Antimicrobial resistance profile of *Staphylococcus aureus isolated from food*

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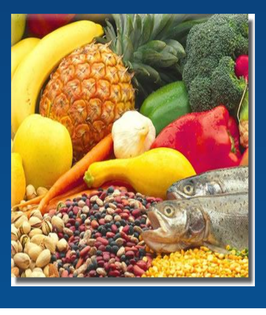


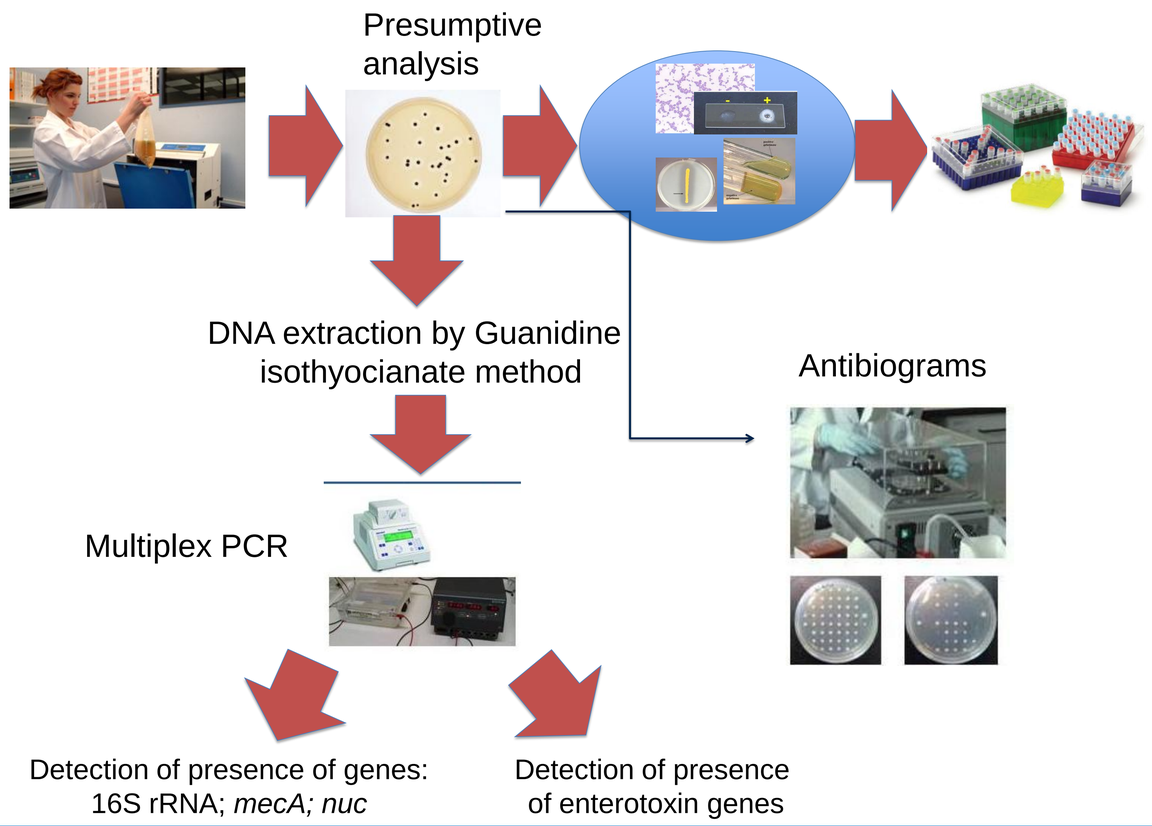
Objectives

The purpose of this study was to evaluate the presence of *S. aureus* in foods, ito determine to what extent isolates are resistant to a range of antibiotics and the proportions of MRSA strains. An indication of the potential degree of virulence was obtained by determinations of the presence of hemolysins, lipase, gelatinase and enterotoxins genes.

Introduction

Staphylococcus aureus is one of the most important pathogens responsible for foodborne intoxication [1,2]. The primary habitat of *S. aureus* is the mucous membranes of the human nasopharynx and animal skin [3]. The presence of *S. aureus* in foods is often related to improper handling by personnel, who are frequently contaminated with or carriers of these microorganisms. Eleven major antigenic types of SEs have been recognised (SEA to SEJ) and their corresponding genes have been reported [1]. Recently, other SE toxins were identified (SEK, SEL, SEM, SEN, SEO, and SEU) and the corresponding genes described, but their role in food poisoning is not clear [1]. In the last decades, the spread of antibiotic resistance in bacteria, including staphylococci, is increasing and may represent a hazard for human health. Among antibiotic resistant staphylococci, multidrug-resistant *S. aureus* strains are of great clinical and public concern since resistances makes the treatment of infections much more difficult. The *mecA* gene is harboured on the staphylococcal chromosomal cassette *mec* (*SCCmec*), a genetic element that integrates site specifically into the *S. aureus* chromosome [4]. MRSA strains are also becoming more frequent in foods [2]. Food may then be considered an excellent way of introducing pathogenic microorganisms into the general population and into immuno-compromised people, and thereby transfer antibiotic-resistant bacteria to the intestinal tract of consumers, very efficiently [2]. It is in the intestine that the transfer of resistance genes can occur between non-pathogenic bacteria and pathogenic or opportunist bacteria [2].

Methods



Results and discussion

1. Isolation of 116 *S. aureus* from different food products, mainly from the north of Portugal, on 2008-2009

2. Confirmation and characterization of *S. aureus*

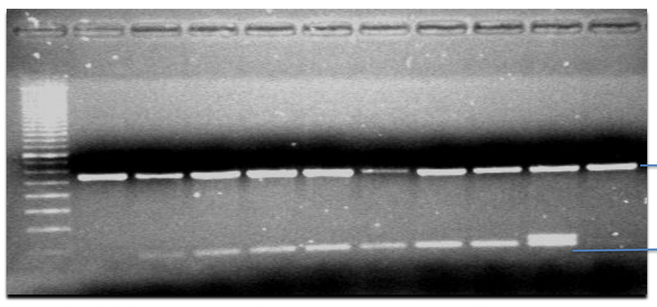


Figure 1: PCR detection of the presence of genes 16S rRNA; *mecA; nuc*

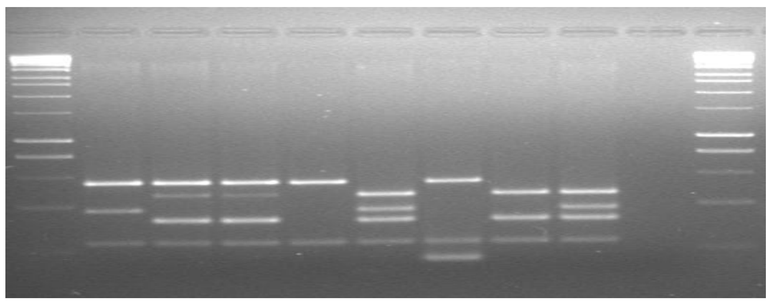


Figure 2: PCR detectiion of the presence of enterotoxin genes

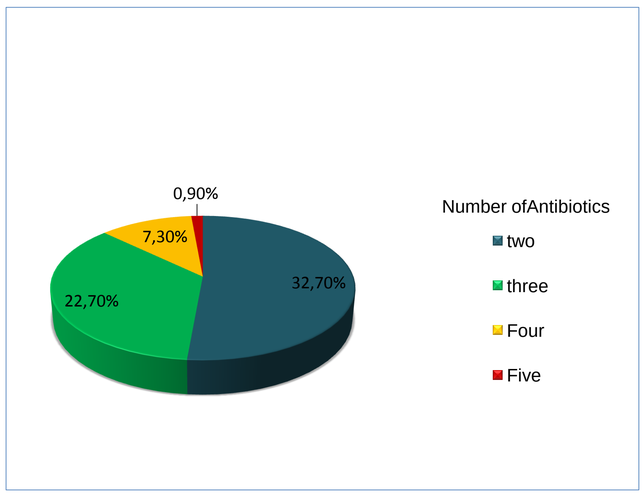


Figure 3: Percentage of *S. aureus* resistant to two or more antibiotics of different classes

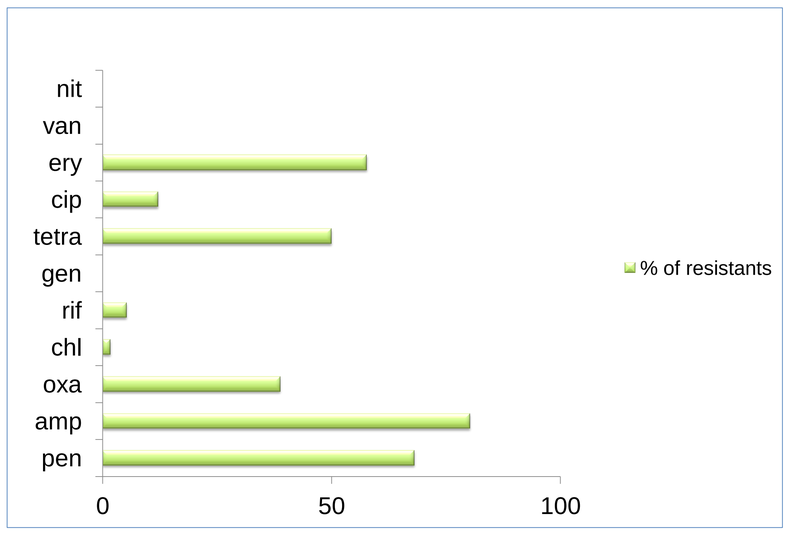


Figure 4: Percentage of resistant of *S. aureus* to eleven antibiotics tested

3. Presence of virulence factors

β-hemolysin, γ-hemolysin, α-hemolysin, lipase and gelatinase were identified for 54.3%, 30.2%, 15.5%, 63.9% and 94.8% of the isolates, respectively.

Conclusions

Staphylococcus aureus is well established as a clinical and epidemiological pathogen; in this study it was demonstrated that the potentially pathogenic role of *S. aureus* as a food-borne pathogen should not be neglected. In conclusion, these results highlight the potentially high risk for consumers in the absence of strict hygienic and preventative measures to avoid the presence of *S. aureus* isolates and SEs production in foods, emphasising the need for improved hygiene practices during food processing and also during the distribution and consumption of the final food products.

References

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