

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

Submission date 29/10/2011	Recruitment status No longer recruiting	☒ Prospectively registered ☐ Protocol
Registration date 21/12/2011	Overall study status Completed	☐ Statistical analysis plan ☒ Results
Last Edited 09/05/2018	Condition category Infections and Infestations	☐ 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

University of Cambridge
Department of Medicine
Box 157
Addenbrooke's Hospital
Hills Road
Cambridge
United Kingdom
CB2 0QQ
+44 (0)1223 330 528
sharon@tropmedres.ac

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

Primary study design

Observational

Study design

Observational cohort study

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?
Results article	results	25/10/2017		Yes	No