates (Scherrer et al., 2004; Salaberry et al., 2015; Azara et al., 2017; Martins et al., 2017a; Vitale et al., 2018).

Other virulence factors are bacterial strategies to overcome host defence mechanisms and antimicrobial actions. The ability to produce biofilms and to get ways to resist antimicrobials are some of these strategies (Murray et al., 2017).

Different virulence factors may play divergent roles in SCM caused by *Staphylococcus* (Salaberry et al., 2015). These factors increase the damage to the mammary gland and hinder the mastitis treatment (Azara et al., 2017).

2.2.3.1 – Enzymes

Staphylococci produce a wide variety of enzymes in order to invade the body and evade immune mechanisms.

Coagulase reacts with prothrombin in the blood producing staphylothrombin, which then convert fibrinogen to fibrin, resulting in the formation of clots. These clots protect the bacterium from phagocytosis and other host defence elements (Constable et al., 2016). Coagulase can be present in the cell wall or be freely secreted by the bacterium (Babu et al., 2014). The detection of coagulase is performed on the laboratory to differentiate CPS from CNS, generally using a tube coagulase test. There are different methods to identify this enzyme, the molecular ones being the most effective. This enzyme is encoded by the *coa* gene, which can be detected by polymerase chain reaction (PCR) (Babu et al., 2014).

The thermostable nuclease enzyme is also a virulence factor present in some staphylococci, which hydrolyzes DNA and RNA in host cells, causing tissue destruction and spreading of staphylococci (Foster, 2005). It may promote their evasion from neutrophil extracellular traps (NETs), which are DNA strands networks with antimicrobial proteins which allow neutrophils to lyse the micro-organisms in the extracellular environment, without phagocytizing them (Berends et al., 2010; Kenny et al., 2017). This enzyme also degrades environmental DNA (eDNA) and has been associated with biofilm regulation (Mann et al., 2009; Kiedrowski et al., 2011). It is encoded by the *nuc* gene, which was considered the gold standard for the identification of *S. aureus* (Kateete et al., 2010) and is still used for that purpose, although it is present in other staphylococci species (Schleifer and Bell, 2009; Hirota et al., 2011) and some *S. aureus* not carrying this gene have been described (van Leeuwen et al., 2008; Xu et al., 2015).

2.2.3.2 – Biofilm production

Biofilms are bacterial multi-layered cluster embedded in an extracellular matrix composed by exopolysaccharide, proteins, and environmental DNA (eDNA) (Büttner et al., 2015). Thereby, the sessile bacterium is protected against cellular and humoral defence mechanisms of the host, also getting higher resistance to antimicrobial agents used for the mastitis treatment (Barrio et al., 2000; Cucarella et al., 2004). According to Melchior et al. (2006), biofilm fixation and production are important factors also to emphasize other *Staphylococcus* virulence mechanisms.

According to Cramton et al. (1999), two sequential steps are involved in biofilm formation, cells adhesion to a solid substrate followed by cell-cell adhesion. For the first step, a polysaccharide capsular adhesin (PS/A) and a polysaccharide intercellular adhesin (PIA) may be involved (Lavery et al., 2013). Bacterial cells aggregation is expressed by a cationic glucosamine-based lipopolysaccharide. In some cases, proteins may function as alternative aggregating substances. Surfactant peptides were recognized as key factors involved in generating the 3D structure of a staphylococcal biofilm between cell disruptive forces, which casually may lead to the detachment of entire cell clusters (Otto, 2008). Inside the biofilm, the quorum sensing (QS) is the process through which bacteria produce and detect signalling molecules and, thus, coordinate the population's behaviour in biofilm. This

phenomenon plays a crucial role using self-inducing signalling molecules, which when accumulate to a threshold concentration activate a transcriptional regulator, which in turn regulate various genes expression, affecting the bacterial virulence (Kong et al., 2006; Rutherford and Bassler, 2012).

The PS/A and PIA are encoded by the *ica*ADBC genes of the intercellular adhesion operon *ica* (Lavery et al., 2013). In *Staphylococcus* species, this operon is also suggested to participate in cell-cell adhesion (Cramton et al., 1999; O'Toole et al., 2000) and has been found in both *S. aureus* and *S. epidermidis*, suggesting that the initial stages in biofilm formation would be similar between these two species (Cramton et al., 1999). For *S. epidermidis*, the ability to produce an exopolysaccharide matrix has been considered the defining virulence factor (Fey and Olson, 2010).

The *icaA* and *icaD* genes have a significant role in biofilm formation in *S. aureus* (Vasudevan et al., 2003). These genes have been considered essential factors for intercellular adhesion (Nourbakhsh and Namvar, 2016). However, in the absence of these genes a biofilm-associated protein (*bap*), encoded by *bap* gene, or biofilm homologous protein, encoded by *bhp* gene, may alternatively be responsible for biofilm production (Cucarella et al., 2004; Martins et al., 2017a). The *bap* gene was first identified in *S. aureus* isolated from mastitis (Cucarella et al., 2001). The biofilm-associated protein is a member of the surface proteins group that share several important structural and functional characteristics in the biofilm formation, besides having a role in bacterial infectious processes (Lasa and Penadés, 2006).

According to Cucarella et al. (2004) *S. aureus* isolates, which showed stronger biofilm production, had *ica* operon together with the *bap* gene. However, Tormo et al. (2005) found only the *bap* gene in staphylococci with strong biofilm formation. Szweda et al. (2012) reported that *S. aureus* carried only *icaA* and *icaD* genes, but not the *bap* gene, while Martins et al. (2017a) detected only the *bap* gene in some CNS. however, the same authors described 61.6% CNS biofilm producers isolated from sheep milk harbouring any of the *bap*, *bhp* and *ica* operon genes.

2.2.3.3 – Antimicrobial resistance

During bacterial growing, genetic mutations occur naturally in bacteria and some may develop strains resistant to antibiotics (Srivastava and Dutt, 2013). Bacteria may also get resistance genes through horizontal gene transfer: conjugation, when a bacterium carrying resistant genes transfer these genes to other bacteria; transformation, when a DNA fragment from the environment enters a recipient bacterium and transduction when a bacteriophage transfer a DNA fragment from one bacterium to another (Kaiser, 2020).

In a bacterial population, different cells may have different resistance levels. When an antimicrobial is introduced in this population environment, those susceptible to the drug are inactivated and thus only resistant bacteria survive. So, the antimicrobial exerts a selection pressure for resistant strains (U.S. Congress, 1995).

The product of genetic recombination can decrease antibiotic access to cell targets, modify antimicrobial targets or inactivate the molecule, as so inducing bacterial resistance to antimicrobials (Williams, 1999).

β -lactam antimicrobials are inactivated by β -lactamase enzymes, which catalyse the hydrolysis of the β -lactam ring cutting the amide bond (Williams, 1999). In Gram-negative bacteria, these enzymes may be present mainly in periplasmic space and in Gram-positive in the extracellular environment (Bush, 1988). In staphylococci these enzymes are encoded by *blaZ* gene and when encoded from chromosomes, are transferred to the same species, but when encoded by plasmids they are transferable between different species of bacteria.

MRSA resistance is due to the Penicillin-binding proteins mutant, additional PBPs (PBP2a), which encoded by *mecA* gene, as well as its *mecB* and *mecC* homolog (Paterson et al., 2014; Nasution et al., 2018). Recently, a study showed that the acquisition of methicillin resistance by the *mecA* gene was possible by transducing SCCmec type IV and SCCmec type I, by bacteriophages 80 α and 29 for *S. aureus* receptor strains (Scharn et al., 2013).

Many pathogenic bacteria are resistant to tetracyclines due to proteins associated with the membrane that favours efflux, thus taking tetracycline out of the cell. These proteins are encoding by *tet* genes. These genes can be transported for other bacteria by transformation or conjugation. *TetM* genes can be found on the bacterial chromosome and

carried mainly by conjugative transposons. The *tetK* gene is generally carried by small plasmids and can be inserted in SCCmec type III (Ito et al., 2003).

Staphylococcal mastitis isolates from small ruminants have been reported to be resistant to β -lactams with prevalence between 41% and 88% (Agnol et al., 2013; Jamali et al., 2015; Kürekci, 2016; Salaberry et al., 2016; Chu et al., 2017; Ayis and Fadlalla, 2017; Obaidat et al., 2018; Hristov, 2018). Moreover, amoxicillin, a penicillin derivative, is more effective against β -lactamases-producing microorganisms, when used together with clavulanic acid, which inactivates β -lactamases (DGAV, 2013). Obaidat et al. (2018) showed better combined action because only 20% of the *S. aureus*, from small and large ruminants milk, resisted their joint action, while 50% were resistant to individual penicillin. Regarding tetracyclines, 26.3% to 73.7% of staphylococci isolated from small ruminant milk samples also showed resistance (Ayis and Fadlalla, 2017; Obaidat et al., 2018).

2.3 – Propolis

2.3.1 – Origin and properties

The Greeks called propolis at the gates of a city, a word taken by the prefix 'pro' and 'polis' for city (Ghisalberti, 1979). Propolis is a mass produced by honeybees with various resinous substances, from plant sources (Alvarez-Suarez, 2017). Resins are sticky and aromatic plants exudates, secreted in the initial flower development and leaf buds. After removing the resins with their jaws, *Apis mellifera* bees triturate and soften them with the aid of 10-hydroxydocenoic acid, a substance produced in their salivary glands, which they then mix with wax, pollen and microelements, resulting in a glue type, used to fill gaps, both in the breeding wells and in the hive wall, allowing better thermal insulation and preventing the entry of undesirable visitors (Ghisalberti, 1979; Costa and Oliveira, 2005). In addition, bees also use it to completely cover and immobilize small animals and invaders insects, embalming them and preventing their decomposition creating a sterile environment. Propolis was also used by Egyptians to embalm corpses due to its anti-putrefactive properties (Ghisalberti, 1979; Bankova et al., 1996; Castaldo and Capasso, 2002).

This resinous paste has been used for centuries to treat different human diseases. It was recognized for its medicinal properties by Greek and Roman physicians, such as Aristotle, Dioscorides, Pliny and Galen, by Arab doctors in the Middle Age, by the Incas of the Old-World civilizations, and by the London pharmacopeia in the 17th century, who listed propolis as official medicine. Between the 17th and 20th centuries, propolis became very popular in Europe due to its antibacterial activity (Castaldo and Capasso, 2002).

Propolis compounds can exhibit different actions, such as antioxidant, anti-inflammatory (Yildiz et al. 2014), antiulcerogenic (Barros et al., 2008), antitumoral (Frozza et al., 2013), antidiabetogenic (Pacheco et al., 2011), antiatherogenic and anti-angiogenic (Daleprane et al., 2011), immunomodulatory (Castaldo and Capasso, 2002), antifungal (Agüero et al., 2011; Mendonça et al., 2015), antiviral (Nolkemper et al., 2010) namely for human immunodeficiency virus (anti-HIV) (Gekker et al., 2005). Propolis also showed action versus some bacterial virulence factors, such as anti-biofilm (Wojtyczka et al., 2013; Doganli, 2016), anti-quorum sensing (Kasote et al., 2015) and antimotility (Mirzoeva et al., 1997; Josenhans and Suerbaum, 2002).

2.3.2 – Composition

Propolis chemical composition and colour are variable and dependent on the vegetation around the hive (Ghisalberti, 1979; Koru et al., 2007). Moreover, chemical composition variation generates differences in their pharmacological properties (Bueno-Silva et al., 2017; Afrouzan et al., 2018).

Propolis generally consists of 30 to 40% waxes, 5 to 10% volatile oils and aromatic acids, 50 to 60% resins and balsams, and 5% pollen grains. These latter are a source of essential elements, such as magnesium, nickel, calcium, iron, zinc, aluminium, strontium, copper, manganese and small amounts of vitamins B1, B2, B6, C and E, and sugars such as arabinose, fructose, glucose, sucrose and maltose (Ghisalberti, 1979; Bonvehí et al., 1994; Castaldo and Capasso, 2002; Park et al., 2002).

The main pharmacologically active compounds in propolis are: bioflavonoids and derivatives (pinocembrin, pinostrobin, galangin, isalpinine, pinobanksina, isosakuranetin, canferida, quercetin, naringenin, apigenin, chrysin, formononetin, vestitol, neovestitol,

isoliquiritigenin, anthocyanins and medicarpin); other phenolic compounds (terpenes, caffeine and its esters, artemillin C, and its derivatives, ferulic, trans-cinnamic, prenylated p-coumaric); phenolic aldehydes; ketones (chalcone); tannins and fatty acids (Marcucci et al., 2001; Castaldo and Capasso, 2002; Koo et al., 2002; Uzel et al., 2005; Funari and Ferro, 2006; Inui et al., 2014; Bueno-Silva et al., 2017; Afrouzan et al., 2018). Some authors reported that in propolis, phenolic acids are more abundant than flavonoids (Woisky and Salatino, 1998). Several compounds already identified are present in all samples, but other depends on the seasonality and flora where the samples are collected (Castaldo and Capasso, 2002; Vargas et al., 2004; Alencar et al., 2007).

2.3.3 – Components extraction and pharmacological activity

Several factors may affect the antimicrobial action of each propolis extract. Solvent type, propolis concentration and the methodology used for extraction determine the components to be extracted from the original sample (Park and Ikegaki, 1998; Pinto et al., 2001; Castaldo and Capasso, 2002; Silva et al., 2003).

Pinto et al. (2001) studied the Gram-positive bacteria susceptibility, isolated from milk, to propolis extracts produced with different methodologies and solvents, such as water, ethanol, methanol, ethyl acetate and chloroform at a concentration of 100 mg/ml. Ethanolic extract showed the best action followed by the methanolic extract. However, extracts produced with water, ethyl acetate and chloroform did not show any bacterial activity as the pure ethanol and methanol used as controls.

Regarding ethanol extracts, although some antimicrobial activity was observed in extracts produced with 30% to 50% ethanol, the best performance was obtained with concentrations between 60% and 80%. In these highest ethanol concentrations occurs the extraction of the highest percentages of bioactive components, such as phenolics, that are less soluble in water (Park and Ikegaki, 1998; Pinto et al., 2001). However, a proper PEE is safe when its preparation is standardized (Castaldo and Capasso, 2002; Silva et al., 2003).

2.3.4 – Antimicrobial activity

The antibacterial action of propolis is more marked against Gram-positive bacteria than for Gram-negative organisms (Campos et al., 2017).

For *Streptococcus agalactiae*, Takaisi-kikuni and Schilcher (1994) described that propolis components caused cell lysis by disrupting the cell wall, cytoplasmic membrane and cytoplasm, and bacterial inhibition was caused by protein synthesis inhibition and DNA replication impairment. Scazzocchio et al. (2006) described *S. aureus* inhibition of lipase and coagulase enzymes by PEE activity. More recently, Campos et al. (2017) showed by atomic force microscopy that the components present in the propolis extract, interacted with *S. aureus* and *E. coli*, generating an increase in the cell volume, indicating that the action on the bacteria cell wall is the main mechanism that leads to bacterial inhibition. These authors reported that Gram-negative bacteria required a higher EEP concentration for cell wall disruption. Mirzoeva et al. (1997) stated that the caffeic acid component of the propolis extract inhibited motility and increased the membrane ionic permeability of *Bacillus subtilis*.

The cell wall of Gram-negative bacteria is of greater chemical complexity, lower flexibility, and higher lipid content, conferring a higher resistance to propolis activity compared to Gram-positive (Vargas et al., 2004; Campos et al., 2017). Studies show that to overcome the structure of the Gram-negative bacteria membrane, a double propolis extract concentration must be used comparing to Gram-positive (Mirzoeva et al., 1997).

2.3.5 – Propolis synergy with antibiotics

Propolis extracts can be used alone or in combination with antibiotics (Afrouzan et al., 2018). This association produces synergy potentiating the antibiotics antimicrobial effect on various bacteria.

Subinhibitory concentrations of propolis extracts together with antibiotics were analysed to observe their inhibitory action on multidrug resistant microorganisms. The synergistic action demonstrated the propolis potential to improve the action of certain antibiotics, which had been previously undetected (Stepanović et al., 2003).

Other authors also observed good results when PEE sub-inhibitory concentrations were added to ampicillin, gentamicin, and streptomycin against *S. aureus* (Scazzocchio et al., 2006). Ampicillin together with PEE was active against *Listeria monocytogenes* for the treatment of goats and sheep with listeriosis. Its synergy showed more efficiency than antibiotics combination (Ismael et al., 2009). However, in another study, this association showed no action against *S. aureus* (Król et al., 1993).

When PEE was added to chloramphenicol, ceftriaxone and vancomycin showed moderate activity and when together with erythromycin did not show antimicrobial action (Scazzocchio et al., 2006).

Differences in PEE composition could explain divergences in PEE synergies with the same antibiotic, for the same bacterial species, due to the activity of the different compounds present in each propolis sample. Fernandes et al. (2005) observed that the better synergistic results detected were for the PEE together with antibiotics that cause interference in bacterial protein synthesis.

2.3.6 – Propolis components with antimicrobial action

In 1994, Takaisi-Kikuni and Schilcher (1994) showed that propolis antimicrobial activity is due to the synergism between various components, such as phenolic acids, flavonoids, and sugars. Likewise, Mirzoeva et al. (1997), observed the efficacy of some propolis components, such as caffeic acid phenolic ester (CAPE), quercetin, naringenin and caffeic acid against Gram-positive and some Gram-negative bacteria. This synergy has the greatest effect on bacterial cells when they are actively growing.

Other authors refer the main propolis compounds commonly found with potential antimicrobial action, both for Gram-positive and Gram-negative bacteria, are flavonoids (pinocembrin, pinostrobin chalcone, isalpinine, pinobanksina, quercetin, naringenin, galangin and chrysin), phenolic and terpene compounds (Castaldo and Capasso, 2002; Uzel et al., 2005; Afrouzan et al., 2018).

Several studies show different compounds are characteristic of specific regions of resin collection by bees. Red coloured propolis has biologically active compounds that have not been reported in other propolis types (Trusheva et al., 2006; Alencar et al., 2007). Isoflavonoid medicarpin compound found in red propolis, by Inui et al. (2014), showed

better antimicrobial activity against *S. aureus*, *B. subtilis* and *P. aeruginosa* than other compounds.

Green PEE displayed better antimicrobial activities against *S. aureus* resistant and sensitive to methicillin (MRSA and MSSA) compared to *Baccharis dracunculifolia* extracts (vegetable source for green propolis production) and artepillin C (compound found in Green propolis and *B. dracunculifolia*). The better EEP activity may be related to the synergy between these constituents or between these and others present in the sample (Veiga et al., 2017). This research confirms the results from the late 20th century by Król et al. (1993) and Bankova et al. (1996), which related a synergism among propolis constituents showing better antimicrobial activity altogether, when compared to the isolated compounds. This synergistic potential was also confirmed by Bittencourt et al. (2015).

2.3.7 – Propolis components with antibiofilm action

Glycosyltransferases (GTFs) are enzymes important for biofilm development (Islam et al., 2008). These enzymes are involved in the synthesis of the glucan polysaccharide, which can provide binding sites for bacteria (Schilling and Bowen, 1992). Potent inhibitors of GTF activity have been found in propolis extracts such as flavone and flavonol, with apigenin being the most effective constituent for this action (Koo et al., 2002).

On the other hand, substances with QS inhibitory functions were proposed by Brackman and Coenye (2015), as promising antimicrobial agents. Quorum Sensing process develops following different systems such as autoinducing peptide (AIP) in Gram-positive bacteria, acyl-homoserine lactone (AHL) in Gram-negative bacteria and the autoinducer-2 (AI-2) existing in both bacteria types. Savka et al. (2015) observed that the components found in propolis inhibited the QS system AHL of Gram-negative bacteria, emphasizing that the extracts that showed higher amounts of flavanones and dihydroflavonols, flavones and flavonols, cinnamic acid derivatives and fatty acids showed the best results in inhibiting this system and, consequently, inhibiting biofilm.

Polyphenol tannins (condensed and hydrolysable), often found in propolis, are also denoted as possible antibiofilm compounds for Gram-negative bacteria, but in higher concentrations (Trentin et al., 2013) compared to Gram-positive bacteria for which a

concentration as low as 0.2 $\mu\text{g} / \text{mL}$ was effective to inhibit the biofilm formation. Antibiofilm activity may also be due to flavonoids (kaempferol, myricetin, pinocembrin, apigenin, genistein and quercetin), which were present in greater amount in the studied sample (Veloz et al., 2015).

2.3.8 – *In vitro* antimicrobial activity of propolis against staphylococci from small ruminants milk

Aqueous and ethanolic green propolis extracts were evaluated for staphylococci susceptibility on isolates from goat's milk. Both extracts were efficient, however, the ethanol extract showed greater activity (Santos Neto et al., 2009). Likewise, Silva et al. (2012), showed satisfactory antibacterial results of brown propolis extract for *Staphylococcus* sp. Propolis antimicrobial studies against goat and sheep mastitis pathogens are scarce.

2.3.9 – *In vivo* antimicrobial activity of propolis in small ruminants

Studies on the use of propolis to improve small ruminants performance are on the rise and showing positive results. In 1983, Havsteen (1983) described that flavonoids administered orally are metabolized and expelled in the urine. Thus, the propolis addition to sheep rations (Silva et al., 2015), goats (Lana et al., 2007) and cows (Aguiar et al., 2014) did not show a negative effect on the nutrients digestibility and could be used as a reliable antimicrobial compound as a food complement for ruminants not affecting normal rumen parameters.

Selem (2012) described that red PEE added to a Tifton hay substrate base (50:50) significantly decreased SCC while increasing fat, protein and lactose together with milk production, improving sheep health during breeding season and performance of lambs. This author also stated that the isoflavonoids were the components responsible for the propolis biological activity. Morsy et al. (2016) administrated red propolis extracts, orally, (3g/sheep/day) for 21 days before the expected lambing date. These authors also observed that the isoflavonoids present in the propolis extract decreased SCC and significantly increased total protein and sheep energy status thus improving milk production. The

authors concluded that propolis extract prepartum administration was positively supported in the transition from pregnancy to lactation, with health benefits for the ewes and the lambs.

A propolis based intramammary formulation was assessed for tolerance and efficacy on 100 goats in intensive milk production. Samples were analysed for milk composition, SCC, and microbiological culture. The formulation was applied three times and the antimicrobial, immunostimulatory and anti-inflammatory activity was observed in 1% to 3% propolis concentrations. The authors suggest that the intramammary formulation has the potential to gradually replace antibiotics, with the advantage that propolis does not require a withdrawal period and repeated use does not cause antimicrobial resistance (Bačić et al., 2016).

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Chapter 3

3. Virulence Factors in *Staphylococcus* Associated with Small Ruminant Mastitis: Biofilm Production and Antimicrobial Resistance Genes

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Virulence Factors in *Staphylococcus* Associated with Small Ruminant Mastitis: Biofilm Production and Antimicrobial Resistance Genes

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Abstract

Small ruminant mastitis is a serious problem, mainly caused by *Staphylococcus* spp. Different virulence factors affect mastitis pathogenesis. The aim of this study was to investigate virulence factors genes for biofilm production and antimicrobial resistance to β -lactams and tetracyclines in 137 staphylococcal isolates from goats (86) and sheep (51). The presence of *coa*, *nuc*, *bap*, *icaA*, *icaD*, *blaZ*, *mecA*, *mecC*, *tetK*, and *tetM* genes was investigated. The *nuc* gene was detected in all *S. aureus* isolates and in some coagulase-negative staphylococci (CNS). None of the *S. aureus* isolates carried the *bap* gene, while 8 out of 18 CNS harbored this gene. The *icaA* gene was detected in *S. aureus* and *S. warneri*, while *icaD* only in *S. aureus*. None of the isolates carrying the *bap* gene harbored the *ica* genes. None of the biofilm-associated genes were detected in 14 isolates (six *S. aureus* and eight CNS). An association was found between *Staphylococcus* species and resistance to some antibiotics and between antimicrobial resistance and animal species. Nine penicillin-susceptible isolates exhibited the *blaZ* gene, questioning the reliability of susceptibility testing. Most *S. aureus* isolates were susceptible to tetracycline, and no cefazolin or gentamicin resistance was detected. These should replace other currently used antimicrobials.

Keywords: mastitis; staphylococci; virulence factors; genes; biofilm; antimicrobial resistance

1. Introduction

Mastitis is the inflammation of the mammary gland, mainly due to intramammary infection (IMI). In small ruminants, this disease is considered a serious economic issue due to the mortality of lactating females, cost of treatment, reduced milk yield and quality [1,2], as well as a public health concern associated with risk of consumer food poisoning [3,4].

Several pathogens can cause mastitis in small ruminants; however, species of staphylococci are the most frequently isolated microorganisms from goat and sheep milk [2,5–8]. *Staphylococcus aureus* is one of the main pathogens associated with mastitis in small ruminants [9]. Incidence of clinical mastitis in sheep due to this bacterium may reach 20% with a mortality rate between 25% and 50%, and the affected mammary halves in surviving animals are frequently destroyed. Chronic mastitis may cause a 25 to 30% reduction in milk yield from the affected udder [10].

Coagulase negative staphylococci (CNS), although not as virulent as *S. aureus*, often cause subclinical mastitis in small ruminants [5,11–13]. This type of infection, most times not detected by the farmer, clearly reduces milk production, also changing milk composition, indirectly impairing the milk product's properties [14]. CNS are the most prevalent pathogens of the mammary gland in goats and sheep with subclinical mastitis, affecting 60% to 80.7% in goats and 45% to 48% in sheep [1]. Other authors have reported as much as 70.1% of subclinical mastitis in sheep is caused by CNS [5].

Virulence factors are bacterial molecules that enhance their capacity to establish and to survive within the host and, thus, contribute to bring damage to the host. Staphylococci possess a wide array of virulence factors [15]. Coagulase enzyme acts on plasma fibrinogen to form fibrin clots that protect the microorganisms from phagocytosis and shelter them from other cellular and soluble host defence mechanisms. This enzyme, encoded by the *coa* gene, is commonly used to distinguish coagulase positive staphylococci (CPS), namely *S. aureus*, *S. intermedius*, and *S. pseudintermedius*, from CNS species [16]. Nevertheless, this gene has been found also in species known as CNS such as *S. epidermidis*, *S. chromogenes*, and *S. hominis* [17]. The *coa* gene has also recently been associated with biofilm production [18].

The staphylococcal nuclease is a thermostable nuclease encoded by the *nuc* gene [19], which hydrolyzes DNA and RNA in host cells, causing tissue destruction and spreading of staphylococci [20], also promoting the escape of microorganisms when retained by neutrophil extracellular traps (NETs), allowing the bacteria to evade this host defence mechanism [21,22]. For decades, the *nuc* gene has been considered the golden standard for *Staphylococcus aureus* identification and is still used presently [23–25]. However, the *nuc* gene has been detected in staphylococci of animal origin other than *S. aureus* [26]. Moreover, the *nuc* encoded staphylococcal thermonuclease is a biofilm inhibitor that degrades the environmental DNA (eDNA) associated with biofilm [27,28].

The production of biofilm is considered a major virulence factor that, besides protecting from host defence mechanisms, also shields bacteria against antimicrobial agents [29]. Furthermore, the persistence of biofilm-producing isolates in the dairy environment enhances the dispersal of virulence factors through the transfer of genetic material to other bacteria [30]. Biofilm major components are an exopolysaccharide matrix, proteins, and eDNA, along with the bacterial cells [31]. The exopolysaccharide, polysaccharide intercellular adhesin (PIA), is also a non-protein adhesin [32] assisting in bacterial adhesion to different surfaces, comprising the first critical event in the establishment of an infection [33]. Staphylococcal PIA is encoded by the *ica* operon [34], and biofilm-associated protein (Bap) is a surface protein connected to the cell wall encoded by the *bap* gene [35].

Antimicrobial resistance (AMR) is a major problem hampering the treatment of an ever increasing range of infections caused by bacteria [36]. Staphylococci resistance has been reported for different antimicrobials used for mastitis control in small ruminants [7,36–38]. Genes often described in *Staphylococcus* spp. isolated from the milk of small ruminants are *bla_Z* and *mecA*, responsible for β -lactam resistance and *tetK* and *tetM*, accounting for tetracycline resistance [39–41]. The presence of resistant bacteria in contaminated food products may lead to the transfer of resistance genes to the indigenous microbiota in the human gut [42].

The aim of this study was to identify *Staphylococcus* species isolated from small ruminants' milk samples and investigate the presence of genes encoding virulence factors

associated with both biofilm (*coa*, *nuc*, *bap*, *icaA*, and *icaD*) and antimicrobial resistance to β -lactams (*blaZ*, *mecA*, and *mecC*) and tetracyclines (*tetK* and *tetM*).

2. Results and Discussion

2.1. Bacteriological Results

From the 646 milk samples collected from goats (508) and sheep (138), bacteriological cultures resulted positive in 191 samples: 131 goat milk and 60 sheep milk. A total of 137 staphylococcal isolates were recovered, of which 86 were isolated from goat and 51 from sheep milk samples.

2.2. Staphylococci Identification

Excellent (96 to 99% probability) and very good (93 to 95% probability) identification was observed for most *Staphylococcus*. Unidentified isolates and isolates with low discrimination results were confirmed by 16S rRNA gene sequencing. Concerning goat milk samples, four *S. aureus*, one *Staphylococcus* sp., and 12 different CNS species were found: *S. caprae* (25), *S. chromogenes* (10), *S. epidermidis* (11), *S. simulans* (8), *S. warneri* (7), *S. capitis* (4), *S. lentus* (4), *S. hominis* (4), *S. hyicus* (3), *S. auricularis* (2), *S. haemolyticus* (2), and *S. equorum* (1). On the other hand, 31 *S. aureus* and seven different CNS species were recovered from sheep milk samples: *S. chromogenes* (9), *S. epidermidis* (3), *S. auricularis* (2), *S. haemolyticus* (2), *S. simulans* (2), *S. lentus* (1), and *S. rostri* (1). *Staphylococcus rostri* has only been seldom isolated from the milk of a sheep with subclinical mastitis [43,44]. In the CNS group, *S. caprae* was the most found species and was isolated only from goat's milk samples. It is a commensal organism that prevails in the skin of the goat udder [19]. This species is most commonly found in cases of goat mastitis [37,45–47], but it was also isolated from sheep [5,48], buffalo [17], and cow's milk [49]. In this study, other *Staphylococcus* species were only isolated from goats: *S. warneri*, *S. capitis*, *S. hominis*, *S. hyicus*, and *S. equorum*. This was probably because the sheep sampling was smaller, since all these species have been isolated before from sheep milk by several other authors [44].

2.3. Biofilm Production

Of the 137 *Staphylococcus* isolates analyzed, 103 were biofilm producers (75%). Biofilm forming isolates belong to the following species: *S. aureus* (29/35), *S. caprae* (22/25), *S. chromogenes* (12/19), *S. epidermidis* (11/14), *S. warneri* (7/7), *S. simulans* (6/10), *S. auricularis* (4/4), *S. capitis* (3/4), *S. lentus* (3/5), *S. haemolyticus* (2/4), *S. hominis* (2/4), *S. equorum* (1/1), and *Staphylococcus* sp. (1/1). All *S. epidermidis* goat isolates were found to produce biofilm in the present study, in accordance with the findings of others authors that reported *S. epidermidis* as the most commonly found species in biofilm-associated human infections [50]. However, none of the sheep *S. epidermidis* isolates were biofilm producers. In fact, other studies had already reported only 8% of biofilm-producing isolates among sheep mastitis *S. epidermidis* [51].

2.4. Genes Associated to Biofilm

We investigated the presence of *coa* and *nuc* genes in all 137 staphylococcal isolates, mainly for identification purposes and due to historical reasons. In fact, the ability of a strain to produce coagulase, encoded by the *coa* gene, is the basis of the primary classification of staphylococci in coagulase-positive or coagulase-negative [16]. All *S. aureus* isolates (35) harbored the *coa* gene, as well as isolate B200E1, not identified to the species level. Based on this result, this isolate was probable also *S. aureus*. Therefore, the 101 *Staphylococcus* isolates not carrying the *coa* gene were confirmed as CNS. Furthermore, in the present study, different amplicons of the *coa* gene with band sizes ranging from 400 to 900 bp were detected (Figure 3.1), as already reported by others [52–55]. In fact, the *coa* gene also has a discriminatory power between isolates because of the heterogeneity of its 3' variable region containing 81-bp tandem short sequence repeats (SSR) [56–58].

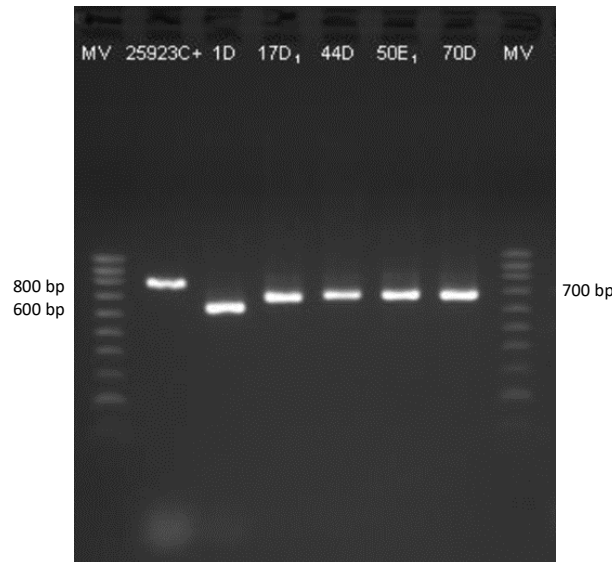


Figure 3.1. Agarose gel electrophoresis of *S.aureus coa* gene PCR products. NZYDNA Ladder V (200-1000 bp) (NZYTech, Lisbon, Portugal).

The *nuc* gene was detected in 67 out of 137 isolates (48.9%), of which only 35 are *S. aureus*. The other *nuc* positive isolates include: *S. chromogenes* (8), *S. warneri* (4), *S. auricularis* (3), *S. caprae* (3), *S. hyicus* (3), *S. lentus* (3), *S. epidermidis* (2), *S. simulans* (2), *S. capitis* (1), *S. haemolyticus* (1), *S. hominis* (1), and *Staphylococcus* sp. (1). Furthermore, an association was found between the *Staphylococcus* species and the presence of the *nuc* gene ($\chi^2=70.968$, $df=14$, $P<0.001$). In fact, all *S. aureus* harbour the *nuc* gene, while most CNS (70/101) do not. However, the *nuc* gene was also detected in more than 50% of the isolates in some CNS species: *S. warneri* (4/7), *S. lentus* (3/5), *S. auricularis* (3/4), and *S. hyicus* (3/3).

The presence of the *nuc* gene was used in the past to identify *S. aureus* [23,25]. The *nuc* gene is present in most *S. aureus* isolates, however some isolates not carrying this gene have been described [59,60]. Moreover, the *nuc* gene has also been detected in other species of *Staphylococcus*, both CPS and CNS [61,62].

For the detection of the biofilm production genes, *bap*, *icaA* and *icaD*, the 44 *nuc*-positive biofilm-producing isolates were selected. *nuc*-positive biofilm-producing staphylococci and biofilm-associated genes are shown in Table 3.1.

Table 3.1. *nuc*-positive biofilm-producing staphylococci isolates and biofilm-associated genes.

Isolate	Origin	Animal	Bacterial species	<i>coa</i>	<i>nuc</i>	<i>bap</i>	<i>icaA</i>	<i>icaD</i>
1D	PT	goat	<i>S. aureus</i>	+	+	-	+	+
13D1	PT	goat	<i>S. warneri</i>	-	+	-	-	-
17D1	PT	goat	<i>S. aureus</i>	+	+	-	-	+
44D	PT	goat	<i>S. aureus</i>	+	+	-	+	+
47D2	PT	goat	<i>S. chromogenes</i>	-	+	+	-	-
50E1	PT	goat	<i>S. aureus</i>	+	+	-	+	+
54E1	PT	goat	<i>S. warneri</i>	-	+	+	-	-
54E2	PT	goat	<i>S. warneri</i>	-	+	-	+	-
55D1	PT	goat	<i>S. capitis</i>	-	+	-	-	-
60D2	PT	goat	<i>S. chromogenes</i>	-	+	+	-	-
65D	PT	goat	<i>S. caprae</i>	-	+	-	-	-
70D	PT	sheep	<i>S. aureus</i>	+	+	-	-	+
71E	PT	sheep	<i>S. aureus</i>	+	+	-	-	-
72D	PT	sheep	<i>S. aureus</i>	+	+	-	-	+
72E	PT	sheep	<i>S. aureus</i>	+	+	-	-	+
83D	PT	sheep	<i>S. aureus</i>	+	+	-	-	-
B51E	BR	goat	<i>S. chromogenes</i>	-	+	-	-	-
B64	BR	goat	<i>S. chromogenes</i>	-	+	-	-	-
B76E	BR	goat	<i>S. chromogenes</i>	-	+	+	-	-
B101	BR	goat	<i>S. warneri</i>	-	+	-	+	-
B159D	BR	goat	<i>S. chromogenes</i>	-	+	+	-	-
B159E	BR	goat	<i>S. chromogenes</i>	-	+	+	-	-
B190D	BR	goat	<i>S. auricularis</i>	-	+	-	-	-
B209D2	BR	goat	<i>S. simulans</i>	-	+	+	-	-
B209E	BR	goat	<i>S. simulans</i>	-	+	-	-	-
B219D3	BR	sheep	<i>S. auricularis</i>	-	+	-	-	-
B219D5	BR	sheep	<i>S. aureus</i>	+	+	-	-	-
B223D	BR	sheep	<i>S. aureus</i>	+	+	-	-	-
B250D	BR	sheep	<i>S. auricularis</i>	-	+	+	-	-
CQ152E1	PT	sheep	<i>S. aureus</i>	+	+	-	+	+
CQ185D1	PT	sheep	<i>S. aureus</i>	+	+	-	+	+
CQ196E	PT	sheep	<i>S. aureus</i>	+	+	-	-	+
CQ201E	PT	sheep	<i>S. aureus</i>	+	+	-	-	+
CQ268D1	PT	sheep	<i>S. aureus</i>	+	+	-	-	+
CQ270E1	PT	sheep	<i>S. aureus</i>	+	+	-	-	-
CQ285D	PT	sheep	<i>S. aureus</i>	+	+	-	-	+
CQ286D	PT	sheep	<i>S. aureus</i>	+	+	-	-	+
CQ290D1	PT	sheep	<i>S. aureus</i>	+	+	-	-	+
CQ290D2	PT	sheep	<i>S. aureus</i>	+	+	-	-	+
CQ296D	PT	sheep	<i>S. aureus</i>	+	+	-	-	+
CQ335E	PT	sheep	<i>S. aureus</i>	+	+	-	-	-
CQ336E2	PT	sheep	<i>S. aureus</i>	+	+	-	-	+
CQ349D	PT	sheep	<i>S. aureus</i>	+	+	-	-	-
CQ354D	PT	sheep	<i>S. aureus</i>	+	+	-	-	+

PT-Portugal; BR-Brazil.

The *bap* gene was amplified in eight isolates: *S. chromogenes* (5), *S. auricularis* (1), *S. simulans* (1), and *S. warneri* (1). None of the *S. aureus nuc*-positive biofilm-producing isolates carries the *bap* gene. In fact, the *bap* gene has been reported mainly in *S. aureus* strains isolated from cattle [24,63,64]. However, Martins et al. [65] have detected the *bap* gene in four sheep milk *S. aureus* isolates. In our study, 8 out of 18 CNS *nuc*-positive biofilm producing isolates harbored the *bap* gene. The *bap* gene encodes a cell wall associated protein named Bap (for biofilm associated protein), which enhances biofilm formation as it mediates bacterial primary attachment to abiotic surfaces and intercellular adherence [35]. Other studies have reported the presence of the *bap* gene in several CNS isolates [66].

The presence of the *icaA* gene was detected in seven isolates: *S. aureus* (5) and *S. warneri* (2). On the other hand, the *icaD* gene was present in 19 *S. aureus* isolates. Furthermore, five *S. aureus* isolates carried both *icaA* and *icaD* genes simultaneously. Xu, Tan, Zhang, Xia, and Sun [59] detected the *icaD* gene in 20 out of 28 *S. aureus* bovine mastitis isolates, while it was not detected in any of the 76 CNS analyzed. The same authors reported the absence of the *icaA* gene in all analyzed staphylococcal isolates [59]. No isolate carrying the *bap* gene harbored the *ica* operon genes, as reported before by other authors [67]. However, Marques et al. [68] found one single bovine mastitis *S. aureus* isolate (out of 20) that simultaneously carried *bap*, *icaA*, and *icaD*.

None of the three biofilm-associated genes were detected in 14 of the *nuc*-positive biofilm-producing isolates: *S. aureus* (6) and CNS (8). Other authors have also reported the absence of *bap*, *icaA*, and *icaD* genes in biofilm-producing *S. aureus* [24,69,70]. Despite no association being found between the presence of the *nuc* gene and biofilm production, most biofilm-producing isolates harbored the *nuc* gene (53.4%), while it was only detected in about 35% of the non-producers. Nevertheless, Kiedrowski, Kavanaugh, Malone, Mootz, Voyich, Smeltzer, Bayles, and Horswill [28] described an inverse correlation between Nuc thermonuclease activity and biofilm formation and confirmed the important role for eDNA in the *S. aureus* biofilm matrix.

Apparently, CNS produce biofilm mainly via Bap, as already suggested by Zuniga et al. [71], who found the *bap* gene to be more frequently present in CNS when compared to CPS.

Meanwhile, most *S. aureus* seem to form biofilm through PIA since they harbor the *icaA* and *icaD* genes. Other authors have reported that a low prevalence of the *bap* gene in *S. aureus* indicates that the *ica* operon-dependent mechanism may be the main responsible for the adhesion and biofilm formation in this species [68]. Notwithstanding, it has been reported that biofilm synthesis in *S. aureus* can also be encoded by the *bap* gene [72].

Other biofilm formation mechanisms in staphylococci not harboring the classical biofilm-production genes, *bap*, *icaA*, and *icaD*, need to be explored. Furthermore, some of the isolates not carrying *bap*, *icaA*, and *icaD* also did not harbor the *coa* gene, which has been reported as associated with biofilm formation [18]. However, the *nuc* gene might be an important factor to consider since all 44 isolates were biofilm producers and harbored the *nuc* gene, although Nuc has been referred to as a biofilm inhibitor [27,28].

2.5. Antimicrobial Resistance

Out of 137 staphylococcal isolates analyzed for antimicrobial susceptibility, 15 were multidrug resistant, 36 were non-susceptible to two antimicrobial categories, and 61 to one antimicrobial category, according to the classification proposed by Magiorakos et al. [73]. Moreover, no antimicrobial resistances were detected in 24 staphylococcal isolates. Staphylococci isolated from milk from small ruminants with mastitis are known for their multiresistance [74]. In this work, the multidrug resistant (MDR) isolates belonged to the following species: *S. aureus* (8), *S. lentus* (3), *S. chromogenes* (2), *S. caprae* (1), and *S. warneri* (1). Contrarily, Taponen and Pyorala [75] reported that multiresistance was more common in CNS than in *S. aureus* from bovine mastitis. Susceptibility patterns of CPS and CNS isolates are shown in Figure 3.2. For most antimicrobials tested, a higher percentage of resistant isolates was observed among CNS when compared to CPS. Vasileiou et al. [76] also reported more resistant CNS isolates than *S. aureus*. However, mastitis caused by CNS responds much better to antimicrobial treatment than *S. aureus* mastitis [75]. Staphylococcal isolates were mainly non-susceptible to streptomycin (50/137), penicillin (38/137), ampicillin (34/137), lincomycin (33/137), oxacillin (22/137), cloxacillin (21/137), and tetracycline (17/137), as previously reported [77] (Figure 3.2). Moreover, most CPS isolates were non-susceptible to streptomycin and lincomycin. On the other hand, CNS isolates were mostly non-susceptible to the β -lactams and tetracyclines. In addition, an

association was found between *Staphylococcus* species and antimicrobial resistance to penicillin ($\chi^2 = 45.981$, $df = 14$, $p < 0.001$), ampicillin ($\chi^2 = 48.327$, $df = 14$, $p < 0.001$), streptomycin ($\chi^2 = 137.705$, $df = 28$, $p < 0.001$), lincomycin ($\chi^2 = 156.536$, $df = 28$, $p < 0.001$), cephalexin ($\chi^2 = 57.219$, $df = 28$, $p < 0.05$), and tetracycline ($\chi^2 = 51.626$, $df = 28$, $p < 0.05$).

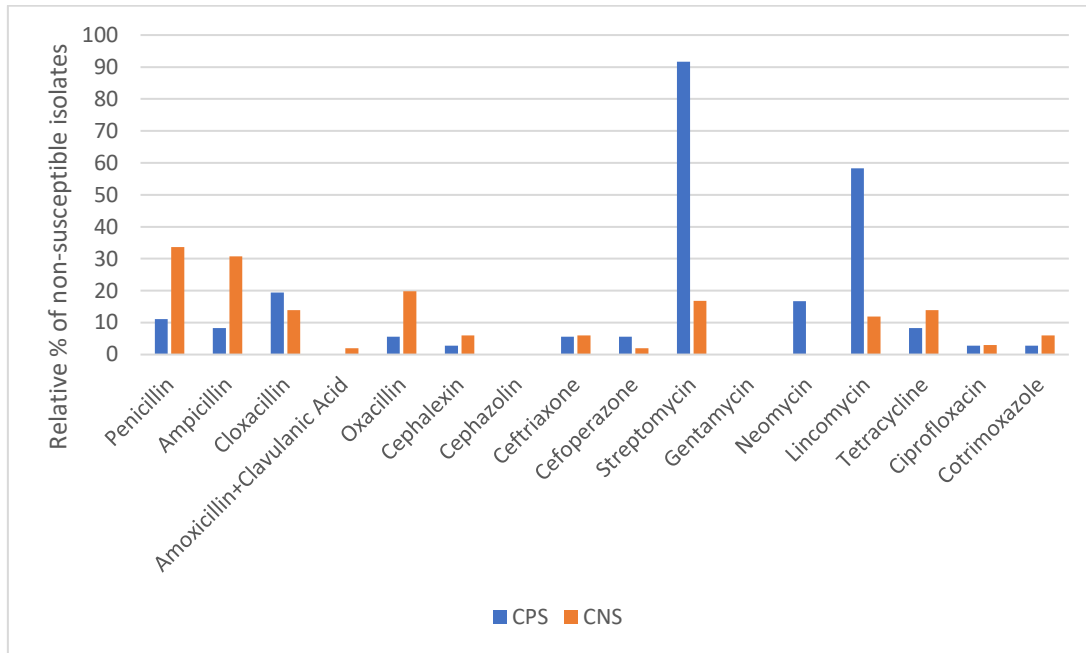


Figure 3.2. Susceptibility patterns of CPS (n=36) and CNS (n=101) isolates to antimicrobials.

Regarding the results shown by the correspondence analysis, most *S. caprae* and *S. capitis* isolates were resistant to penicillin and ampicillin, while all other staphylococci were mostly susceptible to these antimicrobials (Figure 3.3). Most *S. aureus* isolates exhibited an intermediate susceptibility pattern to streptomycin and lincomycin [78]. Additionally, all *S. hyicus* isolates were resistant to streptomycin, while *S. lentus* and *S. rostri* were resistant to lincomycin (Figure 3.3).

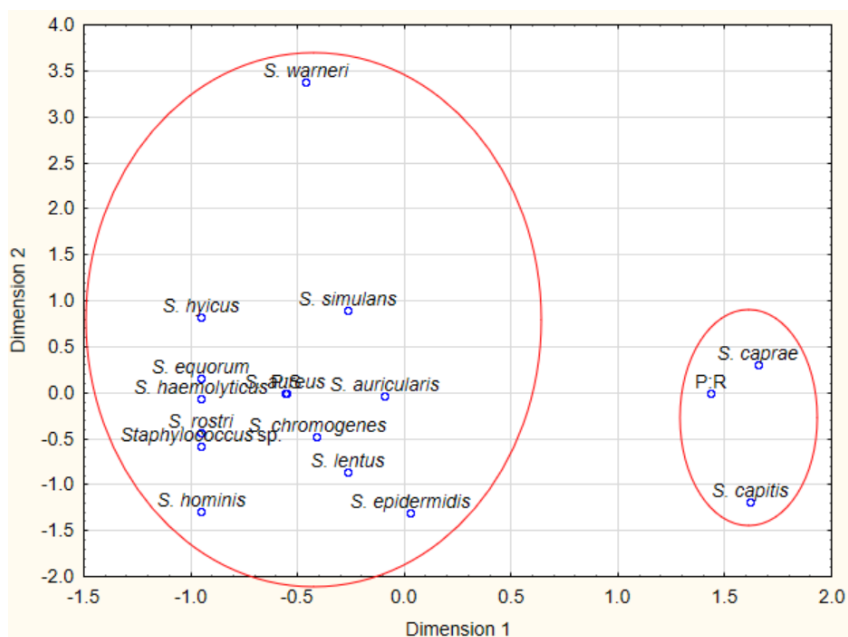


Figure 3.3. CA biplots of the relationship between bacterial species and tolerance to the antimicrobials penicillin (P), ampicillin (AMP), streptomycin (S), and lincomycin (MY).

No staphylococci resistant to ceftazolin and gentamycin were identified. Moreover, no non-susceptible *S. aureus* isolates were found to amoxicillin + clavulanic acid. A number of CNS isolates, although resistant to penicillinase-labile penicillins, were susceptible to amoxicillin + clavulanic acid, which was expected due to the inhibitory action of clavulanic acid against β -lactamases [79]. Regarding CNS isolates, none were found to be resistant to neomycin.

One *S. aureus* and one CPS *Staphylococcus* sp. were found to be resistant to oxacillin, while CNS oxacillin resistant isolates belonged to eight species: *S. chromogenes* (5), *S. caprae* (4), *S. lentus* (3), *S. simulans* (3), *S. epidermidis* (2), *S. auricularis* (1), *S. hominis* (1), and *S. warneri* (1). Other authors previously reported the presence of methicillin resistant coagulase-negative staphylococci (MR-CNS) [80,81].

Regarding tetracycline, most *S. aureus* isolates (32/35) were susceptible, while nonsusceptible isolates belonged to the following CNS species: *S. caprae* (4), *S. haemolyticus* (3), *S. lentus* (2), *S. capitis* (1), *S. hominis* (2), *S. rostri* (1), and *S. warneri* (1). Tetracycline has been widely used in veterinary medicine, and other studies have reported a higher percentage of resistant isolates: 42.8% [82] and 28.9% [45]. On the contrary, our results show a relatively low percentage of non-susceptible isolates (12.4%). In recent

years, there has been an abusive use of more recent antimicrobial molecules, such as cephalosporins and quinolones, that may justify the observed reversal in the patterns of resistance to tetracyclines. To avoid the use of critically important antimicrobials for human medicine, tetracyclines, gentamycin, or cefazolin, a first-generation cephalosporin, may be an option for the control of mastitis in small ruminants. However, there should be a tight control over the development of antimicrobial resistances.

Interestingly, an association between resistance to some antibiotics and animal species was found: penicillin ($\chi^2 = 26.931$, $df = 1$, $p < 0.001$), ampicillin ($\chi^2 = 26.818$, $df = 1$, $p < 0.001$), oxacillin ($\chi^2 = 6.241$, $df = 1$, $p < 0.05$), streptomycin ($\chi^2 = 26.231$, $df = 2$, $p < 0.001$), and lincomycin ($\chi^2 = 20.831$, $df = 2$, $p < 0.001$). For example, isolates from goats (G) were more resistant than sheep (S) isolates to β -lactams, penicillin (G-43%; S-2%), ampicillin (G-39%; S = 0%), and oxacillin (G-22%; S-6%). These differences might be due to different management systems, as suggested by Barrero-Domínguez et al. [45], who reported sheep and goat staphylococcal isolates with the same pulsotypes to exhibit distinct resistance patterns.

2.6. Antimicrobial Resistance Genes

The 44 biofilm producing isolates were selected for the detection of antimicrobial resistance genes involved in the resistance to β -lactams and tetracyclines, namely, *blaZ*, *mecA*, *mecC*, *tetK*, and *tetM*. Table 3.2 shows the antimicrobial genes detected in each isolate, along with its antimicrobial resistance profile.

The *blaZ* gene was detected in 15 staphylococcal isolates belonging to the following species: *S. chromogenes* (7), *S. aureus* (3), *S. warneri* (2), *S. auricularis* (1), *S. caprae* (1), and *S. simulans* (1). Unexpectedly, nine penicillin-susceptible isolates harbor the *blaZ* gene, namely *S. chromogenes* (5), *S. warneri* (2), *S. auricularis* (1), and *S. simulans* (1). El Feghaly et al. [83] also reported penicillin-susceptible isolates harboring the *blaZ* gene and concluded that conventional methods for susceptibility testing such as Kirby-Bauer penicillin disk diffusion may not be reliable. According to CLSI [78], there may be rare isolates of staphylococci containing β -lactamase genes, which may result negative in

phenotypic β -lactamase detection. Additionally, all isolates resistant to penicillin must be considered resistant to all penicillinase-labile penicillins [78].

No staphylococcal isolates harboring the *mecA* or *mecC* genes were detected, although two isolates were found to be non-susceptible to oxacillin and cloxacillin simultaneously, one only to oxacillin and seven to cloxacillin alone. According to the CLSI (2016), oxacillin disk diffusion testing is not reliable for detecting methicillin resistance, at least in *S. aureus*, and cefoxitin should be used for disk diffusion testing. However, Barrero-Domínguez, Luque, Galán-Relaño, Vega-Pla, Huerta, Román, and Astorga [45] also did not detect the *mecA* gene in a cefoxitin-resistant MRSA strain. Thus, other resistance mechanisms cannot be excluded, namely, overproduction of β -lactamase, modified penicillin-binding proteins, distinct SCCmec elements, as well as putative *mecA* mutations [84,85]. Furthermore, Becker et al. [86] have recently reported the presence of a *mecB* gene in a MRSA strain, negative for both *mecA* and *mecC* genes. However, concerning *mecC* detection in our study, we cannot conclude that the isolates with a negative PCR result did not harbor the *mecC* gene, since no positive control strain was available.

An association was found between the resistance to penicillin ($\chi^2 = 11.650$, $df = 1$, $p < 0.05$) and ampicillin ($\chi^2 = 15.828$, $df = 1$, $p < 0.001$) and the presence of the antimicrobial resistance gene *blaZ*. The association between resistance to penicillin and ampicillin and the presence of the antimicrobial resistance gene *blaZ* has been reported before by other authors [87,88]. However, no association was detected between the resistance to oxacillin and cloxacillin and the presence of the antimicrobial resistance gene *mecA* for this subgroup of 44 isolates.

Only one *S. aureus* isolate carrying the *tetK* and another one carrying the *tetM* gene were identified. Both showed resistance to tetracycline. A *S. warneri* tetracycline-resistant isolate did not harbor either *tetK* or *tetM* (Table 3.3). El-Razik, Arafa, Hedia, and Ibrahim [82] found a *S. intermedius* isolate showing intermediate resistance to tetracycline, not harboring *tetK*, *tetL*, *tetM*, and *tetO* genes.

Table 3.2. *nuc*-positive biofilm-producing staphylococcal isolates, phenotypic resistance to selected antimicrobials and their associated antimicrobial resistance genes.

Isolate	Origin	Animal	Bacterial species	P	AMP	OB	AMC	OXA	TET	<i>blaZ</i>	<i>mecA</i>	<i>mecC</i>	<i>tetK</i>	<i>tetM</i>
1D	PT	goat	<i>S. aureus</i>	R	R	R	S	S	S	+	-	-	-	-
13D1	PT	goat	<i>S. warneri</i>	S	S	S	S	S	S	-	-	-	-	-
17D1	PT	goat	<i>S. aureus</i>	R	R	R	S	S	R	+	-	-	-	+
44D	PT	goat	<i>S. aureus</i>	R	R	S	S	S	S	+	-	-	-	-
47D2	PT	goat	<i>S. chromogenes</i>	R	R	R	R	R	S	+	-	-	-	-
50E1	PT	goat	<i>S. aureus</i>	S	S	S	S	S	S	-	-	-	-	-
54E1	PT	goat	<i>S. warneri</i>	S	S	R	S	S	S	+	-	-	-	-
54E2	PT	goat	<i>S. warneri</i>	S	S	R	S	R	S	-	-	-	-	-
55D1	PT	goat	<i>S. capitis</i>	S	S	S	S	S	S	-	-	-	-	-
60D2	PT	goat	<i>S. chromogenes</i>	R	R	S	S	S	S	+	-	-	-	-
65D	PT	goat	<i>S. caprae</i>	R	R	S	S	S	S	+	-	-	-	-
70D	PT	sheep	<i>S. aureus</i>	S	S	S	S	S	S	-	-	-	-	-
71E	PT	sheep	<i>S. aureus</i>	S	S	R	S	S	S	-	-	-	-	-
72D	PT	sheep	<i>S. aureus</i>	S	S	S	S	S	S	-	-	-	-	-
72E	PT	sheep	<i>S. aureus</i>	S	S	S	S	S	S	-	-	-	-	-
83D	PT	sheep	<i>S. aureus</i>	S	S	S	S	S	S	-	-	-	-	-
B51E	BR	goat	<i>S. chromogenes</i>	S	S	S	S	S	S	+	-	-	-	-
B64	BR	goat	<i>S. chromogenes</i>	S	S	S	S	S	S	+	-	-	-	-
B76E	BR	goat	<i>S. chromogenes</i>	S	S	S	S	S	S	+	-	-	-	-
B101	BR	goat	<i>S. warneri</i>	S	S	S	S	S	R	+	-	-	-	-
B159D	BR	goat	<i>S. chromogenes</i>	S	S	S	S	S	S	+	-	-	-	-
B159E	BR	goat	<i>S. chromogenes</i>	S	S	S	S	S	S	+	-	-	-	-
B190D	BR	goat	<i>S. auricularis</i>	R	S	S	S	S	S	-	-	-	-	-
B209D2	BR	goat	<i>S. simulans</i>	S	S	S	S	S	S	-	-	-	-	-
B209E	BR	goat	<i>S. simulans</i>	S	S	S	S	S	S	+	-	-	-	-
B219D3	BR	sheep	<i>S. auricularis</i>	S	S	S	S	S	S	-	-	-	-	-
B219D5	BR	sheep	<i>S. aureus</i>	S	S	S	S	S	S	-	-	-	-	-
B223D	BR	sheep	<i>S. aureus</i>	S	S	S	S	R	S	-	-	-	-	-
B250D	BR	sheep	<i>S. auricularis</i>	S	S	S	S	S	S	+	-	-	-	-
CQ152E1	PT	sheep	<i>S. aureus</i>	S	S	S	S	S	S	-	-	-	-	-
CQ185D1	PT	sheep	<i>S. aureus</i>	S	S	S	S	S	S	-	-	-	-	-
CQ196E	PT	sheep	<i>S. aureus</i>	S	S	S	S	S	S	-	-	-	-	-
CQ201E	PT	sheep	<i>S. aureus</i>	S	S	S	S	S	S	-	-	-	-	-
CQ268D1	PT	sheep	<i>S. aureus</i>	S	S	R	S	S	S	-	-	-	-	-
CQ270E1	PT	sheep	<i>S. aureus</i>	S	S	R	S	S	S	-	-	-	-	-
CQ285D	PT	sheep	<i>S. aureus</i>	S	S	S	S	S	S	-	-	-	-	-
CQ286D	PT	sheep	<i>S. aureus</i>	S	S	S	S	S	S	-	-	-	-	-
CQ290D1	PT	sheep	<i>S. aureus</i>	S	S	R	S	S	S	-	-	-	-	-
CQ290D2	PT	sheep	<i>S. aureus</i>	S	S	S	S	S	S	-	-	-	-	-
CQ296D	PT	sheep	<i>S. aureus</i>	S	S	S	S	S	R	-	-	-	+	-
CQ335E	PT	sheep	<i>S. aureus</i>	S	S	S	S	S	S	-	-	-	-	-
CQ336E2	PT	sheep	<i>S. aureus</i>	S	S	S	S	S	S	-	-	-	-	-
CQ349D	PT	sheep	<i>S. aureus</i>	S	S	S	S	S	S	-	-	-	-	-
CQ354D	PT	sheep	<i>S. aureus</i>	S	S	S	S	S	S	-	-	-	-	-

Penicillin (P), ampicillin (AMP), cloxacillin (OB), amoxicillin + clavulanic acid (AMC), oxacillin (OXA), tetracyclines-tetracycline (TET).

3. Materials and Methods

3.1. Milk Samples Collection and Bacteriological Analyses

A total of 328 small ruminants (258 goats and 70 sheep), belonging to 23 both traditional and industrial dairy farms in Portugal and Brazil, were used to collect 646 half-udder milk samples (508 from goats and 138 from sheep).

Milk samples were aseptically collected in a sterile bottle after the teat was carefully disinfected with 70% ethanol and the first flush was rejected. The samples were kept refrigerated and transported to the laboratory. Ten microliters of each milk sample were plated onto MacConkey agar (Oxoid, Hampshire, UK, CM0007) and onto blood agar (BA) (Oxoid, Hampshire, UK; CM0271 with 5% sheep blood) and incubated at 37 °C for 24 h to 48 h.

Colonies from BA were transferred to brain heart infusion agar (BHI) (Oxoid, Hampshire, UK, CM1136) and again incubated at 37 °C for 24h for primary identification of the *Staphylococcus* genus through morphological and biochemical characteristics, namely, colony morphology, Gram staining, and catalase reaction, according to Markey et al. [89].

Identification of the species level of all isolates was performed by automated compact system VITEK 2 (bioMérieux, Marcy l’Etoile, France) using GP ID cards following the manufacturer’s instructions. Biochemical identification was confirmed by 16S rRNA gene sequencing whenever necessary, using the primers described previously [90].

3.2. Phenotypic Characterisation of Staphylococcal Isolates

3.2.1. Biofilm Detection

Biofilm production was evaluated following the procedures described by Merino et al. [91] with some modifications. In brief, isolates were grown overnight in trypticase soy broth (TSB) at 37 °C. This overnight culture was diluted 1:40 in TSB supplemented with 0.25% glucose, and 200 mL of this cell suspension was used to inoculate microplates. After 24 h of incubation at 37 °C, the microplates were washed three times with 200 µL H₂O, dried in an inverted position, and stained with 100 µL of 0.25% crystal violet for 2 to 3 min at room temperature. Afterwards, the microplates were rinsed again three times with H₂O,

dried, the dye dissolved in 200 μ L ethanol-acetone (80:20), and the absorbance measured at 620 nm. Each assay was performed in triplicate and repeated three times. *Staphylococcus epidermidis* ATCC 12,228 and ATCC 35,984 were used as negative and positive controls, respectively. A blank control was also used.

3.2.2. Antimicrobial Sensitivity Test

The antimicrobial sensitivity test (AST) was performed as described before [77] following the performance standard M02-A11 [92]. Resistance to 16 antimicrobials, belonging to six antimicrobial categories, according to Magiorakos et al. [73], was evaluated: (1) β -lactams-penicillin (P), ampicillin (AMP), cloxacillin (OB), amoxicillin + clavulanic acid (AMC), oxacillin (OXA), cephalexin (CL), cefazolin (KZ), ceftriaxone (CRO), cefoperazone (CFP); (2) aminoglycosides-streptomycin (S), gentamycin (CN), neomycin (N); (3) lincosamides-lincomycin (MY); (4) tetracyclines-tetracycline (TET); (5) fluoroquinolones-ciprofloxacin (CIP); and (6) folate pathway inhibitors-cotrimoxazole (sulfamides + trimethoprim) (STX).

For the interpretation of AST results, the CLSI clinical breakpoints M100-S25 were used [78]. Isolates showing intermediate resistance, now called “susceptible increased exposure” [93], were considered non-susceptible. Moreover, isolates resistant to three or more antimicrobial categories were considered multidrug resistant [73].

3.3. Molecular Characterisation of *Staphylococcal* Isolates

The presence of *coa* and *nuc* genes was investigated in all staphylococcal isolates. *Nuc*-positive biofilm-producing isolates were selected for the detection of the biofilm production genes, *bap*, *icaA*, and *icaD*, and the antimicrobial resistance genes *blaZ*, *mecA*, *tetK*, and *tetM*. The presence of the *mecC* gene was investigated only for *nuc*-positive biofilm-producing isolates, which were simultaneously resistant to oxacillin and cloxacillin and did not harbor the *mecA* gene.

3.3.1. Rapid DNA Extraction

Total DNA was extracted as described previously [94]. Bacterial cultures were grown for 24 h in BHI (Oxoid, Hampshire, UK, CM1136). After this period, they were transferred to microtubes with 200 μL of ultrapure water and centrifuged at 12,000x g for two minutes. Two hundred microliters of sterile saline solution (8.5%) were added to the pellet and centrifuged again at 12,000x g for two minutes. Subsequently, 100 μL of 0.05 M NaOH was added to the pellet and boiled for four minutes, then placed immediately on ice. Afterwards, 600 μL of ultrapure water was added to the microtubes and centrifuged at 4000x g for three minutes. Subsequently, 400 μL were transferred to a new microtube and stored at -20 $^{\circ}\text{C}$ until use.

3.3.2. PCR Amplification

All amplifications were done in a PTC1148C-MJ Mini thermocycler (BioRad, Hercules, CA, USA).

Amplified DNA fragments were stained with 1X Red Gel (Biotium, Fremont, CA, USA) and run on 1.5% (w/v) agarose gels with 0.5X TBE (Tris-borate-EDTA) buffer. Different NZYDNA Ladders (NZYtech, Lisbon, Portugal) were used as molecular weight markers, depending on the size of the PCR products.

Agarose gels were photographed under ultraviolet light using the Gel Doc XR+ Gel Documentation System (BioRad Universal Hood II, Philadelphia, PA, USA).

For all PCR amplifications, 50 μL PCR reactions were prepared with 5 μL of DNA template, 1 U GoTaq DNA polymerase (Promega, Madison, WI, USA), 1X Green Go Taq Flexi buffer (Promega, WI, USA), 1.5 mM MgCl_2 (Promega, WI, USA), 0.2 mM each dNTP (VWR, part of Avantor, Radnor, PA, USA), and 15 pmol each primer (STAB VIDA, Caparica, Portugal). Specific and individual modifications or optimizations were done whenever necessary.

The primers used for amplification of the different genes are listed in Table 3.3.

Table 3.3. Primer sequences for amplification of the different genes.

Gene	Primer	Sequence	Reference
<i>coa</i>	coa-F	5' - ATA GAG ATG CTG GTA CAG G - 3'	[55]
	coa-R	5' - GCT TCC GAT TGT TCG ATG C - 3'	
<i>coa</i>	coa2-F	5' – ATA CTC AAC CGA CGA CAC CG - 3'	[54]
	coa2-R	5' – GAT TTT GGA TGA AGC GGA TT - 3'	
<i>nuc</i>	nuc-F	5' – GCG ATT GAT GGT GAT ACG GTT - 3'	[95]
	nuc-R	5' – AGC CAA GCC TTG ACG AAC TAA AGC - 3'	
<i>bap</i>	bap-F	5' – CCC TAT ATC GAA GGT GTA GAA TTG CAC - 3'	[35]
	bap-R	5' – GCT GTT GAA GTT AAT ACT GTA CCT GC - 3'	
<i>icaA</i>	icaA-F	5' – CCT AAC TAA CGA AAG GTA G - 3'	[96]
	icaA-R	5' – AAG ATA TAG CGA TAA GTG C - 3'	
<i>icaD</i>	icaD-F	5' – AAA CGT AAG AGA GGT GG - 3'	[96]
	icaD-R	5' – GGC AAT ATG ATC AAG ATA C - 3'	
<i>blaZ</i>	blaZ-F	5' – AAG AGA TTT GCC TAT GCT TC - 3'	[97]
	blaZ-R	5' – GCT TGA CCA CTT TTA TCA GC - 3'	
<i>mecA</i>	mecA-F	5' – AAA ATC GAT GGT AAA GGT TGG C - 3'	[98]
	mecA-R	5' – AGT TCT GCA GTA CCG GAT TTG C - 3'	
<i>mecC</i>	mecC-F	5' – GAA AAA AAG GCT TAG AAC GCC TC – 3'	[99]
	mecC-R	5' – GAA GAT CTT TTC CGT TTT CAG C – 3'	
<i>tetK</i>	tetK-F	5'GTAGCGACAATAGGTAATAGT3'	[59]
	tetK-R	5' GTAGTGACAATAAACCTCCTA 3'	
<i>tetM</i>	tetM-F	5'AGTGGAGCGATTACAGAA3'	[59]
	tetM-R	5'CATATGTCCTGGCGTGTCTA3'	

For the detection of the *coa* gene, different primer sequences were used. *Staphylococcus aureus* ATCC 25923 was used as positive control. The first pair of primers, *coa*-F and *coa*-R, amplified a 676 bp fragment [55]. The amplification program was as follows: 3 min at 95 °C, and 35 cycles of 30 s at 94 °C, 30 s at 55 °C, 30 s at 72 °C, and finally, 5 min at 72 °C. The second pair of primers, *coa2*-F and *coa2*-R, amplified a fragment of 1517 bp [54]. The amplification program comprised an initial denaturation of 45 s at 94 °C, followed by 29 cycles at 94 °C for 20 s, 55 °C for 1 min, and 72 °C for 90 s, and a final extension step of 2 min at 72 °C.

For the amplification of the *nuc* gene, primers *nuc*-F and *nuc*-R, amplifying a 267 bp DNA fragment, were used [95]. *S. aureus* ATCC 25923 was used as positive control and *S. epidermidis* ATCC 12228 as negative control. The amplification program was the following: 5 min at 94 °C, followed by 37 cycles, consisting of 94 °C for 1 min, 55 °C for 30 s, and 72 °C for 30 s, ending with a final extension step at 72 °C for 7 min.

For detecting the *bap* gene, primers *bap*-F and *bap*-R were used for the amplification of a 971 bp fragment [35]. No positive control strain was available. The amplification program was as follows: 94 °C for 2 min, followed by 35 cycles of 94 °C for 45 s, 56.5 °C for 45 s, and 72 °C for 50 s, and finally, 72 °C for 5 min.

Primers *icaA*-F and *icaA*-R were used for the amplification of a 1315 bp fragment of the *icaA* gene [96]. *S. epidermidis* ATCC 35984 was used as positive control. The following amplification program was used: 92 °C for 5 min, followed by 30 cycles of 92 °C for 45 s, 49 °C for 45 s, and 72 °C for 1 min, and a final extension step of 7 min at 72 °C.

For the *icaD* gene, primers *icaD*-F and *icaD*-R were used to amplify a 381 bp fragment [96]. *S. epidermidis* ATCC 35984 was used as positive control. The same amplification program as for *icaA* was used, except for the extension step within the cycles, which was 72 °C for 30 s.

The presence of the *blaZ* gene was detected using primers *blaZ*-F and *blaZ*-R, which amplified a 517 bp fragment [97]. *Staphylococcus aureus* ATCC 29213 was used as positive control and *S. aureus* ATCC 25923 as negative control [100]. The amplification program was as follows: 94 °C for 4 min, followed by 37 cycles of 94 °C for 1 min, 50.5 °C for 30 s, and 72 °C for 30 s, and finally, 72 °C for 5 min [97].

To detect the *mecA* gene, primers *mecA*-F and *mecA*-R were used to amplify a fragment of 532 bp [98]. *Staphylococcus epidermidis* ATCC 35984 was used as positive control [101] and *S. aureus* ATCC 25923 as negative control [102]. The following amplification program was used: 94 °C for 2 min, followed by 29 cycles of 94 °C for 30 s, 55 °C for 30 s, and 72 °C for 30 s, and a final extension of 5 min at 72 °C.

Primers *mecC*-F and *mecC*-R were used to amplify a 138 bp fragment [99]. No positive control strain was available. The following amplification program was used: 95 °C for 2 min, followed by 30 cycles of 94 °C for 30 s, 50 °C for 30 s, and 72 °C for 30 s, and a final extension of 10 min at 72 °C.

Primers *tetK*-F and *tetK*-R were used to amplify a 360 bp fragment of the *tetK* gene [59]. No positive control strain was available. For the amplification of the *tetM* gene, *tetM*-F and *tetM*-R were used to amplify a fragment of 158 bp [59]. No positive control strain was available. The amplification program for both *tet* genes was: 94 °C for 2 min, followed

by 29 cycles of 94 °C for 30 s, 55 °C for 30 s, and 72 °C for 30 s, with a final step of 5 min at 72 °C.

3.4. Data Analysis

The chi-square test of association was used: to assess the relationship between the presence of the *nuc* gene with *Staphylococcus* species; to investigate if the presence of the *nuc* gene was associated with biofilm production; to check if the resistance to antimicrobials was associated with bacterial species and with the animal species from which these were isolated. For the abovementioned analyses, all 137 isolates were considered.

For the subgroup of 44 *nuc*-positive biofilm-producing isolates, the chi-square test of association was performed to evaluate the putative relationship between phenotypic resistance to antimicrobials and the presence of four resistance genes.

Multiple correspondence analysis (MCA) was used as an exploratory data analysis technique to detect a structure in the relationships between bacterial species and resistance to selected antimicrobials, divided either into two (susceptible and resistant) or three classes (susceptible, intermediate, and resistant), depending on the antimicrobial.

All statistical analyses were performed using the software STATISTICA Version 12 (StatSoft, Inc., Tulsa, OK, USA).

4. Conclusions

Mastitis aetiology showed to be diverse in the two small ruminant species studied. The most abundant species was *S. caprae*, which, however, was only present in goats.

The *nuc* gene was detected in 67 isolates, of which only 35 were *S. aureus*. Most CNS did not harbor this gene; however, it was detected in more than 50% of *S. warneri*, *S. lentus*, *S. auricularis*, and *S. hyicus*. Although many studies still consider the *nuc* gene as the sole character to identify *S. aureus*, our results have clearly demonstrated that this gene is insufficient, because it is present in numerous staphylococcal isolates other than *S. aureus*.

Most staphylococci were biofilm producers. The *bap* gene was only detected in CNS, while *ica* operon genes were mainly detected in *S. aureus* isolates, suggesting that CNS produce biofilm mainly via Bap, and most *S. aureus* form biofilm through PIA. Furthermore, biofilm-producing staphylococcal isolates not harboring the classical biofilm-production genes *bap*, *icaA*, and *icaD* carry the *nuc* gene. Therefore, the role of the Nuc thermonuclease in staphylococci biofilm formation needs to be further investigated.

Antimicrobial resistance seems to be a growing concern in the treatment of sheep and goat mastitis, with only a low number of isolates (18%) not showing any antimicrobial resistances. Furthermore, CNS were generally more resistant to antimicrobials than CPS. Additionally, an association between animal species and resistance to some antimicrobials was found, suggesting different managing systems for the two species.

All staphylococcal isolates were susceptible to cefazolin and gentamycin. Furthermore, all *S. aureus* isolates were shown to be susceptible to amoxicillin + clavulanic acid and most (32/35) to tetracycline. The use of these antimicrobials to control mastitis may be encouraged to avoid the use of others critically important for human medicine that are currently being used, such as third generation cephalosporins and quinolones. Nevertheless, antimicrobial susceptibility tests cannot be neglected, as the development of resistant strains is always a problem.

Regarding antimicrobial resistance genes, nine penicillin-susceptible isolates exhibited the *blaZ* gene, highlighting the poor reliability of conventional methods for susceptibility testing. Moreover, no staphylococcal isolates harboring the *mecA* or *mecC* genes were detected among those found to be non-susceptible to oxacillin. Hence, other methicillin resistance mechanisms need to be explored.

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Chapter 4

4. The use of propolis for mastitis control

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The use of propolis for mastitis control

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Abstract

Propolis is a resinous mass produced by honeybees for the protection of the honeycomb. Propolis has become very popular in Europe due to its antibacterial activity. Recently propolis activity against bacterial biofilms was reported. Mastitis control greatly depends on the use of antimicrobials. Antimicrobial resistance and bacterial ability to produce biofilm increase microbial survival and contribute to pathogens' persistence in the farm. Furthermore, the transfer of resistance genes from mastitis causing pathogens to bacteria belonging to the human natural microbiota fully justifies the search for alternative products with antimicrobial activity. The aim of this study was to assess propolis components accountable for bactericidal and antibiofilm activities against *Staphylococcus* spp. isolated from the milk of sheep and goats with mastitis. Ten propolis batches (seven from Brazil and three from Portugal) were collected in different regions and were used to produce 30% propolis ethanol extracts (PEE). Total phenolics, flavonoids, anthocyanins and condensed tannins contents were assessed. Thirty-five *Staphylococcus aureus* and 104 coagulase-negative staphylococci (CNS) were analysed for *in vitro* susceptibility to PEE and minimum bactericidal concentration (MBC) was performed with a 96-pins microplate replicator. These PEE were also assessed for biofilm formation inhibition and biofilm disruption on 44 biofilm producing *Staphylococcus* isolates. To identify the propolis components, which are probably associated with antimicrobial and antibiofilm activities,

statistical analyses were performed. Total phenolics content varied from 67.6 to 365.4 mg GAE/g extract, flavonoids content from 54.8 to 141.2 mg QE/g extract, anthocyanins content between not detected and 47.6 mg/g extract, and condensed tannins content between 36.9 and 395.6 mg ECC/g extract. All 139 staphylococci analysed (100%) showed to be susceptible to all PEEs, except Brown4, with concentrations varying between 0.026 and 13.37 mg/mL. Concerning antibiofilm activity, nine PEE inhibited biofilm formation in most of the 44 biofilm-forming isolates. The mean inhibition percentage for each PEE, varied between 33.5 and 80.2%. Regarding biofilm disruption, all ten PEEs partially or totally destroyed the biofilm produced by all 44 staphylococci isolates. The mean PEE activity on biofilm disruption varied between 28.4 and 79.5%. According to these results, propolis deserves to be considered for the control of mastitis.

Keywords: antibiofilm, antimicrobial, mastitis, propolis

1. Introduction

Propolis is a resinous mass produced by honeybees *Apis mellifera* for the protection of the honeycomb. The word *propolis* derives from the Greek *pro* (at the entrance to) and *polis* (community) and refers to a substance for the defense of the hive. Propolis is made of materials collected by worker bees from the leaf buds of numerous plant species and substances actively secreted by plants, or exuded from plant wounds, enriched with bee salivary and enzymatic secretions (Castaldo and Capasso 2002).

Plant secondary metabolites can be divided into three groups: (i) flavonoids and other phenolic and polyphenolic compounds, (ii) terpenoids and (iii) nitrogen-containing alkaloids and sulphur-containing compounds (Crozier et al., 2007). They seem to have a key role in protecting plants from herbivores and microbial infection, among other functions. Secondary metabolites are used for dyes, fibres, glues, oils, waxes, flavouring agents, drugs and perfumes, and they are viewed as potential sources of new natural drugs, antibiotics, insecticides and herbicides (Croteau et al., 2000).

Propolis is rich in flavonoids and other phenolic compounds and may also contain terpenoids (Huang et al., 2014). It has been used around the world in the preparation of medicines to treat different pathologies and more recently became very popular in Europe due to its antibacterial activity (Wojtyczka et al., 2013; Santana et al., 2012; Lu et al., 2005). Recently propolis activity against bacterial biofilms was reported (De Marco et al., 2017; Veloz et al., 2015; Wojtyczka et al., 2013; Doganli, 2016).

Mastitis in small ruminants is responsible for decreased milk yield (Gelasakis et al., 2016; Oravcová et al., 2018), and changed milk composition, which affects cheese-making aptitude and quality of the products (Rovai et al., 2015a; Rovai et al. 2015b ; Raynal-Ljutovac et al., 2007; Paschino et al., 2018). Mastitis control is based on hygienic management of animals, but also greatly depends on the use of antimicrobials. However, some researchers report high rates of antimicrobial resistance (AMR) in pathogens isolated from ewes and goats with subclinical mastitis (Onni et al., 2011; Šiugždaitė et al., 2016; Viridis et al. 2010). Furthermore, the transfer of resistance genes from mastitis causing pathogens to bacteria belonging to the human natural microbiota (Woolhouse et al. 2015) fully justifies the search for alternative products with antimicrobial activity.

Brackman and Coenye (2015) estimated that biofilms are associated with 80% of microbial infections. Biofilm major components are an exopolysaccharide matrix (slime), proteins and environmental DNA (eDNA) along with the bacterial cells (Buttner, Dietrich, and Rohde 2015). Regarding mastitis pathology, bacterial ability to produce biofilm increases microbial survival and contribute to pathogens' persistence in the farm (Gomes et al., 2016). Although some studies showed that *S. aureus* isolated from cows with persistent and non-persistent intramammary infection did not differ in biofilm-forming ability *in vitro* (Pereyra et al., 2016), other reports state that *S. aureus* strains persisting in the bovine mammary gland through the dry period produced significantly more biofilm *in vitro* than strains that do not persist after calving (Veh et al., 2015). Moreover a strong biofilm forming *S. aureus* isolated from bovine mastitis produced significantly more acute mastitic lesions in mammary glands of mice inoculated than a weak biofilm-forming *S.*

aureus strain (Gogoi-Tiwari et al., 2017). In sheep, Vasileiou et al., (2018) reported 80.4% of all cases of staphylococcal subclinical mastitis due to slime producing strains.

The need to control biofilm associated with mammary infection seems to be of major importance. As revised by Melchior and co-workers (2006) several researchers have shown that bacteria growing in a biofilm can become 10–1 000 times more resistant to antimicrobials than the same strain planktonic growing bacteria. Likewise, Costerton (1999) refers to biofilm-forming bacteria as resisting to host defence mechanisms and surviving in the presence of disinfectants and/or antibiotics at concentrations 1000 to 1500 times higher than concentrations that kill planktonic cells of the same species.

In previous studies we showed that propolis ethanol extracts may have a strong bactericidal activity against *Staphylococcus aureus* and coagulase-negative staphylococci (CNS) isolated from sheep and goats with mastitis (Queiroga et al., 2018). We also showed propolis ethanol extracts (PEE) inhibitory action on biofilm formation and PEE ability to eliminate established biofilms (Laranjo et al., 2018). A key aspect to keep in mind, considering mastitis treatment, is that the disruption of biofilm must be associated with bacterial inhibition, since the disassemble of biofilm would be responsible for the release of living bacteria that would colonize additional body sites (Buttner et al., 2015).

The aim of this study was to assess propolis components accountable for bactericidal and antibiofilm activities against *Staphylococcus* spp. isolated from the milk of sheep and goats with mastitis.

2. Methods

2.1. Propolis Collection and Origin

Seven batches of raw propolis (one Green, two Red and four Brown) were collected in apiaries of four Brazilian (BR) States with different climates and vegetation (Table 4.1, Figure 4.1A).

Table 4.1. Propolis collection and origin information

Propolis	Country	Location	Latitude	Longitude	Production	Vegetation
Green	BR	Minas Gerais SE	-20,2752	-45,2535	propolis honey	<i>Baccharis dracunculifolia</i> <i>Eucalyptus</i> sp.
Red1	BR	Alagoas NE	-9,4237	-35,5342	propolis	<i>Schinus terebinthifolius</i> <i>Rhizophora mangle</i> <i>Dalbergia ecastophyllum</i>
Red2	BR	Alagoas NE	-9,4237	-35,5342	propolis	<i>Schinus terebinthifolius</i> <i>Rhizophora mangle</i> <i>Dalbergia ecastophyllum</i>
Brown1	BR	Ceará NE	-5.74312	-39,6285	honey	<i>Schinus terebinthifolius</i> <i>Ziziphus joazeiro</i> <i>Mimosa hostilis</i> <i>Macrosiphonia velame</i> <i>Scoparia dulcis</i>
Brown2	BR	Ceará NE	-5.74312	-39,6285	honey	<i>Schinus terebinthifolius</i> <i>Ziziphus joazeiro</i> <i>Mimosa hostilis</i> <i>Macrosiphonia velame</i> <i>Scoparia dulcis</i>
Brown3	BR	Minas Gerais SE	-21,0137	-46,7439	propolis honey	<i>Eucalyptus</i> sp. <i>Copaifera langsdorffii</i> <i>Pinus pinea</i> <i>Vernonia polysphaera</i> <i>Baccharis dracunculifolia</i>
Brown4	BR	Pernambuco NE	-9,2189	-40,4530	honey	<i>Schinus terebinthifolius</i> <i>Schinopsis brasiliensis</i> <i>Anadenanthera macrocarpa</i> <i>Spondias tuberosa</i> <i>Prosopis juliflora</i> <i>Tamarindus indica</i>
Brown5	PT	Alentejo S	38,5774	-7,8614	honey	<i>Quercus suber</i> <i>Baccharis dracunculifolia</i>
Brown6	PT	Norte N	41,5153	-6,87799	honey	<i>Lavandula stoechas</i> among others
Brown7	PT	Algarve S	37,2859	-8,55594	honey	<i>Cistus ladanifer</i> <i>Arbutus unedo</i> <i>Lavandula stoechas</i> <i>Thymus serpyllum</i> <i>Eucalyptus</i> sp.

The Green propolis and Brown3 were collected in the cities of Formiga and Jacuí-MG in southeastern Brazil (SE), respectively. The Brown1 and Brown2 propolis were obtained in the city of Mombaça-CE in the northeast of Brazil (NE), in two apiaries 7 Km apart. The apiary where Brown2 propolis was collected was near a stream and the apiary where Brown1 propolis was collected had only a water box 600 m away. Brown4 propolis was collected in the city of Petrolina, PE backcountry (NE) and Red1 and Red2 propolis were obtained in the same apiary in Marechal Deodoro-AL (NE), with a two years gap between harvests (Red1 in 2014 and Red2 in 2012) and were kept at -20°C until extract preparation.

Three batches of raw propolis were collected in apiaries from diverse Portugal (PT) regions (NUTS 2), with different climates and vegetation (Table 4.1, Figure 4.1B). Brown5 was collected in Évora city in the Alentejo region (S), Brown6 was collected near the Macedo de Cavaleiros city in the North (N) and Brown7 near Monchique, district of Faro in the South (S).

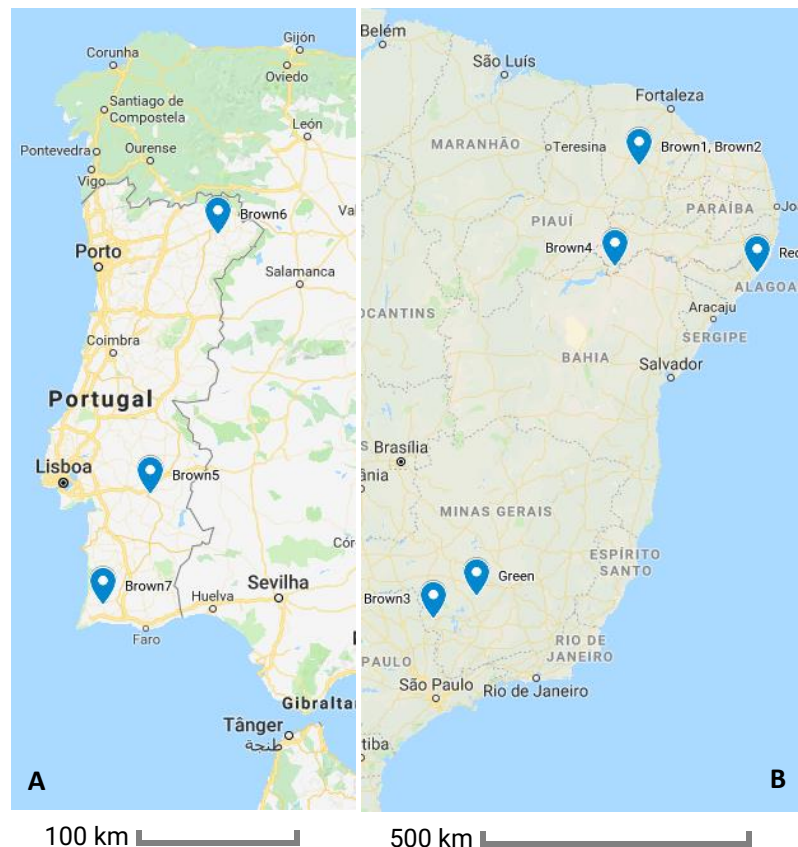


Figure 4.1. Maps showing the collection sites of propolis samples: A-map of Portugal showing three propolis collection sites; B-map of Brazil showing the collection sites of seven propolis samples.

According to Abou-Shaara (2014), bees harvest resins in an area of about 2 km around the hive. Location of collection and vegetation around the apiary, as by beekeepers information, are shown in the Table 4.1.

2.2. Propolis Ethanol Extracts Preparation

Propolis ethanol extracts were prepared according to the official standards for extracts production in Normative Instruction No 3, 19/01/2001, published by the Department of Inspection of Animal Products of the Ministry of Agriculture, Livestock and Food Supply, Brazil (Brazil, 2001). Cold maceration of 300 g of raw propolis in 700 mL of 70° ethanol was performed, resulting in 30% PEE. The preparations were kept at room temperature, protected from light, for 45 days. After this period, extracts were filtered with a sterile funnel and filter paper and kept refrigerated at 4°C, in amber bottles, until use.

2.3. Propolis Ethanol Extracts Major Chemical Groups

Total phenolic, flavonoids, condensed tannins and anthocyanins contents of PEE were determined by spectrophotometric methods. For total phenolic assessment each PEE was diluted to 1mg/mL solution and the determination was performed by the spectrophotometric method of Folin-Ciocalteu (Slinkard and Singleton 1977) with modifications, using gallic acid as standard phenolic compound. Fifty µL of each ethanolic solution was added to 20 µL of de Folin-Ciocalteu and 870 µL distilled water and stirred for 1 min. Sixty µL of Na₂CO₃ (15%) were added and the mixture stirred for 30 seconds, resulting in a final concentration of 50 µg/mL for each sample.

After two hours rest in the absence of light, 300 µL of each solution were transferred to 96-well microtiter plates and readings were recorded at 760 nm. The analyses were performed in triplicate and total phenolic content was determined by interpolating the absorbance of the samples against a calibration curve constructed with gallic acid standards (5.0 to 30.0 µg/mL) and expressed as milligrams of equivalent acid gallic for gram of extract (mg GAE/g), considering the mean standard error. The equation of gallic acid calibration

curve was $y = 0.054x + 0.192$, with the correlation coefficient $r^2 = 0.995$, where x is the concentration of gallic acid and y is the absorbance at 760 nm.

Total flavonoid content was determined using the method of Vermerris and Nicholson (2006) with modifications. Briefly, 500 μL of 5% methanol aluminium chloride (AlCl_3) were mixed with suitable volumes of samples and the volume was made up to 1,000 μL with distilled water. After 10 minutes, absorbance was measured in UV-Vis ELISA spectrophotometer at 425 nm in 96-well microtiter plates. The analyses were performed in triplicate and total flavonoid content was determined by interpolating the absorbance of the samples against a calibration curve constructed with standard solutions of quercetin (from 2.5 to 30.0 $\mu\text{g}/\text{mL}$) and expressed as equivalent milligrams of quercetin per gram of PEE (mg QE/g), considering mean standard error. The equation of quercetin calibration curve was $y = 0.0625x - 0.0023$, with the correlation coefficient $r^2 = 0.997$, where x is the concentration of quercetin and y is the absorbance at 425nm.

Condensed tannins content determination was performed using colorimetric method based on the reaction of vanillin with tannins in acidic medium (Vermerris and Nicholson, 2006). Briefly 300 μL of a vanillin solution in 70% sulfuric acid (1% w/v, freshly prepared) was added to the samples, diluted in ethanol and incubated at 20°C in a water bath for 15 minutes. The absorbance was measured in 96-well plates on an Elisa UV-Vis spectrophotometer at 500 nm. Analyses were performed in triplicate and the content of condensed tannins (proanthocyanidins) was determined by interpolating the absorbance of the samples against a calibration curve constructed with solutions of the catechin standard at various concentrations (5.0 to 40.0 $\mu\text{g}/\text{mL}$) and expressed as milligram epicatechin content per gram of extract (mg ECC/g), considering the standard error of the mean (SEM). The equation of the catechin calibration curve was: $y = 0.0133x + 0.2241$, with the correlation coefficient $r^2 = 0.989$, where x is the catechin concentration and y is the absorbance at 500 nm.

Determination of the anthocyanin content was performed by the differential pH method (Giusti and Wrolstad, 2001). Anthocyanin pigments undergo reversible structural transformations with a change in pH manifested by strikingly different absorbance spectra.

The pH-differential method is based on this reaction and permits accurate and rapid measurement of the total anthocyanins by differences in spectrophotometer absorbance values.

Dilutions of the samples were prepared in triplicate, one with 0.025M potassium chloride buffer pH 1, and the other with 0.4M sodium acetate buffer pH 4.5. The pH was adjusted with concentrated hydrochloric acid using a pH meter. Dilutions were allowed to equilibrate for 15 minutes and samples were read in a 510 nm and 700 nm in glass cuvettes in a UV-visible spectrophotometer (LAMBDA 45, Perkin Elmer). The absorbances of the dilutions were calculated using the following equation:

$$A = (A_{510\text{nm}} - A_{700\text{nm}}) \text{ pH}1.0 - (A_{510\text{nm}} - A_{700\text{nm}})$$

Monomeric anthocyanins concentration of the original sample was calculated by the following formula:

$$\text{Monomeric anthocyanins (mg/L)} = (A \times \text{WM} \times \text{FD} \times 1000) / (\epsilon \times 1)$$

Where WM is the molecular weight, FD is the dilution factor and ϵ is the molar absorptivity of cyanidin-3-glycoside. (MW = 449g, ϵ = 26,900).

2.4. Propolis Ethanol Extracts Chemical Profile

The ultra-high-pressure liquid chromatography along with quadrupole time of flight mass spectrometry (UPLC-QTOF MS^E) experiments were performed to identify some individual compounds from PEE. The UPLC-Photo Diode Array (PDA) phenolic profile of PEE was recorded at 290 nm and the compounds were tentatively identified by UPLC-QTOF-MS/MS as flavonoids (flavonol/flavone, isoflavone, flavanone and chalcones), non-flavonoids phenolics and triterpenes, based on their characteristic UV-vis spectra peaks and mass detection as well as the accurate mass measurement of the precursor and product ions.

Chromatographic analyses were carried out as follows. One hundred mg of each propolis sample were solubilized in 0,5 mL of HPLC grade methanol and 0.5 mL of MilliQ

water pH 2.0 (adjusted with HCl). This solution was eluted in a Strata SPE-C18 cartridge (San Diego, CA, USA) previously activated. After washing with MilliQ water, 2.0 mL of methanol were used three times to elute the compounds of interest and evaporated. Five mg of each extract was solubilized in the mobile phase, filtered through a 0.45 μm Millipore membrane.

The XEVO-G2XSQTOF mass spectrometer (Waters, USA) was connected to the Acquity UPLC system (Waters, USA) via an electrospray ionization interface (ESI). The chromatographic separation of compounds was performed on the ACQUITY UPLC with a conditioned autosampler at 4 °C using a Waters Acquity UPLC BEH C18 (2.1 mm \times 50 mm, 1.7 μm) (Waters, USA).

The mobile phase consisting of water with 0.1% formic acid (Sigma, USA) in water (solvent A) and acetonitrile (Sigma, USA) 0.1% formic acid (solvent B) was pumped at a flow rate of 0.4 mL min⁻¹.

The gradient elution program was as follows: 0-5 min, 5-10% B; 5-9 min, 10-95% B. The injection volume was 5-10 μL . MS analysis was performed on the Xevo G2 QTOF, a quadrupole time-of-flight tandem mass spectrometer coupled with an electrospray ionization source in negative ion mode. The scan range was from 50 to 1200 m/z for data acquisition.

In addition, MS^E experiments were carried which allows both precursor and product ion data to be acquired in one injection. Source conditions as follows: capillary voltage, 3.0 kV; sample cone, source temperature, 120 °C; desolvation temperature 250 °C; cone gas flow rate 50 Lh⁻¹; desolvation gas (N₂) flow rate 800 Lh⁻¹. All analyses were performed using the lockspray, which ensured accuracy and reproducibility.

Leucine-enkephalin (5 ng·mL⁻¹) was used as a standard or reference compound to calibrate mass spectrometers during analysis. All the acquisition and analysis of data were controlled using Waters MassLynx v 4.1 software.

2.5. Bacterial Isolates

Milk samples were aseptically collected from different mammary glands of sheep and goats, belonging to different flocks, with clinical and subclinical mastitis. Clinical mastitis was recognized based on udder and/or milk changes and subclinical mastitis was assessed according to milk somatic cell discharge using California mastitis test (CMT), which results were recorded as negative, “traces” (T), 1+, 2+ and 3 +. Clinical mastitis (CM) was considered the highest grade of mammary inflammation.

Milk samples were immediately refrigerated until processed, within no more than 12 hours. Bacteriological analyses were undertaken according to the National Mastitis Council methodology (2004) and isolates were identified to the species level using API-Staph (Biomérieux) or Vitek 2 Compac (Biomérieux).

A total of 139 staphylococci field isolates, 35 *Staphylococcus aureus*, 104 coagulase-negative staphylococci (CNS) and seven reference strains: five *S. aureus* (ATCC 25923, ATCC 29213, COL, FRI 472, and FRI 913) and two *S. epidermidis* (ATCC 12228, and ATCC 35984) were used to assess antimicrobial activity of PEE.

For PEE antibiofilm activity assessment, 44 biofilm producing *Staphylococcus* field isolates (26 *S. aureus*, seven *S. chromogenes*, four *S. warneri*, three *S. auricularis*, two *S. simulans*, one *S. caprae*, one *S. capitis*), and one biofilm-producing reference *S. epidermidis* strain (ATCC 35984) were included in this study. Biofilm production was evaluated according to Merino et al. (2009) with some modifications, as previously described (Laranjo et al., 2018).

2.6. Antimicrobial and Antibiofilm Assessment

In vitro antimicrobial activity of propolis ethanol extracts was performed according to the CLSI protocol M07-A9 (2012), as described by Queiroga and co-workers (2018). Minimum bactericidal concentration (MBC) was determined with a 96-pin microplate replicator (Boekel Scientific) which inoculates approximately 10 µl of each dilution onto a 150 mm diameter Petri dish with Mueller-Hinton Agar (Queiroga et al., 2018).

To investigate the *in vitro* activity of PEE against biofilms produced by staphylococci isolates, the inhibitory action on biofilm formation and the PEE ability to eliminate established biofilms were evaluated in terms of % of affected isolates and mean % of inhibition and disruption, respectively. The inhibitory effect on biofilm formation was assessed by growing isolates' suspensions with half minimum bactericidal concentration (1/2 MBC) from each PEE, as previously described (Laranjo et al., 2018). To evaluate the PEE ability to eliminate established biofilms, the same isolates were grown to produce biofilms, which were, then, exposed to the action of the corresponding 1/2 MBC of PEE (Laranjo et al., 2018).

2.7. Data Analysis

These analyses were performed in order to tentatively answer the following questions: (1) Does the ability of a *Staphylococcus* isolate to produce biofilm affect mammary inflammation? (2) Is the ability of a *Staphylococcus* isolate to produce biofilm important for its resistance to PEE? (3) Which PEE has shown the best bactericidal activity, biofilm inhibition and biofilm disruption performances? (4) Which PEE components are associated with their antimicrobial action? (5) Which PEE components are associated with their ability to inhibit or to disrupt biofilm?

Data for PEE major components were submitted to analysis of variance (ANOVA). Significant differences ($P < 0.05$) were determined according to Tukey's Honest Significant Difference (HSD) test. Chi-square test of association was used to assess the association between bacterial species and biofilm production ability and the association between mammary gland inflammatory intensity and biofilm production. An ANOVA was performed to evaluate the effect of biofilm production on minimal bactericidal concentration.

In order to assess the best PEE activities, namely minimal bactericidal concentration, percentage of biofilm inhibition and percentage of biofilm disruption, an ANOVA was performed, with significant differences ($P < 0.05$) determined according to Tukey's HSD test.

In addition, Box-whisker plots were performed to represent the distribution of the different PEE activities.

Data for antimicrobial and antibiofilm actions of PEE were analysed by Spearman's correlations for a significance level of $P=0.05$. Data for antimicrobial and antibiofilm activities of each PEE were submitted to an ANOVA to assess PEE individual compounds accountable for those activities. Significant differences ($P<0.05$) were determined according to Tukey's HSD test.

The software Statistica™ v.12.0 software (StatSoft Inc, Tulsa, OK, USA, 1984–2014) was used for all statistical analyses.

3. Results

3.1. Propolis Ethanol Extracts Major Chemical Groups

Table 4.2. Propolis ethanol extracts (PEE) major chemical groups concentration.

PEE	Total phenolics (mg GAE/g)	Flavonoids (mg QE/g)	Anthocyanins (mg/g)	Tannins (mg ECC/g)
Green	283.6 ^c ± 7.5	64.9 ^a ± 1.6	7.1 ^a ± 0.5	287.9 ^e ± 5.7
Red1	232.1 ^b ± 3.7	55.5 ^a ± 1.4	22.6 ^{ab} ± 13.4	256.2 ^d ± 1.1
Red2	312.1 ^c ± 95.3	96.1 ^b ± 0.9	47.6 ^b ± 8.0	216.1 ^c ± 1.0
Brown1	232.9 ^b ± 6.7	109.1 ^d ± 1.7	11.8 ^a ± 2.1	188.6 ^b ± 2.7
Brown2	216.2 ^b ± 4.3	124.5 ^e ± 1.2	11.8 ^a ± 1.7	395.6 ^f ± 7.7
Brown3	305.9 ^c ± 9.2	141.2 ^f ± 3.8	5.8 ^a ± 0.7	247.2 ^d ± 5.0
Brown4	246.6 ^b ± 11.3	103.7 ^{cd} ± 5.0	9.4 ^a ± 0.3	199.2 ^{bc} ± 2.2
Brown5	345.5 ^d ± 1.2	86.3 ^b ± 1.3	ND	48.5 ^a ± 0.1
Brown6	365.4 ^d ± 0.5	92.3 ^{bc} ± 1.5	ND	50.9 ^a ± 0.2
Brown7	67.6 ^a ± 2.8	54.8 ^a ± 1.7	ND	36.9 ^a ± 0.4

SEM - standard error of the mean; ND – not detected; Values are expressed as means ± SEM. Different letters in each column mean significant differences for $P<0.05$.

Chemical composition of the propolis ethanol extracts (PEE) was determined for the 10 PEE. Total phenolics content varied from 67.6 to 365.4 mg GAE/g, flavonoids content ranged from 54.8 to 141.2 mg QE/g, anthocyanins content varied between not detected, in

the Portuguese PEE (Brown5, Brown6, and Brown7), to 47.6 mg/g, and condensed tannins content ranged from 36.9 to 395.6 mg ECC/g (Table 4.2).

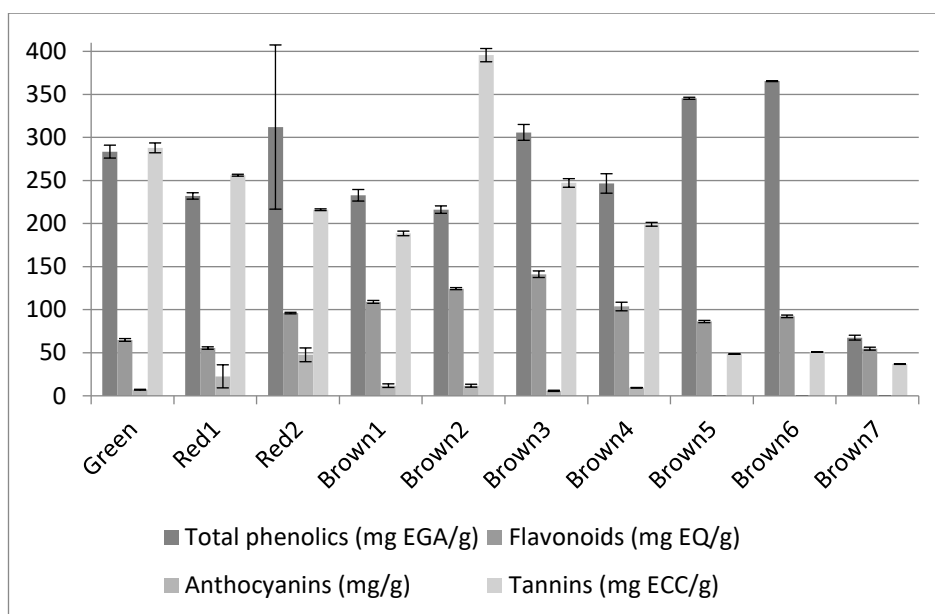


Figure 4.2. Propolis ethanol extracts (PEE) major components.

There are significant differences between the total phenolics, flavonoids, anthocyanins, and condensed tannins contents of the studied PEE ($P < 0.001$). A positive correlation was found between anthocyanins and tannins ($P < 0.05$). Moreover, significant differences in the content of flavonoids and anthocyanins were found for distinct propolis colour. Red propolis PEE have a significantly higher content in anthocyanins compared to green and brown propolis PEE ($P < 0.05$) (Figure 4.2).

3.2. Propolis Ethanol Extracts Chemical Profile

The chemical profile of the 10 PEE was assessed by UPLC-QTOF-MS/MS as exemplified in Figure 4.3 for Green PEE. The peaks not cited are from unidentified compounds. The identification of individual compounds in the different PEE allowed their grouping into six (I-VI) groups as shown in Table 4.3: I-Green; II-Red1 and Red2; III-Brown1 and Brown2; IV-Brown3 and Brown 4; V-Brown5 and Brown 6; and VI-Brown7.

All individual compounds that were identified are flavonoids (chalcones, flavanones, flavanonols, flavones, flavonols, isodihydroflavones, isoflavans), non-flavonoid phenolics and triterpenes.

Green propolis PEE (group I) has two flavonoids and eight non-flavonoid phenolics (among which seven phenolic acids). Red propolis PEE (group II) has nine flavonoids. Brown propolis PEE are divided into four groups: group III (Brown1 and Brown2) PEE has 25 flavonoids; group IV (Brown3 and Brown4) PEE has one flavonoid and four triterpenes; group V (Brown5 and Brown6) PEE has 12 flavonoids and four non-flavonoids phenolics (among which one phenolic acid); and group VI (Brown7) has six flavonoids.

The most widespread individual compounds across the PEE are naringenin (Red1, Red2, Brown1 and Brown2), kaempferol methyl ether and quercetin dimethyl ether (Brown1, Brown2, Brown5 and Brown6), all flavonoids, which were detected in four out of 10 PEE, followed by pinobanksin, chrysin and acacetin, found only in the three Portuguese brown propolis. All other individual compounds are found in two PEE, with the exception all Green PEE compounds, which are exclusive.

3.3. *Staphylococcus* Species and Biofilm Production

Regarding biofilm production ability, according to the Chi-square test of association, an association was found between bacterial species and biofilm production ability ($\chi^2 = 60.671$, $df = 13$, $P < 0.001$) (Table 4.4).

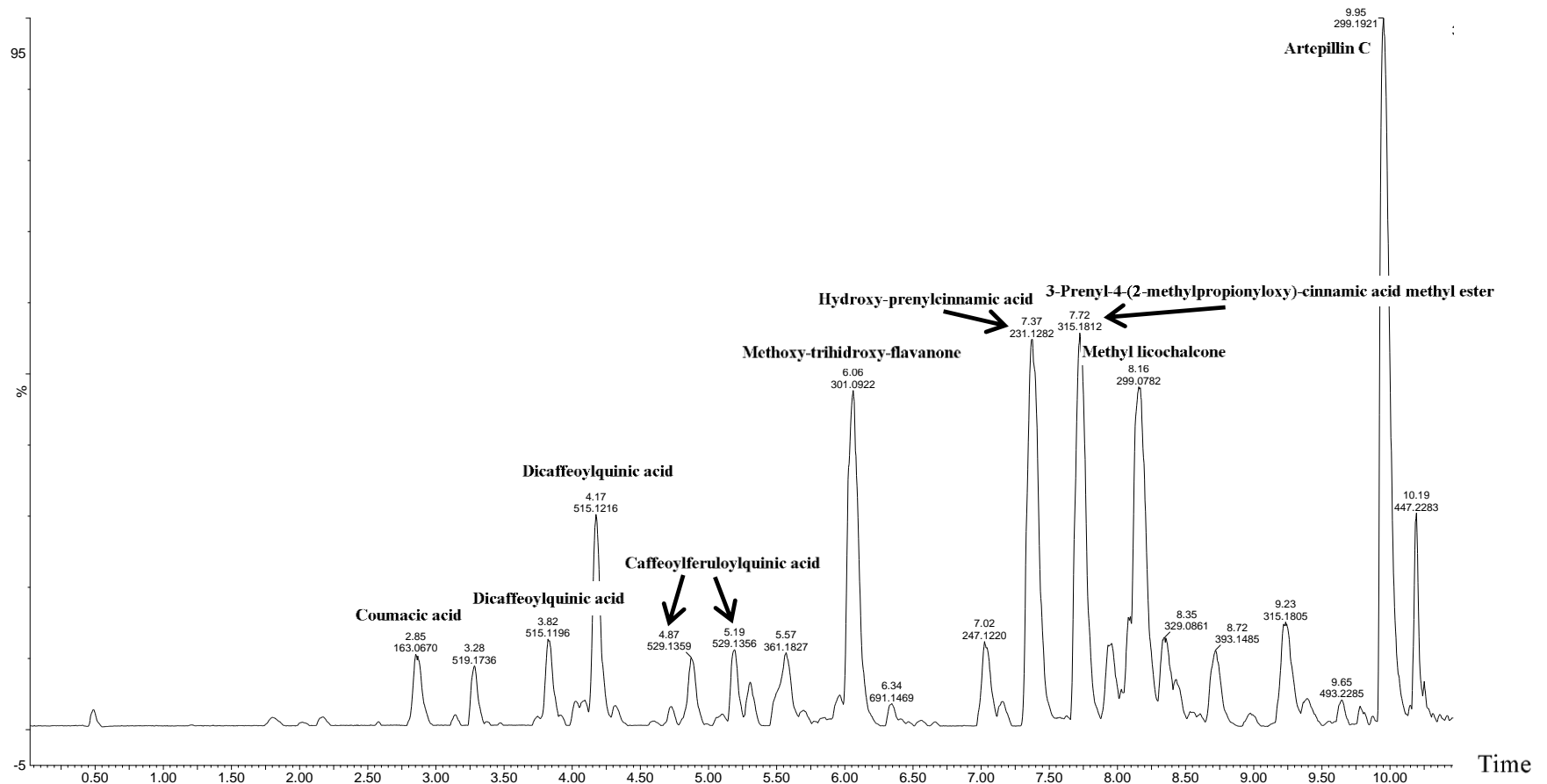


Figure 4.3. UPLC-QTOF-MS/MS profile of Green PEE.

Table 4.3. Identification of some propolis individual compounds

λ_{\max} (nm)	[M-H]- (m/z)	[M-H]- (m/z) calculated	Compound	Green	Red1	Red2	Brown1	Brown2	Brown3	Brown4	Brown5	Brown6	Brown7
308	163.0419	163.0400	Coumaric acid	x									
326	515.1196	515.1195	Dicaffeoylquinic acid (1)	x									
325	515.1227	515.1195	Dicaffeoylquinic acid (2)	x									
325	529.1359	529.1352	Caffeoylferuloylquinic acid (1)	x									
328	529.1356	529.1352	Caffeoylferuloylquinic acid (2)	x									
290	301.0771	301.0717	Methoxy-trihidroxy-flavanone	x									
314	231.1026	231.1026	Hydroxy-prenylcinnamic acid	x									
312	315.1601	315.1601	3-Prenyl-4-(2-methylpropionyloxy)- cinnamic acid methyl ester	x									
364	299.0782	299.0924	Methyl licochalcone	x									
313	299.1658	299.1652	Hydroxy-diprenylcinnamic acid (artepillin C)	x									
274, 314	255.0662	255.0661	Liquiritigenin		x	x							
283	283.0692	283.0611	2'-Hydroxyformononetin		x	x							
284	285.0863	285.0768	Pinobanksin methyl ether		x	x							
372	255.0627	255.0640	Isoliquiritigenin		x	x							
297	267.0792	267.0662	Formononetin/Isoformononetin		x	x							
280	271.0950	271.0611	Vestitol		x	x							
277, 339	283.0793	283.0611	Biochanin A		x	x							
280	271.0943	271.0611	Naringenin *		x	x	x	x					
279	285.1091	285.0768	Vestitone		x	x							
283	285.0757	285.0768	Trimethoxy flavanone				x	x					
373	301.0356	301.0354	Quercetin *				x	x					

λ_{max} (nm)	[M-H]- (m/z)	[M-H]- (m/z) calculated	Compound	Green	Red1	Red2	Brown1	Brown2	Brown3	Brown4	Brown5	Brown6	Brown7
246	315.0500	315.0510	Quercetin methyl ether				x	x					
287	301.0342	301.0717	Trihydroxy-methoxy-flavanonol				x	x					
356	315.0500	315.0510	3-O-Methyl-quercetin				x	x					
356	345.0602	345.0616	Myricetin dimethyl-ether				x	x					
364	285.0405	285.0404	Herbacetin				x	x					
343	299.0541	299.0561	Kaempferol methyl ether (1)				x	x					
361	315.0504	315.0510	Isorhamnetin *				x	x					
346	299.0545	299.0561	Kaempferol methyl ether (2)				x	x			x	x	
287	315.0500	315.0874	Aromadendrin dimethyl ether				x	x					
345	329.0654	329.0667	Quercetin dimethyl ether (1)				x	x					
361	329.0657	329.0667	Quercetin dimethyl ether (2)				x	x					
369	285.0742	285.0404	Hydroxy-methoxy-chalcone				x	x					
296	301.0700	301.0717	Trihydroxy-methoxy-flavanone				x	x					
275	269.0800	269.0819	Hydroxy-methoxy-flavanone				x	x					
333	313.0703	313.0718	Kaempferol dimethyl ether (1)				x	x					
358	329.0642	329.0667	Quercetin dimethyl ether				x	x			x	x	
341	343.0805	343.0823	Quercetin trimethyl ether				x	x					
287	285.0741	285.0768	7-O-methyl naringenin (sakuranetin) *				x	x					
339	283.0605	283.0612	Dihydroxy methoxy flavone				x	x					
346	313.0703	313.0718	Kaempferol dimethyl ether (2)				x	x					
364	269.0814	269.0819	Dihydroxy methoxy chalcone				x	x					
286	299.0914	299.0925	Naringenin dimethyl ether				x	x					
ND	339.1237	339.1238	Trihydroxy-phenyl-flavonone						x	x			

λ_{max} (nm)	[M-H]- (m/z)	[M-H]- (m/z) calculated	Compound	Green	Red1	Red2	Brown1	Brown2	Brown3	Brown4	Brown5	Brown6	Brown7
ND	767.4587	767.4587	Triterpene hexoside derivative						x	x			
ND	373.2704	373.2748	Steroid derivative						x	x			
ND	471.3481	471.3480	Triterpene acid derivative (1)						x	x			
ND	469.3313	469.3329	Triterpene acid derivative (2)						x	x			
322	179.0623	179.0349	Caffeic acid								x	x	
289	285.0654	285.0768	Pinocembrin-methyl ether								x	x	
357	315.0721	315.0510	Quercetin-methyl ether								x	x	
290	271.0662	271.0611	Pinobanksin								x	x	x
294, 325	247.0379	247.0975	Caffeic acid isoprenyl ester								x	x	
266, 313	253.0756	253.0506	Chrysin								x	x	x
325	283.0845	283.0975	Caffeic acid phenylethyl ester								x	x	
354	269.0668	269.0455	Galangin								x	x	
292	313.0817	313.0717	Pinobanksin- <i>O</i> -acetate								x	x	
326	283.0817	283.0617	Acacetin								x	x	x
325	295.0832	295.0975	Caffeic acid cinnamyl ester								x	x	
292	341.1254	341.1394	Pinobanksin- <i>O</i> -butyrate or isobutyrate								x	x	
290	355.1385	355.1550	Pinobanksin-3- <i>O</i> -pentanoate or-2-methylbutyrate								x	x	
290	403.1329	403.1550	Pinobanksin- <i>O</i> -phenylpropionate								x	x	
339	269.0714	269.0455	Apigenin										x
289	255.0926	255.0662	Pinocembrin										x
345	313.0936	313.0717	Kaempferol-dimethyl-ether (3)										x

Compared with references (Almeida et al., 2017; Carvalho et al., 2011; Dausch et al., 2008; Falcão, Tomás, et al., 2013; Falcão, Vale, et al., 2013; Ferreira et al., 2017).

* Compared with standard samples.

Table 4.4. *Staphylococcus* species and biofilm production ability.

<i>Staphylococcus</i> species	Biofilm production		Total
	positive	negative	
<i>S. aureus</i>	26	9	35
<i>S. warneri</i>	4	3	7
<i>S. caprae</i>	1	23	24
<i>S. simulans</i>	2	10	12
<i>S. auricularis</i>	3	1	4
<i>S. epidermidis</i>	0	14	14
<i>S. capitis</i>	1	3	4
<i>Staphylococcus</i> sp.	0	2	2
<i>S. lentus</i>	0	5	5
<i>S. chromogenes</i>	7	12	19
<i>S. hominis</i>	0	4	4
<i>S. hyicus</i>	0	3	3
<i>S. equorum</i>	0	1	1
<i>S. haemolyticus</i>	0	5	5
Total	44	95	139

Most (74%) *S. aureus* isolates (26/35) have the ability to produce biofilm, while all *S. epidermidis* (14/14), *S. simulans* (12/12), *S. lentus* (5/5), *S. haemolyticus* (5/5), *S. hominis* (4/4), *S. hyicus* (3/3) and *S. equorum* (1/1) are non-producers. *S. caprae* isolates are mostly non-producers (23/24) and 37% *S. chromogenes* isolates (7/19) produce biofilm.

3.4. Biofilm Effect on Mammary Inflammation and on In vitro Susceptibility to PEE

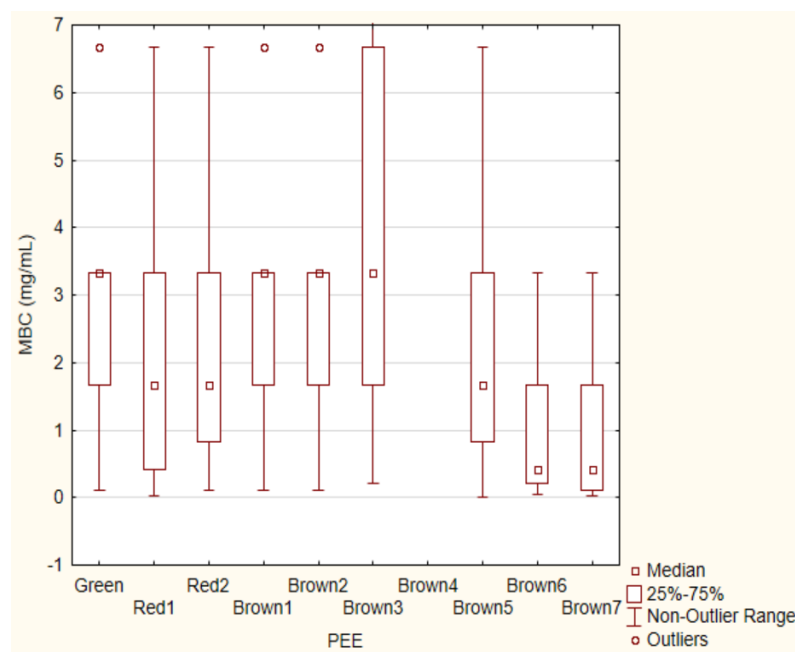
Regarding biofilm production effect on mammary inflammation, for a group of 139 staphylococci field isolates (Table 4.5), there is an association between mammary gland inflammatory intensity, according to CM/CMT, and biofilm production ($\chi^2 = 24.042$, $df = 5$, $P < 0.001$). The most exuberant inflammatory reactions (CM and 3+) as assessed by CMT seem to have been caused by biofilm-producing pathogens. The ability of a *Staphylococcus* isolate to produce biofilm does not seem to influence its susceptibility to PEE ($P > 0.05$).

Table 4.5. Biofilm production effect on mammary inflammation

Biofilm production	Mammary inflammation intensity						Total
	CM	3+	2+	1+	T	neg	
positive	8	13	10	7	3	3	44
negative	4	8	20	39	17	7	95
Total	12	21	30	46	20	10	139

3.5. PEE/PEE Components and Bactericidal Activity

The PEE with the worst bactericidal activity is Brown4, which significantly different from all other PEE ($P < 0.05$). Although not significantly different from all PEE, except Brown4, Brown7 is the PEE with the best bactericidal action. This PEE has six flavonoids: apigenin, pinobanksin, chrysin, pinocembrin, acacetin, kaempferol-dimethyl-ether (Table 4.3). The bactericidal activity of the different PEE is shown on Figure 4.4 with a box-whisker distribution plot.

**Figure 4.4.** Box-whisker plot of PEE antimicrobial activity.

For the 139 staphylococci field isolates studied there is a positive correlation between the content in flavonoids, anthocyanins and condensed tannins and the minimal bactericidal concentration (MBC) ($P < 0.05$). The concentration of these major chemical

groups is directly proportional to the MBC, meaning that the less flavonoids, anthocyanins and condensed tannins, lower the MBC and the more effective the PEE.

Nevertheless, when considering the PEE chemical profiles, the presence of individual compounds showed to positively influence the antibacterial activity, for all identified phenolic compounds (n=61), from which 49 are flavonoids. On the other hand, the presence of triterpenes negatively influences the antimicrobial activity ($P>0.05$).

3.6. PEE/PEE Components and Antibiofilm Activity

3.6.1. Biofilm inhibition

Table 4. 6. Mean biofilm inhibition percentage of different PEE

PEE	Mean biofilm inhibition percentage
Brown2	80.2 ^a
Brown3	77.4 ^a
Brown1	72.9 ^{ab}
Red2	72.2 ^{ab}
Red1	67.8 ^{ab}
Green	65.2 ^{ab}
Brown5	58.6 ^{ab}
Brown7	53.4 ^{bc}
Brown6	33.5 ^c
Brown4	0.0 ^d

Different letters denote significantly different means ($P<0.05$).

Regarding PEE inhibition activity, Brown2 PEE showed to be the best PEE, although not significantly different from Brown3, Brown1, Red2, Red1, Green and Brown5. Brown4 showed to be the worst PEE significantly different from all other PEE (Table 4.6).

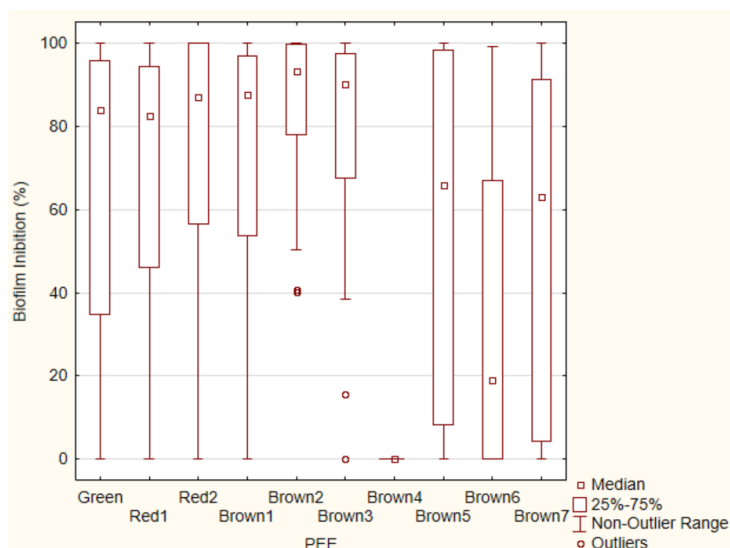


Figure 4.5. Box-whisker plot of PEE biofilm inhibition.

PEE biofilm inhibition percentage is shown on Figure 4.5 with a box-whisker distribution plot. For the 44 biofilm producing *Staphylococcus* field isolates, biofilm mean % of inhibition is positively correlated with the content in major chemical groups flavonoids, anthocyanins and condensed tannins ($P < 0.05$). Regarding the PEE chemical profiles, the presence of different individual compounds showed different influence on biofilm inhibition (Table 4.7).

Considering the 65 individual compounds identified on the studied PEE, 31, all flavonoids, showed to be associated with inhibitory effect on biofilm formation. All triterpenes identified, four non-flavonoid phenolics and 11 flavonoids are associated with a decrease in biofilm inhibition, when present on PEE. No influence on this ability was shown by eight non-flavonoid phenolics and seven flavonoids.

Table 4.7. Effect of the presence of individual compounds on the inhibition of biofilm formation

Increase in inhibition %	Decrease in inhibition %	No influence
Liquiritigenin	Trihydroxy-phenyl-flavanone	Coumaric acid
2'-Hydroxyformononetin	Triterpene hexoside derivative	Dicaffeoylquinic acid (1)
Pinobanksin methyl ether	Steroid derivative	Dicaffeoylquinic acid (2)
Isoliquiritigenin	Triterpene acid derivative (1)	Caffeoylferuloylquinic acid (1)
Formononetin/Isoformononetin	Triterpene acid derivative (2)	Caffeoylferuloylquinic acid (2)
Vestitol	Caffeic acid	Methoxy-trihidroxy-flavanone
Biochanin A	Pinocembrin-methyl ether	Hydroxy-prenylcinnamic acid

Naringenin	Quercetin-methyl ether	3-Prenyl-4-(2-methylpropionyloxy)-cinnamic acid methyl ester
Vestitone	Pinobanksin	Methyl licochalcone
Trimethoxy flavanone	Caffeic acid isoprenyl ester	Hydroxy-diprenylcinnamic acid (artepillin C)
Quercetin	Chrysin	Kaempferol methyl ether (2)
Quercetin methyl ether	Caffeic acid phenylethyl ester	Quercetin dimethyl ether
Trihydroxy-methoxy-flavanonol	Galangin	Apigenin
3-O-Methyl-quercetin	Pinobanksin-O-acetate	Pinocembrin
Myricetin dimethyl-ether	Acacetin	Kaempferol-dimethyl-ether (3)
Herbacetin	Caffeic acid cinnamyl ester	
Kaempferol methyl ether (1)	Pinobanksin-O-butyrate or isobutyrate	
Isorhamnetin	Pinobanksin-3-O-pentanoate or-2-methylbutyrate	
Aromadendrin dimethyl ether	Pinobanksin-O-phenylpropionate	
Quercetin dimethyl ether (1)		
Quercetin dimethyl ether (2)		
Hydroxy-methoxy-chalcone		
Trihydroxy-methoxy-flavanone		
Hydroxy-methoxy-flavanone		
Kaempferol dimethyl ether (1)		
Quercetin trimethyl ether		
7-O-methyl naringenin (sakuranetin)		
Dihydroxy methoxy flavone		
Kaempferol dimethyl ether (2)		
Dihydroxy methoxy chalcone		
Naringenin dimethyl ether		

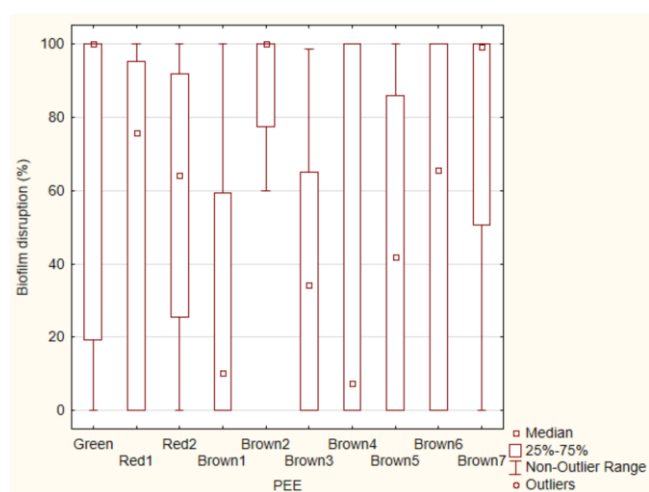
3.6.2. Biofilm Disruption

Concerning PEE disruption activity, Brown2 PEE showed to be the best PEE, although not significantly different from Brown7, Green, Red2, Red1 and Brown6. Brown1 showed to be the worst PEE also not significantly different from Brown3, Brown5, Brown4, Brown6 and Red1 (Table 4.8). PEE biofilm disruption percentage is shown on Figure 4.6 with a box-whisker distribution plot. Biofilm mean % of disruption is positively correlated with the content in condensed tannins and negatively correlated with total phenolics and flavonoids ($P < 0.05$). The presence of different individual compounds showed different influence on biofilm disruption (Table 4.9).

Table 4.8. Mean biofilm disruption percentage of different PEE

PEE	Mean biofilm disruption percentage
Brown2	79.5 ^a
Brown7	72.4 ^{ab}
Green	67.8 ^{abc}
Red2	56.0 ^{abcd}
Red1	55.5 ^{abcde}
Brown6	54.4 ^{abcde}
Brown4	45.4 ^{bcde}
Brown5	44.4 ^{cde}
Brown3	37.6 ^{de}
Brown1	28.4 ^e

Different letters denote significantly different means ($P < 0.05$).

**Figure 4.6.** Box-whisker plot of PEE biofilm disruption.**Table 4.9.** Effect of the presence of individual compounds on the biofilm disruption

Increase in disruption %	Decrease in disruption %	No influence
Coumaric acid	Trihydroxy-phenyl-flavanone	Liquiritigenin
Dicafeoylquinic acid (1)	Triterpene hexoside derivative	2'-Hydroxyformononetin
Dicafeoylquinic acid (2)	Steroid derivative	Pinobanksin methyl ether
Caffeoylferuloylquinic acid (1)	Triterpene acid derivative (1)	Isoliquiritigenin
Caffeoylferuloylquinic acid (2)	Triterpene acid derivative (2)	Formononetin/Isoformononetin
Methoxy-trihydroxy-flavanone		Vestitol
Hydroxy-prenylcinnamic acid		Biochanin A
3-Prenyl-4-(2-methylpropionyloxy)-cinnamic acid methyl ester		Naringenin
Methyl licochalcone		Vestitone
Hydroxy-diprenylcinnamic acid (artepillin C)		Trimethoxy flavanone
Apigenin		Quercetin
Pinocembrin		Quercetin methyl ether
Kaempferol-dimethyl-ether (3)		Trihydroxy-methoxy-flavanonol
		3-O-Methyl-quercetin

		Myricetin dimethyl-ether
		Herbacetin
		Kaempferol methyl ether (1)
		Isorhamnetin
		Kaempferol methyl ether (2)
		Aromadendrin dimethyl ether
		Quercetin dimethyl ether (1)
		Quercetin dimethyl ether (2)
		Hydroxy-methoxy-chalcone
		Trihydroxy-methoxy-flavanone
		Hydroxy-methoxy-flavanone
		Kaempferol dimethyl ether (1)
		Quercetin dimethyl ether
		Quercetin trimethyl ether
		7-O-methyl naringenin (sakuranetin)
		Dihydroxy methoxy flavone
		Kaempferol dimethyl ether (2)
		Dihydroxy methoxy chalcone
		Naringenin dimethyl ether
		Caffeic acid
		Pinocembrin-methyl ether
		Quercetin-methyl ether
		Pinobanksin
		Caffeic acid isoprenyl ester
		Chrysin
		Caffeic acid phenylethyl ester
		Galangin
		Pinobanksin-O-acetate
		Acacetin
		Caffeic acid cinnamyl ester
		Pinobanksin-O-butyrate or isobutyrate
		Pinobanksin-3-O-pentanoate or-2-methylbutyrate
		Pinobanksin-O-phenylpropionate

From all individual compounds identified, eight non-flavonoid phenolics and five flavonoids showed to be associated with biofilm disruption effect. All triterpenes identified and one flavonoid are associated with a decrease in biofilm disruption activity. No influence on this ability was shown by 43 flavonoids and four non-flavonoid phenolics.

4. Discussion

The present study evaluated 10 propolis ethanol extracts (PEE) with the purpose of assessing the influence of their composition on bactericidal, biofilm inhibition and biofilm

disruption activities against *Staphylococcus* species isolated from the milk of sheep and goats with mastitis.

Regarding PEE chemical composition, a positive correlation was found between anthocyanins and condensed tannins ($P < 0.05$). A strong relationship between tannin and anthocyanin was also demonstrated in wine (Kilmister et al., 2014). According to the same authors, the fruit anthocyanin concentration correlates with wine tannin concentration and wine colour (Kilmister et al., 2014). According to the same authors, the fruit anthocyanin concentration correlates with wine tannin concentration and wine colour. Similarly, a correlation was found in the present study between anthocyanin content and propolis colour with significantly higher values for red propolis samples.

Total phenolics, flavonoids and condensed tannins contents for Red1 and Red2 PEE were significantly different ($P < 0.05$). These two propolis batches were collected in the same apiary with a two years gap between harvests. Other authors report total polyphenols and flavonoids variations depending on the month of collection (Isla et al., 2009; Montenegro et al., 2001) and quantitative and qualitative variations in the composition of the polyphenol-rich extracts from propolis collected in the same month along three different years (Veloz et al., 2015). As mentioned by Costa et al., (2013), propolis composition and quality depends on the region vegetation and on other environmental factors.

Individual compounds identified in the studied PEE are mostly flavonoids and other phenolics compounds. Naringenin, kaempferol methyl ether and quercetin dimethyl ether were detected in four out of 10 PEE, pinobanksin, chrysin and acacetin were found in the three Portuguese brown propolis. These three compounds were found only in the Portuguese propolis. Apigenin, acacetin, and kaempferol derivatives were found before in Portuguese propolis sample (Falcão, Vale, et al., 2013).

Several authors have reported that Asian, African, and European PEE predominantly contain phenolics and flavonoids, such as naringenin, galangin, pinocembrin, apigenin, quercetin, cinnamic acid and its esters, kaempferol, chrysin, cinnamyl caffeate, cinnamylidene acetic acid, caffeic acid, p-coumaric acid, aromatic acids and their esters, among others (Huang et al., 2014; AL-Ani et al., 2018).

In this work, Green PEE Individual compounds are mainly non-flavonoid phenolics. The composition of Brazilian Green propolis includes flavonoids and cinnamic acid derivatives (Park, Alencar, and Aguiar 2002). In fact, in green propolis, p-coumaric acid and artepillin C are reported to be typical components of green Brazilian propolis (Machado et al., 2016). Green propolis are very typical and significantly differ from other types of propolis, as also confirmed by the results obtained for our Green PEE.

The typical Brazilian Red propolis composition (Daugusch et al., 2008) includes liquiritigenin, daidzein, dalbergin, isoliquiritigenin, formononetin and biochanin A. This composition is similar to that of our Red1 and Red2 PEE.

According to Zaccaria et al., (2017), flavonoids are the major components of European brown propolis, with flavones (chrysin and apigenin), flavanones (pinocembrin) and flavonols (galangin) being the most common individual compounds (Volpi and Bergonzini 2006), which is in agreement with the composition of our Portuguese brown PEE.

Concerning bacterial species and biofilm production ability, most *S. aureus* isolates produce biofilm, while most coagulase-negative staphylococci are non-biofilm producers. Similarly, only 8% *S. epidermidis* isolates expressed the capacity to produce biofilm, using tissue culture plate (TCP) method, in a study comprising 109 *S. epidermidis* isolates from milk samples collected from 90 sheep belonging to 14 different flocks (Queiroga, Duarte, and Laranjo 2018). Nevertheless, studies on bovine mastitis isolates, using the same methodology for biofilm assessment, report different results, with higher percentage of biofilm producer CNS, namely 37.5% biofilm producing *S. epidermidis* to 18.8% biofilm producing *S. aureus* (Oliveira et al., 2006), 31.3% biofilm producing CNS (Simojoki et al., 2012), and 85.1% biofilm producing CNS (Tremblay et al., 2013).

Considering the effect of biofilm on mammary inflammation, the results showed a significant association between mammary gland inflammatory intensity, according to CM/CMT, and biofilm production. These results are in agreement with other studies in bovine mastitis caused by *S. aureus* (Cucarella et al., 2004; Zuniga et al., 2015) and in the mouse model mammary gland inoculated with *S. aureus* (Gogoi-Tiwari et al., 2017). However, also in bovine mastitis causing CNS, biofilm production was not associated with the intensity of inflammation (Simojoki et al., 2012) and in a study on sheep mastitis *S.*

epidermidis biofilm effects on inflammatory changes, this association was not detected (Queiroga et al., 2018).

According to our results, Brown7 PEE shows the lowest content in flavonoids, anthocyanins and condensed tannins. This is the PEE with best antimicrobial activity, while the one with less antimicrobial action is Brown4 (Queiroga, Andrade, and Laranjo 2018), which exhibited high values for those components in this work. Moura (2000) found greater antimicrobial activity in extracts of propolis collected in NE Brazil, with lower flavonoid contents. Similar results were mentioned for propolis, also from NE Brazil, with low levels of flavonoids and phenolic compounds, which showed highly efficient bacteriostatic and bactericidal activity in comparison to propolis found in the Southeast (SE) of Brazil (Cabral et al., 2012). Nonetheless, Bonvehí and Gutiérrez (2012) reported a strong correlation between the total phenolic and flavonoids content and antimicrobial activity in propolis from Spain. Also Uzel et al., (2005) refer high flavonoids content propolis and significant antimicrobial action on Gram-positive bacteria. Silva et al., (2006) found a strong linear relationship between total phenol contents and the growth inhibition of *S. aureus* in one group of extracts, but in the other group this relationship was weaker. Additionally, no direct correlation between the content in total phenolics and flavonoids and MIC was reported in propolis from Brazil (Silva et al., 2006) and Greece and Cyprus (Kalogeropoulos et al., 2009).

The propolis flavonoid contents has been related with its antimicrobial activity (Cushnie and Lamb 2005; Marcucci, Ferreres, and Garcı 2001; Yong Kun Park and Ikegaki 1998), namely due to inhibition of nucleic acid synthesis, inhibition of cytoplasmic membrane function and inhibition of energy metabolism (Cushnie and Lamb 2005). Nevertheless, other propolis components may as well cause bacterial inhibition, some are also phenolic compounds (Bankova 2009; Bogdanov 2017).

Our results have shown that higher contents in total phenolics and flavonoids (including anthocyanins and condensed tannins) are related to a lower bactericidal activity. Nevertheless, all flavonoids and other phenolics identified in this work are associated with a higher bactericidal activity. In fact, the concentration in total phenolics and flavonoids does not directly reflect all biological activities, antimicrobial activity included, of PEE (Cabral et al., 2012). The methods used for the determination of total phenolics and

flavonoids are not accurate and may under- or overestimate their content depending on the PEE composition in individual compounds (Cabral et al., 2012). This may justify the fact that in the present study, although total flavonoid content is associated with a lower bactericidal activity, the presence of each individual flavonoid (n=49) positively influences antimicrobial activity. Manner et al., (2013) studied the anti-*S. aureus* biofilm activity of 500 natural and synthetic flavonoids and stated that they had different degrees of activity, some highly active although more than 80% (443) were declared inactive. Furthermore, the synergism of propolis components regarding antimicrobial activity, compared to isolated compounds, has been reported before (Król et al., 1993; Vassya Bankova 2009), and could also be partly responsible for this apparent discrepancy.

The antimicrobial activity of propolis is generally attributed to flavonoids and phenolic acids and their esters. In particular, the antimicrobial activity of Iranian propolis may be due to the presence of the most effective flavonoid agents, including pinocembrin (Afrouzan et al., 2018). In Croatian PEE, apigenin, chrysin, pinocembrin, and kaempferol were found to be significantly correlated with antimicrobial activity. Additionally, it has been shown that flavonoids, and particularly kaempferide, and pinocembrin, interfere with bacterial RNA polymerase and cause its inhibition (Gajger et al., 2017). Similarly, Uzel et al., (2005) refer that pinocembrin is among the most potent microbicidal compounds in propolis. In the present work, Brown7 PEE, which showed the best bactericidal activity, is the only one where pinocembrin was detected.

Bankova et al., (1995) suggested that the biological activities of Brazilian propolis could be due to the high levels of phenolic acids, whereas flavonoids might be responsible for the activity of European propolis extracts (Hegazi et al., 2000).

Regarding the antibiofilm role of PEE, the present results have shown a remarkable inhibitory effect on staphylococcal biofilm formation. Other authors have reported an effect on biofilm inhibition from Poland PEE, which were efficient against all 10 *Staphylococcus epidermidis* isolates Wojtyczka et al., (2013). Brown2 is the best PEE for its ability to inhibit the formation of biofilm, while Brown4 is the worst, as reported in a previous study (Laranjo et al, 2018).

On the other hand, regarding the ability of PEE to disrupt the newly formed biofilm, a positive association was found between condensed tannins and biofilm mean percentage

of disruption, and a negative association between total phenolics and flavonoids and biofilm mean % of disruption. Brown2 PEE exhibited the higher content on condensed tannins and in a previous study had shown the best performance in terms of mean % of disruption (Laranjo et al., 2018).

PEE Brown4 showed the lowest performance of all studied PEE: antimicrobial and in biofilm production (Laranjo, Andrade, and Queiroga 2018; M.C. Queiroga, Andrade, and Laranjo 2018). This might be related to the different chemical composition of the Brown4 PEE, composed mainly of triterpenes. According to the ANOVA performed, triterpenes negatively influence bactericidal activity, biofilm inhibition and biofilm disruption for *Staphylococcus* spp. Nevertheless, tannins (condensed and hydrolysable) are capable of inhibiting the formation of biofilms in Gram-negative bacteria, rupturing the bacterial membrane and making it difficult to produce exopolysaccharide matrix (Trentin et al., 2013).

In this study, biofilm mean % of inhibition is positively correlated with the content in flavonoids, anthocyanins and condensed tannins. On the other hand, biofilm mean % of disruption is positively correlated with the content in condensed tannins and negatively correlated with total phenolics and flavonoids. Moreover, all individual compounds which presence is related to biofilm formation inhibition do not influence biofilm disruption and all individual compounds which presence is related to biofilm disruption do not influence biofilm formation.

Inhibition of biofilm formation by propolis extracts has been attributed to flavonoids and total phenolic contents, regarding *S. aureus* biofilm (Doganli 2016) and *Streptococcus mutans* biofilm (Veloz et al., 2015). Doganli (2016) studied the antibiofilm activity of three different propolis extract, both inhibitory and disruption activities and reported that extracts with the higher amount of phenolic contents were the ones that revealed the best biofilm reduction rates, stating that there is a notable consistency between the phenolic content and the biofilm inhibition rate/antibiofilm activity. However, an anti-*S. aureus* biofilm screening comprising 500 flavonoids, including both the inhibitory and disruption abilities, based on viability results, showed that in general, many flavonoids had strain-specific effects, and their biofilm disruption percentages were lower than inhibition percentages (Manner et al., 2013).

Our results strongly suggest that propolis is a promising product for mastitis control which also addresses One Health protection. The treatment of mastitis with antimicrobial alternatives is a priority to reduce the growing trend towards antimicrobial resistance (AMR) and its harmful repercussions on animal health and public health. The use of propolis for mastitis treatment and prevention has been addressed by other researchers. In 1980, Mirolyubov and Barskov described a propolis based intramammary preparation that improved the degree of restoration of milk yield and reduced bacterial counts in mammary secretion. More recently, one other intramammary propolis formulation has been developed, which reduced intramammary infection prevalence from 28.6% to 4.8% after two applications (Bačić et al., 2016a; Bačić et al., 2016b; Mačešić et al., 2016). Wang et al. (2016) studied the effect of Chinese propolis in a cell culture of bovine mammary epithelial cells and described that the treatment of the cells, prior to infection with mastitis pathogens, enhanced expressions of antioxidant genes and decreases in expressions of proinflammatory cytokines compared to non-treated challenged cells. Additionally, synergism between propolis extracts and antimicrobials, such as gentamicin, and those acting on cell wall synthesis, like vancomycin and oxacillin, has been reported (AL-Ani et al., 2018; Runyoro et al., 2017).

5. Conclusions

The ability of a *Staphylococcus* isolate to produce biofilm seems to affect mammary inflammation, as evaluated by CMT/CM. However, the ability of a *Staphylococcus* isolate to produce biofilm does not seem to be important for its resistance to PEE.

Brown7 is the PEE with the best bactericidal activity, while Brown2 is the PEE that showed the best antibiofilm activity, both inhibiting the formation and disrupting the preformed biofilm.

The antibiofilm activity is probably important for a good efficiency in the treatment and prevention of intramammary infections, but it will be absolutely necessary that the PEE also has antimicrobial action; otherwise there is a risk of releasing viable bacteria that could spread the infection.

The presence of all PEE individual phenolics identified in the present study enhanced bactericidal activity, whereas triterpenes negatively influenced the antimicrobial activity.

As to antibiofilm activities, triterpenes also showed to be related with decreased activity, while diverse effects are associated with different flavonoids and other phenolic compounds.

Further studies to determine the concentration of each individual PEE compound are needed to better correlate these with the biological activities of propolis.

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Chapter 5

5. Antimicrobial action of propolis extracts against staphylococci

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Antimicrobial action of propolis extracts against staphylococci

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Abstract

One Health is a worldwide strategy of healthcare for humans, animals, and the environment. Antimicrobial resistance is a serious global problem, recently recognised by the World Health Organization. Prudent, responsible use of antimicrobials should be a concern for both human and veterinary doctors. Concerning animal health and its repercussion in human health, antimicrobials and disinfectants have been widely used for the control of mastitis. This practice induces a selective pressure for resistant bacterial strains, which is deleterious for public health associated with milk consumption. Antimicrobial resistance genes have been detected in pathogens associated to small ruminants' mastitis. These genes may be transferred to the indigenous microbiota of humans. The presence of disinfectant resistance genes has also been reported in staphylococci from both ovine and caprine milk. Propolis is a resinous substance produced by honeybees using different types of plants. It is used to seals holes and cracks in the beehive, contributes to an aseptic internal environment, maintains the hive's internal temperature, and prevents predators from entering the beehive. Propolis has been used as a natural medicine for its antiseptic, antimicrobial, antioxidant, anti-inflammatory, and other immunomodulatory properties. The aim of the present study was to investigate the *in vitro* activity of propolis ethanol extracts (PEE) against staphylococci isolated from mastitic milk of sheep and goats. Antimicrobial susceptibility was assessed for 16 antimicrobials (ampicillin, gentamicin, lincomycin, trimethoprim/sulfamethoxazole, penicillin, streptomycin, tetracycline, cloxacillin, neomycin, cefazolin, cefoperazone, cephalixin, amoxicillin+clavulanic acid, oxacillin, ceftriaxone, and ciprofloxacin) by the disk

diffusion method. Ten PEE from propolis samples collected both in Portugal (three brown), and Brazil (one green, two red, and four brown) were evaluated for their antimicrobial action against 146 staphylococci: 35 *S. aureus*, and 104 coagulase-negative staphylococci isolates, together with seven reference strains. Antimicrobial activity of PEE was assessed on polystyrene flatbottomed microtiter plates in triplicate by the microdilutions methodology for concentrations between 0.0065 and 214 mg/mL. All staphylococci isolates revealed susceptibility to all but one of the studied PEE. Minimal bactericidal concentration for most isolates was 3.34 mg/mL. According to our results, propolis may be an important alternative to the use of antimicrobials, with remarkable advantages for public health.

Keywords: *Staphylococcus*; antimicrobial resistance; One Health

1. Introduction

One Health is a worldwide strategy of healthcare for humans, animals, and the environment, shared by the World Health Organization (WHO), the Food and Agriculture Organization of the United Nations (FAO), and the World Organisation for Animal Health (OIE). Addressing the rising threat of antimicrobial resistance (AMR) requires a holistic and multisectoral approach, because antimicrobials used to treat various infectious diseases in animals may be the same or similar to those used for humans. Resistant bacteria arising in humans, animals or the environment may spread from one to the other, and from one country to another. According to the WHO, antimicrobial resistance is the ability of a microorganism (like bacteria, viruses, and some parasites) to stop an antimicrobial (such as antibiotics, antivirals, and antimalarials) from working against it. As a result, standard treatments become ineffective, infections persist, and may spread to others.

Antimicrobials and disinfectants have been widely used for the control of mastitis in small ruminants, a practice with severe consequences for human health. The massive use of antimicrobials induces a selective pressure for resistant bacterial strains, which is deleterious for public health associated with milk consumption.

Mastitis, the inflammation of the mammary gland, which is mostly caused by bacteria, is highly prevalent in dairy herds [1]. *Staphylococcus* spp. are the main aetiological

agents of mastitis in small ruminants [2, 3]. The prophylaxis and treatment of mastitis is currently mostly dependent on the use of antimicrobials, which exert pressure selection over resistant and multi-resistant strains [4-6]. A recent study showed a noticeable increase in antimicrobial resistance, over a period of ten years, in *Staphylococcus aureus* isolates from goats and sheep milk [7].

These resistant bacteria may worsen the problem of mastitis, but in addition, they may be threatening for human health. Their access to the consumer through milk and dairy products may be responsible for the transfer of resistance genes to the microorganisms of the indigenous microbiota in the gut of humans [8].

The search for control measures and antimicrobial alternatives to decrease intramammary infections are needed to reduce losses in the dairy sector; to increase the motivation and profitability of farmers and, last, but not least, to protect public health.

One possible alternative is propolis, a natural antimicrobial. Propolis is a resinous mass produced by *Apis mellifera* bees by manipulating resins harvested in several plants with their salivary gland secretions, which they use to close the hive to difficult the access of invaders. Its biological properties are related to the chemical composition, which differs in its structure and concentration depending on the region of production, availability of sources for resin harvesting, genetic variability of the queen bee and technique used for production [9].

The biological activity of propolis has been used in traditional medicine since ancient times. Different solvents have already been tested for extracting propolis components and to produce extracts [10, 11]. Propolis has been shown to possess several properties, such as: antioxidant action, anti-inflammatory [12], antiulcerogenic [13], antitumoral [14], antidiabetogenic [15], antiatherogenic and anti-angiogenic [16], immunomodulatory [17], antifungal [18, 19], antiviral [20], namely for human immunodeficiency virus (anti-HIV) [21], anti-bacterial [22, 23] and acting versus some virulence factors, such as antibiofilm [24, 25] and antimotility [26, 27].

The aim of the present study was to evaluate the *in vitro* activity of propolis ethanol extracts (PEE) against staphylococci isolated from mastitic milk of sheep and goats.

2. Materials and methods

2.1 *Staphylococci isolates*

Thirty-five *Staphylococcus aureus* and 104 coagulase-negative staphylococci (CNS) were isolated from small ruminant milk samples. Seven references strains were also used: five *S. aureus* (ATCC 25923, ATCC 29213, COL, FRI 472, and FRI 913) and two *S. epidermidis* (ATCC 12228, and ATCC 35984).

2.2 *Antimicrobial Sensitivity Test (AST) - disk diffusion method*

The AST followed the performance standard M02-A11 CLSI [28] using the Kirby Bauer diffusion method. Bacterial cultures were suspended in sterile saline solution whose turbidity was adjusted at 0.5 of the MacFarland scale (1×10^8 cfu/mL) and confirmed in turbidimeter (DensiChek, bioMérieux). The suspension was inoculated onto the surface of Muller-Hinton agar (MHA) plates (Oxoid, CM0337) and after 5 minutes at room temperature, antimicrobial disks were applied with the aid of a disk dispenser (Oxoid, ST 6090). The plates were incubated at 37 °C for approximately 24 hours and the inhibition zone diameter was measured. The list of 16 antimicrobials studied, used in intramammary antibiotics preparations, are grouped according to their chemical structure and their mode of action in **Table 5.1**.

Table 5.1. Antibacterial agents, their classes, and their corresponding mode of action.

Antimicrobials	Class	Mode of action	
Penicillin	β -LACTAMS	Cell wall inhibitors	
Ampicillin			Semisynthetic penicillins
Cloxacillin			
Amoxicillin + Clavulanic Acid			
Oxacillin			
Cephalexin	Cephalosporins		
Cefazolin	Generation I•		
Ceftriaxone	Generation III•		
Cefoperazone			
Streptomycin	Aminoglycosides		Protein synthesis inhibitors
Gentamycin			
Neomycin			
Lincomycin	Lincosamides		
Tetracycline	Tetracyclines		
Ciprofloxacin	Fluoroquinolones	DNA replication inhibitor	
Cotrimoxazole (Sulfamides + Trimethoprim)	Chemotherapeutic agents	Competitive inhibitor	

2.3 *Propolis Ethanol Extracts (PEE)*

Ten propolis samples, seven from Brazil (Green, Red1, Red2, Brown1, Brown2, Brown3, and Brown4), and three from Portugal (Brown5, Brown6, and Brown7) were collected from apiaries located in different regions.

Propolis ethanol extracts were prepared according to the official standards for extracts production in Normative Instruction Nº 3, 19/01/2001, published by the Department of Inspection of Animal Products of the Ministry of Agriculture, Livestock and Food Supply, Brazil [29]. Cold maceration of 300 g of raw propolis in 700 mL of 70% ethanol was performed, resulting in a 30% PEE. The preparations were kept at room temperature, protected from light, for 45 days. After this period, extracts were filtered with a sterile funnel and filter paper. Extracts were kept under refrigeration at 4 °C, in amber bottles, until use [46].

2.4 *In vitro antimicrobial activity of propolis extracts*

In vitro antimicrobial activity of propolis ethanol extracts was performed according to the CLSI protocol M07-A9 [30]. A total of 150 µL of 30% PEE were added to 150 µL of Mueller-Hinton Broth (MHB) (Oxoid, CM0405), in polystyrene flat-bottomed 96-well microtiter plates, in triplicate, by the microdilutions methodology for concentrations between 0.0065 and 214 mg/mL. Ethanol (70%) was used as a control, to ensure that the resulting antimicrobial action was not due to the ethanol used for extract production.

A suspension with a turbidity equivalent to a 0.5 McFarland standard (1×10^8 cfu/mL) was made for each bacterial culture using a turbidimeter (DensiChek, bioMérieux), and was further diluted to reach a concentration of 5×10^5 cfu/mL after added to extract. Microplates were incubated at 37°C for approximately 24 hours. In order to determine the minimum bactericidal concentration (MBC), a 96-pin microplate replicator (Boekel Scientific) was used to inoculate approximately 10 µL of each dilution onto a 150 mm diameter Petri dish with Mueller-Hinton Agar (MHA) (**Fig. 1**). Analyses were performed in triplicate, and Petri dishes incubated for 24 hours at 37 °C. The MBC is defined as the lowest dilution that inactivated the inoculum visibly.

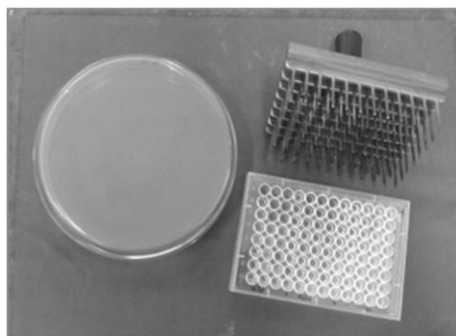


Figure 5.1. Minimum Bactericidal Concentration (MBC) methodology: polystyrene flat-bottomed 96-well microtiter plates, 96-pin microplate replicator; and 150 mm diameter Petri dish.

3. Results

3.1 Antimicrobial susceptibility test of staphylococci

Staphylococci isolates and reference strains have shown distinct resistance rates to the tested antimicrobials. Thirty eight percent of all 146 staphylococci were non-susceptible to streptomycin, 30% to penicillin, 27% to ampicillin and lincomycin, 16% to cloxacillin and oxacillin and 13% to tetracycline. Less than 10% of all staphylococci were found to be resistant to all other antimicrobials (**Fig. 2**). Nevertheless, at least one resistant *Staphylococcus* to each antimicrobial was found.

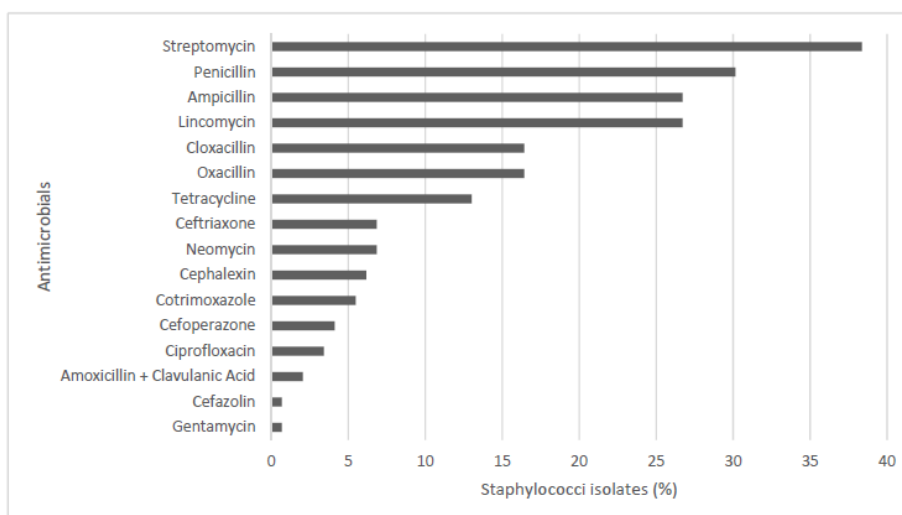


Figure 5.2. Antimicrobial resistance of 146 staphylococci isolates and reference strains.

3.2 Antimicrobial activity of PEE against staphylococci

Bacterial activity is shown in **Fig. 3**. Identifications per column are shown from left to right: 1st, 2nd and 3rd are triplicates of dilutions of Brown1 extract; 4th, 5th and 6th are triplicates of dilutions of the Red2 extract; 7th, 8th and 9th are triplicates of Brown3 dilutions; 10th is ethanol control (70% ethanol dilutions with inoculum); 11th negative control (MHB culture medium only) and 12th positive control (culture medium with inoculum). Different dilutions of each PEE are positioned in different rows.

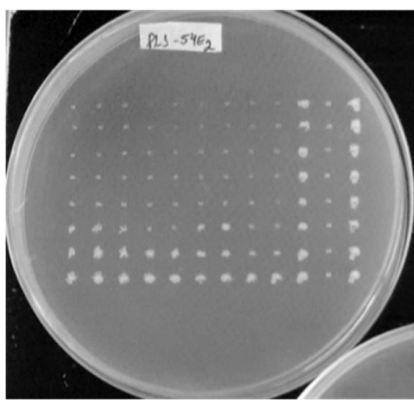
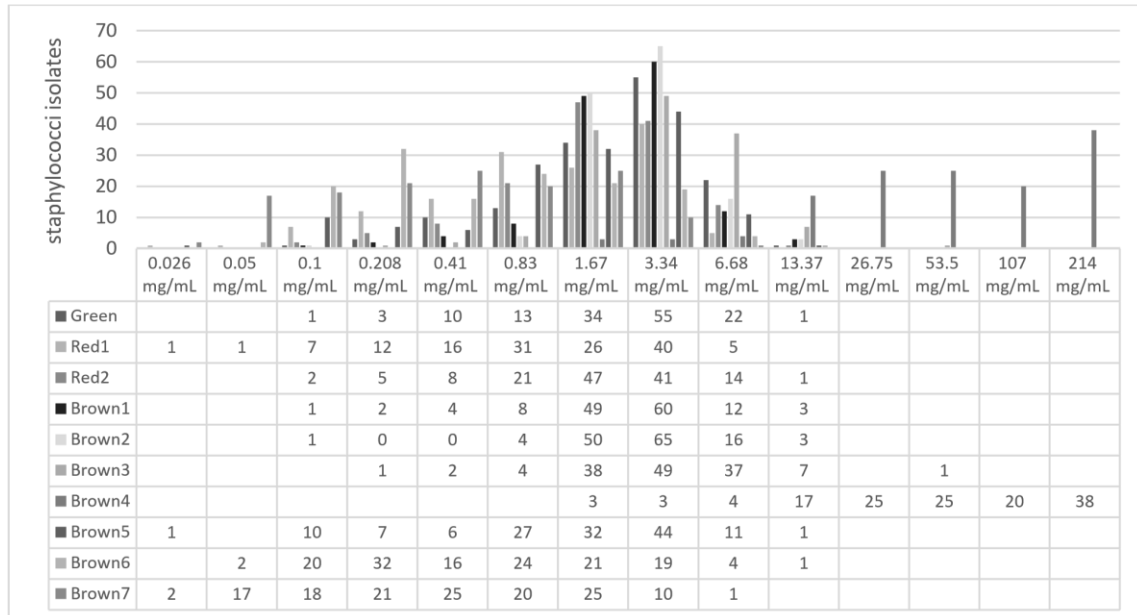


Fig. 5.3 Minimum Bactericidal Concentration (MBC): Petri dish showing the growth of a bacterial isolate in the presence of Brown1, Red2 and Brown3 PEE.

All 139 staphylococci isolates revealed susceptibility to all but one of the studied PEE, in concentrations ranging between 0.026 and 13.37 mg/mL. Furthermore, the inhibitory activity was bactericidal. Most PEE minimal bactericidal concentration for most isolates was

3.34 mg/mL. Brown4 was the only PEE that showed less antimicrobial activity against the studied isolates (**Figure 5.4**).

Figure 5.4. Minimum inhibitory concentration of 10 PEE against 139 staphylococci isolates.



All but one isolate were inhibited with concentrations between 0.208 and 13.37 mg/mL of the nine PEE. The concentration of 13.37 mg/mL, of these nine PEE, is adequate to inhibit *Staphylococcus* isolates. Red1 and Brown7 PEE were bactericidal to all isolates at the concentration of 6.68 mg/mL. Red1, Brown5, 6 and 7 extracts showed bactericidal activity with the lowest concentrations. This last one, Brown7, collected in PT, showed to inhibit more isolates at all concentrations (**Figure 5.5**), showing the best performance. Following best performance was for Brown6, then Red1 followed by Brown5. Brown1 and Brown2 PEE showed quite similar antimicrobial activity. Green PEE showed an inhibitory activity not much different from Brown1, Brown2 and Brown3 PEE.

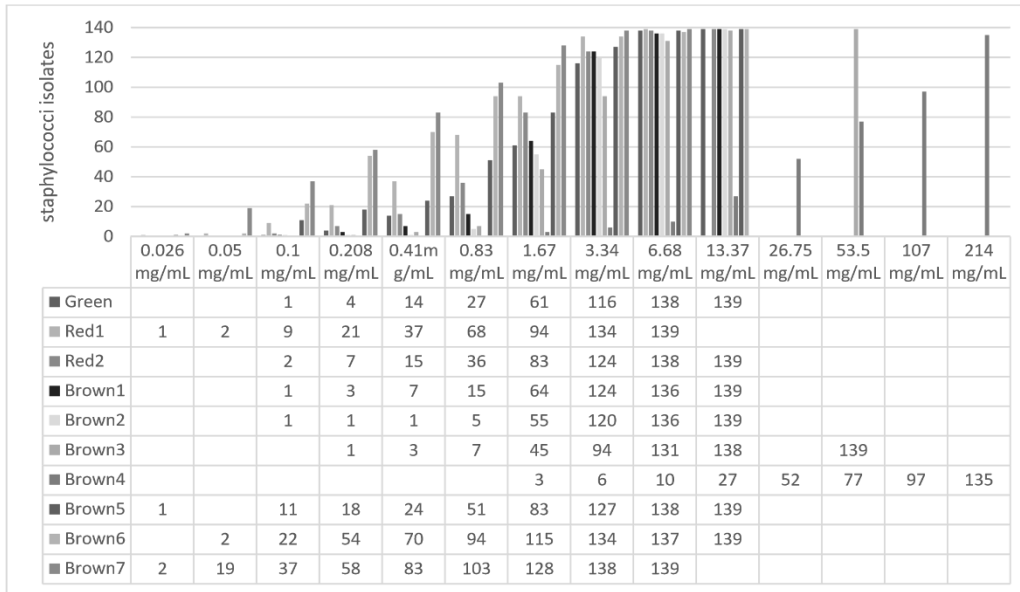


Figure 5.5. Antimicrobial activity of 10 PEE against 139 staphylococci isolates.

Regarding the antimicrobial activity of the PEE against the studied reference strains (Figure 5.6), all strains showed sensitivity to the same nine PEE, in concentrations between 0.1 and 13.37 mg/mL, and 5 *S. aureus* (71.4%) revealed sensitivity to Brown4 extract, between 107 and 214 mg/mL concentrations. Two reference strains (*S. epidermidis* ATCC 12228 and 35984) showed Brown4 resistance, which was the one that showed less antimicrobial activity against all the strains tested. PEE Brown6 and 7 showed antimicrobial activity at lower concentrations.

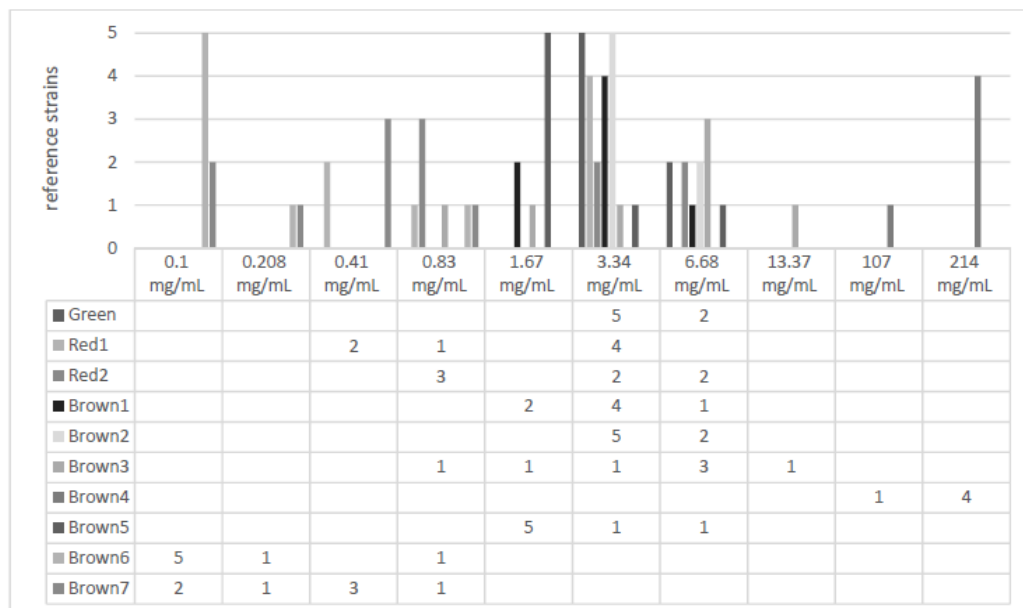


Figure 5.6. Minimum inhibitory concentration of 10 PEE against reference strains.

4. Discussion

In this study, resistance rate was higher to streptomycin (38%), followed by penicillin (30%), ampicillin and lincomycin (27%). Although antimicrobial resistance is not particularly high for all tested antimicrobials, it is noteworthy that resistant isolates were found to all antimicrobials and that 16% isolates showed resistance to cloxacillin and oxacillin, which is mostly relevant, as methicillin resistant staphylococci are a real scourge for public health. Staphylococci isolated from the milk of small ruminant with mastitis with low resistance patterns have been mentioned by other researchers [4, 31]. Nevertheless, some reports indicate *S. aureus* from ewes' subclinical mastitis with a high rate of resistance to ampicillin, cefalotin, cephalexin, gentamicin, streptomycin, erythromycin, oxytetracycline and sulphonamide with a percentage from 50.0 to 100.0 [32]. Additionally, Onni *et al.* [33] reported 38% *S. epidermidis* associated with ovine mastitis (n = 50) resistant to penicillin.

Except for Brown4 PEE, all the other PEE showed inhibitory activity against all staphylococci isolates. Furthermore, all ten PEE are bactericidal, which is a very important feature of propolis. For example, essential oils (EO) of Aromatic and Medicinal Plants (AMP) have been tested for their antimicrobial effect against staphylococci, and they were found to be only bacteriostatic [34].

Due to bacterial resistance to antimicrobials, researchers are exploring the natural components of propolis for their antimicrobial properties [35]. Plant compounds have been shown not to be prone to develop acquired bacterial resistance even after prolonged exposure [36].

The antimicrobial activity of propolis has been addressed before by other authors [22-24, 37-39]. The antibacterial activity of PEE over the bacterial cell wall was confirmed through atomic force microscopy (AFM) images. Furthermore, it is possible to differentiate the degenerative ability of propolis against Gram-negative and Gram-positive bacteria. In fact, PEE were found to be more effective against the Gram-positive *S. aureus* [40].

Propolis extracts can be used alone or in combination with antimicrobials [35]. This mixture represents a synergy that potentiates the antimicrobial power of antibiotics against various microorganisms. Minimal inhibitory concentrations (MIC) of penicillin G, doxycycline, streptomycin, cloxacillin, chloramphenicol, cephradine, ampicillin, and

polymyxin B were established, in the absence of PEE, against *S. aureus*. When PEE was added at concentrations of up to 600 µg/ml to antimicrobial solutions, a high synergistic effect was observed in the anti-bacterial activity of streptomycin and cloxacillin, and a moderate synergistic effect with other antibiotics, but no action was noticed when at the junction with ampicillin [41]. On the contrary, the good performance of a mixture of propolis with ampicillin, was observed by Ismael et al. [42], *in vivo*, when treating sheep and goats affected with *Listeria monocytogenes*. The animals treated with this mixture showed the best result, compared to the mixture of cefotaxime antibiotics, cefotaxime alternative with gentamicin and trimethoprim-sulfadimethoxine combination. The author also noted that treatments with combinations of propolis and antibiotics were more effective than those treatments with only antibiotics. Better synergistic results between PEE and antimicrobials were observed with chloramphenicol, gentamicin, netilmicin, tetracycline and clindamycin, antibiotics (causers interference in protein synthesis of bacteria), than those antibiotics that show other forms of action in the inactivation of the bacterium [43].

Resistant and multi-resistant microorganisms to antibiotics were submitted to analysis with sub-inhibitory concentrations of PEE together with antimicrobials. The results of the synergistic action demonstrated the potential of propolis to improve the action of certain antimicrobials, which had been previously undetected [44]. Scazzocchio *et al.* [45] also evaluated sub-inhibitory concentrations of PEE added to different antimicrobials. These showed divergent activities against *S. aureus*. When sub-inhibitory concentrations were added to ampicillin, gentamicin and streptomycin showed high antimicrobial potency against this strain, when added to chloramphenicol, ceftriaxone and vancomycin showed moderate activity and when added to erythromycin did not show antimicrobial action.

Our results have clearly demonstrated that propolis may be highly efficient as antimicrobial for staphylococci. Its use alone or in combination with antimicrobials may be an important alternative for the control of small ruminant mastitis, with remarkable advantages for public health.

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Chapter 6

6. Antibiofilm activity of propolis extracts

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Antibiofilm activity of propolis extracts

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Abstract

Propolis is a resinous substance produced by honeybees with plant ingredients, which is used to fill gaps in the hive to prevent the entry of undesirable visitors and to provide better thermal insulation. It has been used for centuries to treat different pathologies and more recently became very popular in Europe due to its antibacterial activity. Biofilm is a multi-layered cluster of bacteria embedded in an extracellular polysaccharide matrix, which is known to increase bacterial ability to colonise inert materials and to protect bacteria from body defence mechanisms and antimicrobials, contributing to the establishment of persistent infections. Bacteria of the genus *Staphylococcus* are responsible for a plethora of infections in humans and animals and are the main etiological agents of mastitis in ruminants. The production of biofilm by these bacteria increases their resistance to antimicrobials, greatly hindering the treatment of infections. This study aims to investigate the in vitro activity of propolis ethanol extracts (PEE) against biofilms produced by staphylococci isolated from the milk of small ruminants with mastitis. The inhibitory action on biofilm formation and the PEE ability to eliminate established biofilms were evaluated. Ten PEE were produced from seven samples of propolis harvested in several regions in Brazil (one green, two red and four brown) and three samples collected in different regions in Portugal (all brown). These PEE were assessed for biofilm formation inhibition and biofilm disruption ability on 45 biofilm producing *Staphylococcus* isolates (26 *S. aureus*, seven *S. chromogenes*, four *S. warneri*, three *S. auricularis*, two *S. simulans*, one *S. caprae*, one *S. capitis*, and one *S.*

epidermidis) on polystyrene flat-bottom microtiter plates. All PEE showed antibiofilm activity against some *Staphylococcus* isolates. Generally, PEE are more effective in inhibiting biofilm formation, than in destroying the formed biofilm. According to these results, propolis deserves to be considered for the control of infections caused by biofilm producing staphylococci.

Keywords: *Staphylococcus*; propolis; biofilm; mastitis.

1. Introduction

Propolis is a resinous mass, rich in flavonoids and other phenolic compounds, produced by honeybees *Apis mellifera* for the protection of the honeycomb. Propolis may display different colours due to the biodiversity of plants used for its production. It has earned the attention of many researchers due to its antimicrobial action (1–3), but also due to its synergistic effect in combination with antibiotics (4). Besides antimicrobial activity, propolis has other biological properties, like antiviral, antifungal, antitumor, anti-inflammatory and antioxidant ones, and is used in traditional medicine since Antiquity (5–7). Recently antibiofilm activity of propolis has been described (3,8) and anti-quorum sensing was also stated (9).

Inflammation of the mammary gland, known as mastitis, is a serious problem for milk producers, both bovine and small ruminant, as it is responsible for lowering milk yield and quality (10). *Staphylococcus* spp. are recognized worldwide as a frequent cause of intramammary infections in small ruminants (11–19). Some of these bacteria also produce enterotoxins accountable for public health threats (20–22). Treatment and control of mastitis due to *Staphylococcus* spp. is challenging due to antimicrobial resistance (22–24) and bacterial ability to produce biofilm (26,27). Biofilm hampers mastitis control as it increases microbial survival and contribute to pathogens' persistence in the farm (25). Biofilm production has been considered responsible for antimicrobial resistance and for persistent mastitis (28–33). Its major components are an exopolysaccharide matrix (slime), proteins and environmental DNA (eDNA) along with the bacterial cells (34).

Propolis may replace or reduce the use of antibiotics in veterinary medicine due to its antimicrobial action, but also due to its antibiofilm activity. This study aims at investigating the *in vitro* antibiofilm activity of propolis ethanol extracts (PEE) against

biofilm produced by staphylococci isolated from the milk of small ruminants with mastitis. The study includes the assessment of PEE inhibitory action on biofilm formation and PEE ability to eliminate established biofilms.

2. Materials and methods

2.1 Propolis ethanol extracts

Ten different batches of raw propolis, seven from Brazil (Green, Red1, Red2, Brown1, Brown2, Brown3 and Brown4) and three from Portugal (Brown5, Brown6 and Brown7) were collected in apiaries located in different regions with different climates and vegetation (data not shown). Propolis ethanol extracts were prepared as follows (35). Cold maceration of 300 g of raw propolis in 700 mL of 70% ethanol was performed, resulting in 30% PEE. The preparations were kept at room temperature, protected from light, for 45 days. After this period, extracts were filtered through a sterile funnel and filter paper. Extracts were kept refrigerated at 4°C, in amber bottles, until use.

2.2 Bacterial isolates

Forty-four biofilm producing *Staphylococcus* field isolates (26 *S. aureus*, seven *S. chromogenes*, four *S. warneri*, three *S. auricularis*, two *S. simulans*, one *S. caprae*, one *S. capitis*) collected from different mammary glands of sheep and goats, belonging to different flocks, with clinical and subclinical mastitis, were included in this study. Milk samples were aseptically collected and immediately refrigerated until processed, within no more than 12 hours. Bacteriological analyses were undertaken according to the National Mastitis Council methodology (36) and isolates were identified to the species level using Vitek 2 Compac (Biomérieux).

2.3 Biofilm production

Biofilm production was assessed according to Merino et al. (37) with some modifications. Bacteria were grown overnight in Trypticase Soy Broth (Oxoid, CM0129) with 1% glucose (TSBg) at 37°C. Bacterial cultures were diluted in sterile TSBg until the turbidity reached 0.5 of the MacFarland scale (approximately 1×10^8 CFU/mL), according to the turbidimeter reading (DensiChek, bioMérieux), and again diluted 1:20 to reach 5×10^6 CFU/mL (38). One hundred microliters of these suspensions were added to 100 μ L of

sterile TSBg in flat bottom sterile 96-well polystyrene microtiter plates. A non-biofilm producer *Staphylococcus epidermidis* ATCC 12228 was used as negative control, *S. epidermidis* ATCC 35984 as positive control and non-inoculated TSBg as sterility control. Plates were incubated overnight at 37°C. The wells were gently washed three times with 200 µL of distilled water, dried in an inverted position, and stained with 100 µL 0.25% gentian violet for 3 min at room temperature. Wells were rinsed again, 200 µL of alcohol-acetone (80:20) were added and the optical density was read at 620 nm in an ELISA plate reader (BioRad). Each assay was performed in triplicate and repeated three times. Results were recorded as follows: optical readings (OR) average value of the triplicates, subtracting the average value for the negative control (NC) in the same microplate according to the following formula: $OD = (\sum OR1, OR2, OR3)/3 - (\sum NC1, NC2, NC3)/3$

No production of biofilm (isolate OD \leq negative control OD), weak biofilm formation (negative control OD < isolate OD \leq 2 X negative control OD), moderate biofilm formation (2 X negative control OD < isolate OD \leq 4 X negative control OD) and strong biofilm formation (isolate OD > 4 X negative control OD).

2.4 Effect on biofilm formation

Isolates were grown overnight at 37°C in 3 ml TSBg and 5×10^6 CFU/mL suspensions were prepared. One hundred microliters of these suspensions were added to 100 µL of half minimum bactericidal concentration (1/2 MBC) from each PEE (diluted in Mueller Hinton broth) into each well of 96- well polystyrene flat-bottomed microtiter plates. The bactericidal activity of the extracts towards the different isolates was previously determined (see Chapter “Antimicrobial action of propolis extracts against staphylococci” in this book) and half MBC was used in this assay, so that bacteria wouldn't be inactivated. TSBg along with 0.5 CBM of each extract, previously determined for each isolate, were used as a sterility control. After incubation for 24 h at 37°C, plates were washed and stained as for the biofilm production assay. Absorbance was settled at 620 nm and the biofilm density was determined as described previously. Each assay was performed in triplicate and repeated three times. These results were compared with the results of the biofilm formation assay and the PEE inhibitory action on the biofilm formation was established as a percentage of inhibition.

2.5 Effect on established biofilms

To evaluate the PEE ability to eliminate established biofilms, the same isolates were grown as biofilms using polystyrene flat-bottomed microtiter plates. After 24 h of incubation at 37°C, the wells were washed three times with distilled water and 200 µL of the corresponding half MBC of PEE were added. Non-inoculated MBC of each PEE for each isolate and TSBg were used as sterility controls. After incubation on the regular conditions, microplates were again washed and stained following the described procedure. Absorbance was determined at 620 nm and the formation of biofilm was determined as described previously. Each assay was performed in triplicate and repeated three times. These results were compared with the results of the biofilm formation assay and the PEE activity on the biofilm disruption was established as a percentage.

3. Results

3.1 PEE effect on biofilm formation

Nine PEE showed the ability to inhibit or stop biofilm-formation in 74.4% of the isolates analysed. The mean inhibition for each PEE, varied between 52.6 and 86.1%. Brown1, 2 and 3 Brazilian PEE showed higher activity compared to the Brown5, 6 and 7 Portuguese PEE, but Brown4 Brazilian PEE showed no activity against any of the tested isolates (**Figure 6.1**).

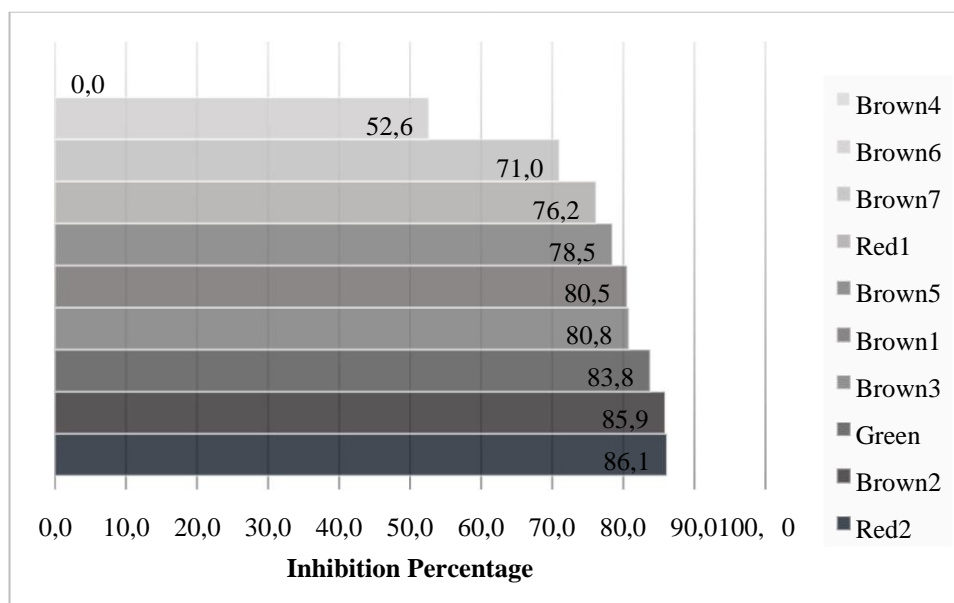


Figure 6.1. Mean inhibition percentage for each propolis ethanol extract.

Twenty-six *S. aureus* isolates were biofilm producers and only Brown2 PEE showed to inhibit biofilm formation of all isolates. The percentage of biofilm inhibition for each *S. aureus* isolate ranged from 54.4 to 88.8%. Biofilm of *S. epidermidis* ATCC 35984, used as a positive control, was susceptible to eight PEE and its percentage of inhibition varied between 62 and 96.3% (Table 6.1).

Table 6.1. PEE effect on biofilm formation: number of isolates, and respective percentage, and mean inhibition percentage by species for each PEE.

Isolates/Species	<i>S. aureus</i>	<i>S. auricularis</i>	<i>S. caprae</i>	<i>S. capitis</i>	<i>S. chromogenes</i>	<i>S. epidermidis</i>	<i>S. simulans</i>	<i>S. warneri</i>	Total N/Mean %
N	26	3	1	1	7	1	2	4	45
Inhibited by PEE Green (N)	20	3	1	0	5	1	2	3	35
Inhibited isolates (%)	76.9	100.0	100.0	0.0	71.4	100.0	100.0	75.0	80.6
% of Inhibition	88.8	73.6	100.0	0.0	85.4	65.1	56.9	76.4	83.8
Inhibited by PEE Red1 (N)	24	3	1	0	5	1	2	4	40
Inhibited isolates (%)	92.3	100.0	100.0	0.0	71.4	100.0	100.0	100.0	91.8
% of Inhibition	85.7	59.3	80.3	0.0	56.8	62.0	85.5	54.0	76.2
Inhibited by PEE Red2 (N)	23	2	1	1	6	1	1	3	38
Inhibited isolates (%)	88.5	66.7	100.0	100.0	85.7	100.0	50.0	75.0	85.7
% of Inhibition	85.8	92.1	81.0	80.3	91.0	95.1	98.5	71.7	86.1
Inhibited by PEE Brown1 (N)	24	3	1	0	7	1	2	3	41
Inhibited isolates (%)	92.3	100.0	100.0	0.0	100.0	100.0	100.0	75.0	93.7
% of Inhibition	82.6	97.1	98.9	0.0	72.9	96.3	68.2	62.8	80.5
Inhibited by PEE Brown2 (N)	26	2	1	0	7	1	2	3	42
Inhibited isolates (%)	100.0	66.7	100.0	0.0	100.0	100.0	100.0	75.0	96.6
% of Inhibition	88.6	86.4	79.9	0.0	85.9	79.0	91.6	62.1	85.9
Inhibited by PEE Brown3 (N)	25	3	1	1	7	1	2	3	43
Inhibited isolates (%)	96.2	100.0	100.0	100.0	100.0	100.0	100.0	75.0	96.0
% of Inhibition	78.5	91.5	99.5	82.9	83.3	69.9	83.8	77.8	80.8
Inhibited by PEE Brown4 (N)	0	0	0	0	0	0	0	0	0
Inhibited isolates (%)	0	0	0	0	0	0	0	0	0.0
% of Inhibition	0	0	0	0	0	0	0	0	0.0
Inhibited by PEE Brown5 (N)	23	1	1	0	7	1	0	1	34
Inhibited isolates (%)	88.5	33.3	100.0	0.0	100.0	100.0	0.0	25.0	88.1
% of Inhibition	84.2	48.0	90.7	0.0	64.5	89.8	0.0	50.5	78.5
Inhibited by PEE Brown6 (N)	16	1	1	0	5	0	2	3	28
Inhibited isolates (%)	61.5	33.3	100.0	0.0	71.4	0.0	100.0	75.0	67.8
% of Inhibition	54.4	85.2	81.1	0.0	47.2	0.0	40.0	40.6	52.6
Inhibited by PEE Brown7 (N)	21	1	1	0	6	1	2	2	34
Inhibited isolates (%)	80.8	33.3	100.0	0.0	85.7	100.0	100.0	50.0	80.7
% of Inhibition	78.4	34.5	61.2	0.0	53.9	63.5	75.9	67.2	71.0

3.2 PEE effect on established biofilms

All ten PEE showed to partially or totally destroy the biofilm produced by 45 staphylococci isolates. The mean PEE activity percentage on biofilm disruption varied between 51.4 and 92.0% (**Figure 6.2**).

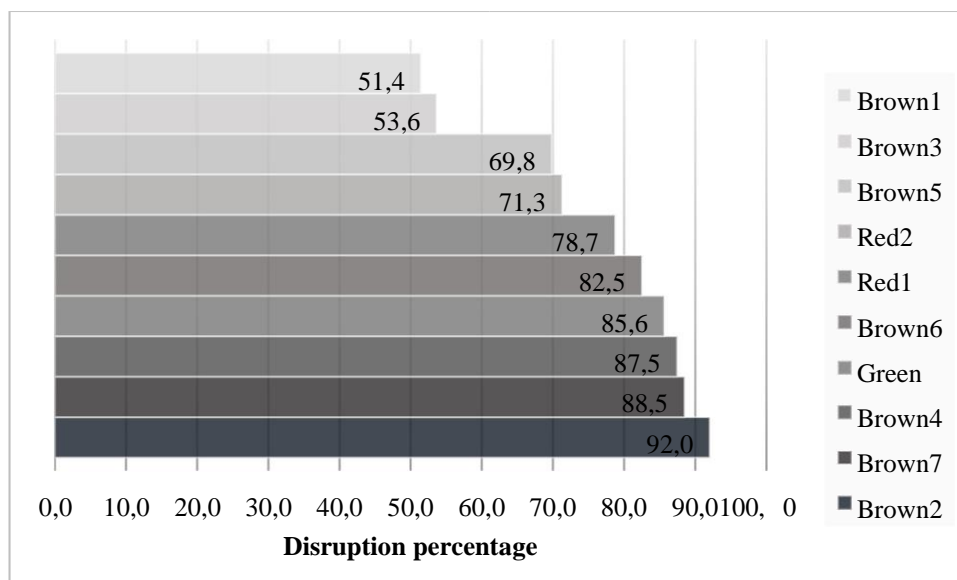


Figure 6.2. Mean activity percentage on biofilm disruption for each propolis ethanol extract.

The percentage of biofilm disruption ranged from 0 to 100% (**Table 6.2**). Propolis Ethanol Extract Brown 2 showed biofilm disruption activity against 88.4% of *S. aureus* isolates but did not affect biofilm from *S. epidermidis* and *S. capitis*.

Generally, PEE are more effective in inhibiting biofilm formation, than in destroying the formed biofilm, with the exception of Green, Brown4, Brown6, and Brown 7. PEE Brown1, Brown2 and Brown3 were able to inhibit more than 40 out of 45 isolates (88.9%). However, these were not the best PEE in disrupting the established biofilm. Brown7, Green and Red were the most effective PEE in destroying biofilm. Brown4, while completely unable to inhibit biofilm formation, was still able to disrupt the established biofilm in more than 50% of the isolates. Antibiofilm activity is summarised in Figure 6.3.

Table 6.2. PEE effect on established biofilms: number of isolates, and respective percentage, and mean activity percentage on biofilm disruption by species for each PEE.

Isolates/Species	<i>S. aureus</i>	<i>S. auricularis</i>	<i>S. caprae</i>	<i>S. capitis</i>	<i>S. chromogenes</i>	<i>S. epidermidis</i>	<i>S. simulans</i>	<i>S. warneri</i>	Total N/Mean %
N	26	3	1	1	7	1	2	4	45
Affected by PEE Green (N)	19	3	1	1	6	1	2	3	36
Affected isolates (%)	73.0	100.0	100.0	100.0	85.7	100.0	100.0	75.0	81.3
% of Disruption	93.4	23.3	58.6	100.0	95.5	100.0	100.0	68.9	85.6
Affected by PEE Red1 (N)	20	1	1	0	5	1	1	3	32
Affected isolates (%)	76.9	33.3	100.0	0.0	71.4	100.0	50.0	75.0	75.1
% of Disruption	70.7	54.9	98.0	0.0	97.1	79.3	100.0	96.3	78.7
Affected by PEE Red2 (N)	19	3	1	1	5	1	2	4	36
Affected isolates (%)	73.0	100.0	100.0	100.0	71.4	100.0	100.0	100.0	81.8
% of Disruption	62.8	74.2	85.6	73.1	66.9	100.0	98.7	90.1	71.3
Affected by PEE Brown1 (N)	12	2	1	0	6	1	2	2	26
Affected isolates (%)	46.1	66.6	100.0	0.0	85.7	100.0	100.0	50.0	65.4
% of Disruption	32.0	86.2	83.6	0.0	65.9	87.2	70.3	36.8	51.4
Affected by PEE Brown2 (N)	23	2	1	0	7	0	2	3	38
Affected isolates (%)	88.4	66.6	100.0	0.0	100.0	0.0	100.0	75.0	89.2
% of Disruption	94.4	52.2	81.3	0.0	91.5	0.0	100.0	100.0	92.0
Affected by PEE Brown3 (N)	16	2	1	1	6	1	2	3	32
Affected isolates (%)	61.5	66.6	100.0	100.0	85.7	100.0	100.0	75.0	73.6
% of Disruption	40.9	81.4	75.9	29.1	71.0	62.4	84.3	45.6	53.6
Affected by PEE Brown4 (N)	17	1	0	0	3	1	1	1	24
Affected isolates (%)	65.3	33.3	0.0	0.0	42.8	100.0	50.0	25.0	60.3
% of Disruption	84.1	100.0	0.0	0.0	100.0	100.0	73.6	95.9	87.5
Affected by PEE Brown5 (N)	14	1	1	0	7	0	2	3	28
Affected isolates (%)	53.8	33.3	100.0	0.0	100.0	0.0	100.0	75.0	71.8
% of Disruption	52.7	43.2	97.7	0.0	98.2	0.0	98.9	64.0	69.8
Affected by PEE Brown6 (N)	14	1	1	0	7	0	2	4	29
Affected isolates (%)	53.8	33.3	100.0	0.0	100.0	0.0	100.0	100.0	75.4
% of Disruption	70.8	41.3	99.8	0.0	99.1	0.0	100.0	91.5	82.5
Affected by PEE Brown7 (N)	20	2	1	1	6	0	2	4	36
Affected isolates (%)	76.9	66.6	100.0	100.0	85.7	0.0	100.0	100.0	82.9
% of Disruption	88.3	69.2	100.0	76.8	92.5	0.0	100.0	87.4	88.5

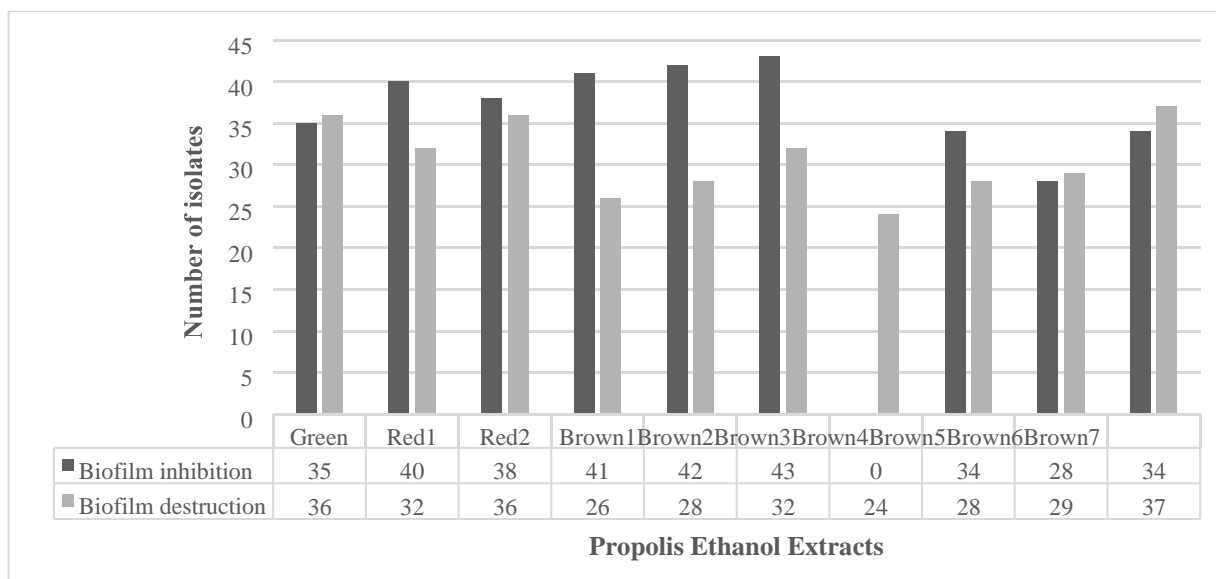


Figure 6.3. PEE effect on biofilm formation and on established biofilms: number of isolates affected by each PEE.

4. Discussion

Nine PEE showed ability to prevent biofilm formation and all the tested PEE revealed biofilm disruption aptitude. It should be noted that the concentration of PEE used in these trials was half the minimum bactericidal concentration for each bacterial isolate. The dosage of PEE to be used in clinical situations should be at least the MBC, therefore twice the amount used here, hence the antibiofilm activity should be better than the one here presented.

The need to control biofilm associated with mammary infection seems to be of major importance. As revised by Melchior *et al.* (30) several researchers have shown that bacteria growing in a biofilm can become 10 to 1000 times more resistant to antimicrobials than planktonic growing bacteria of the same strain. Concerning the pathology of the mammary gland, although some authors refer that the *in vitro* biofilm-forming ability of a given strain was not related to its clinical origin, considering cows with persistent and non-persistent intramammary infection (39), others mention that *S. aureus* strains persisting in the bovine mammary gland through the dry period produced significantly more biofilm *in vitro* than strains that do not persist after calving (33). Furthermore, mice inoculated with a bovine mastitis strong biofilm forming *S. aureus*

isolate produced marked acute mastitis lesions while the damage was significantly less severe in mammary glands of mice infected with a weak biofilm-forming *S. aureus* strain (40). Results from a study on staphylococci causing subclinical mastitis in sheep confirmed the significance of slime producing strains in the aetiology of this affection, with 80.4% of all cases of staphylococcal subclinical mastitis caused by slime producing strains (26).

A key aspect to keep in mind is to ensure that the PEE has antimicrobial activity. Since an action on the disassemble of biofilm without the concomitant bacterial inhibition would be responsible for the release of living bacteria that would colonise additional body parts (34). All ten PEE are bactericidal in appropriate concentrations (see Chapter “Antimicrobial action of propolis extracts against staphylococci” in this book).

Other studies have shown that propolis extracts were able to inhibit *Pseudomonas aeruginosa* biofilm formation (41) and stated an inhibitory effect of propolis extracts on biofilm formation by *Streptococcus mutans* (42) with some propolis components displaying a potent inhibition of glucosyltransferase activity, which is an enzyme that catalyses the formation of biofilm (43). Biofilm formation ability by *Staphylococcus epidermidis* strains in the presence of PEE was significantly inhibited by incubation time and was observed after 12 and 24 hours of incubation (3).

Furthermore, some investigators showed quorum sensing inhibitory activity of distinct propolis samples (9,44). Quorum sensing is the phenomenon through which bacteria, within a biofilm, use signalling molecules, autoinducers, that when accumulate to a threshold concentration activate a transcriptional regulator, which in turn regulates the expression of various genes, including virulence factors and thus is one of the essential factors that regulate bacterial virulence and pathogenicity (45,46). This plays an important role in biofilm development, resistance, and virulence. Therefore, the interruption of QS can be an effective strategy to control disease-causing pathogens.

Biofilm formation is accompanied by significant genetic and subsequent physiological changes in the microorganisms resulting in a loss of sensitivity to virtually all classes of antibiotics (30). As mostly studied in *S. aureus* and to some degree in *S. epidermidis*, quorum sensing is achieved by activating the accessory gene regulator (*agr*) that results in the production of a regulatory mRNA molecule termed RNAIII, which activates multiple toxin genes (47).

Biofilm production ability can greatly hinder conventional antimicrobial therapy suggesting the need of alternative control approaches such as the use of propolis. According to our results some PEE have antibiofilm activity against small ruminants' mastitis causing *Staphylococcus* spp. biofilm and might, therefore, be a promising approach for disease control either as alternative to antibiotics or in combination with antibiotics taking advantage of synergistic effect (48).

Studies to isolate and identify the specific propolis compounds responsible for the bioactivity are needed.

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Chapter 7

7. General discussion and future perspectives

7.1 – General discussion

7.1.1 – *Staphylococcus* identification

With the aim of assessing propolis as an alternative to traditional antimicrobials for the control of small ruminant mastitis, we collected milk samples from 70 sheep and 258 goats with mastitis. Our collection of 137 staphylococci isolates included *S. aureus* and 13 CNS species, 12 identified in goats and seven in sheep milk samples. Six *Staphylococcus* species were isolated from both animal species. *Staphylococcus caprae*, *S. warneri*, *S. capitis*, *S. hominis*, *S. hyicus* and *S. equorum* were found only in goat's milk. *S. caprae* was mostly found in goat's milk, as was reported by other authors (Bergonier and Berthelot, 2003; Peixoto et al., 2010; Gosselin et al., 2018), despite having also been isolated from sheep's milk (Martins et al., 2017). The other species, on the other hand, are commonly found in sheep's milk (Zafalon et al., 2018; Vasileiou et al., 2018). An isolate of the species *S. rostri* was found in sheep's milk in this work. As far as we know, this species had only

been once isolated from the milk of a sheep with mastitis (Persson et al., 2017). No data were found in the literature related to goat's mastitis, *S.rostri* being more commonly found in cow's milk (Jenkins et al., 2019; Wuytack et al., 2020).

The difference in the number of isolates in the different chapters, as in chapters 4, 5 and 6, is due to the fact of some isolates had not been sequenced in the year of publication of the articles. In chapter 3 there is the correct quantity of all isolates analyzed in this study.

Biochemical identification with the automated compact system VITEK 2 (bioMérieux, F) showed excellent to very good results for most isolates and 16S rRNA gene sequencing was only necessary for four isolates. Nevertheless, the presence of *coa* and *nuc* genes was investigated in all staphylococci isolates, as these are genes frequently assessed to differentiate *S. aureus* from CNS. Our isolates were found to be polymorphic regarding the *coa* gene, showing fragments between 400 and 900 bp in length. Likewise, this gene was also amplified from *S. aureus* of small ruminants and humans isolates with variations from 300 to 800 bp (Vimercati et al., 2006; Mahmoudi et al., 2017). Soltan Dallal et al. (2016), found polymorphism between 500 and 1000 bp of *S. aureus* isolated from food samples. The *coa* gene had been reported as polymorphic before and these polymorphisms are known to be strain-specific (Soltan Dallal et al., 2016).

The *nuc* gene was detected in 48.9% of the analysed staphylococci isolates. All 35 *S. aureus* carried the *nuc* gene (100%). However, this gene was also detected in 22.6% of CNS. Although this gene is often used to identify *S.aureus*, this is not a reliable technique according to our results. These findings agree with those of other authors which detected this gene in other species of *Staphylococcus*, both CPS and CNS (Hirotaiki et al., 2011; Silva et al., 2003). Moreover, Leeuwen et al. (2008) did not detect it in MRSA.

The *nuc* gene is an important virulence factor for bacterial survival (Olson et al., 2013), as it defeats the host defences (Berends et al., 2010) and it is an indicator of biofilm dispersion (Mann et al., 2009). In the present study we found an association between *Staphylococcus* species and the presence of the *nuc* gene. This gene was detected in more than 50% of *S. warneri* (4/7), *S. lentus* (3/5), *S. auricularis* (3/4), and *S. hyicus* (3/3) isolates. This feature may eventually affect the pathogenesis of mastitis due to those pathogens.

7.1.2 – Biofilm production and biofilm-associated genes

To detect whether the isolates were capable of forming biofilm, the polystyrene microtiter plates method was used, according to Merino et al. (2009). This is considered one of the most effective phenotypic methods (Stiefel et al., 2016; Salina et al., 2020), showing a 96.7% agreement with molecular methods (Melo et al., 2012). Of the biofilm-forming isolates, 59% were *S aureus* and 41% CNS. Ebrahimi et al. (2014) also found a higher percentage of phenotypic biofilm formation to *S. aureus* than CNS in sheep isolates.

Considering biofilm as a relevant virulence factor for mastitis, our studies disclosed an association between mammary gland inflammatory intensity and biofilm formation. However, no association was found between this feature and bacterial susceptibility to PEE (Chapter 4). Other authors have mentioned *S. aureus* ability to produce biofilm as a virulence factor affecting mastitis pathogenesis (Felipe et al., 2017).

Regarding biofilm associated genes, the *bap* gene was only present in CNS, while *icaA* and *icaD* genes were mainly detected in *S. aureus*. Other studies showed that the *bap* gene is more often detected in CNS species than CPS (Salaberry et al., 2015; Martins et al., 2017). In the present study the isolates carrying the *bap* gene did not harbour the *ica* operon genes. Likewise, Szweda et al. (2012) reported no isolate carrying both the *bap* and *ica* operon genes. However, in bovine mastitis, 56% of CPS harboured *icaA*, *icaD* and *bap* genes together, unlike CNS (Salina et al., 2020).

Some isolates studied, including *S. aureus* and CNS, did not evidence any of the three biofilm-associated genes. The same absence of *bap*, *icaA* and *icaD* genes in biofilm-producing *S. aureus* was reported (Khoramian et al., 2015; Vitale et al., 2019; Torres et al., 2019). The *nuc* gene was detected in 53.4% biofilm-producing isolates, while in only about 35% of the non-producers, although we did not find any association between the presence of this gene and biofilm production. We might wonder about the role of the Nuc thermonuclease in staphylococci biofilm formation. Nevertheless Mann et al. (2009) suggested its role as a promoter of biofilm dispersal. Investigating biofilm formation mechanisms in strains that do not harbour *bap* or *ica* genes is important to have a better understanding of the resources used by bacteria in the production of this virulence factor.

7.1.3 – Antimicrobial susceptibility and resistance genes

The detection of staphylococci susceptibility profile to antimicrobials available for mastitis control was evaluated. Some staphylococci isolates were multidrug resistant. This constitutes a potential risk for consumers (Omshaba et al., 2020). Antimicrobials resistance acquired by staphylococci is a reality, as well as its transfer to human microbiota. In addition, these microorganisms can reach the human population through a variety of routes, including through food of animal origin (Kuile et al., 2016). *Staphylococcus* isolated from bovine milk samples, carrying the *mecA* gene and phenotypic resistant were transmitted to humans (Lee, 2003). *BlaZ* gene was found in *Staphylococcus* isolated from goat cheese (Aragão et al., 2019), as well as *mecA* gene was detected in *Staphylococcus* isolated from Kurd cheeses samples (Hachiya et al., 2017).

Non-susceptibility of the isolates to β -lactam antimicrobials was mostly observed. Other studies describe less efficacy of these antimicrobials over the years (Virdis et al., 2010; França et al., 2012; Santos et al., 2020), highlighting the possibility of resistance acquisition by this genus. The resistance is individual and develops through mutations and rearrangements in the staphylococcal genome or also through the acquisition of resistance determinants. The increased antibiotic pressure, together with genetic variants, contributes to this virulence factor (Vasileiou et al., 2019). Accordingly, *blaZ* was the antimicrobial resistance gene mostly detected in this work. Some of these isolates showed susceptibility to some or all β -lactam antimicrobial analysed, however one must be aware that carrying the *blaZ* gene demands to consider the isolate resistant to all penicillins and semi-synthetic penicillins. Similar results were found by Ferreira et al. (2017). The most reliable way to detect if the isolate produces β -lactamase is through the detection of *blaZ* gene (Pitkälä et al., 2007). In the present study some penicillin-susceptible isolates harboured the *blaZ* gene. Some *Staphylococcus* may present this gene and not show resistance phenotypically (CLSI, 2016). El Feghaly et al. (2012) also stated that commonly used phenotypic sensitivity methods may not be reliable.

The presence of the *mecA* and *mecC* genes was not confirmed in isolates non-susceptible to oxacillin. Although in most studies all *mecA*-positive isolates showed oxacillin resistance (Obaidat et al., 2017), some reports mention oxacillin-resistant isolates not carrying the *mecA* gene Shah et al. (2017). Other resistance mechanisms are possible, as

the presence of the recently described *mecB* gene (Becker et al., 2018) or overproduction of β -lactamase, modified penicillin-binding proteins, distinct SCCmec elements, as well as putative *mecA* mutations (Xu et al., 2008; Paterson et al., 2014).

Curiously, *mecA*-positive *S. aureus* showing susceptibility to oxacillin, which were classified as oxacillin-susceptible *mecA*-positive *Staphylococcus aureus* (OS-MRSA) was mentioned by Pu et al. (2014). Goering et al. (2019), demonstrated that oxacillin susceptibility was associated with mutations in the *mecA* gene and that subinhibitory exposure of the isolate to oxacillin restored its resistance.

Regarding tetracycline resistance, the few *S. aureus* isolates assessed harboured either the *tetK* or the *tetM* gene. However, conclusions cannot be drawn due to the few samples genotypically analysed. Liu et al. (2017), observed correlations between *S. aureus* resistant phenotypes and genotypes for tetracycline. In the present study one CNS isolate phenotypically resistant to this antimicrobial did not carry either *tetK* or *tetM* gene. Other authors reported non-susceptible *S. intermedius* not carrying *tetK*, *tetL*, *tetM*, and *tetO* genes (El-Razik et al., 2017). However, Mama et al. (2019), found these genes in tetracycline-resistant CNS.

Gentamicin and cefazolin inhibited the growth of all tested isolates. Gentamicin is an aminoglycoside, generally used for Gram negative bacteria, however it showed an excellent performance against different species of *Staphylococcus* in this study. Other authors reported very good results with staphylococci isolates from buffalo, goat and sheep mastitis (Santos et al., 2020). Cefazolin is a first generation cephalosporin, although it is not reserved for human use, such as those of third and higher generations, it should not be a molecule of first choice. Kumari et al. (2020) referred 10% of cefazoline-resistant *S. aureus*.

7.1.4 – Antimicrobial and antibiofilm activity of Propolis

Seven propolis batches from Brazil and three from Portugal were used to produce propolis ethanol extracts, which were characterized by UPLC-QTOF MS^E. We used UPLC-Photo Diode Array (PDA) to detect phenolic profile and UPLC-QTOF-MS / MS to identify different compounds. As expected, diverse PEE showed differences in composition. This is due to the vegetable biodiversity (Tolêdo et al., 2011) found in each country, also resulting

in the propolis differences colour. The variety of individual compounds found allowed to separate the PEE into 6 groups in this work, green (Group I), red (Group II) and brown (Group III, IV from Brazil and Group V and VI from Portugal). Flavonoids (chalcones, flavanones, flavanonols, flavones, flavonols, isodhydroflavones, isoflavans), non-flavonoid phenolics and triterpenes were the constituents identified.

Green propolis is known, in different countries, for diverse activities due to its peculiar components (Machado et al., 2012; Szliszka et al., 2012; Chen et al., 2018). All Green PEE individual components were exclusive, in this study. This may be due to the components of its main botanical source, Asteraceae *Baccharis dracunculifolia* (Park et al., 2002), which were also found in this PEE.

Red coloured propolis is found in several states from Brazil, but its constituents are not always the same as those found in its probable botanical source *Dalbergia ecastophyllum*, according to López et al. (2013). The constituents found in this vegetable by Silva et al. (2007), in the same Brazilian state, differ from those detected in this study as well as from other supposed sources *Schinus terebinthifolius* (Kassem et al., 2004) and *Rhizophora mangle* (Kandil et al., 2004). The compounds detected in our Red PEE possibly come from sources not yet known.

Substantial differences were found in different groups of Brown PEE. The of group III had a greater number of constituents and showed none in common with group IV, which had fewer compounds. This may be due to the biodiversity found in Brazil. On the other hand, groups V and VI PEE, produced with propolis from Portugal, showed three similar components (pinobanksin, chrysin and acacetin). Interestingly, no work was found mentioning these three compounds in the botanical source indicated here by beekeepers as the vegetable sources surrounding the apiaries. However, pinobanksin and chrysin are found in species of the genus *Pinus* (Nisula, 2018), a plant commonly found in Portugal (Ratola et al., 2010), which may be the main botanical source of these components.

Regarding the antimicrobial activity, all 10 PEE showed actions against the analysed staphylococci. Green and red PEE inhibited most bacteria at a concentration of 3.34 mg/mL. Similar results were also found for MRSA and MSSA by Veiga et al. (2017) and Bueno-Silva et al. (2017) for the same types and sources of PEE, respectively.

Among the Brown coloured PEE, Brown7 (PT) inhibited the isolates in the lowest concentrations (0.026 mg/mL), whereas PEE Brown4 (BR) was not inhibitory or only in much higher concentrations. Brown7 propolis was harvested in the South of Portugal and the PEE contains the flavonoids pinobanksin, chrysin, acacetin, apigenin, pinocembrin and kaempferol-dimethyl-ether in its composition. According to Falcão et al. (2013), the propolis from this region are rich in kaempferol derivatives similar to *Cistus ladanifer* exudates, a shrub commonly found in the Mediterranean area. Velikova et al. (2000) also found pinobanksin, chrysin and pinocembrin in propolis samples from Mediterranean region and these showed better action on bacteria than on fungi. Kasote et al. (2015) referred pinobanksin, detected in South African propolis, active against Gram-positive bacteria.

Pinobanksin derivatives are components presents in propolis that keeps the hive free from intruders (Alotaibi et al., 2019). This bioflavonoid was also detected in group V (PT) and II (BR) PEE, which showed antimicrobial activities similar to Brown7. Castaldo and Capasso (2002) believe that pinobanksin is one of the main propolis compounds with antimicrobial properties, in addition to pinocembrin and galangin. Boisard et al. (2015), on the other hand, observed antimicrobial effect against MRSA and MSSA due to the synergism of some French propolis compounds, including pinobanksin.

Concerning antibiofilm activity, Brown2, from Brazil, showed to inhibit biofilm formation with the lowest PEE concentration. Regarding Brown4 PEE, chapter4 and chapter6 denote slight discrepancies in results because chapter6 shows percentage averages and chapter4 shows results of statistical analyses.

Brown4 PEE did not show any inhibitory effect on the biofilm formation, but presented compounds similar to Brown3, mostly triterpenes derivates. Silva et al., (2019) refers that triterpenes and some derivatives show antibiofilm activity against *S. aureus* and *S. epidermidis*, stating that the ideal antibiofilm compound must lack antimicrobial activity. In the present study, the presence of triterpenes negatively influences the antimicrobial activity, however Catteau et al. (2018) summarizes the activity of some triterpenoid derivatives as anti-staphylococcal and as modifiers of resistance agents when combined with antibiotics.

Brown7 (PT) inhibited biofilm formation even though significantly different from the PEE that showed the best action. This PEE components act more in growth inhibition of the bacteria than in the antibiofilm action, however it showed the two activities. Meto et al. (2020), also found the antimicrobial and antibiofilm actions, only for Gram-negative bacteria, of a sample of propolis from Albania containing several components similar to those found in Brown7, such as pinocembrin, apigenin, chrysin and pinobanksin.

Regarding the PEE disruption of the formed biofilm, Brown2 (BR) and Brown7 (PT) showed the best results, although not owning common components.

In our study, all flavonoids, detected in any PEE, positively influenced bactericidal activity, however some (apigenin, pinocembrin and kaempferol-dimethyl-ether) did not influence the inhibition of biofilm formation, while others (pinobanksin, chrysin, acacetin) contributed to decreased biofilm inhibition. Apigenin, pinocembrin and kaempferol-dimethyl-ether, on the other hand, increased the disruption of the formed biofilm and pinobanksin, chrysin, acacetin did not influence either actions. Thus, suggesting that the antibiofilm action is given to the synergy of several compounds.

We confirm that each PEE can have different components and that it is probably their synergy that causes the two activities antimicrobial and antibiofilm, as generally each component is not able to achieve both activities.

With this work we demonstrated the antimicrobial and antibiofilm activity of PEE against *Staphylococcus* spp., showing a promising contribution for the control of mastitis in goats and sheep. The use of PEE, in replace or combined with antimicrobials, may help to decrease the selection pressure for resistant and multi-resistant staphylococci while fighting small ruminant mastitis.

7.2 – Perspectives for future studies

Finding antimicrobials to control mastitis is a challenge difficult to overcome. Bacteria are able to acquire antimicrobial resistance genes at every opportunity. Natural alternative products with antimicrobial and antibiofilm activity such as propolis may be an interesting and promising option to consider.

The present study has provided useful insights on the potential of propolis against mastitis pathogens. The individual antimicrobial and antibiofilm activity against staphylococci must be evaluated for the different propolis components. Furthermore, more studies to determine the concentration of individual PEE compound are needed to better correlate these with the biological activities of propolis. Moreover, propolis extracts were found to be efficient bactericides and contribute to biofilm inhibition or destruction that may be helpful in the control of mastitis.

The use of propolis alone or in combination with antimicrobials may be an important alternative for the control of small ruminant mastitis, with remarkable advantages for public health and contributing to the reduction of antimicrobial residues in the environment. These results should however be complemented with *in vivo* studies.

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