Grey matter volume, psychotic disorders, and heredity of alcohol use disorder: Reconceptualization by B-SNIP Biotypes

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Introduction

B-SNIP: The Bipolar and Schizophrenia Network for Intermediate Phenotypes revealed different levels of dysfunction patterns through EEG and cognitive testing.[1]

Psychotic disorders: Structural[2] and functional[3] deficits are well-known in schizophrenia (SCZ) and reported in B-SNIP biotypes.

Alcohol misuse: Drinking can result in grey matter (GM) atrophy[4] and abnormal default mode (DMN)[5] and central executive (CEN)[6] network activation.

Heredity: Structural and functional deficits have been associated with heredity and genetics among both psychotic[7] and alcohol use disorders[8] including genetic overlap[9].

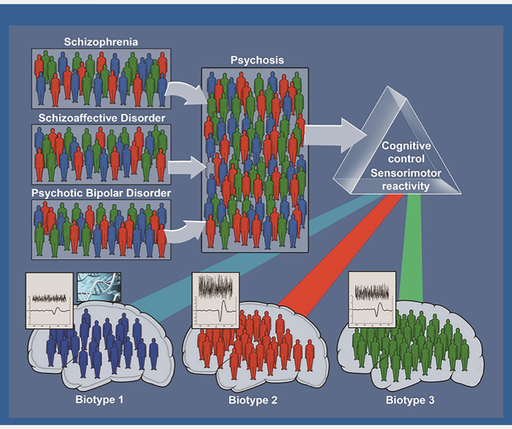
Questions

1. How can B-SNIP structural anatomic data be used to further understand the biomarker of GMV in relation to disorders on the psychosis spectrum?
2. How can this research enhance the conceptual understanding of the B-SNIP Biotypes, as well as increase understanding of vulnerability and comorbidity, by additionally analyzing the influence of family history of AUD on GMV?

Method

Measures *(secondary data analysis)*

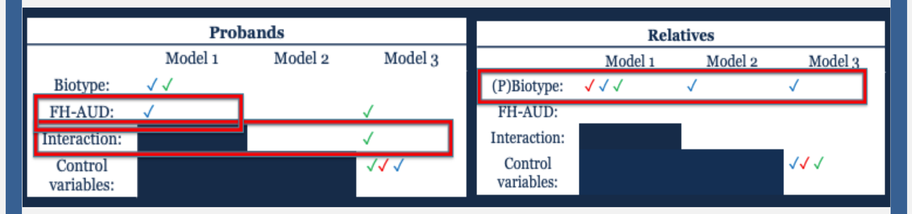
- Structural Clinical Interview for DSM-IV-TR (SCID)
- Study specific survey for presence of alcohol use disorder (AUD) family history (FH-AUD+/-)
- Biotypes determined through clustering methods using electrophysiological and cognitive data



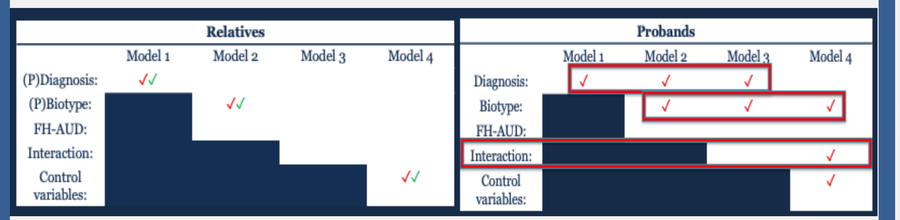
These 'biotypes' may have greater biological validity… than diagnostic categories limited to observable symptoms."[10]

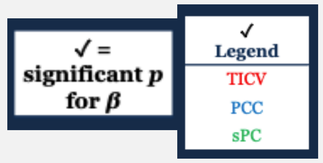
Results

Biotype Analysis



Combination Analysis





Discussion

- Proband Biotype was a consistent predictor of GMV in probands and relatives.
- Biotype was a more useful predictor than conventional DSM diagnosis.
- FH-AUD+/- and the interaction between FH-AUD+/- and Biotype were predictors in probands.
- The interaction was significant in the CEN (sPC) and TICV, but not the DMN (PCC).
- *Clinical implication:* executive functioning impairment via influence of Biotype and FH-AUD+/- on the CEN.

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Acknowledgment

Data and/or research tools used in the preparation of this poster were obtained from the National Institute of Mental Health (NIMH) Data Archive (NDA). NDA is a collaborative informatics system created by the National Institutes of Health to provide a national resource to support and accelerate research in mental health. Dataset identifier(s): 10.15154/1519195. This poster reflects the views of the authors and may not reflect the opinions or views of the NIH or of the Submitters submitting original data to NDA.

Method

Participants

- Probands (n = 347) and their first-degree relatives (n = 346)
- Proband diagnoses: Schizophrenia, schizoaffective disorder, or bipolar disorder with psychotic features

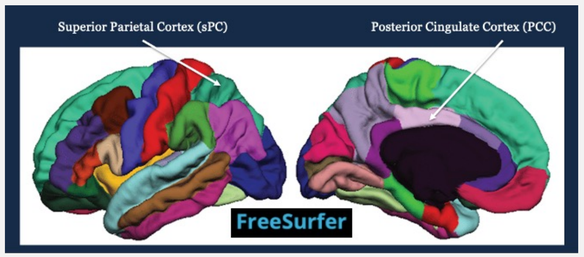
Gender:	59% female
Age:	M = 39 (SD = 13.9)
Race/ethnicity:	62% white
Education (years):	M = 13.9 (SD = 2.5)
FH-AUD+:	43% probands | 44% relatives
Antipsychotic use:	89% probands

Procedure

- Participants were categorized by B-SNIP Biotype (1-3) and DSM categories, and identified as FH-AUD+/-

Regions of Interest

- Superior parietal cortex (sPC) -> CEN
- Posterior cingulate cortex (PCC) -> DMN
- Total intracranial volume (TICV) -> global effect



Statistical Analyses

1. Biotype, FH-AUD+/-
2. Biotype, FH-AUD+/-, interaction
3. Biotype, FH-AUD+/-, interaction, control variables

Biotype Only

1. Diagnosis
2. Diagnosis, Biotype, FH-AUD+/-
3. Diagnosis, Biotype, FH-AUD+/-, interaction
4. Diagnosis, Biotype, FH-AUD+/-, interaction, control variables

- Control variables: age, sex, education, ethnicity, and antipsychotic medication use among probands only

Combination: Biotype and Diagnosis