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Do genetic influences on abuse and dependence overlap? Explorations using cannabis and alcohol diagnoses

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Do genetic influences on abuse and dependence overlap? Explorations using cannabis and alcohol diagnoses.

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ABSTRACT

INTRODUCTION

Sample

- The Vietnam Era Twin Study Registry (VETS) is a national registry of male-male twin pairs in which both individuals were in the military during the Vietnam-era
  - 8,169 individuals completed a telephone diagnostic interview in 1992
    - 3537 complete twin pairs (MZ=1923, DZ=1529, unknown zygosity=85)
    - 1095 singletons (MZ=467, DZ=578, unknown zygosity=50)
  - Respondents with known zygosity were included in the present analyses

SAMPLE, cont.

Race	
Caucasian	94%
African-American	6%
Other	< 1 %

Marital Status	
Married	77%
Widowed	< 1%
Separated	2%
Divorced	13%
Single	7%

Educational Level	
< High school	3%
High school	31%
Some college	26%
Voc./Tech. degree	16%
Bachelor’s degree	13%
Some graduate work	4%
Graduate degree	7%

NOTE: race and educational level were asked in 1987; marital status was asked in a 1992 interview

MEASURES

- Alcohol use:
  - Drinkers (at least once a month for 6+ months, or 5+ lifetime)
  - DSM-III-R abuse
  - DSM-III-R dependence
- Cannabis use:
  - Ever tried
  - DSM-III-R abuse
  - DSM-III-R dependence
- See Table 1 for percentages of respondents who have used the substances and the mean age of initiation

Table 1

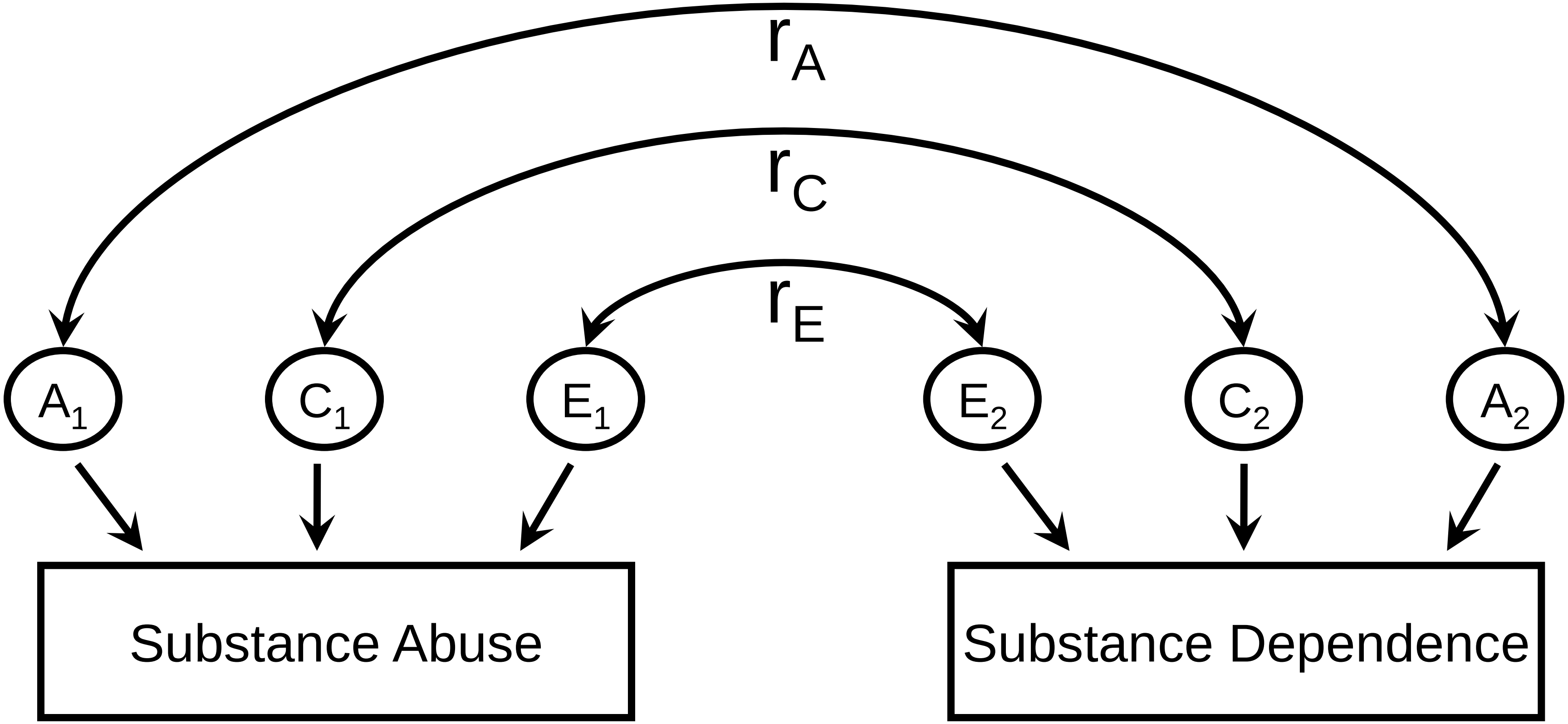
	% of sample (n=8169)		Mean age of initiation
Drinkers	91%	(n=7440)	18.4 yrs
Alcohol abuse ever (w/ or w/out depend.)	59%	(n=4388)	---
Alcohol abuse only (no depend.)	21%	(n=1543)	---
Alcohol dependence (w/ or w/out abuse)	39%	(n=2916)	---
Ever tried cannabis	48%	(n=3884)	20.0 yrs
Cannabis abuse ever (w/ or w/out depend.)	26%	(n=998)	---
Cannabis abuse only (no depend.)	14%	(n=531)	---
Cannabis dependence (w/ or w/out abuse)	14%	(n=540)	---

ANALYSES

- Bivariate quantitative genetic analyses were conducted separately for alcohol abuse/dependence and cannabis abuse/dependence
- The variables included for each substance were:
  - Having ever had an abuse diagnosis
  - Having ever had a dependence diagnosis
- The basic model is depicted in Figure 1
- The significance of overlap between variables was tested by dropping the paths from A_1, C_1, and E_1 to variable 2
- The significance of influences specific to variable 2 was tested by dropping the paths A_2, C_2, and E_2 to variable 2

Figure 1

Bivariate Model



A = additive genetic　　C = shared environment　　E = nonshared environment

RESULTS

- Alcohol abuse and dependence were best explained by a model that included additive genetic (A) and nonshared environmental (E) influences
  - Proportions of variance are shown in Table 2
- Cannabis abuse and dependence were best explained by a model that included additive genetic (A), shared environmental (C), and nonshared environmental (E) influences,
  - Proportions of variance are shown in Table 3
  - Note that the shared environmental parameter only reached statistical significance for cannabis dependence

Table 2

Proportions of Variance for Alcohol

* indicates p < .05

Table 3

Proportions of Variance for Cannabis

	Cannabis Abuse	Cannabis Dependence
Genetic	.32* (.03-.43)	.38* (.24-.52)
Shared Environmental	.06 (.00-.31)	.14* (.0003-.37)
Nonshared Environmental	.62* (.51-.73)	.48* (.37-.60)

* indicates $p < .05$

RESULTS, cont.

- For cannabis, correlations between genetic (and environmental) influences on abuse overlapped highly with those on dependence, with all correlations estimated at 0.75 or greater (see Table 5)

Table 4

Genetic and Environmental Correlations between alcohol abuse and alcohol dependence

* indicates significant at p < .05
(note that the confidence intervals for correlations can range from -1 to +1)

Table 5

Genetic and Environmental Correlations between cannabis abuse and cannabis dependence

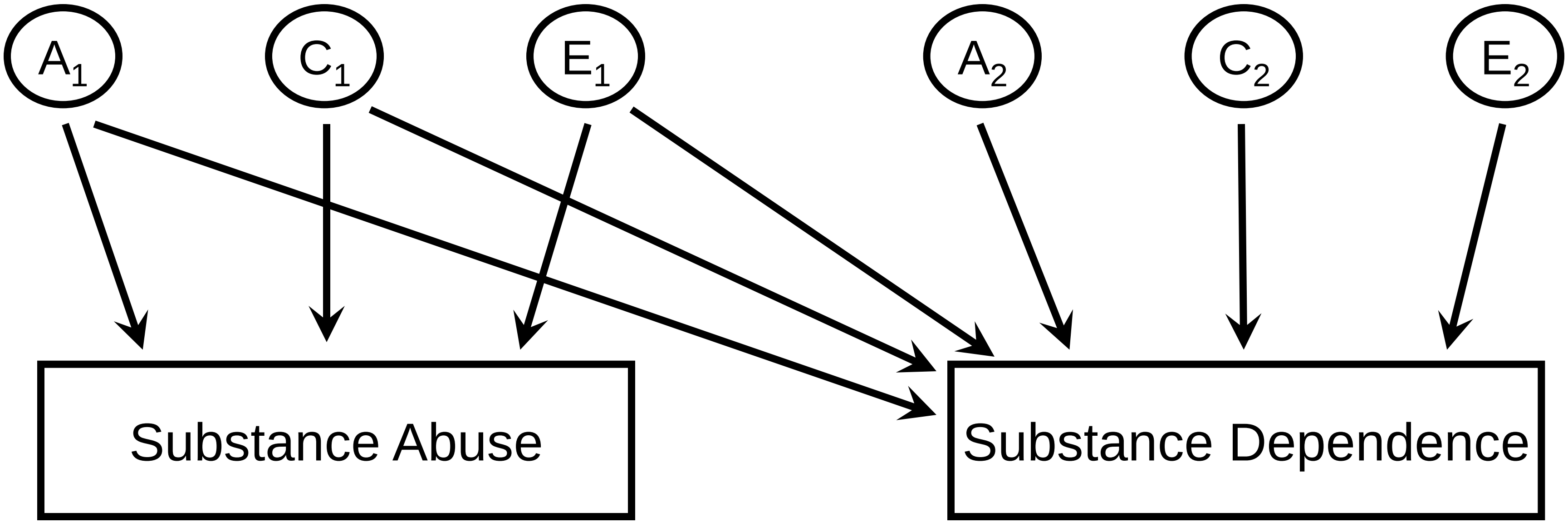
Genetic	1.00* (0.77-1.00)
Shared environmental	1.00* (0.01-1.00)
Nonshared environmental	0.75* (0.68-0.83)

* indicates significant at p < .05
(note that the confidence intervals for correlations can range from -1 to +1)

CONCLUSIONS

Figure 1

Bivariate Model



A_1 C_1 E_1 A_2 C_2 E_2

Substance Abuse

Substance Dependence

A = additive genetic C = shared environment E = nonshared environment

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