



Schizophrenia and bipolar disorder show both common and distinct changes in cortical interneuron markers



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ABSTRACT

Schizophrenia and bipolar disorder are often viewed as distinct clinical disorders, however there is substantial overlap in their neuropathologies. While compromised cortical interneurons are implicated in both diseases, few studies have examined the relative contribution of the distinct interneuron populations to each psychotic disorder. We report reductions in somatostatin and vasoactive intestinal peptide mRNAs in prefrontal and orbitofrontal cortices in bipolar disorder ($n = 31$) and schizophrenia ($n = 35$) compared to controls ($n = 34$) and increased calbindin mRNA in schizophrenia. We show, at the molecular level, shared deficits in interneuron markers in schizophrenia and bipolar disorder, and a unique interneuron marker increase in schizophrenia.

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1. Introduction

Schizophrenia and bipolar disorder may be biologically distinct or, as suggested by overlap in symptoms, genetic risk factors, and affected signaling pathways, may be on a continuum of underlying neuropathology (Craddock and Owen, 2010). Indeed, cortical interneuron pathology may be shared between individuals with schizophrenia and bipolar disorder, as GABAergic dysregulation is thought to contribute to altered gamma band oscillations and cognitive deficits in both (Hall et al., 2011; Lewis et al., 2012). Abnormalities in several cortical transcripts and proteins, including reduced glutamic acid decarboxylase 67 kDa (Akbarian et al., 1995; Guidotti et al., 2000; Volk et al., 2000; Knable et al., 2002; Torrey et al., 2005; Woo et al., 2008; Thompson et al., 2009) and various interneuron biochemical markers are found, suggesting that inhibitory neurotransmission is diminished in both schizophrenia and bipolar disorder (Benes et al., 1991; Beasley and Reynolds, 1997; Caberlotto and Hurd, 1999; Cotter et al., 2002; Hashimoto et al., 2003; Pantazopoulos et al., 2007; Hashimoto et al., 2008; Morris et al., 2008; Morris et al., 2009; Fung et al., 2010; Sibille et al., 2011; Wang et al., 2011). However, before we conclude the degree of overlap in the cortical interneuron

deficit across these two clinically distinct diseases, more comparative studies using similar techniques across diagnostic groups with a wider panel of interneuron makers are needed.

Interneurons are heterogeneous cells with different subtypes inhibiting pyramidal neurons by primarily targeting the cell body and/or axon initial segment (cholecystokinin, parvalbumin), or by targeting the dendrites [e.g. somatostatin, neuropeptide Y (NPY)] (Markram et al., 2004). Interneurons may also directly inhibit other interneurons [e.g. vasoactive intestinal peptide (VIP)] (Pi et al., 2013). Thus, examining these interneuron subtypes more specifically and comparatively will determine the degree and nature of the cortical interneuron pathology in bipolar disorder and schizophrenia and will determine if they can be considered different manifestations of a similar underlying neurobiological deficit, or if they are qualitatively different.

Several previous studies have examined the expression of interneuron markers in both schizophrenia and bipolar disorder (Cotter et al., 2002; Sakai et al., 2008; Wang et al., 2011). However, whether a unique profile of interneuron deficits can be distinguished for each disorder across two functionally distinct cortical regions is unknown. We examined the relative change in expression of seven interneuron biochemical marker mRNAs (parvalbumin, cholecystokinin, somatostatin, NPY, calbindin, VIP, and calretinin) in two brain regions: the dorsolateral prefrontal cortex (DLPFC) and orbitofrontal cortex (OFC). We hypothesized there may be both shared and distinct alterations in interneuron mRNA expression in the two diseases.

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2. Experimental/materials and methods

2.1. Post-mortem brain samples

Studies were carried out with approval of the University of New South Wales Human Research Ethics Committee, (#HREC07261). RNA from postmortem DLPFC (BA46) and lateral OFC cases was obtained from the Stanley Medical Research Institute Array Cohort (Table 1).

2.2. qPCR analysis

Due to availability of RNA, the examined cohort consisted of 34 controls, 31 bipolar disorder, and 35 (DLPFC) or 34 (OFC) schizophrenia subjects. cDNA was synthesized as previously described (Weickert et al., 2010). Transcript levels were measured by qPCR on ABI Prism 7900HT system using TaqMan Gene Expression Assays (Table 2) as previously described (Fung et al., 2010). The geometric mean for 4 housekeeper control mRNAs (TATA box binding protein, β -actin, ubiquitin C, β -2-microglobulin) used for normalization did not vary according to diagnostic group (DLPFC: $F = 1.51$, $df = 2$, 99 , $p = 0.23$; OFC: $F = 0.53$, $df = 2$, 98 , $p = 0.59$).

2.3. Analysis

Where data were not normally distributed, quantities were transformed (square root: cholecystokinin and calretinin in DLPFC, calretinin and NPY in the OFC; log: calbindin in OFC). Group outliers of >2 SD from the mean were removed (0–4 per group, average 1.57 outliers per group, 4.67%, Supplementary Table 1). Demographic variables that correlated with gene expression across the cohort (Pearson's correlation on normally distributed data, Supplementary Table 2) were used as covariates in ANCOVA analyses of differential gene expression between diagnostic groups where warranted, otherwise one-way ANOVAs were used to determine diagnostic differences (LSD post-hocs). Statistical analyses were performed using IBM SPSS Statistics, Version 20.

3. Results

3.1. Interneuron mRNAs are altered in the DLPFC of schizophrenia and bipolar disorder subjects

Several interneuron transcripts were changed in the DLPFC according to diagnostic group (Fig. 1). Somatostatin mRNA was reduced in schizophrenia (20.9%, $p = 0.021$) and in bipolar disorder (34.7%, $p < 0.001$) DLPFC relative to healthy controls (overall ANOVA, $F = 7.17$, $df = 2$, 93 , $p = 0.001$). VIP was reduced 17.8% in schizophrenia subjects ($p = 0.018$) compared to controls and 32.6% in bipolar patients compared to controls ($p < 0.001$, overall ANOVA $F = 9.10$, $d = 2$, 92 , $p < 0.001$). Conversely, calbindin mRNA expression was increased in people with schizophrenia relative to both controls (22.7%, $p = 0.001$) and bipolar

Table 2
TaqMan gene expression assays.

Gene name	Gene symbol	TaqMan assay ID
<i>Interneuron marker</i>		
Parvalbumin	PV	Hs161045_m1
Somatostatin	SST	Hs356144_m1
Calbindin	CB	Hs1077197_m1
Calretinin	CR	Hs242372_m1
Neuropeptide Y	NPY	Hs173470_m1
Cholecystokinin	CCK	Hs174937_m1
Vasoactive intestinal peptide	VIP	Hs929575_m1
<i>Housekeeper</i>		
TATA box binding protein	TBP	Hs00427620_m1
β -actin	ACTB	Hs99999903_m1
Ubiquitin C	UBC	Hs00824723_m1
β -2-microglobulin	B2M	Hs99999907_m1

subjects (22.5%, $p = 0.002$), and unchanged between bipolar and control subjects ($p > 0.05$, overall ANCOVA covarying for age, $F = 7.40$, $df = 2$, 89 , $p = 0.001$). Parvalbumin, cholecystokinin and calretinin mRNAs did not show significant changes across diagnostic groups by ANOVA (all $F < 1.05$, $p > 0.05$). As there was a trend for overall change in NPY mRNA (ANOVA $F = 2.85$, $df = 2$, 94 , $p = 0.063$) combined with our prior findings of reduced NPY mRNA in schizophrenia (Fung et al., 2010), we conducted post-hoc analysis, revealing a reduction in NPY mRNA in schizophrenia compared to controls (18.8%, $p = 0.035$), and reduced NPY mRNA in bipolar disorder relative to controls at the level of significance (17.6%, $p = 0.05$).

3.2. Interneuron mRNAs are altered in the OFC of schizophrenia and bipolar disorder subjects

Somatostatin mRNA was reduced in schizophrenia (23.9%, $p = 0.004$), and in bipolar disorder relative to controls (29.9%, $p = 0.001$; overall ANOVA $F = 7.216$, $df = 2$, 90 , $p = 0.001$) (Fig. 2). There was a trend for a diagnostic group difference in VIP mRNA ($F = 2.54$, $df = 2$, 89 , $p = 0.085$), with reduction in bipolar relative to controls (16.2%, $p = 0.043$) and a trend toward reduction in schizophrenia relative to controls (13.6%, $p = 0.079$). Calbindin mRNA was increased in schizophrenia relative to bipolar disorder OFC (27.4%, $p = 0.016$, overall ANOVA $F = 3.33$, $df = 2$, 91 , $p = 0.040$), and tended to decrease in bipolar relative to controls, but this did not quite reach statistical significance (15.3%, $p = 0.06$). No other interneuron marker mRNAs were significantly changed between groups ($F < 1.15$, $p > 0.05$).

4. Discussion

Our results indicate that bipolar disorder and schizophrenia share significant interneuron pathology, with the largest and most consistent

Table 1
Stanley array cohort demographics (based on DLPFC).

	Control group $n = 34$	Bipolar disorder group $n = 31$	Schizophrenia group $n = 35$
Age (years) (range)	43.8 (31–60)	44.9 (19–64)	42.6 (19–59)
Gender	9F/25M	16F/15M	9F/26M
Hemisphere	16L/18R	17L/14R	17L/18R
pH (\pm SD)	6.61 \pm 0.27	6.46 \pm 0.28	6.47 \pm 0.24
PMI (hours) (\pm SD)	29.5 \pm 13.0	36.6 \pm 18.1	31.4 \pm 15.4
RIN (\pm SD)	8.30 \pm 0.69	8.32 \pm 0.84	8.47 \pm 0.56
Manner of death	Natural = 34	Natural = 17, suicide = 14	Natural = 28, suicide = 7
Age of onset (years) (\pm SD)	–	24.8 \pm 8.95	21.3 \pm 6.07
Duration of illness (years) (\pm SD)	–	20.2 \pm 9.89	21.3 \pm 10.1
Lifetime antipsychotics (fluphenazine equivalents, mg)	–	10,296.8 \pm 23,865	85004.3 \pm 100,335
Antidepressant use	Yes = 0, no = 34	Yes = 18, no = 13	Yes = 9, no = 26

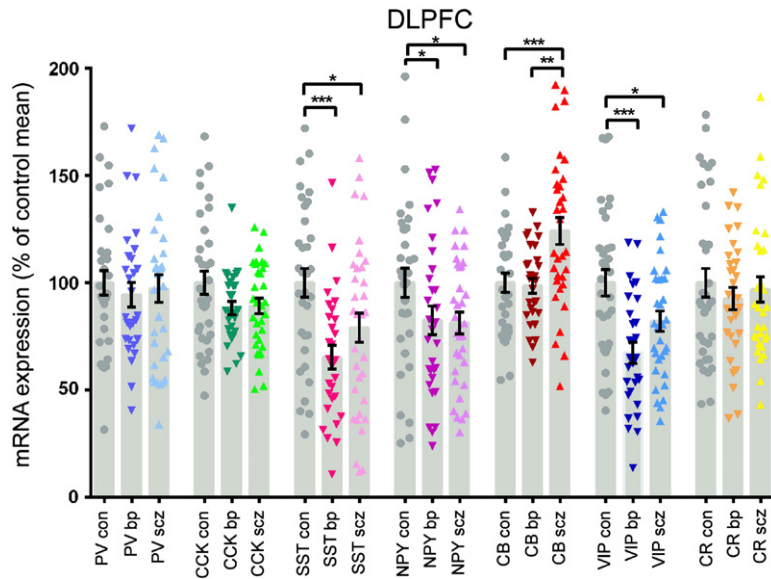


Fig. 1. Expression of interneuron marker mRNAs are altered in the dorsolateral prefrontal cortex (DLPFC) of schizophrenia (scz, light data points) and bipolar disorder (bp, dark data points) subjects compared to controls (con, gray data points). Error bars represent standard error. PV = parvalbumin, CCK = cholecystokinin, SST = somatostatin, NPY = neuropeptide Y, CB = calbindin, VIP = vasoactive intestinal peptide, CR = calretinin. * $p < 0.05$, ** $p < 0.005$, *** $p < 0.001$.

reductions in VIP and somatostatin mRNAs. These abnormalities are evident across both regions studied suggesting that interneuron deficits are not restricted to the DLPFC (implicated by deficits in working memory and cognitive control), but also include the frontal cortical areas associated with social–emotional function (OFC). Our finding of reduced somatostatin, VIP and NPY mRNAs in the DLPFC in schizophrenia replicate our previous finding (Fung et al., 2010) and those of others that also show reduced somatostatin (Hashimoto et al., 2008; Morris et al., 2008) and NPY mRNA (Morris et al., 2009), implicating dendrite targeting interneurons as pathological in both psychotic disorders. A meta-analysis of microarray data comparing patients with schizophrenia and bipolar disorder with psychosis to affective disorder patients without psychosis found both somatostatin and NPY mRNAs reduced in the psychotic group, suggesting that these transcripts may be associated with psychotic features of these disorders (Choi et al., 2008). Interestingly, however, the reduction in somatostatin mRNA is of greater magnitude in bipolar disorder than schizophrenia, while psychotic and cognitive symptoms tend to be less severe in

bipolar disorder (Caletti et al., 2013), suggesting additional factors also contribute to symptom severity.

Surprisingly, we found frontal cortical parvalbumin mRNA was unaltered in both schizophrenia and bipolar disorder in contrast to previous studies that consistently demonstrate reduction in parvalbumin mRNA in the cortex (Cotter et al., 2002; Hashimoto et al., 2003; Hashimoto et al., 2008; Fung et al., 2010; Sibille et al., 2011) and reductions of cell number, cell density and parvalbumin expression in hippocampus (Zhang and Reynolds, 2002; Knable et al., 2004; Konradi et al., 2011), parahippocampal region (Wang et al., 2011) and entorhinal cortex (Pantazopoulos et al., 2007). The most significantly altered mRNAs that we report in the frontal cortex (somatostatin, VIP and NPY) in schizophrenia overlap with those showing the greatest magnitude of change in our earlier report in the DLPFC (Fung et al., 2010). While our previous study also found parvalbumin mRNA reduced, the magnitude of this change was less than that of somatostatin, VIP and NPY mRNAs. This indicates that, while much attention has focused on parvalbumin

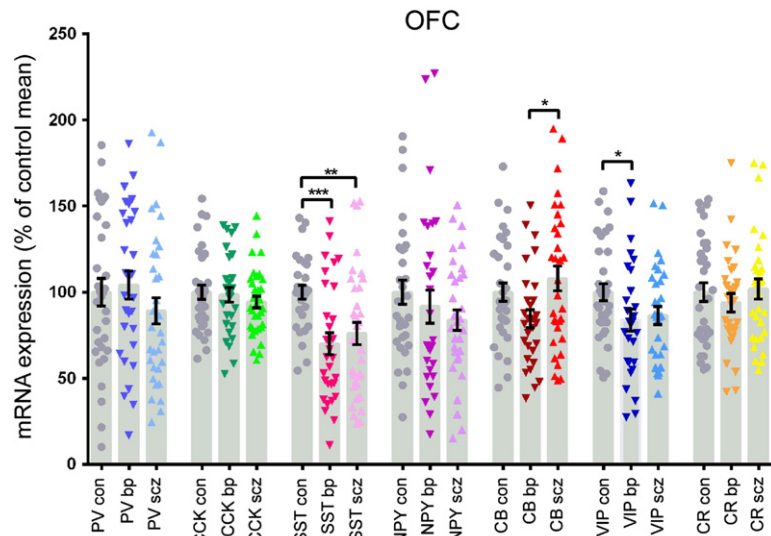


Fig. 2. Expression of interneuron marker mRNAs are altered in the orbitofrontal cortex (OFC) of schizophrenia (scz, light data points) and bipolar disorder (bp, dark data points) subjects compared to controls (con, gray data points). Error bars represent standard error. PV = parvalbumin, CCK = cholecystokinin, SST = somatostatin, NPY = neuropeptide Y, CB = calbindin, VIP = vasoactive intestinal peptide, CR = calretinin. * $p < 0.05$, ** $p < 0.005$, *** $p < 0.001$.

abnormalities in schizophrenia and in animal models of schizophrenia-like behaviors, deficits in other interneuron subtypes may be more profound or widespread, at least in the frontal cortex, in schizophrenia and bipolar disorder.

We were able to identify one qualitative distinction in interneuron marker mRNA change in people with schizophrenia from those with bipolar disorder. In schizophrenia, we find increased calbindin mRNA replicating our previous finding in a different cohort (Fung et al., 2010). While calbindin may be co-expressed with somatostatin and other interneuron markers (Kawaguchi and Kubota, 1996), it can also be found in pyramidal neurons (Hof and Morrison, 1991). However, since earlier reports demonstrated an increase in density of non-pyramidal calbindin immunopositive neurons in the frontal cortex of people with schizophrenia (Daviss and Lewis, 1995), our finding of increased calbindin mRNA expression may also reflect an interneuronal increase in calbindin that may be compensatory for reductions in other interneuron markers.

Alternatively, in human frontal cortex development, calbindin mRNA expression shows a dramatic upregulation early in childhood, prior to the peak in VIP and parvalbumin mRNA expression (Fung et al., 2010). Thus, the elevated levels of calbindin mRNA that we find in schizophrenia could reflect an immature phenotype of cortical interneurons that persists into adulthood in schizophrenia, and would be consistent with the theory of delayed or arrested development of cortical interneurons in schizophrenia (Catts et al., 2013; Volk and Lewis, 2013). The increase in calbindin mRNA that we find in schizophrenia but not bipolar disorder may suggest differences in the underlying developmental trajectories of these disorders.

Our study adds to a growing body of literature suggesting that the molecular neuropathologies of schizophrenia and bipolar disorder display substantial overlap, including that much interneuron pathology is shared between the disorders and may be conserved across distinct frontal brain regions (e.g. Thompson et al., 2009; Thompson Ray et al., 2011; Sinclair et al., 2012). However an interneuron subtype-specific alteration (increase in calbindin mRNA) in the DSM-IV defined schizophrenia group only demonstrates that there are also unique differences to the interneuron pathology in these major mental illnesses and may indicate the existence of unique “biotypes” within the psychosis spectrum.

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Contributors

SJF, MW and CSW designed the study. SJF and SGF performed the analysis and SJF wrote the first draft of the manuscript. All authors contributed to and have approved the final manuscript.

Conflict of interest

The authors declare that they have no conflicts of interest.

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Appendix A. Supplementary data

Supplementary data to this article can be found online at <http://dx.doi.org/10.1016/j.schres.2014.02.021>.

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