ABSTRACT

The emergence of multidrug-resistant bacteria in animals and their products has highlighted the considerable value of the potential transfer of resistance to the human population via the food chain. The objective of this work was to study the antibiotic resistance profile of staphylococci of human and animal origin and to compare the two profiles in order to define an effective therapeutic and preventive strategy. This work was carried out on a set of 97 strains of staphylococci isolated from animal and human biological liquids. The isolation and identification was done by conventional methods. The determination of the minimum inhibitory concentrations (MIC) was studied by the reference method (dilution in agar medium) and VITEK® 2 with respect to eight (8) antibiotic molecules. The results were interpreted according to the ACFSM criteria (2001). The results showed higher resistance of human bacteria to penicillin (72.22% vs. 30.23%) erythromycin (50% vs. 18.6%) and gentamicin (33.33% vs. 9.3%) compared to animal bacteria. On the other hand, the resistance to fosfomycin of staphylococci of animal origin was higher (60.46%) compared to human strains (38.89%). Indeed, it seems that vancomycin and rifampicin are the antibiotics of choice against these pathogenic strains in veterinary and human medicine.

Keywords: Staphylococcus, human, animal, antibiotic, resistance.

INTRODUCTION

Staphylococci, members of our skin ecosystem, are opportunistic and invasive pathogenic bacteria, known as pyogenic cocci (Lowy, 1998), responsible for a variety of human and animal infections. S. aureus, the most virulent species of the genus Staphylococcus, has emerged as one of the most important human pathogens, representing one of the main causes of hospital and community infections (Lyon and Skurray, 1987).

However, the study of the epidemiology of this species has attracted interest in recent years due to their importance in veterinary and human medicine due to the increase in infectious episodes caused by this multidrug-resistant pathogenic microorganism, particularly methicillin-resistant strains of S. aureus (MRSA), as well as the emergence of an animal-associated clone (MRSA-L) and their increasingly demonstrated zoonotic potential (Lozano and al., 2016).
The emergence of these antibiotic-resistant bacteria has become a global public health problem affecting human and veterinary medicine (Chardon and Brougere, 2014). The bacterial resistance that occurs in these animals can be transmitted to humans not only through food, but also through other routes such as water, environmental contamination and direct contact with animals.

Raw milk from animals may occasionally play a role in the transmission of these antibiotic-resistant pathogenic bacteria to humans (Pal, 2012). The first report of MRSA in farm animals was published in the early 1970s, when these bacteria were isolated from milk of dairy cows with mastitis in Belgium (Petinaki and Spiliopoulou, 2012).

The emergence of this resistance in animals and their products has highlighted the considerable value of the potential transfer of resistance to the human population via the food chain (Vasquez and al., 2017).

Monitoring the antibiotic resistance of zoonotic and commensal bacteria in food-producing animals and their food is a prerequisite for understanding the emergence and spread of resistance (EFSA, 2014).

In view of this global concern, it is essential to conduct studies in order to understand and control the spread and increase of antibiotic resistance in staphylococci. It is in this context that our study aims to study the antibiotic resistance profile of staphylococci of human and animal origin and to compare the two profiles in order to better define an effective therapeutic and preventive strategy.

MATERIAL AND METHODS

This work was carried out on a set of 97 strains of staphylococci isolated from animal and human biological fluids.

The isolation of bacteria of animal origin was made from raw sheep's and cow's milk, that looks healthy and shows no macroscopic changes. The bacteria of human origin were isolated from various biological fluids (blood, urine, pus) taken from the medical analysis laboratory of the public health department of the city of Tebessa, in the east of Algeria.

The isolation and identification were done by conventional methods. Biological liquids had been bacterially cultured at 37°C for 24-48 hours on a non-selective Nutrient Agar medium (Biomerieux, France). Based on the results of Gram staining, the sample was sown on a Chapman medium (Biomerieux, France). Pure crops have been identified on the Mini APITM systems (Biomerieux, France) and the VitekTM system (Biomerieux, France).

The determination of minimum inhibitory concentrations (MIC) was studied by the reference method (dilution in agar medium) and VITEK 2® with respect to eight (8) antibiotic molecules. The discs use came from the Biomerieux laboratory (France). The results were interpreted according to the criteria of the Antibiogram Committee of the French Society of Microbiology (AC-FSM) 2018.

RESULTS

In this study, many strains of staphylococci were isolated with S. aureus predominating in humans and animals (Table 1). The frequency of this species was 81.48% and 37.02% for samples of human and animal origin respectively. In addition, S. xylosus had a similar frequency to S. aureus of animal origin (37.02%).
Other species of staphylococci should be noted; *S. haemolyticus* (5.56%), *S. saprophyticus* (9.26%), *S. homnis* (3.70%) for strains of human origin and *S. haemolyticus* (2.33%), *S. epidermidis* (18.61%), *S. homnis* (2.33%) and *S. lentus* (2.33%) for strains of animal origin.

Table 1. Distribution of Staphylococcus species according to their origin of sampling.

| Bacteria | Animal (n=43) | Human (n=54) |
|----------|--------------|--------------|
|          | Species      | Number | Frequency | Number | Frequency |
| CPS      | *S. aureus*  | 16     | 37.20     | 44.0   | 81.48     |
|          | *S. haemolyticus* | 1     | 2.33     | 3.0    | 5.56     |
|          | *S. epidermidis* | 8     | 18.61    | 0.00   | 0.00     |
|          | *S. saprophyticus* | 0     | 0.00     | 5.0    | 9.26     |
|          | *S. homnis*  | 1     | 2.33     | 2.0    | 3.70     |
|          | *S. xylosus* | 16    | 37.20    | 0.00   | 0.00     |
|          | *S. lentus*  | 1     | 2.33     | 0.00   | 0.00     |

CSP: Coagulase Positive Staphylococcus, CSN: Coagulase Negative Staphylococcus, n: number.

Figure 1. Resistance profile of staphylococci according to the origin of samples. (E) Erythromycin (15 mcg), (TE) Tetracycline (30 mcg), (GEN) Gentamicin (10 mcg), (VA) Vancomycin (30 mcg), (Fos) Fosfomycine (200 mcg), (P) Penicillin (1u), (Rif) Rifampicin (5 mcg) and (Lin) Lincomycin (15 mcg).
It is interesting to note that this study revealed the resistance of staphylococci against certain antibiotics tested (figure 1), the most important in humans are penicillin (72.22%), erythromycin (50%) and lincomycin (40.74%) in humans.

In contrast, staphylococci of animal origin have been less resistant to these antibiotics. They showed a resistance frequency of (30.23%) for penicillin, (18.6%) for erythromycin and (37.2%) for lincomycin, as well as remarkable resistance to fosfomycin (60.47%). However, complete (100%) susceptibility of these strains to vancomycin has been reported.

The results of the antibiotic resistance study of the group of CSN isolated from human samples (figure 2) showed the high resistance of CSN to most of the antibiotics tested ranging from 40% for tetracyclin, vancomycin to 100% for penicillin. Furthermore, we noted the complete sensitivity (100%) of these strains to gentamicin and lincomycin.

For S. aureus of animal origin (figure 3), vancomycin had 100% activity. However, they showed significant resistance to fosfomycin (70.07%) and lincomycin (40.74%). S. aureus of human origin were less resistant than CNS for penicillin (65.0%), but showed significant resistance to gentamicin (40.9%) and lincomycin (50%).

For animal strains of S. aureus, they showed a high sensitivity to vancomycin (100%), gentamicin (87.5%) and penicillin (81.25%).

Figure 2. Resistance profile of coagulase- negative staphylococci (CNS) according to the sampling origin. (E) Erythromycin (15 mcg), (TE) Tetracycline (30 mcg), (GEN) Gentamicin (10 mcg), (VA) Vancomycin (30 mcg), (Fos) Fosfomycine (200 mcg), (P) Penicillin (1u), (Rif) Rifampicin (5 mcg) and (Lin) Lincomycin (15 mcg).
Figure 3. Resistance profile of S. aureus according to their sampling origin. (E) Erythromycin (15 mcg), (TE) Tetracycline (30 mcg), (GEN) Gentamicin (10 mcg), (VA) Vancomycin (30 mcg), (Fos) Fosfomycine (200 mcg), (P) Penicillin (1u), (Rif) Rifampicin (5 mcg) and (Lin) Lincomycin (15 mcg).

DISCUSSION AND CONCLUSION

The resistance profile study of staphylococci (S. aureus and CNS) to antibiotics revealed the efficacy of vancomycin and rifampicin against these pathogenic strains, whether of animal or human origin.

In Algeria, the use of rifampicin in human medicine has been relatively abandoned in favor of new molecules, which could explain the restoration of its efficacy (Alioua, 2014).

In hospitals, vancomycin remains the appropriate antibiotic for the treatment of staphylococcal infections even MRSA infections. However, the selection of glycopeptide resistant strains is a concern, particularly with the isolation of some strains with reduced susceptibility to vancomycin.

Although CNS strains of human origin showed significant resistance to gentamicin and lincomycin, S. aureus were completely sensitive (100%) to both molecules. In Algeria, analysis of the results of staphylococci resistance to gentamicin, in particular MRSA, showed a marked increase in resistance, which was around 7% in 2006 (Ramdani-ouguessa and al., 2006) and 34% in 2011 (Antri and al., 2010).

The high sensitivity of Staphylococci of animal origin to vancomycin, rifampicin, erythromycin and gentamicin is mainly due to the limited use of these molecules in veterinary medicine, especially in the treatment of mastitis.

For penicillin, tetracycline, and fosfomycin, the different strains studied showed variable resistance according to spe-
cies (S. aureus, CNS) and strain origin (animal or human). This can be explained, on the one hand, by the fact that the treatment of Staphylococcus infections relies essentially on these antibiotics, and their availability on the Algerian market, as well as their accessibility without medical prescription. On the other hand, the less frequent use of these antibiotics in veterinary medicine as compared to human medicine.

In human medicine the majority of S. aureus strains tested are resistant to penicillin. Boukhatem et al., (2015) found that 90% of S. aureus produce penicillinase. They have strong adaptive power and can develop mechanisms of resistance to anti-staphylococci (Boukhatem and al., 2015).

However, the efficacy of fosfomycin was remarkable, active on 98.9% of MRSA (Alioua, 2014). In France, the susceptibility of strains of staphylococci, particularly MRSA, to fosfomycin increased from 66.7 to 94.9% between 1993 and 2009 in France (ONERBA, 2011). The resistance of strains to lincomycin suggests the same resistance mechanism (MLSgB phenotype) that confers resistance to macrolides, lincosamides, and streptogramines B (Convalin and al., 2006).

Indeed, infectious diseases are very frequent in animals and their treatments are very often administered probabilistically. The lack of means and the urgency of animal management push clinicians to prescribe broad-spectrum molecules such as tetracyclines and quinolones outside these antibiotics are likely to select more multi-resistant bacteria.

Despite the certain danger that these types of bacteria represent for human health, it seems imperative to raise as much awareness as possible about the need to reduce the use of antibiotics in veterinary medicine as soon as possible.

Surveillance of these pathogenic bacteria in humans, animals (pets, livestock and wildlife) and food provides a powerful tool to better understand the epidemiology of this microorganism, host-pathogen interactions, to identify virulence factors and factors predisposing to the development of this type of zoonotic infection and to establish appropriate control measures.

DISCLOSURE OF CONFLICTING INTERESTS

The author declares that there is no conflict of interest to disclose.

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