



SNP-based assay for analysis of MRSA

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Description of Technology

This assay is a rapid and reproducible approach for epidemiological analysis of methicillin-resistant *Staphylococcus aureus* (MRSA) clinical isolates. The assay identifies different strains on EMRSA-15, which is a major cause of hospital acquired MRSA infections in the UK and in other parts of the world.

Epidemiological analysis of hospital outbreaks is critical to inform effective infection control procedures but existing typing methodologies have limited capacity to discriminate closely-related strains, and are often poorly reproducible between laboratories. Unlike established methods the DNA sequence-based method is ideally suited for inter-laboratory comparison of identified genotypes, and its flexibility lends itself to supplementation with additional SNPs (single nucleotide polymorphisms) or markers for the identification of novel *S. aureus* strains in other regions of the world.

This SNP-based assay is based on genome analysis of 17 Scottish EMRSA-15 strains that have been fully sequenced allowing identification of SNPs. The assay has been validated by genotyping all EMRSA-15 bacteraemia isolates collected during a 12 month period from healthcare facilities in the East of Scotland, resulting in the identification of 19 distinct genotypes among the 43 isolates examined. Unlike other established methods such as PFGE, the method is ideally suited for inter-laboratory comparison of identified genotypes, and the flexibility of the SNP-based assay lends itself to supplementation with additional SNPs or markers for the identification of novel MRSA strains in other regions of the world.

Key Benefits

- Successfully distinguishes between closely related strains of EMRSA-15
- Unlike PFGE the SNP based method is well suited for comparison between labs

Potential Applications

- Enables epidemiological analysis of hospital outbreaks of EMRSA-15

Key Publications

- Holmes A, McAllister G, McAdam PR, Hsien Choi S, Girvan K, Robb A, Edwards G, Templeton K, Fitzgerald JR. (July 2013) Genome-wide single nucleotide polymorphism-based assay for high-resolution epidemiological analysis of the methicillin-resistant *Staphylococcus aureus* hospital clone EMRSA-15. *Clinical Microbiology and Infection*, Vol: E-pub 9 August 2013.
- McAdam P, Fitzgerald JR *et al.* (Apr 2013) A genomic portrait of the emergence, evolution, and global spread of a methicillin-resistant *Staphylococcus aureus* pandemic. *Genome Research*, Vol: 23 Pages: 653-664.

Open Technology

A protocol explaining the assay procedure will be provided following acceptance of the University's Open Technology standard terms and conditions.

University Services Available

University researchers are also able to offer additional commercial services related to this technology, such as collaborative research or consultancy. Please get in touch if you wish to discuss this further.