SUPER – Finnish study for the hereditary mechanisms behind psychotic illnesses

Information for researchers interested in using stored samples and data

1. Introduction

The Finnish SUPER Survey on Genetic Mechanisms of Psychotic Disorders is part of the International Stanley Global Neuropsychiatric Genomics Initiative. Institute for Molecular Medicine Finland (FIMM), University of Helsinki, is leading the study in Finland. The objective of the study is to better understand the genetic and biological background of psychotic disorders in order to provide more accurate information for the development of new therapeutic interventions.

The study was commenced with a pilot study in three regions in Finland (Oulu, Tampere and Kuopio) in the fall of 2015. In 2016, the study was expanded to cover all five University hospital regions in Finland (Oulu, Tampere, Kuopio, Helsinki and Turku) and sample and data collection continued until the end of 2018. The aim was to collect samples from a minimum of 10,000 Finnish patients diagnosed with psychotic illnesses accompanied with an extensive data collected by health examinations, interviews and questionnaires. The questionnaire and interview consist of questions related to life history, previous important life events (such as major childhood events, traumas, and abuse), current status of living, education, employment, comorbidities, current health (sleep, daily functioning) and medication. Participants also performed a Cantab- reaction test and a PAL (Paired association learning) test to assess cognitive performance.

Total number of participants in the SUPER study was over 10 500, of which more than 9 300 consented also for THL Biobank, which allows the use of these samples and data also in biobank research.

2. Ethical considerations

Coordinating Ethical Committee of the Helsinki and Uusimaa Hospital Region approved the SUPER Study 16 July 2015 (pilot) and 9 February 2016 (full study). All participants of the SUPER Study signed an informed consent that permits the use of collected samples and data for the original study of psychiatric disorders. In parallel to SUPER Study, most participants (~91%) signed an informed consent for THL Biobank, which allows the use of these samples and data also in biobank research.

3. Selection of study subjects

Finnish patients diagnosed with psychotic illnesses, classified by ICD-10 diagnostic codes F20-F29, F30.2, F31.2, F31.5, F32.3 and F33.3 were recruited for the study.

The recruitment and selection of study subjects was based on three different strategies:

1. Patients presenting with psychotic illness at hospitals, healthcare centers, mental health centers and private healthcare contractors (i.e. assisted living services) were contacted during their normal treatment.
2. Suitable subjects were identified from National Higher Special Refund Entitlement Register by The Social Insurance Institution of Finland (KELA), which sent a recruitment letter for suitable participants.
3. Care Register for Health Care (HILMO) was used to identify subjects with specialized health care contact due to a psychotic disorder. They were initially contacted through their treating unit directly or via a recruitment letter.

The exclusion criteria were:

1. being younger than 18 years of age
2. being unable to give informed consent as evaluated by the trained research personnel or attending physician

4. SUPER Study samples and data available for biobank research

Samples and data of the SUPER Study will be transferred gradually to THL Biobank to prioritize the research interests of the original study. SUPER Study may, at its own discretion, also provide additional data from its own databases through THL Biobank to biobank research projects before the requested data has been transferred to THL Biobank. All collected and measured information

from the participants, including confirmed diagnoses, questionnaire and interview data, results of Cantab- reaction test and test results of Paired association learning test (PAL) to assess cognitive performance will be gradually transferred to the biobank starting in 2023.

4.1. Samples currently available for biobank research:

The following samples are available from more than 9 300 sample donors.

- **DNA**
- **serum** (processed within 60 min after sampling)
- **plasma** (EDTA, processed within 60 min after sampling)
- **PBMC** (subset of 4900, consented separately, processed 24h after sampling)
- **Blood/Paxgene** (subset of 1450)

Sample collection and processing details:

The study nurses were trained to perform sampling and sample processing in a similar manner in all research areas. The protocol was evaluated in all areas twice a year by the training teachers. Fasting was not required, but fasting time was documented. Additionally, possible infections (or fever) within the last 7 days was documented. Blood samples were collected by venipuncture for DNA extraction and for serum (Vacutainer STII 10/8 ml gel, BD) and plasma (Vacutainer EDTA K2 10/10 ml, BD) samples. In cases where venipuncture was not possible, saliva sample (DNA OG-500, Oragene) was collected for DNA extraction. Serum and plasma were let to settle for 30 min and then centrifuged, aliquoted in 0,5 ml fractions (Fluid X tubes) and frozen (-20^{0}C) on site within 60 min after sampling. Serum and plasma samples were shipped in dry ice within three months for long term storage in -185^{0}C. The study participants were additionally consented for extra blood sample (10ml) for isolation of peripheral blood mononuclear cells (PBMC). PBMC were isolated by Ficoll-Paque method within 24 h after sampling and stored in *LN2 vapor phase.* DNA extraction was performed using PerkinElmer Janus Chemagic 360i Pro Workstation with CMG-1074 kit. This workstation uses patented magnetic bead technology with fully automated liquid handling. Saliva samples were incubated in +50 °C o/n before DNA extraction. Saliva samples were processed using Chemagen Chemagic MSM I robot with CMG-1035-1 kit. DNA was eluted in 400 µl 10mM Tris-EDTA elution buffer (PerkinElmer).

4.2. Phenotype and omics data currently available for biobank research

The updated list of data variables can be uploaded from the **variable descriptions -file** found on the right panel of the Super Research collection page:

For availability of genome-wide genotypes and sequencing data, see more information in the **'THL Biobank Omics data availability table'** at the THL Biobank research collection page.

5. Registry data

Information from the Finnish national health registries, such as Care Register for Health Care (HILMO), Cancer Register, Cause-of-Death Register and Drug Imbursement Registers etc., can be linked to sample donors by separate application process and project-specific permission from Findata.

(Contact THL Biobank for help: admin.biobank (at) thl.fi).

6. Research group

The director of the Finnish Super study
Professor Aarno Palotie

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