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O1100 Another gaze into the crystal ball: predicting *Staphylococcus aureus* traits from whole-genome sequencing data

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Background: Whole genome sequencing (WGS) is becoming the method of choice for rapid and accurate identification and characterization of bacteria. However, the challenge remains to translate the produced data in relevant and easy to interpret epidemiological information. Here, we describe and validate the use of two different commercially available software tools enabling this translation for *Staphylococcus aureus*: SeqSphere+ and the genotyping functionality implemented in the BioNumerics software platform, respectively.

Materials/methods: A panel of 279 *S. aureus* isolates, representing the diversity of German *S. aureus* population, was characterized using traditional phenotypic and genotypic methods. Antibiotic susceptibility towards 19 antibiotics was determined using broth microdilution. *spa*-types were determined using PCR and Sanger sequencing. All isolates were subjected to WGS (Illumina technology) and raw data was assembled using three different assembly algorithms (A5, SPAdes and Velvet). Resulting assemblies were analyzed using SeqSphere$^+$ and BioNumerics, respectively. Besides cgMLST/wgMLST, *spa*-type, MLST and resistance genes were predicted from WGS data and results were compared to those obtained by traditional methods.

Results: Regarding *spa*-type and MLST, high concordance rates (93-99%) between predicted and traditionally obtained results were observed. However, *spa*-type prediction based on SPAdes assemblies correlated least with the traditionally obtained results, yielding 93% correlation compared to 99% and 97% for Velvet and A5 based predictions, respectively. Additionally, concordance rates were lower for *spa*-type predictions obtained from BioNumerics: an extra remapping and consensus calling step performed after the assembly might assure more conservative results but in turn would introduce more uncertain bases.

Almost 90% concordance was obtained between traditionally obtained and WGS predicted antibiotic resistance results based on SPAdes and A5 assemblies, whereas only 84% overall concordance was observed for predictions based on Velvet assemblies. Predominantly, *blaZ* and *ermC* genes were frequently split over two contigs, impeding their correct detection. Additionally, resistance to certain antibiotics is acquired through mutational changes, which were currently not screened for.

Conclusions: The use of WGS data in standard bioinformatics pipelines can greatly improve the efficiency and effectiveness of molecular surveillance to predict phenotypic traits. Moreover, these predictions can help to increase our knowledge and understanding of *S. aureus*.