

Introduction

The NIDA Poly-Substance Distribution 4.0 adds Study 23 (Vanyukov) to Dist 3.2 studies. There are n=4453 records (including dummy connectors) in 1880 families (including n=880 singletons). N=3465 subjects have blood samples. N=888 new records were added from Study 23.

Notes

1. Study 12. The twin question was asked only of parents and did not specify zygosity, only twin yes/no.
2. Study 12. Stimulant dep/abuse defined as Study 12 AMPHETAMINE dep/abuse.
3. Study 12. other drug dependence = one or more of Study 12 HALLUCINOGEN_DEPEND, INHALANT_DEPEND, PCP_DEPEND, PSYCHOACTIVE_SUB_DEPEND_NOS, POLYSUBSTANCE_DEPEND
4. Study 12. other drug abuse = one or more of Study 12 HALLUCINOGEN_ABUSE, INHALANT_ABUSE, PCP_ABUSE, PSYCHOACTIVE_SUB_ABUSE_NOS
5. Study12. dummy parent records added to connect nuclear families according to sub_seq 1 = father, sub_seq 2 = mother, sub_seq 3 = proband (child); no dummy parents added to singletons
6. Study 11. Stimulant dependence defined as Study 11 amphetamine dep .
7. Study 11. other drug dependence = one or more of Study 11 hallucinogen, inhalant, PCP, or club drug dependence.
8. Study 11. n=20 families have no members with a drug dependence or abuse diagnosis in clinic data yet are included because one or more family members have genotype data. Study 11 subjects with genotypes are indicated with the variable study11_gen0: 1=has genotype data, 0=no genotypes.
9. Study 11. genotype data. 2 = affected = clinical proband (either in treatment or otherwise considered at-risk). 1 = not proband (subject may have drug use or dependence).
10. Study 11. Documentation. For a description of the Study 11 sample, see Coors ME, et al, Directives for retained DNA: preferences of adolescent patients with substance and conduct problems and their siblings. Am J Bioeth. 2008 October ; 8(10): 77–79.
11. Study 11. The following number of records were removed from the distribution. The specific ids are listed in the file nida_study11_exclusions.sas7bdat.

nida_exclusion	Frequency
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EXCLUDE_IRB	7
EXCLUDE_SUB	47
fam no affected with blood (or geno)	14
family no blood (or geno)	9
geno data dup	14
ind_id discrepancy	23
mfblood dup	17

12. Study 19. Subjects are singleton adoptees so fam_id set to ind_id.
13. Study 19. when both DSM-IIIR and DSM-IV defined for a given subject, dx was coded positive if either system positive. dxsys was set to the diagnostic system for nicotine dependence, the most prevalent dx in this poly drug study. Original study dx and dx systems are preserved in study specific dataset.

14. Study 19. study19_gen0. indicator of presence in candidate gene data. These subjects were included even if no cell line at Rutgers.
15. Study 19. The following number of records were removed from the distribution. The specific ids are listed in the file nida_study19_exclusions.sas7bdat.

nida_exclusion	Frequency
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family no blood or geno	9
geno data dup	1
ind_id discrepancy	1
mfblood dup	3
no clinic data	195
no master id (study 19)	2

16. Study 23. Family design but lacks father and mother ids, only family identifier.
17. Study 23. Age is age at the date blood sample received by RUCDR; set age=0 to missing for n=10 subjects.
18. Study 23. AMPHETAMINE use disorder mapped to stimulant dependence.
19. Study 23. HALLUCINOGEN, INHALANT, PCP use disorder mapped to other drug dependence.
20. Study 23. families were included if at least one family member had a defined diagnosis (including unaffected) and a blood sample, so that control families were included.
21. Study 23. dx are DSM-III-R lifetime diagnoses