REFErence Repository for healthy livers (REFER trial)

No registrations found.

Ethical review	Positive opinion
Status	Recruiting
Health condition type	-
Study type	Observational non invasive

Summary

ID

NL-OMON28065

Source
Nationaal Trial Register

Brief title
REFER

Health condition

gallstones, NAFLD, Liver disease

Sponsors and support

Primary sponsor: AMC
Source(s) of monetary or material Support: N/A

Intervention

Outcome measures

Primary outcome

1. Presence of NAFLD/NASH parameters in liver biopsy using histology (NASH-CRN / Steatosis Activity and Fibrosis Score Steatosis) and liver RNA sequencing.

Secondary outcome

1. Presence of bacterial DNA, histology and inflammatory genes (RNA seq) liver and abdominal adipose tissue depots as well as metabolites in plasma, feces and urine
2. Fecal and oral microbiota composition
3. Dietary, psychological and satiety lists and excreted metabolites
4. Clinical data (body weight, body composition), waist circumference and blood pressure
5. Genomic DNA (buffy coat)

Study description

Background summary

The current estimated global prevalence of non-alcoholic fatty liver disease (NAFLD) is 25 – 30% and is diagnosed in up to 80% of individuals with obesity and type 2 diabetes (T2D) 1,2. The rapidly growing prevalence of NAFLD and lack of effective treatment options to tackle this potentially debilitating disease, will further increase obesity-related burden on public health and economies.
In order to develop appropriate, non-invasive diagnostic methods and treatment options, it is critical to deeply investigate the complex pathophysiology of NAFLD. Genome-wide analysis of large cohorts (containing hundreds of patients to insure the robustness of results), is required to obtain insight in hepatic metabolism in NAFLD 3. A number of such genome-wide transcriptomic studies have indeed characterized alterations in hepatic gene expression in individuals with NAFLD and its more severe, progressive form non-alcoholic steatohepatitis (NASH) 4 5 6 7. Nevertheless, these studies have thus far not been able to define a predictive transcriptome signature for NAFLD. Multiple confounding factors such as differences in genetic origin, sex and unappreciated environmental factors, including the gut microbiota, might have contributed to this.
Our research question therefore is how omics data of several biological layers are different between men and women with and without NAFLD and to what extent these signatures contribute to NAFLD development.
To answer this question, we will establish liver transcriptomic, fecal metagenomic and plasma metabolomics profiles of otherwise healthy men and women. Therefore, we will set up a cross-sectional cohort and include non-obese, otherwise healthy individuals scheduled for cholecystectomy. Using state-of-the-art sequencing and systems biology approaches, we can integrate plasma/urinary metabolomics, liver and adipose transcriptomic and fecal metagenomics data to create a unique much needed signature of healthy individuals (men and women). This database will be integrated in our large cohort of obese men and women with and without NAFLD (BARIA study METC 2015_357).

Study objective

How omics data of several biological layers are different between men and women with and without NAFLD and to what extent these signatures contribute to NAFLD development.

Study design

all time points are at the day of surgery (cross-sectional).

Contacts

Public
Amsterdam UMC locatie AMC
Stijn Meijnikman

0205661925
Scientific
Amsterdam UMC locatie AMC
Stijn Meijnikman

0205661925

Eligibility criteria

Inclusion criteria

- 18-65 years of age
- BMI < 30 kg/m2
- Individual should be able to give informed consent

Exclusion criteria

- Type 2 diabetes mellitus
- Prior bariatric surgery
- Inflammatory bowel disease
- Primary lipid disorder
- Known genetic basis for insulin resistance or glucose intolerance
- Ethanol intake > 2 U/week
- Pregnancy, females who are breastfeeding
- Hepatitis B and/or C
- Liver cirrhosis
- Auto-immune hepatitis
- Wilson disease3/ alpha 1-antitripsine deficiency
- Hemochromatosis

Study design

Design

Study type:	Observational non invasive
Intervention model:	Other
Allocation:	Non controlled trial
Masking:	Open (masking not used)
Control:	N/A , unknown

Recruitment

NL

Recruitment status:	Recruiting
Start date (anticipated):	01-10-2020
Enrollment:	200
Type:	Anticipated

IPD sharing statement

Plan to share IPD: No

Ethics review

Positive opinion

Date:	06-10-2020
Application type:	First submission

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
NTR-new	NL8983
Other	METC AMC : METC 2020_130

Study results