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Identifying genetic determinants of outcome in multiple sclerosis

Submission date	Recruitment status	[X] Prospectively registered
22/04/2023	Recruiting	[_] Protocol
Registration date	**Overall study status**	[_] Statistical analysis plan
04/05/2023	Ongoing	[_] Results
Last Edited	**Condition category**	[_] Individual participant data
20/03/2026	Nervous System Diseases	[X] Record updated in last year

Plain English summary of protocol

Background and study aims
Multiple sclerosis (MS) is what scientists call an “autoimmune” disease. In such diseases the immune system is faulty and mistakenly attacks part of the body. In MS, this faulty attack is directed against the central nervous system (CNS); that is against the brain and the spinal cord. The damage caused by MS results in increasingly severe neurological disability that is known as disease “progression”. The rate at which this irreversible damage develops varies greatly between patients. Some become markedly disabled very quickly, while others develop little or no disability even after years. This study will examine the DNA code from people with MS in order to identify genetic factors that influence how quickly progression develops in the disease. That is, to identify changes in the DNA sequence that influence the outcome of the disease.

Who can participate?
People with MS who have had their disability recorded at least once using a clinical assessment called the Extended Disability Status Scale (EDSS). The EDSS is frequently measured in MS research studies and is now also often measured as part of routine clinical care.

What does the study involve?
The study involves the genetic analysis of DNA donated by participants. The DNA will be extracted either from venous blood or saliva collected from participants. The analysis of the DNA will be undertaken in the laboratory. The genetic data emerging from the laboratory analysis will be correlated with the demographic and clinical details collected about the participants.

What are the possible benefits and risks of participating?
This is an observational study in which the only intervention is the collection of venous blood. This collection will be undertaken by professional appropriately trained staff. The collection of venous blood is a routine procedure with no meaningful risk. The study will also involve the sharing of data about participants between the researchers involved in the study. All data sharing in the study will be undertaken in accordance with best practice and legal requirements such as GDPR. There are no benefits to participants from taking part in the study other than the knowledge that they are helping to bring effective treatments closer for future generations of patients.

Where is the study run from?
The University of Cambridge (UK)

When is the study starting and how long is it expected to run for?
September 2026 to September 2030

Who is funding the study?
Funding for the study is not yet confirmed

Who is the main contact?
Prof. Stephen Sawcer, sjs1016@cam.ac.uk

Contact information

Type(s)
Principal investigator

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Additional identifiers

Integrated Research Application System (IRAS)
324856

Protocol serial number
A096498

Study information

Scientific Title
Progression in Multiple Sclerosis

Acronym
PIMS

Study objectives
The primary aim of this study is to identify genetic variants influencing the clinical course of multiple sclerosis

Ethics approval required
Old ethics approval format

Ethics approval(s)
Not provided at time of registration

Study design
Genome wide association screen

Primary study design
Observational

Study type(s)
Other

Health condition(s) or problem(s) studied
Multiple sclerosis

Interventions
The researchers will undertake array-based genome-wide genotyping in DNA extracted from patients' venous blood or saliva

Intervention Type
Genetic

Primary outcome(s)
Disability measured using the Extended Disability Status Scale (EDSS) and age-corrected to generate the Age-Related Multiple Sclerosis Severity (ARMSS) Score. All available measures of the ARMSS will be considered in the analysis as observed at any timepoint in the disease course.

Key secondary outcome(s))
TIme to event measures including time to EDSS 6.0 and time to confirmed disability worsening. These variables will be assessed in the sub-group of patients with EDSS measured at multiple timepoints.

Completion date
30/09/2030

Eligibility

Key inclusion criteria
1. A locally confirmed diagnosis of multiple sclerosis
2. At least one measure of Extended Disability Severity Score (EDSS)
3. Able to give valid informed consent

Participant type(s)
Patient

Healthy volunteers allowed
No

Age group
Adult

Sex
All

Total final enrolment
0

Key exclusion criteria
1. Patients with Radiologically or Clinically Isolated Syndrome (RIS or CIS)
2. Comorbidities causing significant disability likely to have confounded the reliability of the EDSS
3. Inclusion in the discovery cohort of the recently completed first progression GWAS

Date of first enrolment
01/03/2026

Date of final enrolment
30/09/2028

Locations

Countries of recruitment
United Kingdom

England

Study participating centre
Addenbrookes
Addenbrookes Hospital
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Sponsor information

Organisation
Cambridge University Hospitals NHS Foundation Trust

ROR
https://ror.org/04v54gj93

Funder(s)

Funder type
Other

Funder Name
Not yet confirmed

Results and Publications

Individual participant data (IPD) sharing plan

It is the researchers' intention to store the data generated in this study (demographic, clinical and genetic) in a genomics data repository such as the European Genome-Phenome Archive (EGA, https://ega-archive.org/). Anonymised data will be available when the results of the study are published by application to the Data Access Committee (DAC) via the repository. All participants will consent to data sharing with bona fide third-party researchers undertaking appropriate biomedical research.

IPD sharing plan summary

Stored in publicly available repository