

Molecular studies in a family with eosinophilic esophagitis (EoE)

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Ethical review	Approved WMO
Status	Recruitment stopped
Health condition type	Gastrointestinal tract disorders congenital
Study type	Observational invasive

Summary

ID

NL-OMON37139

Source

ToetsingOnline

Brief title

Molecular studies in a family with EoE

Condition

- Gastrointestinal tract disorders congenital
- Gastrointestinal inflammatory conditions
- Allergic conditions

Synonym

allergic esophagitis, Eosinophilic esophagitis

Research involving

Human

Sponsors and support

Primary sponsor: Academisch Medisch Centrum

Source(s) of monetary or material Support: Ministerie van OC&W

Intervention

Keyword: EoE, Family, Genetic, Molecular

Outcome measures

Primary outcome

The linkage to one or more chromosomal regions and identification of associated gene(s) in the EoE family.

Secondary outcome

Clinical characteristics of EoE patients in this family.

Study description

Background summary

EoE is a rapidly increasing disorder which usually presents with dysphagia. The pathophysiology remains largely unexplained. An allergic pathway is suggested by the observation that a large proportion of EoE patients has an atopic constitution and elementary diets have been shown to have a beneficial effect. Familial clustering indicates that genetic factors play a role as well in the pathophysiology. EoE shows a sibling risk ratio (*S) of approximately 80, which is high compared to other atopic diseases such as asthma (*S about 2). So far, only few Genome Wide Association Studies (GWAS) have been performed aiming to identify loci associated with EoE. GWAS have shown associations with CCL26 (encoding for eotaxin-3) in 14% of EoE patients, and with TGFB1, TSLP, and FLG in smaller percentages of patients. No replication studies have yet been performed to confirm these associations. No pathological mutations have been described in EoE patients.

We reason that performing molecular analyses in a well-defined family with multiple affected members with EoE may allow identification of genes associated with EoE, especially if linkage and sequencing studies are combined.

Study objective

- 1) To identify chromosomal regions associated with the EoE-phenotype in a family with multiple affected family members. Subsequently these regions will be sequenced to detect causative gene(s).
- 2) To describe the clinical characteristics of EoE-patients within this family.

Study design

We will perform linkage analysis in one family with EoE-patients in multiple generations. Suggestive chromosomal regions identified by linkage analysis will be further investigated by Sanger sequencing or next generation sequencing, depending on the number and the size of the identified regions. Clinical information will be obtained from a questionnaire.

Study burden and risks

Peripheral blood drawing will be performed once and does not bring along any mentionable risks

Filling out the questionnaire will take 20 minutes.

Contacts

Public

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Trial sites

Listed location countries

Netherlands

Eligibility criteria

Age

Adults (18-64 years)

Elderly (65 years and older)

Inclusion criteria

- Adult family members fulfilling criteria for EoE
- Adult family members without EoE
- Written informed consent

Exclusion criteria

None

Study design

Design

Study type:	Observational invasive
Intervention model:	Other
Allocation:	Non-randomized controlled trial
Masking:	Open (masking not used)
Control:	Active
Primary purpose:	Basic science

Recruitment

NL	
Recruitment status:	Recruitment stopped
Start date (anticipated):	01-10-2013
Enrollment:	9
Type:	Actual

Ethics review

Approved WMO	
Date:	14-08-2012
Application type:	First submission
Review commission:	METC Amsterdam UMC

Study registrations

Followed up by the following (possibly more current) registration

No registrations found.

Other (possibly less up-to-date) registrations in this register

No registrations found.

In other registers

Register	ID
CCMO	NL41358.018.12