

# Study of MRSA (Methicillin-resistant Staphylococcus aureus) carriage and infection in the United Kingdom

|                                        |                                                          |                                                                                                   |
|----------------------------------------|----------------------------------------------------------|---------------------------------------------------------------------------------------------------|
| <b>Submission date</b><br>29/10/2011   | <b>Recruitment status</b><br>No longer recruiting        | <input checked="" type="checkbox"/> Prospectively registered<br><input type="checkbox"/> Protocol |
| <b>Registration date</b><br>21/12/2011 | <b>Overall study status</b><br>Completed                 | <input type="checkbox"/> Statistical analysis plan<br><input checked="" type="checkbox"/> Results |
| <b>Last Edited</b><br>09/05/2018       | <b>Condition category</b><br>Infections and Infestations | <input type="checkbox"/> Individual participant data                                              |

## Plain English summary of protocol

### Background and study aims

Staphylococcus aureus is a germ (bacterium) that lives on the skin and in the nose of approximately 30 in 100 people. Methicillin-resistant Staphylococcus aureus (MRSA) is a type of S.aureus that has become resistant to penicillin and similar antibiotics. Over the past few decades the incidence of MRSA infections has increased and certain strains of MRSA have become dominant in hospitals. The UK Department of Health has instituted mandatory surveillance of MRSA blood stream infections (bacteraemias) and this has resulted in a reduction in MRSA bacteraemia. However, MRSA continues to cause a considerable burden of illness and death. One of the problems in controlling MRSA infection is that we do not understand why certain MRSA strains are more successful than others or exactly how they are transmitted between patients and between hospitals. Understanding these factors will help us to identify potential control points for intervention.

### Who can participate?

All individuals with MRSA carriage or infection admitted to the study hospitals may participate in the study. Participants may be any age and male or female.

### What does the study involve?

We are conducting a study to look at genetic diversity and geographical distribution of MRSA in the UK. This will be achieved by collecting clinical and laboratory information and bacterial isolates from 3,300 patients with MRSA carriage and infection. We are collecting bacterial samples from these patients and performing genetic tests (whole genome sequencing) to determine the genetic differences between strains. We are examining patient movements within a hospital and between hospitals in the UK. By combining this information we hope to learn more about genetic differences in MRSA and transmission pathways. All clinical data and bacterial samples are being collected as part of routine clinical care. There are no study-specific interventions although all patients will receive treatment for MRSA colonisation or infection as part of routine clinical care.

What are the possible benefits and risks of participating?

There are no benefits to the individual patient in taking part. However, information that is obtained from the study may help to inform local infection control practices and public health policy. The risks of participation are negligible as no additional samples will be taken and no additional procedures will be performed.

Where is the study run from?

The study is being conducted by the University of Cambridge. The lead site will be the Cambridge University Hospitals NHS Foundation Trust and additional sites have been identified in England. Bacterial isolates are being sequenced at the Wellcome Trust Sanger Institute.

When is the study starting and how long is it expected to run for?

The study started in April 2012 and is expected to run for 2 years.

Who is funding the study?

The study is being funded by UK Clinical Research Collaboration (UKCRC) Translational Infection Research Initiative, the Health Protection Agency and the NIHR Cambridge Biomedical Research Centre (UK).

Who is the main contact?

Professor Sharon Peacock  
sharon@tropmedres.ac

## Contact information

### Type(s)

Scientific

### Contact name

Prof Sharon Peacock

### Contact details

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## Additional identifiers

### Protocol serial number

MRSA 001

## Study information

**Scientific Title**

Study of MRSA carriage and infection in the United Kingdom: an observational cohort study

**Study objectives**

1. Can we use bacterial whole genome sequencing to determine MRSA phylogeography and transmission pathways in the United Kingdom?
2. Can we use phenotypic drug susceptibility (antibiograms) to track MRSA transmission within hospitals?
3. What are the relationships between clinical features, bacterial phenotype, and bacterial genotype in patients with MRSA carriage and infection in the UK?

**Ethics approval required**

Old ethics approval format

**Ethics approval(s)**

Cambridge South Research Ethics Committee, 24/11/2011

**Study design**

Observational cohort study

**Primary study design**

Observational

**Study type(s)**

Prevention

**Health condition(s) or problem(s) studied**

Methicillin-resistant Staphylococcus aureus (MRSA)

**Interventions**

Observational cohort study of patients with MRSA infection or colonisation hospitals in the United Kingdom.

There are no study-specific interventions although all patients will receive treatment for MRSA colonisation or infection as required

**Intervention Type**

Other

**Phase**

Not Specified

**Primary outcome(s)**

1. Baseline clinical and demographic information
2. Outcome at hospital discharge
3. Antibiotic resistance profiles
4. Bacterial sequence data

**Key secondary outcome(s)**

No secondary outcome measures

**Completion date**

01/01/2013

## Eligibility

**Key inclusion criteria**

1. Patients with MRSA colonisation or infection
2. Male or female participants
3. Aged 1 day or above (no upper age limit)

**Participant type(s)**

Patient

**Healthy volunteers allowed**

No

**Age group**

Adult

**Sex**

All

**Key exclusion criteria**

1. No evidence of MRSA colonisation or infection
2. No bacterial isolate available for sequencing

**Date of first enrolment**

01/01/2012

**Date of final enrolment**

01/01/2013

## Locations

**Countries of recruitment**

United Kingdom

England

**Study participating centre**

**University of Cambridge**

Cambridge

United Kingdom

CB2 0QQ

## Sponsor information

**Organisation**

Cambridge University Hospitals NHS Foundation Trust (UK)

**ROR**

<https://ror.org/04v54gj93>

**Funder(s)****Funder type**

Government

**Funder Name**

UK Clinical Research Collaboration (UKCRC) Translational Infection Research Initiative (TIRI)

**Funder Name**

Medical Research Council (MRC) ref: G1000803

**Alternative Name(s)**

Medical Research Council (United Kingdom), UK Medical Research Council, Medical Research Committee and Advisory Council, MRC

**Funding Body Type**

Government organisation

**Funding Body Subtype**

National government

**Location**

United Kingdom

**Funder Name**

Health Protection Agency (HPA) (UK)

**Alternative Name(s)**

HPA

**Funding Body Type**

Government organisation

**Funding Body Subtype**

National government

**Location**

United Kingdom

**Funder Name**

NIHR Cambridge Biomedical Research Centre (UK)

## Results and Publications

**Individual participant data (IPD) sharing plan**

Participant level data are not available. The whole genome sequences from this study have been deposited in the European Nucleotide Archive (<https://www.ebi.ac.uk/ena>) under study accession number PRJEB3174.

**IPD sharing plan summary**

Not expected to be made available

**Study outputs**

| Output type                     | Details | Date created | Date added | Peer reviewed? | Patient-facing? |
|---------------------------------|---------|--------------|------------|----------------|-----------------|
| <a href="#">Results article</a> | results | 25/10/2017   |            | Yes            | No              |