

Survey of Genes Encoding Staphylococcal Enterotoxins, Toxic Shock Syndrome Toxin 1, and Exfoliative Toxins in Members of the *Staphylococcus sciuri* Group

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Received 3 March 2005/Returned for modification 18 April 2005/Accepted 28 June 2005

Genes encoding staphylococcal enterotoxins (*sea* to *see*, *seg*, and *seh*), toxic shock syndrome toxin 1 (*tst*), and exfoliative toxins (*eta* and *etb*) were not detected in a large panel of 48 *Staphylococcus sciuri* group isolates tested. This strongly suggests that production of the staphylococcal exotoxins by these bacteria is highly unlikely.

Staphylococcal enterotoxins (SEs), toxic shock syndrome toxin 1 (TSST-1), and exfoliative (epidermolytic) toxins (ETs) are staphylococcal exotoxins responsible for the pathogenesis of food poisoning, toxic shock syndrome, and scalded skin syndrome, respectively. The production of these toxins has been extensively studied and well-documented for *Staphylococcus aureus*. It has also been shown that other coagulase-positive staphylococcal species, such as *S. intermedius* and *S. hyicus*, produce similar toxins (1, 2). As far as coagulase-negative staphylococci (CoNS) are concerned, although detection of ETs and TSST-1 in different CoNS species has been reported (12–14), a number of studies failed to detect staphylococcal toxins in these bacteria (2, 3, 5, 8). In addition to the five classical antigenic types of SE (SEA to SEE), a number of additional SEs have recently been reported (5, 9, 10). The newly described ETs have been reliably established for *S. aureus* isolates only.

Members of the *S. sciuri* group, *S. sciuri*, *S. lentus*, and *S. vitulinus*, are coagulase-negative, novobiocin-resistant, oxidase-positive staphylococci. These bacteria colonize skin and mucosal surfaces of various domestic and wild animals and are frequently isolated from different food products of animal origin. They have also been isolated from soil, sand, and water and from a hospital environment. Members of the *S. sciuri* group are not considered common human pathogens, but their clinical significance is apparently increasing. A number of recent studies have reported different infections caused by these bacteria, such as endocarditis, peritonitis, septic shock, endophthalmitis, urinary tract infection, pelvic inflammatory disease, and wound infections (see references 6 and 11 and references therein).

Little has been reported on the production of major staphy-

lococcal exotoxins by members of the *S. sciuri* group; furthermore, a majority of the studies available tested only a few isolates. While a number of the studies showed no toxin production in these bacteria (2, 3, 5, 8), it has been reported that as many as 20% of *S. sciuri* and 66.6% of *S. lentus* strains tested were capable of enterotoxin production (12). The presence of the *see* gene has also been reported for *S. lentus* (14). Genes encoding more recently described SE types were not detected in *S. lentus* and *S. vitulinus* (5), while to date no data are available for *S. sciuri*.

The 48 *S. sciuri* group strains we analyzed were reported previously but not investigated for characteristics presented in this study. Twenty-eight strains were recovered from various human clinical samples (11), while the remaining 20 strains were recovered from an inanimate hospital environment (6). All strains were identified by conventional methods, and the identity was confirmed by PCR amplification of the 16S to 23S rRNA intergenic spacer region. Strains isolated from human samples were identified as *S. sciuri* (23 strains), *S. lentus* (3 strains), and *S. vitulinus* (2 strains), while all 20 strains isolated from the hospital environment were identified as *S. sciuri*. All strains were screened for the presence of genes encoding the five classical enterotoxins A, B, C, D, and E (*sea*, *seb*, *sec*, *sed*, and *see*, respectively) and the two more recently described enterotoxins SEG and SEH (*seg* and *seh*), TSST-1 (*tst*), and exfoliative toxins A and B (*eta* and *etb*) by using previously described primers (4, 7, 9, 10). All results obtained by PCR methods in laboratories involved in this survey were finally confirmed in the Scottish MRSA Reference Laboratory, Glasgow, Scotland. Detection of *seg* and *seh* genes was performed in the Scottish MRSA Reference Laboratory only.

A majority of the studies which established production of staphylococcal exotoxins in CoNS, including the *S. sciuri* group members, were performed by immunological methods (12–14). On the other hand, a majority of the studies which searched for the presence of genes encoding production of toxins found CoNS isolates tested to be toxin negative (2, 3, 5). Although

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the number of strains tested was small and thus may present certain limitations for these studies, the results were still largely consistent. As far as *S. sciuri* group members are concerned, only the *see* gene responsible for ETE production was found in a single *S. lentus* strain isolated from goats' milk and cheese (14).

Since false-positive results have been noted with immunoassays (14, 15), we decided on a more reliable approach and searched for the presence of the toxin genes. None of the 48 *S. sciuri* group isolates harbored the *sea*, *seb*, *sec*, *sed*, *see*, *seg*, or *seh* gene or the *tst*, *eta*, or *etb* gene. Therefore, the results we obtained are in agreement with the results of other studies based upon toxin gene amplification. We suggest that the relatively high proportions of toxin-producing *S. sciuri* group strains found in some of the previous studies might have been related to nonspecific immunoassay reaction results.

To the best of our knowledge, this is the first study which searched for the presence of genes encoding all major staphylococcal toxins as well as newly described SEs in all members of the *S. sciuri* group. The study included the largest series of isolates tested so far for *S. sciuri*, which is considered the clinically most important species within the group, and for the first time investigated the presence of genes encoding newer SEs in this species. The results presented strongly suggest that production of the major staphylococcal exotoxins, as well as more recently described SEs, by members of the *S. sciuri* group is highly unlikely.

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