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O0985 Whole genome sequences of Staphylococcus aureus in correlation with chronic rhinosinusitis and healthy participants

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Background: Chronic rhinosinusitis (CRS) which are caused by infections are generally caused by invasion of respiratory pathogens or by the dominance of respiratory pathogens those colonising the upper respiratory tract (URT). *Staphylococcus aureus* has been identified as the primary pathogen associated with CRS in URT. Here, we analysed the genome sequence data of *S. aureus* and non-*aureus Staphylococcus* from CRS patients and healthy participants, CRS and control groups, respectively.

Materials/methods: Fourteen *S. aureus* identified by MALDI-TOF (7 strains from CRS group and 7 strains from control group) were whole genome sequenced (WGS) using Ilumina HiSeq2000. These isolates were representative *S. aureus* isolates selected by rep-PCR (Diversilab) from 90 participants. The genome data were *de novo* assembled using CLC Genomic Workbench (Ver 8.0). The gene annotation was performed through RAST. Analysis of the WGS data included species identification, sequence type (ST), virulence and antibiotic resistance genes.

Results: Of the 14 *S. aureus*, ten strains were confirmed as *S. aureus,* two *S. capitis* and two *S. warneri*. *S. aureus* ST45 were identified in one participant of control group and two of CRS group. Other identified STs from the CRS group were ST72, 109, 149 and 1027. ST5, 30, 508 were identified from the control group. Interestingly, *S. aureus* ST45 colonised well in the oropharynx. Beta-lactam resistance encoded by *blaZ* were identified in nine *S. aureus* and one *S. capitis*. *mecA* gene encoding beta-lactam resistance was only identified in one *S. aureus* from the CRS group. Aminoglycoside resistance gene (*spc*) was identified in two *S. aureus* strains. Higher number of genes responsible for adhesion (20-25 gene) were identified amongst *S. aureus* in comparison to *S. capitis* and *S. warneri* (13-14 genes). Similarly, the number of iron acquisition encoding genes identified in *S. aureus* (40-47 genes) were nearly double than in *S. capitis* and *S. warneri* (20-27 genes).

Conclusions: Colonisation of *S. aureus* in URT with high number of genes encoding for adhesion, iron acquisition and antibiotic resistance may contribute to the severity of CRS. *S. capitis* and *S. warneri* showed less genomic properties as pathogenic *Staphylococcus* in comparison to *S. aureus*.