Phenomics & Genomics of Clozapine Pharmacotherapy: To a better understanding of the backgrounds of clozapine use

Gepubliceerd: 11-06-2015 Laatst bijgewerkt: 13-01-2025

To assess whether the genetic architecture of this severe therapy-resistant SCZ phenotype differs from the broad DSM-based SCZ phenotype.

Ethische beoordeling	Positief advies
Status	Werving gestart
Type aandoening	-
Onderzoekstype	Observationeel onderzoek, zonder invasieve metingen

Samenvatting

ID

NL-OMON20386

Bron
NTR

Verkorte titel
CLOZIN Current

Aandoening

Genetics of clozapine use because of schizophrenia, schizo-affective disorder, schizophreniform disorder

Ondersteuning

Primaire sponsor: Dr. J. Luykx
Overige ondersteuning: Research funds dr. Luykx

Onderzoeksproduct en/of interventie

Uitkomstmaten

Primaire uitkomstmaten

First, in a discovery cohort a case-control genome-wide association study (GWAS) will be performed on 2000 CLZ using subjects (cases) and >30,000 already available SCZ patients (controls, drawn from the most recent Psychiatric Genomics Consortium analysis, . We hereby aim to reveal potential differences in the genetic architecture between the severe CLZ-SCZ phenotype and the broad SCZ phenotype.

Toelichting onderzoek

Achtergrond van het onderzoek

Clozapine (CLZ) is generally prescribed if at least two trials of antipsychotic agents have not led to satisfactory clinical improvement, thereby implying that patients on CLZ generally suffer from more severe and/or persistent symptoms than patients suffering from schizophrenia spectrum disorders (SCZ) on other antipsychotic agents. Unraveling the (functional) genetic variation underlying this severe SCZ phenotype therefore has the potential to deepen our understanding of the biological underpinnings of SCZ beyond the boundaries of DSM-based consensus criteria. Such knowledge in turn has the potential to shape future pharmacotherapeutic research. We here hypothesize that targeting this phenotype in genome-wide association studies and next-generation sequencing studies will signal genetic risk loci implicated in this severe SCZ phenotype. In the future, this may lead to early detection of severe SCZ, which in turn will enable tailoring of pharmacotherapeutic strategies to such SCZ subtypes.

In addition, we use the data with our other protocol (NTR 5257) to create a prediction model for clozapine response and side effects.

Doel van het onderzoek

To assess whether the genetic architecture of this severe therapy-resistant SCZ phenotype differs from the broad DSM-based SCZ phenotype.

Onderzoeksopzet

One visit

Onderzoeksproduct en/of interventie

None

Contactpersonen

Publiek

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Wetenschappelijk

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Deelname eisen

Belangrijkste voorwaarden om deel te mogen nemen (Inclusiecriteria)

-he/she currently uses CLZ

-he/she has received a diagnosis of schizophrenia, schizophreniform disorder, schizoaffective disorder or psychosis not otherwise specified

-his/her age must be ≥18 years old

-he/she must be able to speak and read the Dutch language

-he/she must be mentally competent and have decisional capacity with regard to a decision

to participate in the current study

Belangrijkste redenen om niet deel te kunnen nemen (Exclusiecriteria)

- admission to a psychiatric unit involuntarily in the context of an ‘inbewaringstelling’ (IBS)

- a history of Parkinson’s disease

Onderzoeksopzet

Opzet

Type:	Observationeel onderzoek, zonder invasieve metingen
Onderzoeksmodel:	Anders
Toewijzing:	N.v.t. / één studie arm
Blindering:	Open / niet geblindeerd
Controle:	N.v.t. / onbekend

Deelname

Nederland

Status:	Werving gestart
(Verwachte) startdatum:	01-07-2015
Aantal proefpersonen:	2500
Type:	Verwachte startdatum

Voornemen beschikbaar stellen Individuele Patiënten Data (IPD)

Wordt de data na het onderzoek gedeeld: Nee

Ethische beoordeling

Positief advies

Datum:	11-06-2015
Soort:	Eerste indiening

Registraties

Opgevolgd door onderstaande (mogelijk meer actuele) registratie

ID: 50518
Bron: ToetsingOnline
Titel:

Andere (mogelijk minder actuele) registraties in dit register

Geen registraties gevonden.

In overige registers

Register	ID
NTR-new	NL5116
NTR-old	NTR5248
CCMO	NL52726.041.15
OMON	NL-OMON50518

Resultaten

Samenvatting resultaten
None yet