

## ***Comparative analysis of antimicrobial resistance in S.aureus strains associated with Staphylococcal Food Poisoning investigated at the National Reference Laboratory for Staphylococcus, Cantacuzino National Institute of Research, 2009-2013***

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### **Abstract**

Antibiotic resistance can be considered a zoonotic public health problem. Our study aimed at comparing antimicrobial resistance patterns of *S.aureus* strains isolated from food and human hosts, in order to evaluate potential sources of resistant strains or resistance genes of animal and/or human origin.

We analyzed at the National Reference Laboratory for Staphylococcus, Cantacuzino National Institute of Research, 95 strains associated in the 2009-2013 interval with 9 Staphylococcal Food Poisoning (SFP) outbreaks, of which 34 from patients (vomit liquid, coproculture, 31 from food (dairy products, creams, meat products, vegetables) and 30 from human hosts involved in the food chain (nose, throat or skin). Antimicrobial susceptibility testing was performed by using the Kirby Bauer disc diffusion method, according to the CLSI standard.

Antimicrobial Susceptibility Testing to Vancomycin was performed by using the E-test.

We compared rates of resistance in every strain category for each antibiotic. Zone diameters values have been analyzed by using the 19.0 variant of the SPSS program. By using the Ward minimum variance method, we obtained a dendrogram which allowed us to visualize the resistance clusters.

We noticed significant differences between strains isolated from patients, staff and food, regarding rates of resistance to Penicillin (97%, 90%, and 71% respectively). Strains isolated from food showed obvious higher resistance rates than human strains to Tetracycline (64.5% versus approx. 30%), Erythromycin (74 % versus approx. 27%) and Clindamycin (71% versus approx. 25%). We obtained 11 resistance clusters, with strains isolated from food clearly grouping in one of these clusters.

Conclusions: Food represents a distinct source of antimicrobial resistant strains and/or antimicrobial resistance genes that may interfere with antimicrobial resistance background of human origin bacteria. Integrative surveillance of antimicrobial resistance may contribute to better understanding of AR transmission dynamic, which could fundament better public health actions to prevent and/or curbe antimicrobial resistance phenomenon both in animals and humans in our country.

**Keywords:** antimicrobial resistance, *Staphylococcus aureus*, One Health approach