

Comparative Genomics of MRSA Strains

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Abstract

Background: Genome sequences of six strains of Methicillin resistant *Staphylococcus aureus* (MRSA) are becoming available: N315, Mu50 [Kuroda et al.], MW2 [Baba et al.], COL [TIGR], MRSA252 [Sanger], NCTC8325 [Oklahoma]. We propose methods to identify and differentiate their homology, distinguishing orthologues and paralogues with the aim to understand their phylogeny.

Methods: For the genomes, we seek similar regions by whole genome alignment using AVID [Bray et al.] or by homology between two sequences using bl2seq [Tatusova et al.]. As for the genes, we first group homologous ones by database homology search using blast [Altschul et al.] and sequence alignment using gap [GCG], and then compare the genes in a group by multiple sequence alignment using ClustalX [Thompson et al.].

Results: On the genome level, regions unique to some strains were identified as SaPI_n1, IS232, IS1181, Tn554, rRNA operon, etc. On the gene level, *HsdS*, *hlg* and *luk*, *fhu* and *sir*, were each grouped as similar genes. Study on the difference among homologous genes supported the “allelic view” in [Baba et al.].

Conclusion: Our methods enable understanding the evolutionary history of MRSA strains in the levels of genome or gene.

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