CNCR research gets unique boost from U.S. genotyping consortium

In a further appreciation of non-American research the U.S. based Genetic Association Information Network (GAIN) has awarded depression researchers at NTR (Netherlands Twin Register) and NESDA (Netherlands Study on Depression and Anxiety) a genotyping boost. GAIN will provide the means for the whole genome screening of 1000 depression patients and 1000 healthy matched counterparts. This will deliver an amazing billion data points at the CNCR doorstep, promising to provide new clues on the genetic basis of major depression.

The agreement is part of a larger genotyping effort GAIN finances. This unique public-private partnership involves the National Institutes of Health (NIH), Pfizer, Affymetrix and the FNIH, as well as Perlegen Sciences, Abbott and the Broad Institute of Massachusetts Institute of Technology and Harvard University. Private donors have contributed about 26 million dollar (over 20 million euro) to the project to help find genetic causes of genetic diseases. GAIN does so by selecting high quality studies which possess extensive clinical data and offers to perform whole genome analysis on these earlier collected samples.

On October 10, GAIN announced the first round of studies to undergo whole genome analysis. The six rewarded studies involve schizophrenia, AHDH, psoriasis, type I diabetes, bipolar disorder, and major depression. All are 100 percent U.S. projects, except the major depression study, which is rooted in the cohorts of psychiatric patients of the NESDA project and the carefully maintained Netherlands Twin Register.

The principal investigator in the major depression project, is Patrick Sullivan from the University of North Carolina at Chapel Hill. CNCR researcher prof. Dorret Boomsma from the Netherlands Twin Register, has a long standing cooperation with Sullivan. Together they approached the NESDA group and jointly they agreed to submit the request to GAIN together. A lucrative decision, it turns out.

“I feel GAIN especially appreciated our extremely well phenotyped samples”, Boomsma comments. “At NESDA we have a first class patient population, and the NTR excels in providing healthy controls.” “The collaborations of our groups with molecular geneticists within the CNCR and the Centre for Systems Biology (CMSB) are clearly paying off”.

NESDA – a collaborative study between universities in Amsterdam (VU), Leiden and Groningen - will ‘deliver’ samples from 1000 patients suffering from major depression, the NTR will provide the healthy, age matched controls. In the United States these samples will be genotyped, and returning to Amsterdam is information about 500.000 whole genome SNPs – for every of the 2000 samples. Maybe even, Boomsma says, GAIN might ask the researchers to provide 2000 patient samples and 2000 controls, but that is still preliminary. Luckily, within the CNCR and CMSB context researchers are already upgrading databases and bioinformatics facilities to cope with this huge amount of data.

Boomsma is thrilled by the possibilities the information about the SNPs gives the depression researchers. “Genetic research on depression so far has focused on the more laborious linkage approach. SNP based research has been around, but it usually aimed at SNPs in known target genes. This whole genome approach however gives us a lot of statistical power in identifying genotypes involved in depression.”

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Rinze Benedictus

FNIH Press Release about GAIN:
http://www.fnih.org/Biomarkers%20Consortium/GAIN%20Award%20Announcement%20for%2010-10-06ver1.pdf