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EACH study: Evaluation of Array Comparative genomic Hibridisation in prenatal diagnosis of foetal anomalies

Submission date
24/06/2013

Recruitment status
No longer recruiting

Registration date
24/06/2013

Overall study status
Completed

Last Edited
20/10/2017

Condition category
Pregnancy and Childbirth

[_] Prospectively registered
[_] Protocol
[_] Statistical analysis plan
[X] Results
[_] Individual participant data

Plain English summary of protocol
Not provided at time of registration

Contact information

Type(s)
Scientific

Contact name
Prof Stephen Robson

Contact details
Institute of Cellular Medicine
Claremont Road
Newcastle Upon Tyne
United Kingdom
NE1 7RU
+44 (0)191 282 4132
s.c.robson@ncl.ac.uk

Additional identifiers

Protocol serial number
11729

Study information

Scientific Title

EACH study: Evaluation of Array Comparative genomic Hibridisation in prenatal diagnosis of foetal anomalies

Acronym
EACH

Study objectives
All pregnant women are offered ultrasound scans to detect fetal abnormalities, many of which are due to chromosome imbalances. Babies with chromosomal abnormalities have complex problems, usually resulting in developmental disability. Parents faced with this knowledge have to make difficult choices. Testing for chromosome problems involves an 'invasive' procedure (e. g. amniocentesis) which can cause miscarriage. Major chromosomal abnormalities can be detected quickly by a technique called PCR. Less common imbalances require the baby's cells to be grown (karyotyping) which is slow, labour intensive and only detects large (microscopic) imbalances. Array comparative genomic hybridisation (CGH) is a new molecular test that can rapidly detect smaller (sub-microscopic) imbalances. In children with developmental disability, array CGH has detected imbalances in 10% of cases. Limited experience of array CGH on fetal samples suggests it may detect 5-10% more chromosome imbalances than karyotyping. However performing and interpreting arrays is complex. The size of imbalances that can be detected depends on array design and not all imbalances cause problems some are inherited from a parent. Understanding the significance of a newly detected imbalance requires further tests on fetal and parental DNA. This study will recruit 1500 fetuses undergoing karyotyping because of a scan abnormality. Arrays will be performed and interpreted in 7 Genetics laboratories according to agreed guidelines. Clinicians/parents will be informed of large imbalances detected by array CGH but only where the outcome of such imbalance is known (based on the medical literature). In addition to determining if array CGH detects harmful chromosomal imbalances more often, more quickly and at less cost than karyotyping, the study will find out what parents and health professionals think of the new technology.

Ethics approval required
Old ethics approval format

Ethics approval(s)
04/01/2012, ref: 11/NE/0331

Study design
Non-randomised; Interventional; Design type: Diagnosis, Process of Care

Primary study design
Interventional

Study type(s)
Diagnostic

Health condition(s) or problem(s) studied
Topic: Genetics Research and Congenital Disorders, Reproductive Health and Childb; Subtopic: Genetics Research and Congenital Disorders (all subtopics), Reproductive Health and Childb (all Subtopics); Disease: Genetics Research and Congenital Disorders, Reproductive Health & Childbirth

Interventions
Diagnosis & management of care, comparision of karyotyping test with Array CGH; Study Entry: Registration only

Intervention Type
Other

Phase
Not Applicable

Primary outcome(s)
Detection of pathogenic Copy number variants (CNVs); Timepoint(s): detection of pathogenic CNVs and chromosomal imbalances by array CGH and/or karyotyping

Key secondary outcome(s))
Not provided at time of registration

Completion date
01/09/2014

Eligibility

Key inclusion criteria
1. Fetuses (singleton or dichorionic twin) undergoing conventional karyotyping by amniocentesis or Chorionic villus sampling (CVS) for clinical indications with:
1.1. one or more structural anomalies identified on an ultrasound scan* or
1.2. an isolated nuchal translucency (NT) =3.5 mm identified at the 11+2 to 14+1 wk ultrasound screening scan.
* Includes fetal growth restriction (defined as abdominal circumference >2 standard deviations below the mean for gestational age)
2. Only those fetuses with a normal qfPCR result, fetuses with a sex chromosome aneuploidy that is unlikely to explain the ultrasound anomaly e.g. XXX, XXY and XYY will undergo array CGH. This group has the highest risk of unbalanced chromosomal rearrangements [25] and recent array CGH studies suggest that they have the highest risk of pathogenic CNVs.

Cases will be recruited from selected Fetal Medicine Units (FMUs) in England and Wales.
Target Gender: Male & Female; Upper Age Limit 65 years ; Lower Age Limit 16 years

Participant type(s)
Patient

Healthy volunteers allowed
No

Age group
Adult

Sex
All

Key exclusion criteria
1. Single or multiple ultrasound variants (or markers). In this context fetal cerebral ventriculomegaly (atrium = 10 mm) is classed as a structural anomaly not a normal variant.
2. Structural anomaly identified outside the time frame specified in the inclusion criteria
3. Participant declines to take part in the study
4. Participant is under the age of 16 years
5. Participant is unable to read English and understand the study information leaflet
6. Those fetuses with Triploidy, the common aneuploidies (Trisomy 13, 18, 21), or Monosomy X will be excluded from the study

Date of first enrolment
01/05/2012

Date of final enrolment
01/09/2014

Locations

Countries of recruitment
United Kingdom

England

Study participating centre
Institute of Cellular Medicine
Newcastle Upon Tyne
United Kingdom
NE1 7RU

Sponsor information

Organisation
Newcastle upon Tyne Hospitals NHS Foundation Trust (UK)

ROR
https://ror.org/05p40t847

Funder(s)

Funder type
Government

Funder Name
NIHR Evaluation, Trials and Studies Coordinating Centre; Grant Codes: 10/06/03

Results and Publications

Individual participant data (IPD) sharing plan

IPD sharing plan summary
Not provided at time of registration

Study outputs

Output type	Details	Date created	Date added	Peer reviewed?	Patient-facing?
Results article	results	01/02/2017		Yes	No
Participant information sheet	Participant information sheet	11/11/2025	11/11/2025	No	Yes