



Major Depressive Disorder: Stage 1 Genomewide Association in Population-Based Samples.

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Critique

- Unrealistic sample sizes
- Sparse genotyping
- Imhomogeneity of samples
- Epidemiological sampling frame unknown
- Minimal phenotypes

- Controls not "draws from the same population" as cases
- Controls just unaffected, not at low liability
- Cases not directly evaluated by pros
- Replication not intrinsic





Primary phenotype definition

- Major depressive disorder (MDD)
- Dysphoria along with
 - Physical signs & symptoms
 - Impairment
 - Persistent & pervasive
 - Not normal sadness or grief
- Excludes depression due to other psychiatric and medical causes





Importance of MDD

- Common
 - Lifetime prevalence ~15%
 - Increasing importance to psychiatry
- Chronic recurrent for most (~75%)
- Increased mortality (suicide & other)
- Considerable morbidity
 - By 2020, projected to become 2nd leading cause of disability in world





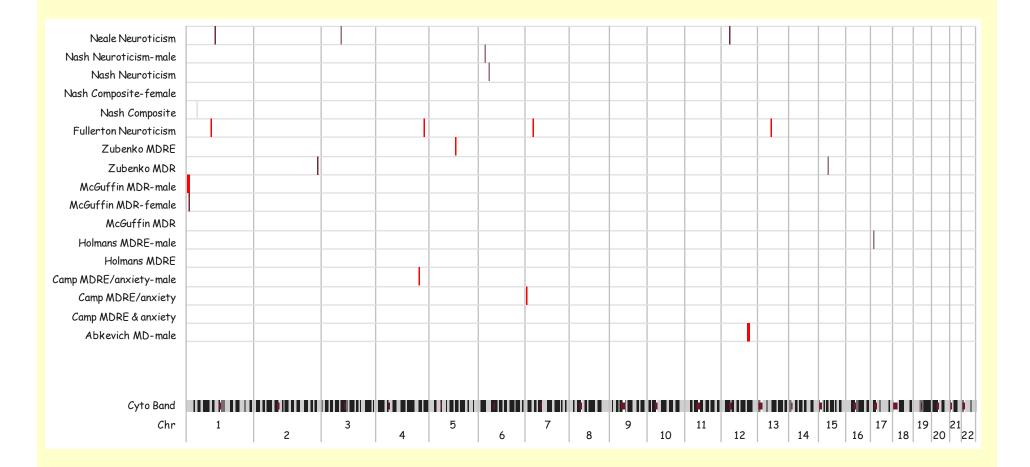
Evidence for genetic influence on phenotype

- Complex trait
- Indirect data from genetic epidemiological studies
 - Twin studies, heritability ~40% (or higher)
 - Adoption studies consistent
 - Familial risk to 1st degree relatives RR=2.8
- Evidence from the Netherlands consistent





Genomewide Linkage Studies (MDD & N)







Genomewide Association Studies

Study	N _{total}	IP?	Ancestry	Status	Comments
GAIN	3,200	No	EUR	In progress	4,600+Stage 2
Pfizer	500	Yes	EUR	Complete	No controls
GSK	2,000	Yes	EUR	?	
Academic 1	3,000	No	EUR	In progress	Pooling
Academic 2	2,000	No	Mixed	?	
Academic 3	2,000	No	Mixed	Planned	





Restrictions on data use

IRB approvals & consents :

- Allow the future use of DNA samples/phenotype data and information derived from them for genetic studies;
- Permit the use of the samples and information derived from them for research on phenotypes other than MDD;
- Do not impose any restrictions on sharing samples and information derived from them with other investigators; and
- Do not restrict the use of the samples and information derived from them in any other way, as long as the anonymity of the participants is guaranteed.





1,600 CASES with MDD: Netherlands Study of Depression and Anxiety (NESDA, <u>www.nesda.nl</u>, 2003-present)

- Collaborative study within the Netherlands (4 academic centers, 2 non-academic centers)
- Longitudinal cohort study following 2,850 persons, 18-65 years
- Five assessments: baseline and after 1, 2, 4 and 8 years
- Designed to be representative for MDD patients → Covers different range of psychopathology and settings





Inclusion & exclusion criteria for MDD cases

Inclusion criteria:

Confirmed MDD diagnosis according to CIDI interview, version 2.1
 Age 18-65 years

Exclusion criteria:

 Insufficient knowledge of Dutch language
 Ancestry other than North-European
 Other psychiatric disorder, e.g. bipolar disorder, OCD, severe addiction, psychosis, mood disorder due to a general medical condition





TOS TWEELINGER STS		SCHOOL OF MEDICINE				
Recruitment of MDD cases						
Community	Primary care	Mental Health Care				
Random sample n=10152 30% refusal	Random GP sample of 19596, from 60 GPs 50% not-returned	Newly admitted MHO patients				
Psychiatric interview n=7076	Screening list (K-10), n=9798 → 42% screen pos n=4115	MDD diagnosis at Intake, n=1390				
▼	9% refusal	7% exclusion				
MDD diagnosis N=640	Phone screen CIDI-SF n=3744 \rightarrow 45% screen pos, n=1684	Phone screen n=1293				
30% refusal 15% dropout	8% exclusion	32% refusal 10% exclusion				
NESDA baseline n=350	NESDA baseline n=1407	NESDA baseline n=750				
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300 MDD cases	800 MDD cases	650 MDD cases				





Key clinical features for MDD

Positive family history(%)	71%
Recurrent episode	2 episodes: 47% 1 episode of >3 years: 31%
Age of onset	>30: 39% 22-30:40% <22: 21%
Any of these	95.1%





CONTROLS: Netherlands Twin Register (NTR)

	1991	1993	1995	1997	2000	2002	2004
Twins	3386	4225	3413	3231	4610	4523	4017
Siblings	n/a	n/a	1481	1517	1474	1454	1264
Fathers	1439	1774	1572	n/a	n/a	1266	1058
Mothers	1607	1920	1688	n/a	n/a	1529	1333
Spouses	n/a	n/a	n/a	n/a	708	1527	945
Total	6432	7919	8154	4753	6795	10299	8617

In total, questionnaire data available for 20,496 individuals.





Selection of 1,600 controls

- DNA, mRNA (challenged/unchallenged) and lymphocytes (immortalized cell lines) present
- Only unrelated individuals are selected
- Proband & parents born in the Netherlands or Western-Europe
- NEVER a high score (> mean + 0.6 SD) on personality traits associated with depression (neuroticism, anxious depression, trait anxiety, borderline personality) in the 15 year follow-up period
- NO reports of clinical depression (YASR/Beck inventories, CIDI interview) or use of antidepressant medication EVER, up to biobanking





Matching of cases and controls

- All cases and controls are drawn from the same population
- Very homogeneous subject ancestries
- Cases and controls come from ongoing prospective studies
- Comparable composition across age, sex, marital status, SES





Matching of cases and controls

	MDD cases (NESDA)	Controls (NTR)
Age (mean \pm SD)	41.6 yrs \pm 12.8	43.9 yrs \pm 13.3
Female	68.9%	66.5%
Married/partner	66.5%	75.8%
Educational level	Lower: 33.3% Middle: 31.4% Higher: 33.5%	Lower: 25.3% Middle: 31.7% Higher: 38.6%
North-European ancestry	100%	100%





Phenotype	NESDA Cases	NTR Controls	GAIN Deposition
CIDI - MDD information (episodes & age of onset)	Yes	n/a	Initial
Depression severity (Inventory of Depressive Symptoms)	Yes	n/a	Initial
Family history of MDD	Yes	Yes	Future
Anxiety severity	Yes	Yes	Initial
Personality (neuroticism & extraversion)	Yes	Yes	Initial
Prospective follow-up	Yes	Yes	n/a
Demography – age, sex, ancestry, marital status, & educational attainment	Yes	Yes	Initial
Stressful life events	Yes	Yes	Future
Leisure time exercise behavior	Yes	Yes	
Licit & illicit substance use	Yes	Yes	Initial
Thyroid function (TSH & free T_3 , 99% of subjects)	Yes	No	Future
Cortisol profile (six time points, 75% of subjects)	Yes	No	Future
Heart Rate Variability (and other indices of autonomic nervous system functioning via VU-AMS system, 95% of subjects)	Yes	No	Future





Future Plans

- Increase Stage 1 sample (N=3,200 now)
 Can increase now to total of 4,600 or 8,000
- "Stage 1b" alternate genotyping
 - Subset of best SNPs
 - Promising SNPs with technical issues
 - Fill in sparse regions
 - "Too hard" MHC & mitochondrial tag SNPs
- Stage 2 N=14,000 & special samples
- Stage 3