

## Project proposal

<i>Project title</i>	Determine which virulence factor/s are important in the spread of pandemic strains of methicillin resistant Staphylococcus aureus via RT-PCR comparison
<i>First Supervisor</i>	Dr <input type="text" value="Simon Gould"/>
<i>Second Supervisor</i>	Prof Mark Fielder
<i>School</i>	Life Sciences
<i>Other member of supervisory team (no more than three KU supervisors in total)</i>	<input type="text"/>
<i>Specific requirements beyond 2:1 degree</i>	<input type="text"/>

### Project summary (max 4,000 characters)

#### MSc by Research

Methicillin resistant Staphylococcus aureus (MRSA) is recognised as a major challenge for healthcare settings worldwide. Strains of MRSA may be classified as local/regional, epidemic or pandemic. To date eight major hospital acquired pandemic MRSA strains have been described, these include; the so called Iberian, Brazilian, Hungarian, New York/Japan, Paediatric, EMRSA-15, EMRSA-16 and Berlin strains. These strains have demonstrated the ability to spread rapidly across continents in challenging conditions, increasing the problem for healthcare establishments further.

Understanding how these strains respond under stressful conditions may reveal the specific adaptations which make them so adept at spreading. Ongoing investigations comparing pandemic genomes against a regional strain, EMRSA-17, have revealed virulence genes, including toxins, extracellular enzymes and adhesion factors, which are found in all isolates tested, indicating that regulation of genes maybe more important than their presence or absence.