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A cluster investigation method for studying dengue virus genetic diversity, immunological responses and entomological dynamics

Submission date
16/07/2008

Recruitment status
Stopped

Registration date
17/07/2008

Overall study status
Stopped

Last Edited
24/07/2013

Condition category
Infections and Infestations

[X] Prospectively registered
[_] Protocol
[_] Statistical analysis plan
[_] Results
[_] Individual participant data
[_] Record updated in last year

Plain English summary of protocol

Background and study aims
Dengue is an infectious disease caused by four types of dengue virus, transmitted by mosquitoes. Dengue can be present with no symptoms at all or as a mild illness with fever, headache and joint aches, but can also be complicated by bleeding and shock. There is no treatment for dengue beyond supportive care and there is no vaccine. The World Health Organization lists dengue fever as one of the most important emerging infectious diseases in the world.

Dengue viruses are highly variable: their genetic material changes slightly each time they replicate within their human or mosquito host. As a result, the millions of individual viruses within a host are all slightly different from each other. We call this the diversity of the virus. The goal of this study is to obtain dengue viruses from patients in hospital with dengue, from the mosquitoes in and around their house and from household members and neighbours that may be infected with or without being sick, and to test if the degree of diversity of the virus in different hosts is related to the severity of illness. The study will also look at the patients immune response in different degrees of dengue severity.

Who can participate?
This study aims to recruit dengue patients of all ages who have a high fever and test positive for dengue virus. This study will recruit between 18-110 dengue patients per year in Binh Thuan province. The actual number will depend on how many cases occur in the province.

What does the study involve?
When a dengue case is reported, study staff will take blood samples from the patient. They will take blood when the patient first arrives, and once per day until his/her fever is gone. These samples will be used for testing of the type of dengue virus, the number of viruses and their diversity, and of the patients immune response. Study staff will also draw blood from household members and neighbours of the patient. This study estimates there will be about 5-10 people

who live close to the patient. Mosquito traps will be placed around houses with a dengue patient. A large black plastic container will also be used to collect mosquito larvae, pupae and eggs. These larvae will be bred and stored for future analysis.

What are the possible benefits and risks of participating?
Family members and neighbours will be tested for dengue by the study staff and referred to the community health station for clinical assessment and follow-up. Taking blood samples may cause mild discomfort and bruising.

Where is the study run from?
The study is run by researchers at the Oxford University Clinical Research Unit (OUCRU) Viet Nam; Binh Thuan Medical College Binh Thuan Province, Viet Nam; and the Academic Medical Center Amsterdam, the Netherlands.

When is the study starting and how long is it expected to run for?
The study will run from July 2008 to October 2011 for a total of 3 years and 2 months. After enrolment of 16 index patients and 39 household contacts/neighbours, the study was stopped due to slow enrolment and problems with study staffing.

Who is funding the study?
The Wellcome Trust (UK).

Who is the main contact?
The Clinical Trials Unit at the Oxford University Clinical Research Unit Viet Nam. +84839241983

Contact information

Type(s)
Scientific

Contact name
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Additional identifiers

EudraCT/CTIS number

IRAS number

ClinicalTrials.gov number

Secondary identifying numbers
ctu03dxfeb08

Study information

Scientific Title
A community-based study using household sampling around dengue index cases for assessing genetic diversity, immunological responses and entomological transmission dynamics

Study objectives
1. Dengue virus exists as quasi-species in vivo and genetic diversity in mosquitoes is less
2. The genetic diversity of dengue virus in an infected index case is larger than the genetic diversity of the virus in asymptomatic subjects
3. The genetic diversity of dengue virus is less or qualitatively different in asymptomatic subjects, infected household member and cases of different severity
4. The antibody responses, viral load and antigenemia are lower in asymptomatic subjects

Ethics approval required
Old ethics approval format

Ethics approval(s)
Ethics approval received from:
1. Oxford Tropical Medicine Research Ethics Committee (OXTREC) (UK) on the 24th April 2008 (ref: 10/08)
2. Binh Thuan Ethics Committee on the 26th May 2005

Study design
Prospective, observational cohort study

Primary study design
Observational

Secondary study design
Cohort study

Study setting(s)
Hospital

Study type(s)
Screening

Participant information sheet
Not available in web format, please use the contact details below to request a patient information sheet

Health condition(s) or problem(s) studied
Dengue fever

Interventions

Patient data and clinical examination will be documented in case record forms (CRF). Blood samples will be collected according to the following schedule:
1. At presentation:
1.1. Blood sample for haematology, biochemistry, serology, NS1 and virology
1.1.1. 2 ml if less than 10 years of age
1.1.2. 5 ml if greater than or equal to 10 years of age
2. Daily follow up until afebrile: 2 - 5 ml blood sample for haematology, biochemistry, serology, NS1 and virology

Updated 24/07/2013: After enrolment of 16 index patients and 39 household contacts /neighbours, the study was stopped due to slow enrolment and problems with study staffing.

Intervention Type
Other

Phase
Not Specified

Primary outcome measure
To study dengue pathogenesis by comparing the genetic diversity of virus populations in dengue cases versus infecting mosquitoes and in asymptomatic subjects versus symptomatic cases of different severity

Secondary outcome measures
To study dengue pathogenesis by:
1. Studying the evolution of dengue virus quasispecies during the course of illness
2. Studying antibody responses, viral load and antigenemia in asymptomatic and symptomatic dengue virus infections of varying severity

Overall study start date
20/07/2008

Completion date
01/10/2011

Reason abandoned (if study stopped)
Participant recruitment issue

Eligibility

Key inclusion criteria
Index cases:
1. All ages, either sex
2. Clinical suspicion of dengue:
2.1. Confirmed fever (i.e. an axillary temperature greater than 38°C at presentation)
2.2. Fever less than 72 hours duration
3. Positive NS1 antigen rapid test (indicative of viraemia)

Sample collection around index case:
All family members and neighbours

Participant type(s)
Patient

Age group
Not Specified

Sex
Both

Target number of participants
Patients 100, controls 100

Key exclusion criteria
Does not meet inclusion criteria

Date of first enrolment
20/07/2008

Date of final enrolment
01/10/2011

Locations

Countries of recruitment
Viet Nam

Study participating centre
The Oxford University Clinical Research Unit (OUCRU)
Ho Chi Minh City
Viet Nam
Q5

Sponsor information

Organisation
University of Oxford (UK)

Sponsor details
Clinical Trials and Research Governance
Manor House
John Radcliffe Hospital
Headington
Oxford

England
United Kingdom
OX3 9DZ

Sponsor type
University/education

Website
http://www.ox.ac.uk/

ROR
https://ror.org/052gg0110

Funder(s)

Funder type
Charity

Funder Name
The Wellcome Trust (UK) (grant ref: 077078)

Results and Publications

Publication and dissemination plan
Not provided at time of registration

Intention to publish date

Individual participant data (IPD) sharing plan

IPD sharing plan summary
Not provided at time of registration