Cone (rod) dystrophy: identification of the molecular defects and clinical consequences

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The purpose of the study is to identify the molecular defects of CORD, to evaluate the clinical course as a function of the molecular defect, and to assess the modifying role of environmental factors.

Ethical review	Approved WMO
Status	Recruiting
Health condition type	Eye disorders congenital
Study type	Observational invasive

Summary

ID

NL-OMON31001

Source
ToetsingOnline

Brief title
Cone (rod) dystrophies: genotype and phenotype

Condition

- Eye disorders congenital

Synonym
(juvenile) macula degeneration of macular/cone dysfunction

Research involving
Human

Sponsors and support

Primary sponsor: Erasmus MC, Universitair Medisch Centrum Rotterdam
Source(s) of monetary or material Support: oogheelkundige fondsen en stichtingen

Intervention

Keyword: cone (rod) dystrophy, genotyping, phenotyping

Outcome measures

Primary outcome

Primary study parameters

These are genetic mutations and haplotypes.

Primary outcome of the study

CORD.

Secondary outcome

Secundary study parameters

Age, sexe, tabacco intake, UV-exposition, intake of anti-oxidants and

omega-3-lipids (DHA en EPA), vascular co-morbidity

Secundary outcome

Visual acuity, age of onset, quantification of color vision defects, photopic

ERG responses, bull's eye maculopathy

Study description

Background summary

Cone (rod) dystrophy: identification of the molecular defects and clinical consequences

Cone (rod) dystrophy(CORD) is a juvenile hereditary macular disorder

characterized by loss of cone photoreceptor cells. The estimated prevalence is 1/10.000. The first symptoms of CORD are decreased visual acuity and color visions defects. This generally leads to functional blindness. Currently, no therapeutical options are available to prevent, stabilize or cure this disease.
CORD is heterogeneous and autosomal dominant, autosomal recessive and X-linked inheritance has been described. Ten genes have been identified: RPGR (X-linked), CNGB3, ABCA4, GUCA1A, GNAT2, CNGA3, RDH5, RIMS1, RCD1, GUCY2D, and 15 additional loci. The attributable risk of these genes to the disease occurrence, however, is low and the cause of the majority of CORD is still unknown.
This lack of knowledge hampers genetic counseling of patients. Patients are not adequately informed about their visual prognosis, can not be treated, and do not know how to improve their lifestyle to alter the course of the disease.

Study objective

The purpose of the study is to identify the molecular defects of CORD, to evaluate the clinical course as a function of the molecular defect, and to assess the modifying role of environmental factors.

Study design

1. 150 CORD probands will be recruited from eye clinics and low vision institutes. The entire clinical chart of each patient will be studied for age of onset, all clinical parameters to diagnose CORD, and visual acuity per 5 years.
2. 200 unrelated controls will be recruited from the same clinics.
3. Analysis of all known genetic mutations with standard procedures.
4. Analysis of unknown mutations with linkage analysis, genome wide SNP arrays, and specific retinal gene arrays.
5. Risk analysis of disease mutations and haplotypes, genotype-fenotype associations, and analysis of gene-environment interactions.

Study burden and risks

The assessment of clinical parameters to diagnose CORD are part of the regular ophthalmologic exam performed by ophthalmologists. Parameters are collected retrospectively by medical charts. If parameters are incomplete, patients will be invited for further diagnostic work-up.

The questionnaire is additional for the patient and will take a maximum of an hour.

Contacts

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Trial sites

Listed location countries

Netherlands

Eligibility criteria

Age
Adults (18-64 years)
Elderly (65 years and older)

Inclusion criteria

<50 years
decreased visual acuity in all three axes
color vision defects
decreased or absent photopic ERG
central scotoma on visual field

Exclusion criteria

> 50 years
normal visual acuity
normal color vision

normal ERG responses
no central scotoma

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:	Recruiting
Start date (anticipated):	01-11-2007
Enrollment:	350
Type:	Actual

Ethics review

Approved WMO

Date:	30-10-2007
Application type:	First submission
Review commission:	METC Erasmus MC, Universitair Medisch Centrum Rotterdam (Rotterdam)

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	NL18730.078.07