

# Investigating risk factors and transmission of acute Hepatitis C: The UK Acute Hepatitis C cohort

<b>Submission date</b> 01/03/2021	<b>Recruitment status</b> No longer recruiting	<input type="checkbox"/> Prospectively registered <input checked="" type="checkbox"/> Protocol
<b>Registration date</b> 05/05/2021	<b>Overall study status</b> Ongoing	<input type="checkbox"/> Statistical analysis plan <input type="checkbox"/> Results
<b>Last Edited</b> 13/12/2024	<b>Condition category</b> Infections and Infestations	<input type="checkbox"/> Individual participant data <input checked="" type="checkbox"/> Record updated in last year

## Plain English summary of protocol

### Background and study aims

Hepatitis C (HCV) is a viral infection transmitted by exposure to infected body fluids. Whilst some people can be exposed to the virus and clear it themselves, the majority of people will develop a long-lasting infection unless they are treated. In some cases, people might not realise they are infected and not have any specific symptoms, but unknowingly transmit the virus to other people. In other cases, HCV can cause cirrhosis of the liver and liver cancer. HCV is a global problem and is a major cause of illness worldwide. Overall, we think that HCV is responsible for roughly 600,000 deaths every year.

Until recently, HCV was very difficult to treat. Earlier treatments were only partly effective and had many side effects. New drug-classes have recently become available and have dramatically changed HCV treatment. These are called directly-acting-antivirals (DAAs). In most cases, these drugs can cure ~95% of infected people. The success of DAAs has led to hope that HCV can be eliminated as a major health problem worldwide.

In this study, we're aiming to study recently acquired HCV infections (acute infections). This means people who have been infected (or re-infected) at some point within the past twelve months. Diagnosing new or acute infections can be very hard. We still don't fully understand how these infections can spread between groups of people – so-called transmission networks.

The main aim of this study is to better understand the ways in which the virus can spread between groups of people. We aim to do this by better understanding the people who are infected, how they were infected and by looking at the virus itself. We hope that this information will help us to design tools to reduce the spread of the infection.

### Who can participate?

Adults (aged 18 years or over) with acute hepatitis C (HCV) infection

### What does the study involve?

Firstly, participants to complete a questionnaire that aims to understand what factors may have

put them at risk for HCV infection and transmission.

Secondly, a blood sample is taken. This sample would be collected in addition to tests that we would routinely recommend for standard clinical care – extra tubes but no extra needles. We would collect this at the first visit and at any subsequent visits participants show any evidence of having been re-infected with HCV. Participants can take part in the study by answering the questionnaire only, without having a blood sample collected. There are a total of four visits over three years.

What are the possible benefits and risks of participating?

There is no direct benefit for participants from taking part in the study, beyond receiving general information about their health. We hope that the knowledge gained from this study will contribute towards efforts to eliminate HCV as a global health problem

This study involves some blood tests. Taking blood samples may sometimes result in slight pain or bruising to the area, and occasionally people can feel faint. Our trained team will be on hand to help in the unlikely event that any problems arise.

Where is the study run from?

1. Imperial College NHS Trust (UK)
2. Guy's & St Thomas' NHS Foundation Trust (UK)

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

August 2020 to November 2023

Who is funding the study?

National Institute for Health Research (NIHR) (UK)

Who is the main contact?

Dr Malick Gibani, [m.gibani@nhs.net](mailto:m.gibani@nhs.net)

## Contact information

### Type(s)

Public

### Contact name

Dr Malick Gibani

### ORCID ID

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# Additional identifiers

## EudraCT/CTIS number

Nil known

## IRAS number

270137

## ClinicalTrials.gov number

Nil known

## Secondary identifying numbers

19SM5527, IRAS 270137

# Study information

## Scientific Title

UK Cohort for Acute Hepatitis C: A prospective, multicentre, observational, cohort study of Acute Hepatitis C in the United Kingdom

## Acronym

UKACH

## Study objectives

To identify and describe cases of acute HCV infection in the United Kingdom

## Ethics approval required

Old ethics approval format

## Ethics approval(s)

Approved 06/02/2020, London - Westminster Research Ethics Committee (The Old Chapel, Royal Standard Place, Nottingham, NG1 6FS, UK; +44 (0)207 104 8237; westminster.rec@hra.nhs.uk), ref: 19/LO/1859

## Study design

Prospective observational multi-centre cohort study

## Primary study design

Observational

## Secondary study design

Cohort study

## Study setting(s)

Hospital

## Study type(s)

Other

## **Participant information sheet**

See additional file ISRCTN10510711\_PIS\_V2.0\_08Dec2020 (added 01/06/2021)

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

Hepatitis C

## **Interventions**

There are two main components to this study. The first is a questionnaire. We ask participants to complete a questionnaire that aims to understand what factors may have put them at risk for HCV infection and transmission. This will involve a series of questions on their personal activities, including those such as drug use, sexual practices and medical procedures. We would ask participants complete a questionnaire each year for the duration of the study (four questionnaires in total), if they of the study visits. The second component of the study is to collect a blood sample. We would use this sample to study the genetic sequence of the HCV virus in detail This will tell us what sub-type or 'family' of virus they are infected with (the genotype) as well as how it is related to other circulating viruses (the phylogeny). We can use the genetic information of the virus to anonymously compare it to other HCV sequences, to explore potential transmission patterns. It may also give us additional information, such as how well different drugs are likely to work.

We would aim to collect about 20ml of blood (equivalent to ~4 small teaspoons). This sample would be collected in addition to tests that we would routinely recommend for standard clinical care – extra tubes but no extra needles. We would collect this at the first visit and at any subsequent visits when participants show any evidence of having been re-infected with HCV. Participants can take part in the study by answering the questionnaire only, without having a blood sample collected. There are a total of four visits over three years.

## **Intervention Type**

Other

## **Primary outcome measure**

Descriptive statistics (n[%]) of participant characteristics (demographics and risk factors) measured using a bespoke questionnaire and review of medical notes and virus characteristics (genotype) at baseline and during follow up as measured by routine Sanger sequencing and Whole Genome Sequencing

## **Secondary outcome measures**

1. Descriptive statistics of risk factors collectively and by individual acquisition risk sub-groups, including but not limited to MSM, PWID, primary infection and re-infection. Analysis will be performed at baseline and at timepoints 12, 24 and 36 months of follow-up, using a bespoke questionnaire and review of medical notes
2. Proportion on patients with acute infection with an undetectable viral load at 3 years post enrolment by; SVR at 12 weeks post completion of DAA treatment; SVR at 24 weeks post completion of DAA treatment by review of medical notes
3. Descriptive statistics of treatment regimens and source (NHSE, clinical trial, self-sourced via internet). Analysis will be performed overall and by acquisition risk sub-group (including but not limited to MSM, PWID, primary infection and re-infection), by review of medical notes and a bespoke questionnaire
4. Descriptive network analysis including clustering and geographic analysis based upon epidemiological data by combing geographic data from questionnaire and whole genome sequence data

5. Proportion of individuals meeting criteria for re-infection at month 12, 24 and 36 of follow up, collectively and by individual subgroup, using a bespoke questionnaire and review of medical notes
6. Proportion of cases under ongoing secondary care follow up defined as attending annual follow up visits in secondary care; Proportion of cases discharged from routine follow up owing to successful treatment; Proportion lost to follow up. Data summarised at timepoints 12, 24 and 36 months of follow-up, using a bespoke questionnaire and review of medical notes
7. Phylogenetic analysis of HCV using whole genome sequencing of HCV isolates presented as maximum likelihood phylogenetic trees; Clustering analysis; Time to most recent common ancestor

**Overall study start date**

01/08/2020

**Completion date**

01/11/2025

## Eligibility

**Key inclusion criteria**

1. Adults (aged  $\geq 18$  years) with acute hepatitis C (HCV) infection
2. Evidence of acute hepatitis C infection or re-infection defined:
  - I. A positive HCV RNA test in the presence of a negative anti-HCV test (antibody and/or antigen and/or HCV RNA) within the past 12 months
  - II. A positive HCV RNA test with an acute clinical hepatitis (jaundice or ALT rise  $>5\times$  ULN) and no other identifiable cause;
  - III. A positive HCV RNA test in patients who had previously achieved spontaneous clearance (anti-HCV positive individuals with two consecutive negative HCV RNA results 24 weeks apart and did not receive treatment), sustained virological response following treatment (negative HCV RNA result 24 (for IFN-based) or 12 weeks (DAA), after stopping treatment or later
  - IV. Evidence of HCV genotype and/or sub-type switch

**Participant type(s)**

Patient

**Age group**

Adult

**Lower age limit**

18 Years

**Sex**

Both

**Target number of participants**

300

**Key exclusion criteria**

Evidence of HCV infection not consistent with the case definition for acute hepatitis C

**Date of first enrolment**

01/11/2020

**Date of final enrolment**

31/10/2023

## **Locations**

**Countries of recruitment**

England

United Kingdom

**Study participating centre****St Mary's Hospital**

Imperial College NHS Trust

London

United Kingdom

W2 1NY

**Study participating centre****Guy's Hospital**

Guy's & St Thomas' NHS Foundation Trust

Great Maze Pond

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## **Sponsor information**

**Organisation**

Imperial College London

**Sponsor details**

Joint Research Compliance Office

Imperial College London and Imperial College Healthcare NHS Trust

Room 215, Level 2, Medical School Building

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England

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cheuk-fung.wong@imperial.ac.uk

**Sponsor type**

University/education

**Website**

<https://www.imperial.ac.uk/research-and-innovation/support-for-staff/joint-research-office/hrs/stakeholders/rgit/>

**ROR**

<https://ror.org/041kmwe10>

## **Funder(s)**

**Funder type**

Government

**Funder Name**

National Institute for Health Research

**Alternative Name(s)**

National Institute for Health Research, NIHR Research, NIHRresearch, NIHR - National Institute for Health Research, NIHR (The National Institute for Health and Care Research), NIHR

**Funding Body Type**

Government organisation

**Funding Body Subtype**

National government

**Location**

United Kingdom

## **Results and Publications**

**Publication and dissemination plan**

The Chief Investigator will co-ordinate dissemination of data from this study. All publications (e. g. manuscripts, abstracts, oral/slide presentations, book chapters) based on this study will be reviewed by any site sub-investigator and by the Sponsor prior to submission. All communication or publications concerning the project, including at a conference or seminar, shall acknowledge the financial contribution of the NIHR.

**Intention to publish date**

01/06/2024

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

The datasets generated during and/or analysed during the current study are available from the corresponding author on reasonable request. De-identified data for exploratory analyses and validation of study results will become available at the time of study publication for a period of 10 years. Whole genome sequencing data will be deposited in a publicly accessible database.

**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="#">Participant information sheet</a>	version V2.0	08/12/2020	01/06/2021	No	Yes
<a href="#">Protocol file</a>	version V2.0	08/12/2020	01/06/2021	No	No
<a href="#">HRA research summary</a>			26/07/2023	No	No