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An Optimization Algorithm Based on the Natural Gold Mining Process is known as the "Collaborative Gold Mining Algorithm"

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Introduction

Infections in humans, including endocarditis, prosthetic device infections (PDI), pleuropulmonary infections, abscesses, meningitis, and urinary tract infections (UTIs), can be brought on by the bacterial pathogen Staphylococcus aureus. The fact that some clonal lineages of this virus might spread from animals to people, potentially causing health problems and financial losses, is another big concern in the food production business . It is an extremely harmful bacteria due to its ability to adapt and resistance to antibiotics. In fact, the World Health Organization (WHO) and the Centers for Disease Control and Prevention (CDC) of the United States both include it among the infections with the highest priority for the development of new antibiotics. Today, whole genome sequencing (WGS) is a popular and effective method for characterising harmful bacteria, such as S. aureus . By looking for the genes that determine these phenotypic traits in the genomes or more specifically in their mobile genetic elements (MGE), it allows for the typing of strains (e.g., using core genome multi locus sequence typing) as well as the prediction, with a certain level of confidence, of their phenotypic characteristics, such as virulence and AMR potential [1-3].

Discussion

Although some investigations have shown a high degree of confidence between AMR phenotypes and genotypic predictions, the correlations sometimes identified are not absolute, necessitating the employment of the conventional microbiological techniques for AMR assessment. WGS is also used to investigate outbreaks. From the three open databases, 29,679 Staphylococcus aureus genomes were obtained in total. ARG-containing chromosomes on 24,765 of these were found. 1,063,861 plasmidic contigs in total were found, of which 21,006 had an ARG. There were a total of 13 CCs found, with the most prevalent ones being CC8 (29%), CC22 (21%), and CC5 (19%) for chromosomes and CC8 (40%), CC5 (15%), CC22 (12%), and CC1 (9%) for plasmids [4,5]. Some of the WGS data (8% of chromosomic and 6% of plasmidic contigs) could not be attributed to any known CC. 52% of the chromosomic contigs and 86% of the plasmidic contigs lacked information on the isolation source (Supplementary Tables S1 and S2, metadata information for each chromosomic or plasmidic contig. From the three open databases, 29,679 Staphylococcus aureus genomes were obtained in total. ARG-containing chromosomes on 24,765 of these were found. 1,063,861 plasmidic contigs in total were found, of which 21,006 had an ARG. There were a total of 13 CCs found, with the most prevalent ones being CC8 (29%), CC22 (21%), and CC5 (19%) for chromosomes and CC8 (40%), CC5 (15%), CC22 (12%), and CC1 (9%) for plasmids [6].

Conclusion

Some of the WGS data (8% of chromosomic and 6% of plasmidic contigs) could not be attributed to any known CC. 52% of the chromosomic contigs and 86% of the plasmidic contigs lacked information on the isolation source (Supplementary Tables S1 and S2, metadata information for each chromosomic or plasmidic contig can be accessed at Supplementary Tables). There were regional variations in the distribution of S. aureus CCs according to continent. In the chromosomes, CC5 made up 56 and 47% of North America and South America, respectively, while CC22 and CC398 made up 32 and 23% of Europe and CC8 made up 28%, 25%, and 23% of Africa, Asia, and Oceania, respectively (Figure 2A). Variable trends between various nations were seen within continents. For instance, in North and South America, the USA, Argentina, Brazil, and Colombia had the highest concentrations of CC5 and CC8 (CC5: 56%, 28%, 53%, and 53%; CC8: 33%, 19%, 11%, and 31%, respectively); CC30 was also prevalent in Argentina (20%).

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