

Systemic Analysis of the mecA Gene Using a Bioinformatics Tool



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Background: The mecA gene, carried by methicillin-resistant *Staphylococcus aureus* (MRSA), allows the bacterium to promote bacterial resistance to antibiotics such as methicillin, penicillin, and other penicillin-like antibiotics. Our objectives are to use a bioinformatics tool to analyze the sequence of the mecA gene, which is spread on the SCCmec genetic element, and to investigate the relationship between each mecA gene.

Methods: From 2008 to 2016, we collected 229 MRSA from bacteremia; we extracted DNA from the MRSA and designed specific primers to target mecA using PCR. The primers used are listed in mec A-1 (5'-GGGATCATAGCGTCATTATTC-3') and mec A-2 (5'-AACGATTGTGACACGATAGCC-3'). We determined whether the mecA gene was present by using electrophoresis and then sequenced the MRSA samples in which it was present. The POWER tool was employed to analyze the mecA gene and compile a pedigree chart.

Results: Using the sequencing data, we created an MRSA database, and the BLAST findings demonstrated that most of the mecA genes were similar, with over 95% identified. The pedigree chart illustrates that there are four groups of mecA genes, and these groups were found to be not differentiated between the sources of the MRSA, whether from communities or hospital-associated infections.

Conclusions: Our findings indicate that even though there were four groups with ancestors in the pedigree chart, no significant difference was found between MRSA from community- and hospital-associated infections. We plan to collect more MRSA samples for analysis and investigate the differences between MRSA groups and MRSA from various geographical regions.

