

Staphylococcus aureus spa types in strains from patients with Staphylococcal Food Poisoning, food chain staff and food, investigated in the 2009-2013 interval at the National Reference Centre for Staphylococcus, Cantacuzino Institute of Research

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Abstract

Molecular typing of Staphylococcus aureus strains is useful for tracking their sources and transmission pathways and for confirming the staphylococcal etiology of the Staphylococcal Food Poisoning (SFP). Our study aimed at comparing spa types of Staphylococcus aureus strains isolated from food, from patients and from staff involved in the food chain, in order to evaluate the implication of food and/or staff as source/ transmission pathway of SFP.

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); spa typing, based on the polymorphism of the gene coding for the staphylococcal Protein A, was performed by analyzing the nucleotides sequence of the spa gene X region, using an ABI 3130 Avant Genetic Analyzer. The sequence was then edited and analyzed by using the Ridom StaphType (Ridom GmbH) software.

The 95 S.aureus strains fall in 35 different spa types, of which 2 spa types newly described (t12656, t12657), registered by Romania in the international data base (<http://spaserver.ridom.de/>); the most frequent spa type overall was t053; in the food strains t053 group was isolated the most frequently (13/31), followed by spa type t458 (4/31); in the staff strains group, the most frequently detected spa type was t053 (4/30), followed by t902 (3/30), while in the patients strains group the most frequently detected spa type was t902 (13/34), followed by t4780 (8/34) and t053 (4/34).

In conclusion, t053 S.aureus strains belonging to the CC5 clonal complex have been identified in food, in staff involved in the food chain and in patients with SFP, while t902 strains have been found only in staff and patient samples, thus confirming the complex interplay between the bacteria and enterotoxin coding genes evolving in livestock, food, food chain staff and patients and supporting the opportunity of integrated surveillance.

Key words: *Staphylococcal Food Poisoning, food, spa types*