**ABSTRACT**

Objective: *Staphylococcus aureus* causes 50% of chronic otitis media (COM) cases. Genotypic makeup of *S. aureus* varies, based on geographical location and type of disease. We studied whether a lineage causing COM reflected a population structure of *S. aureus* in the study field or specific to the disease.

Methods: Between Jan. 2010 and July 2012, 35 strains of *S. aureus*, including 11 MRSA isolates were collected from patients with COM following tympanoplasty. Phylogenetic analysis was performed using multilocus sequence typing (MLST). Previous phylogenics analyses of *S. aureus* from healthy nares were used as a control.

Results: The major clonal complexes of *S. aureus* from healthy nares were CC508, CC188, and CC8. In COM, the most prevalent clonal complex was CC5, followed by CC8. Prevalence of CC59, CC75, and CC121, which are minor strains in nasal cavities, was greater in COM patients. MRSA isolates made up 5 of 8 in CC5 (63%), 5 of 6 in CC8 (83%) and 1 of 4 in CC59 (25%). The study suggests that *S. aureus* lineages from COM patients are different from nares of healthy patients.

**METHODS AND MATERIALS**

Between Jan. 2010 and July 2012, 35 strains of *S. aureus*, including 11 MRSA isolates were collected from patients with COM following tympanoplasty. Phylogenetic analysis was performed using multilocus sequence typing (MLST). PCR and DNA sequencing were performed using chromosomal DNA and primer sets that amplified fragments of the following seven housekeeping genes: arc, aro, gtp, gmk, pta, tpi and yqi. The phylogenetic tree was created with Molecular Evolutionary Genetics Analysis (MEGA) Software, in which a clonal complex (CC) was defined as the occurrence of at least five genes of the seven genes (Fig 1). Previous phylogenics analyses of *S. aureus* from healthy nares were used as a control.

**RESULTS**

The major clonal complexes (CC; lineages sharing: at least 5 of 7 house-keeping genes in MLST) of *S. aureus* from healthy nares were CC508, CC188, and CC8. The prevalence was 17%, 14%, and 10%, respectively, making up a total 40% of all isolates (Fig 2). In COM, the most prevalent clonal complex was CC5 (23%), followed by CC8 (17%). Prevalence of CC5, which included MRSA isolates, in COM was significantly greater than in healthy volunteers (P<0.001, Chi-square for independence test). Prevalence of CC59, CC75, and CC121, which are minor strains in nasal cavities, was also greater in COM patients. In contrast, prevalence of CC188 and CC508, which are major strains in nasal cavities, were lower in COM patients. MRSA isolates made up 5 of 8 in CC5 (63%), 5 of 6 in CC8 (83%) and 1 of 4 in CC59 (25%). The study suggests that *S. aureus* lineages from COM patients are different from nares of healthy patients.

**CONCLUSIONS**

This study demonstrated that *S. aureus* types were disease specific and genotypes from COM patients did not reflect those of nares from healthy volunteers.

**REFERENCES**