Operation of the Schizophrenia Susceptibility Gene, Neuregulin 1, Across Traditional Diagnostic Boundaries to Increase Risk for Bipolar Disorder

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Context: Family and twin data suggest that, in addition to susceptibility genes specific for bipolar disorder or schizophrenia, genes exist that contribute to susceptibility across the traditional Kraepelinian divide. Several studies have provided evidence that variation at the neuregulin 1 (NRG1) gene on chromosome 8p12 influences susceptibility to schizophrenia. The most consistent finding has been that one particular haplotype (the “core” haplotype) is overrepresented in cases compared with control subjects.

Objective: To investigate the possible role of NRG1 in bipolar disorder.

Design: Genetic case-control association analysis.

Setting: Subjects were unrelated and ascertained from general psychiatric inpatient and outpatient services.

Participants: Five hundred twenty-nine patients with DSM-IV bipolar 1 disorder and 1011 controls from the United Kingdom (100% white).

Methods: We genotyped the markers constituting the NRG1 core haplotype in cases and controls and reanalyzed our existing data from 573 DSM-IV schizophrenia cases with this larger set of controls.

Results: We found a significant difference in haplotype distribution between bipolar cases and controls globally (P=.003) and specifically for the core haplotype. Frequencies were 10.2% for bipolar cases and 7.8% for controls (effect size, as measured by odds ratio [OR], 1.37; 95% confidence interval [CI], 1.03-1.80; P=.04). The effect size in our bipolar sample was similar to that in our schizophrenia sample (OR, 1.22; 95% CI, 0.92-1.61). In the bipolar cases with predominantly mood-incongruent psychotic features (n=193), the effect was greater (OR, 1.71; 95% CI, 1.29-2.59; P=.009), as was the case in the subset of schizophrenia cases (n=27) who had experienced mania (OR, 1.64; 95% CI, 0.54-5.01).

Conclusions: Our findings suggest that neuregulin 1 plays a role in influencing susceptibility to bipolar disorder and schizophrenia and that it may exert a specific effect in the subset of functional psychosis that has manic and mood-incongruent psychotic features.

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haps likelihood, that there is not a neat biological distinction between schizophrenia and bipolar disorder. Some workers, such as Crow,7 have argued strongly in support of a continuum approach to psychosis. The likelihood of a genetic overlap across the Kraepelinian divide finds support in several observations from genetic research. First, although family studies have shown substantial consistency in demonstrating that schizophrenia and bipolar disorder tend to “breed true,”8-30 some studies have also shown statistically significant evidence that bipolar disorder occurs at increased frequency in the relatives of probands with schizophrenia13 and that schizophrenia occurs at increased frequency in the relatives of bipolar probands.12 Moreover, schizoaffective disorder has been shown to occur at an increased rate in the families of probands with schizophrenia13 and bipolar disorder,14 and schizophrenia and bipolar disorder have been shown to occur at an increased rate in the families of probands with schizoaffective disorder.15 These family data argue for a more complex relationship between the psychoses than is reflected in the conventional dichotomous view. Second, a recent twin study that used an analysis unconstrained by the diagnostic hierarchy inherent in current classification systems (ie, the principle that schizophrenia trumps mood disorder in diagnosis) demonstrated an overlap in the genetic susceptibility to mania and schizophrenia.15 A graphic illustration of the varied expression of the same set of susceptibility genes is provided by the Maudsley triplets—a set of genetically identical triplets, of whom 2 had an RDC lifetime diagnosis of schizophrenia and the third an RDC lifetime diagnosis of bipolar I disorder.16 Third, genetic linkage studies have identified some chromosomal regions that show convergent or overlapping regions of interest in both disorders, including regions of chromosome 13q, 22q, and 18.17,18 Fourth, recent reports implicating variation at the gene encoding D-amino-acid oxidase activator (DAOA; formerly known as the G72/G30 locus) on chromosome 13q in schizophrenia19,20 and bipolar disorder21,22 suggest that the substantial circumstantial and genetic evidence is starting to gain molecular genetic support.

Given this background, it is important that any gene found to influence susceptibility to schizophrenia should also be examined in bipolar disorder. Herein we report the first study, to our knowledge, of bipolar disorder with polymorphisms in the neuregulin 1 (NRG1) gene. Neuregulin 1 is highly expressed in the brain and is a member of a family of proteins that signal through tyrosine kinase receptors and thereby exert a key role in neurodevelopmental processes in the central nervous system that are thought to be relevant to the pathogenesis of schizophrenia, including (1) neuronal migration and specification, (2) hormonal controls of puberty, (3) regulation of acetylcholine, y-aminobutyric acid, and glutamate, and (4) oligodendrocyte development.23,24 The NRG1 gene maps to chromosome 8p12, a region implicated in several genome scans for schizophrenia (locus SCZD6 [Mendelian Inheritance in Man No. 603013]).25-29 After their initial evidence for linkage of schizophrenia to 8p21-p12 in a large number of multigeneration families from Iceland, Stefansson and colleagues29 performed case-control and family-based association analyses and obtained evidence for association between schizophrenia and several haplotypes at NRG1. The entire exonic sequence of NRG1 was extensively screened for mutations in 184 patients with schizophrenia, but despite identifying a large number of variants, it was not possible to find any that were unambiguously associated with schizophrenia. The most important finding, however, was the identification of a single “core at-risk haplotype” (henceforth referred to as the core haplotype), which was significantly overrepresented in individuals with schizophrenia compared with controls (15.4% vs 7.5%; P=6.7×10−6). This has been replicated in a large case-control sample from Scotland30 and our own sample from the United Kingdom31 demonstrating that the risk haplotype is not specific to the Icelandic population. A study of Japanese schizophrenia cases and controls failed to find significant evidence for association with the core haplotype, but, consistent with other studies, the core haplotype was more common in familial cases than controls (7.7% vs 5.1%).32 Evidence for linkage disequilibrium between schizophrenia and different haplotypes that overlap the core haplotype has been reported in an Irish case-control sample,33 3 Han Chinese samples,34-36 and a South African sample but not in a US sample.37 A recent analysis of the Irish high-density schizophrenia families found no clear-cut evidence of linkage disequilibrium between schizophrenia and haplotypes at NRG1. The full-core haplotype itself was not examined in that study, but sliding window analysis of haplotypes across the core haplotype region showed modest nominally significant evidence for association with some haplotypes.38 A schematic representation of the NRG1 gene and previous findings is shown in Figure 1.

Given that we found supportive evidence for the association with the core haplotype in our schizophrenia sample, we have used our similarly recruited bipolar sample to examine the hypothesis that the core haplotype is also associated with risk for bipolar disorder in general and a subset with phenotypic features related to

In the present study, we have examined the risk of schizophrenia and bipolar disorder by linkage disequilibrium sliding window analysis of haplotypes across the core haplotype. In a large number of multigeneration families from Iceland, Stefansson and colleagues performed case-control and family-based association analyses and obtained evidence for association between schizophrenia and several haplotypes at NRG1. The entire exonic sequence of NRG1 was extensively screened for mutations in 184 patients with schizophrenia, but despite identifying a large number of variants, it was not possible to find any that were unambiguously associated with schizophrenia. The most important finding, however, was the identification of a single “core at-risk haplotype” (henceforth referred to as the core haplotype), which was significantly overrepresented in individuals with schizophrenia compared with controls (15.4% vs 7.5%; P=6.7×10−6). This has been replicated in a large case-control sample from Scotland and our own sample from the United Kingdom demonstrating that the risk haplotype is not specific to the Icelandic population. A study of Japanese schizophrenia cases and controls failed to find significant evidence for association with the core haplotype, but, consistent with other studies, the core haplotype was more common in familial cases than controls (7.7% vs 5.1%). Evidence for linkage disequilibrium between schizophrenia and different haplotypes that overlap the core haplotype has been reported in an Irish case-control sample, 3 Han Chinese samples, and a South African sample but not in a US sample. A recent analysis of the Irish high-density schizophrenia families found no clear-cut evidence of linkage disequilibrium between schizophrenia and haplotypes at NRG1. The full-core haplotype itself was not examined in that study, but sliding window analysis of haplotypes across the core haplotype region showed modest nominally significant evidence for association with some haplotypes. A schematic representation of the NRG1 gene and previous findings is shown in Figure 1.

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schizophrenia in particular. Within current classifications, 1 of the key features of schizophrenia is the presence of psychotic features that are mood incongruent, ie, they are not understandable within the context of mood state.4,5 We therefore hypothesized that the subset of patients with bipolar disorder who experienced predominantly mood-incongruent psychotic features would be most likely to show evidence of an influence of susceptibility from NRG1.

METHODS

SUBJECTS

All of the subjects in these studies were white and of UK origin and provided written informed consent to participate in genetic studies. Protocols and procedures were approved by relevant ethical review panels including the UK West Midlands Multi-Center Research Ethics Committee, Birmingham, England.

BIPOLAR PROBANDS

Cases were recruited through mental health services in England and Wales and met DSM-IV criteria for bipolar 1 disorder (n=529; 38% men; mean age, 48 years [SD, 13 years]; mean age at onset, 26 years [SD, 10 years]). The ICD-10 diagnoses included bipolar disorder (manic) in 512 and schizoaffective disorder (bipolar) in 17; RDC diagnoses, bipolar I disorder in 481 and schizoaffective disorder (bipolar) in 48. A history of psychiatric illness in a first- or second-degree relative was present in 60%. Diagnoses were made by the consensus lifetime best-estimate method on the basis of all available information, including a semistructured interview (Schedules for Clinical Assessment in Neuropsychiatry),41 and review of psychiatric case records, and an OPCRIT checklist was completed.42 Key clinical variables relating to psychosis were rated using the Bipolar Affective Disorder Dimension Scale (BADDS).43 In our sample, bivariate correlation coefficients were 0.89 for the BADDS incongruence dimension shows the best estimate of the overall balance between mood-congruent and mood-incongruent psychotic features. Mood incongruence was defined according to the guidelines in the DSM-IV and BADDS.43 In our sample, bipolar cases had a lifetime occurrence of 1 or more psychotic features in 62% and a lifetime occurrence of predominantly mood-incongruent psychotic features (ie, mood-incongruent features constitute 50% or more of the psychotic features that occur) in 36%. Interrater reliability was high for the measures used in this study. This was formally assessed using 20 cases and resulted in mean k statistics of 0.85, 0.83, and 0.80 for DSM-IV, ICD-10, and RDC diagnoses, respectively. Mean intraclass correlation coefficients were 0.89 for the BADDS incongruence dimension and 0.86 for the psychosis dimension. Formative team reliability meetings took place weekly throughout recruitment.

CONTROLS

Controls (n=1011; 57% men; mean age, 42 years [SD, 12 years]), all white and of UK origin, were collected from 2 sources. One source was the British Blood Transfusion Service. This sample (n=902) did not undergo specific screening for psychiatric illness, but individuals were not taking regularly prescribed psychiatric medications. In England and Wales, blood donors are not remunerated, even for expenses, and are therefore not over-represented by the indigent or the socially disadvantaged in whom the rate of psychosis might possibly rise above a threshold that would influence power.44 The second source was individuals who were recruited from among those attending a family practitioner clinic for nonpsychiatric reasons. This sample (n=109) was screened to exclude a personal history of mood disorder.

GENOTYPING

The core haplotype of Stefansson et al25 can be defined by 1 single nucleotide polymorphism (SNP) and 2 microsatellites that were typed as follows. The SNPNRGR221333 was genotyped using a fluorescence polarization–based primer extension assay45 with the AcycloPrime Kit (Perkin Elmer Life Sciences, Boston, Mass) according to manufacturer’s instructions and an Analyst genotyping platform (LJL Biosystems, Sunnyvale, Calif). The microsatellites 478B14848 and 420M91395 were genotyped after analysis on an ABI3100 capillary sequencer (Applied Biosystems, Foster City, Calif).

STATISTICAL ANALYSIS

Departure from Hardy-Weinberg equilibrium was tested using a x2 goodness-of-fit test. Tests for differences between allele and haplotype frequencies were performed using UNPHASED software, version 2.40.46 The effect of haplotypes was assumed to be additive. The primary analysis was a comparison of the frequency of the core haplotype between patients and controls, allowing a 1-df test that maximizes power to test our hypothesis. We also examined a global haplotype test using the restriction of excluding rare haplotypes (frequencies of <1%). Uncertain haplotypes were estimated using the expectation maximization algorithm within UNPHASED. Two-tailed P values are reported. Nominally significant asymptotic P values were confirmed by permuting the case-control status for 50,000 replicates and observing the maximum test statistic in each case. We undertook testing for population stratification as a potential cause of finding genetic differences between our case and control samples using the program STRUCTURE,39 with 18 SNPs and 20 microsatellites distributed across the autosomes and unlinked to the NRG1 locus.

RESULTS

The controls underwent genotyping for the NRG1 polymorphisms in 2 waves. The first underwent genotyping with our schizophrenia sample (618 controls), with the results reported in Williams et al31; the second underwent genotyping with the bipolar sample (393 controls). Duplicate samples were typed and allele coding was verified. There were no significant deviations from Hardy-Weinberg equilibrium in the separate or in combined control sets. The allele frequencies for each of the 3 markers showed no significant difference between the 2 control sets. Further, the 2 control samples had similar levels of linkage disequilibrium between the loci (data not shown). Pooling the controls yielded a total sample of 1011 control individuals who underwent genotyping for all loci.

There were no significant differences in the allele distributions between bipolar cases and controls for any of the markers. We found a significant difference between
the overall distribution of 3-locus haplotypes between bipolar cases and controls (*P*=.003). Inspection of these haplotypes showed that the largest absolute difference in haplotype frequencies was found for the core haplotype, with the global signal also coming from a series of small differences at several rarer haplotypes (but all having a frequency >1%). Results of our primary analyses of the core haplotype frequency comparisons with controls are presented in the Table. Consistent with our hypothesis, the core haplotype was significantly more common in our bipolar cases than in the controls (odds ratio [OR], 1.37; 95% confidence interval [CI], 1.03-1.80; *P*=.04). The magnitude of this overrepresentation was very similar in the subset of 329 bipolar cases who had lifetime experience of psychotic features (OR, 1.34; 95% CI, 0.94-1.90; *P*=.11), but consistent with our hypothesis, it was increased within the subset of bipolar individuals who had experienced psychotic features that were predominantly mood incongruent (defined by a BADDS incongruence dimension score ≥20; OR, 1.71; 95% CI, 1.29-2.59; *P*=.009). This analysis had been decided a priori, and clinically this corresponds to at least half of the psychotic features experienced during a subject’s lifetime being rated as mood incongruent. Comparing this subset of bipolar cases (ie, with an incongruence dimension score ≥20) against all remaining bipolar cases demonstrated a significant difference in the core haplotype frequency (*P*=.04). All effect sizes were very similar when cases were separately compared against the controls undergoing genotyping in the first or second waves or when cases were separately compared against the subset of blood donor controls or the subset of family practice controls. We explored the effect on the estimate of effect size (measured by the OR) of variation in the preponderance of mood incongruence in psychotic symptoms experienced and found that the estimated OR increased with increasing mood incongruence, as measured by the incongruence dimension of BADDS (Figure 2). For example, when comparing the group of bipolar cases with BADDS incongruence dimension scores greater than or equal to 30, we found an OR of 1.95 (95% CI, 1.11-

### Table. Frequency of the Core Haplotype at NRG1 in Controls, Bipolar Cases, and Schizophrenia Cases

<table>
<thead>
<tr>
<th>Test</th>
<th>Frequency of Core Haplotype, %</th>
<th>Value for Comparison vs Controls</th>
<th>OR (95% CI)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Controls (n = 1011)</td>
<td>7.8*</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Bipolar (n = 529)</td>
<td>10.2</td>
<td>.04</td>
<td>1.37 (1.03-1.80)</td>
</tr>
<tr>
<td>Bipolar-P (n = 329)</td>
<td>10.1</td>
<td>.11</td>
<td>1.34 (0.94-1.90)</td>
</tr>
<tr>
<td>Bipolar-I (n = 193†)</td>
<td>12.3</td>
<td>.009</td>
<td>1.71 (1.29-2.59)</td>
</tr>
<tr>
<td>Bipolar-I (n = 95‡)</td>
<td>14.1</td>
<td>.01</td>
<td>1.95 (1.11-3.41)</td>
</tr>
<tr>
<td>Bipolar-NI (n = 336§)</td>
<td>9.1</td>
<td>.33</td>
<td>1.19 (0.82-1.72)</td>
</tr>
<tr>
<td>Schizophrenia (n = 573)</td>
<td>9.5</td>
<td>.18</td>
<td>1.22 (0.92-1.61)</td>
</tr>
<tr>
<td>Schizophrenia-M (n = 27)</td>
<td>12.2</td>
<td>.29</td>
<td>1.64 (0.54-5.01)</td>
</tr>
<tr>
<td>Schizophrenia-NM (n = 545)</td>
<td>9.2</td>
<td>.24</td>
<td>1.20 (0.90-1.60)</td>
</tr>
<tr>
<td>Schizophrenia-M + bipolar-I (n = 220)</td>
<td>12.2</td>
<td>.007</td>
<td>1.70 (1.15-2.51)</td>
</tr>
<tr>
<td>Schizophrenia-NM + bipolar-NI (n = 881)</td>
<td>9.2</td>
<td>.17</td>
<td>1.20 (0.96-1.51)</td>
</tr>
<tr>
<td>RDC SABP (n = 75)</td>
<td>12.7</td>
<td>.05</td>
<td>1.72 (1.06-2.10)</td>
</tr>
</tbody>
</table>

Abbreviations: BADDS, Bipolar Affective Disorder Dimension Scale; bipolar, bipolar I disorder; CI, confidence interval; core haplotype, “core at-risk haplotype”; NRG1, neuregulin 1 gene; OR, odds ratio; P, with lifetime occurrence of 1 or more psychotic features; RDC, Research Diagnostic Criteria; SABP, schizoaffective disorder of bipolar type.

*It is a property of the estimation algorithms that when estimating control haplotype frequencies, the estimates vary slightly according to the composition of the case sample. Thus, estimates range from 7.7% to 7.9%, according to the analysis.
†Indicates a score greater than or equal to 20 on the incongruence dimension of the BADDS.
‡Indicates a score greater than or equal to 30 on the incongruence dimension of the BADDS.
§Excludes those with a score greater than or equal to 20 on the incongruence dimension of the BADDS.

Figure 2. Variation in estimated odds ratios (ORs) with score on the incongruence dimension of the Bipolar Affective Disorder Dimension Scale (BADDS) for the “core at-risk haplotype” (core haplotype) for bipolar I disorder cases compared with controls. The ORs were estimated for the set of cases with a score equal to or exceeding the BADDS incongruence dimension value shown on the x-axis, compared with the set of controls. Thus, as the incongruence dimension score increases on the x-axis, a successively smaller subset of cases (with greater mood incongruence) is compared against controls. Only cases with lifetime psychotic symptoms and sufficient information to make a consensus judgment about the balance of mood congruence had a rating on the incongruence dimension (n=320) and therefore contributed to this analysis. The significance of the upward trend was tested using a sign test of the direction of changes in the OR with the increase of the incongruence dimension score (compared with the null expectation of a 50% chance of an increase of the OR with each increase of the incongruence dimension score). This demonstrated significance at *P*=.002.
COMMENT

Consistent with our hypotheses, we found significant evidence for the association of the schizophrenia core haplotype at NRG1 with susceptibility to bipolar I disorder, and the pattern of results showed a stronger signal within the bipolar cases in whom psychotic features were predominantly mood incongruent. Further, there was a clear and statistically significant trend for the estimated effect size to increase with the degree of mood incongruence, as measured by the incongruence dimension of the BADDS. These findings are of interest for several reasons.

First, in our large samples recruited using similar methods and ascertainment approaches in the same geographical and clinical locations, we found that the estimated effect size of the core haplotype was very similar in our bipolar and schizophrenia cases, suggesting that NRG1 is not a specific schizophrenia susceptibility gene but instead confers risk across the traditional Kraepelinian dichotomy. An interesting observation in our data was that the small subset of schizophrenia cases in whom at least 1 definite manic episode had occurred (n=27) showed higher estimates for the frequency of the core haplotype, at a level similar to that for the bipolar individuals with predominantly mood-incongruent psychotic features (Table).

Analysis of the set of autosomal microsatellites (n=20) and SNPs (n=18) unlinked to the NRG1 locus using the STRUCTURE program showed no evidence of population stratification (tested under a presumed subpopulation number, k=1, 2, and 3) in our case-control sample (data not shown).

Second, although the 8p12 region has not been implicated in meta-analyses of bipolar disorder genome scans, a recent linkage analysis of psychosis in bipolar pedigrees reported genome-wide significant evidence of linkage in this region. The findings reported herein suggest that NRG1 may be responsible for the linkage signal in that scan.

Third, our phenotype analyses are consistent with the core haplotype at NRG1 exerting some specificity on susceptibility to mania and mood-incongruent psychotic features. It might, therefore, more appropriately be regarded as a schizoaffective susceptibility haplotype. However, it is important to recognize that the effect was not restricted to the 48 bipolar cases meeting formal RDC for schizoaffective disorder but was also present in the additional 145 bipolar cases with predominantly mood-incongruent features not conventionally regarded as schizoaffective under current classifications. Identification of 1 or more variants that have specificity for an intermediate form between the traditional major categories of schizophrenia and bipolar disorder would have major importance for nosology and understanding of pathophysiology of the major psychoses. Indeed, our findings support the view that alternative approaches to classification of the functional psychoses will more closely reflect biology. For example, our data are consistent with the suggestion by Crow of a dimensional or continuum approach to the functional psychosis phenotype, although they are incompatible with his hypothesis that a single gene underlies all psychoses.

Fourth, our findings suggest that in seeking bipolar cases most likely to have an overlap in pathogenesis with schizophrenia, it may not be sufficient simply to examine the subset with lifetime occurrence of psychotic features. Instead, the qualitative similarity of the psychotic features to those seen in schizophrenia is relevant. This argues for the importance of detailed phenotypic characterization of samples.

Fifth, our previously reported schizophrenia sample shows reduced support for the involvement of NRG1 in the pathogenesis of schizophrenia. However, it should be noted that the core haplotype frequency in our schizophrenia cases is very close to that observed in the Scottish sample. The difference in statistical significance comes from the different estimates in control frequency for the core haplotype. The finding of an increased effect in our manic subset of schizophrenia cases should be interpreted cautiously because of the small number of cases in this subset (n=27).

Sixth, it is of interest that the mouse model used by Stefansson et al to provide support for the involvement of NRG1 in schizophrenia has hyperactivity as 1 of the key features, a behavior, perhaps, more characteristic of mania than schizophrenia. Thus, the animal data are at least as supportive of the involvement of NRG1 in bipolar spectrum illness as they are supportive of its involvement in schizophrenia.

Seventh, the presence of a global linkage disequilibrium signal between bipolar cases and controls cannot be entirely explained by the core haplotype, with additional evidence coming from several relatively rare haplotypes, each showing modest differences. This could be the result of multiple, independent, relatively uncommon variants that influence susceptibility to bipolar illness or the result of 1 or a small number of variants occurring on multiple haplotypes. These possibilities are entirely consistent with the current state of understanding of the role of NRG1 in schizophrenia where no causative variants have yet been identified and multiple haplotypes have been reported that are associated with schizophrenia susceptibility within and between samples.
In any case-control study, spurious differences between cases and controls that are unrelated to disease status can be caused by the presence of so-called population structure, which may result in differential sampling of cases and controls from genetically distinct subpopulations. However, we can be confident that this is not the cause of our findings for the following reasons: (1) Results of formal tests for stratification demonstrated no evidence of stratification in our sample. (2) The direction and magnitude of effect is similar to that observed in several other case-control studies of samples from European populations, including Iceland and the United Kingdom. (3) The estimated effect sizes in our sample are closely similar in our blood donor and our family practice controls. (4) The clear and significant relationship between the OR and mood incongruence (Figure 2) is very unlikely to arise from population stratification. Nonetheless it is generally desirable that a finding from a case-control design is explored in family-based association designs that are robust to population stratification. However, there is a practical difficulty in that samples exceeding 800 parent-proband trios would be required to provide 80% power to detect the effect observed in our study (Genetic Power Calculator49; available at: http://statgen.iop.kcl.ac.uk/gpc/). This required sample size substantially exceeds any that are available at present.

No previous reports of studies of NRG1 haplotypes in bipolar disorder have been published to date, and it is clearly important that other groups examine relevant independent samples. However, it will be essential that samples are adequately powered and sufficiently well characterized phenotypically, particularly in relation to the frequency and nature of psychotic symptoms. It will be appropriate to explore the haplotype-phenotype correlations within schizophrenia samples in addition to bipolar disorder samples. Analysis of sets of individuals having schizophrenic features and clear manic episodes will be of particular relevance. Given the findings with NRG1 in schizophrenia, it would be expected that an effect with the core haplotype in bipolar disorder will be most easily replicated in samples of North European origin.

Our findings add to the increasing molecular genetic evidence consistent with the involvement of NRG1 in the pathogenesis of psychotic illness and suggest that this may be the first gene to be identified that confers particular susceptibility to mania and mood-incongruent psychotic features. However, pathogenic variants remain to be identified, and it is important that detailed analyses are undertaken of multiple large samples using phenotypically informed approaches.

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