

Investigation of a Candidate Gene for Schizophrenia on Xq13 Previously Associated With Mental Retardation and Hypothyroidism

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Weak support for linkage of schizophrenia to proximal Xq has previously been reported. In addition, an increased prevalence of thyroid disorder has been noted in families of individuals with schizophrenia. Recently, a gene mapped to Xq13 termed *HOPA* has been found to be associated with mental retardation, hypothyroidism, and depression and to function as a coactivator for the thyroid receptor. We therefore examined the *HOPA* gene in a group of 111 probands from a larger cohort of multiplex families with schizophrenia, several of whom ($n = 53$) also had a family history of hypothyroidism. Four males and two females were found with an alteration in exon 42 of the *HOPA* gene compared with 8/492 males and 18/471 females (942 X chromosomes) compared with consecutively screened newborns ($\chi^2 = 3.92, P < 0.05$). However, when available family members of each of the probands with an exon 42 variation were subsequently screened, the mutation did not segregate with schizophrenia in three of five families, although all 6 probands with an exon 42 variation did have hypothyroidism in either themselves ($n = 3$) or their mothers ($n = 3$) ($P < 0.008$). These findings replicate prior findings demonstrating an association between *HOPA* polymorphisms and hypothyroidism. In addition, the increased frequency of *HOPA* variants in this population may also provide a genetic basis for the familial association of thyroid disease and schizophre-

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INTRODUCTION

A sex chromosome locus for schizophrenia has been previously hypothesized [Crow, 1988; Crow and DeLisi, 1991; DeLisi and Crow, 1989; DeLisi et al., 1988] based on the high frequency of X chromosome anomalies (XXY and XXX) among psychiatric hospital patients with psychosis [DeLisi et al., 1994b], an excess of same sex concordance for schizophrenia within families, and sex differences in age of onset and other clinical characteristics of the disorder. Linkage studies testing this hypothesis were either negative for the entire X chromosome [Okoro et al., 1995; Pulver et al., 1995] or weakly positive pericentromeric [Dann et al., 1997; DeLisi et al., 1994b; Hovatta et al., 1998; Lichtermann et al., 1999; Paterson, 1999; Williams et al., 1998]. In two recent studies extending results to a larger cohort [DeLisi et al., 1994a; Laval et al., 1998], minimally positive peak lod scores of approximately 1.5 were found pericentromeric. In the Laval et al. study, this peak was with marker DXS8032 mapped to Xp11.2 whereas a parallel QTL analysis of asymmetric hand-skill (a presumed measure of cerebral asymmetry) peaked within the Xq21.3 region approximately 20 cM away.

In addition, there is intriguing, though unexplained evidence for a higher frequency of thyroid abnormalities among relatives of patients with schizophrenia, particularly mothers of these patients [DeLisi et al., 1991; MacSweeney et al., 1978]. This increase is not surprising because alterations in thyroid function are associated with severe mental illness. For instance, thyroid abnormalities such as blunted TSH response and hypothyroidism are significantly increased among patients with depression [reviewed in Sachar, 1974] and schizophrenia [Ryan et al., 1994]. Furthermore, hyperthyroidism has long been known to cause an

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acute psychosis [Granet and Kalman, 1978; Greer and Parsons, 1968; Roca et al., 1990]. However, whether there is a genetic basis for this association is unclear.

Recently, exonic variations in exon 42 of an Xq13 gene termed *HOPA* were associated with a syndrome of mental retardation, hypothyroidism, and psychiatric symptoms [Philibert et al., 1998; Philibert et al., 1999]. The association with hypothyroidism became more interesting after another group reported that the *HOPA* gene codes for a thyroid receptor coactivator [Ito et al., 1999]. Given the evidence suggesting some linkage of schizophrenia to proximal Xq and the high prevalence of hypothyroidism in the schizophrenic population, we then hypothesized that alterations in the *HOPA* sequence may be associated with increased risk for schizophrenia or hypothyroidism. Thus, in the present study, we report the results of our initial investigation of this hypothesis and conclude that further studies are clearly merited.

METHODS AND MATERIALS

Clinical

Families with schizophrenia or schizoaffective disorder in at least 2 siblings were identified over a period of approximately 15 years, from 1985 to the present [see DeLisi et al., 1987, 1994a; Garner et al., 1996; Shaw et al., 1998]. Those from the United States and collected within the Department of Psychiatry, SUNY, Stony Brook were screened for a history of multiple medical disorders including thyroid disease in a first-degree relative. Recruitment involved several methods: catchment area screening, systematic contact with health professionals at hospital and out-patient facilities, and advertisement through local and national support organizations for families of the mentally ill [i.e., the National Alliance for Mental Illness (NAMI)].

Diagnoses were made using *DSM-III-R* [American Psychiatric Association, 1987] criteria based on a combination of structured interviews, medical records from all hospitalizations, or other relevant treatment and structured information about each individual obtained from at least one reliable family member. A modified SADS interview was used from 1985–1994 [Schedule for Affective Disorder and Schizophrenia, Spitzer and Endicott, 1978] combined with the SIDP [Structured Interview for Personality Disorders, Pfohl et al., 1990]. From 1994 to the present, these forms were replaced by the newer, comprehensive DIGS interview [Diagnostic Interview for Genetic Studies, Nurnberger et al., 1994] and many of the ill individuals in previously obtained families were reinterviewed using this method.

In stage I of this study, coded blood or DNA samples from 111 unrelated probands (82 male, 29 females) from the aforementioned families were selected for genotyping with respect to *HOPA* exon 42. Of these, 85 were diagnosed with chronic schizophrenia, 22 schizoaffective disorder, depressed or mixed type, and 4 schizoaffective, manic type. Fifty-three of these schizophrenic probands (47 males, 6 females) had either personal and/or family history (first-degree relative) of hypothyroidism (11 probands, 32 mothers of probands, 5 fathers of probands, 19 siblings of probands). The other

58 schizophrenics (37 males, 21 females) did not have personal or family histories of hypothyroidism.

In stage II, DNA sample genotyping was performed on all available DNA from family members of probands who showed an unusual allelic variation in exon 42 of the *HOPA* gene.

Laboratory

Individuals who were blind to diagnostic status conducted all laboratory procedures. When necessary, DNA from blood samples of schizophrenic probands was prepared using a QuiAmp kit (Qiagen, Santa Clarita, CA, U.S.A.). Genotyping of the proband DNA at the exon 42 dodecamer repeat was performed using standard PCR protocols and conditions for radioisotopic genotyping, ³⁵S-dATP internal labeling, 10% DMSO and the following primers: (5' to 3') Forward TGCTTCCTCATCCCCTGCCCTCA and Reverse GGGCTGTAGTCCAGCAGCTACCTG. Cycling parameters were as follows: 95°C × 5 min, then 45 cycles of 95°C × 1 min, 65°C × 30 sec, and 72°C for 1 min. Approximately 3 μl of each of the PCR products were denatured, then loaded on a standard 6% polyacrylamide sequencing gel and electrophoresed for 2–3 hr. The gels were exposed to standard X-ray film and the visualized PCR products sized by comparison to an internal sequencing ladder. Gels were read independently and blindly with respect to sample status by R.P. and H.S.

The frequency of the exon 42 size polymorphism was determined by the sampling consecutive bloodspots provided by the State of Iowa Birth Registry. Briefly, DNA from bloodspots provided from a newborn registry (courtesy of Dr. Jeff Murray) were prepared using a standard QiaAmp kit (Qiagen). This DNA was then genotyped and analyzed as described earlier.

The sequence of *HOPA* exon 42 was delineated by standard methods in all four hemizygous probands and the father of one of the heterozygous probands who was a carrier for the 265 bp allele. Briefly, using the primers and cycling parameters delineated earlier and standard PCR conditions, a PCR product representing exon 42 was amplified, separated on agarose gel, excised from the gel with a razor blade, and then purified using a QUIquick PCR purification kit (Qiagen). The resulting PCR product was then sequenced using standard fluorescent protocols [Philibert et al., 1995].

Chi-square analyses (df = 1) were performed to compare the frequency of unusual variants in unrelated schizophrenic probands to the frequency of these variants in the newborn population.

RESULTS

Three differently sized alleles (238 bp, 253 bp, or 265 bp) for exon 42 of the *HOPA* gene were noted in the 111 probands from the Stony Brook cohort (see Table I). Three males were hemizygous for the 265 bp allele, 1 male was hemizygous for the 238 bp allele, and 2 females were heterozygous for the 265 base pair allele. The remainder of the subjects were either hemi- or homozygous for the more common 253 bp allele.

The frequency distribution of size polymorphisms was also determined in almost 1,000 consecutive new-

TABLE I. Frequency of *HOPA* Exon 42 Size Polymorphisms in Schizophrenic Probands

	With family history of hypothyroidism		Without family history of hypothyroidism	
	Male	Female*	Male	Female*
238 BP	1	0	0	0
253 BP	41	14	37	42
265 BP	3	2	0	0

*Denotes that the number of females have been multiplied by two giving the correct number of X-chromosomes.

borns from the state of Iowa. As Table II demonstrates, the 253 bp allele was the most common. (The X chromosomes of 484 males and 924 females carried this allele.) One female was heterozygous for the 238 bp allele, another female was heterozygous for the 256 bp allele, and 16 females were heterozygous for the 265 bp allele. We are still investigating whether 1 apparently homozygous female is truly homozygous or a partial or full Turner syndrome (X0) subject. For the purposes of this study, her data were excluded. Seven males were hemizygous for the 265 bp allele whereas 1 other male was hemizygous for the 250 bp allele. The remainder of the males and females appeared to be either hemizygous or heterozygous for the common 253 bp allele.

A chi-square analysis comparing schizophrenics to the controls (by all inherited X chromosomes; 1 from each male and 2 from each female) revealed a trend toward an excess of the 265 bp expansion in patients with schizophrenia ($\chi^2 = 2.83$, $P < 0.09$). When all anomalies were considered together ($n = 6$), the resulting chi square was 3.92, $P < 0.05$. However, it should be noted that all of these calculations are based on a few observations of an uncommon allele.

All 6 probands with an alteration in their sequence *HOPA* exon 4 had a history of hypothyroidism in themselves ($n = 3$) or their mother ($n = 3$) (6/53 vs. 0/58; $\chi^2 = 6.94$; $P < 0.008$). Because genotyping only allows alleles to be assessed on the basis of size, all 4 male hemizygotes and the father of 1 of the heterozygous female probands were sequenced with respect to *HOPA* exon 42. As Figure 1 shows, all four 265 bp hemizygotes possessed the same four amino acid polymorphism associated with an Xq13 mental retardation/hypothyroidism/depression syndrome reported previously. In addition, Figure 1 demonstrates that the newly discovered 238 bp variant allele is caused by the deletion of five glutamate residues in exon 42. The impact of these polymorphisms on protein function is not known.

TABLE II. Frequency of *HOPA* Exon 42 Six Polymorphisms in Iowa Newborns

	Male (N = 492)	Female* (N = 942)
238 BP	0	1
250 BP	1	0
253 BP	484	924
256 BP	0	1
265 BP	7	16

*Denotes that the number of females have been multiplied by two giving the correct number of X-chromosomes.

Available DNA from family members of the 5 probands with either the 265 bp expansion variant or the 238 bp deletion variant revealed a pattern of inheritance that segregated with hypothyroidism in each family, but with schizophrenia in only 2 of the 5 families. The 6th proband with an abnormality (265 bp) had hypothyroidism, but her family was not examined by genotyping. Figure 2 indicates the family pattern of inheritance of each allele, schizophrenia, and hypothyroidism.

DISCUSSION

In view of the previous observations, *HOPA* seemed to be a promising candidate gene for schizophrenia. The present study shows a small, but significant, excess of an allelic expansion of this gene among unrelated patients with schizophrenia (6 of 111 unrelated patients). However, when their family members were studied, *HOPA* variations did not significantly segregate with psychosis in the first-degree relatives. Taken together, these data suggest that although these variant polymorphisms may confer increased susceptibility to schizophrenia, they are clearly not a major risk factor for schizophrenia.

On the other hand, these data contribute more evidence about whether the 265 bp variant allele is associated with the pathogenesis of hypothyroidism or merely a neutral polymorphism physically linked to another causative mutation. In the first report [Philibert et al., 1998], only an association of the 265 bp polymorphism and the surrounding gene region with the syndrome was established. Thus, it was unclear whether the 265 bp allele was causal or was simply a neutral polymorphism that segregated with a "causative mutation." Because prior to the current study we had not found the 241 bp variant in any of over 1,000 males that we had studied previously, the finding of another new polymorphism in exon 42 in a family and a patient with hypothyroidism tends to suggest the former possibility. Furthermore, the recent findings by Ito and colleagues [Ito et al., 1999] that *HOPA* functions as a thyroxine receptor coactivator also strongly supports the hypothesis that these polymorphisms can cause thyroid hormone deficiency. Nevertheless, more definitive proof will require the completion of larger linkage disequilibrium and case control studies currently in progress.

The increase in thyroid disease among relatives of patients with schizophrenia, particularly mothers [DeLisi et al., 1991; MacSweeney et al., 1978], may be an important clue to the susceptibility for schizophrenia that still requires an explanation. One possibility could be that a gene for schizophrenia is on the X chromosome, more proximal or distal, but still linked to the *HOPA* gene. This would be consistent with the weak, but positive linkage results previously reported near this region [Dann et al., 1997; DeLisi et al., 1994a; Laval et al., 1998; Williams et al., 1998]. Thus, thyroid disease caused by a variant in the *HOPA* gene would be more likely to be inherited with schizophrenia in families if both are relatively common in the population. Alternatively, the genetic mechanisms that lead to in-

tasks of attention and language at ages 7–9 as compared with matched controls. These findings in humans complement early experiments in rodents that show abnormal neuronal biochemistry and cell maturation with reduced thyroid hormone exposure in utero [Balazs et al., 1971; Eayrs, 1967]. Because schizophrenia susceptibility, whether determined by variable gene sequences, is likely to result from a neurodevelopmental anomaly, these observations could explain why there is an association of schizophrenia with maternal thyroid deficiency and suggest a genetic mechanism through which this effect could be accomplished.

In the prior study, an increased incidence of the 265 bp variant allele was reported in males from three independent mentally retarded and institutionalized cohorts [Philibert et al., 1998]. The overall incidence of the 265 bp allele in these three cohorts of males of European ethnic origin was reported to be between 5–8% whereas in this study the incidence of the allele in males from the over 98% European-derived Iowa population was 1.3%, indicating that the increased relative risk for mental retardation due to this allele is between three- and five-fold. In the current study, 4 males were observed to be hemizygous for the 265 bp allele but none of them have been diagnosed with mental retardation. The incidence of mental retardation in the general population is approximately 1% [Hodapp and Dykens, 1996]. If the calculated relative risk for this gene is approximately three- to five-fold, we would hypothesize that only 1 in 20 to 30 male hemizygotes for the 265 bp allele have mental retardation. Therefore, it is not surprising that none of the 4 probands were observed to have mental retardation in the current study. However, decreased intellectual functioning has been documented to occur in individuals who develop schizophrenia even prior to the onset of psychosis [Davidson et al., 1999]. Although cognitive testing was not performed on the probands with the 265 bp allele in the present study, we nevertheless speculate that some of the diminished intellectual functioning seen in schizophrenia could represent pleiotropic effects of *HOPA* gene variations.

False positive results in association studies can be due to population stratification differences between patients and control groups. Although this might explain our present results, both the Iowa newborn and national U.S. schizophrenia samples consisted of almost all of Caucasians and no known ethnic differences emerged between those in the schizophrenia sample with and without thyroid disorder in their families. However, future studies using parent offspring triads examining the frequency of transmitted versus non-transmitted alleles may be more reliable for avoiding this problem.

In summary, we replicate the prior association of hypothyroidism with exonic polymorphisms in the Xq13 gene *HOPA* in this subset population of schizophrenic/schizoaffective probands. Although the overall allele frequency is higher in this cohort, we do not demonstrate familial segregation of this exonic polymorphism with psychosis. We conclude that further research is needed to examine this and other X-chromosome loci involved with neurodevelopment and their role in the

subsequent development of neuropsychiatric and cognitive disorders.

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