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# A non- synonymous polymorphism in galactose mutarotase (*GALM*) is associated with serotonin transporter binding potential in the human thalamus: Results of a genome-wide association study

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#### **Keywords**

[<sup>11</sup>C]DASB; mood disorder; bipolar; GALM; PET

Positron emission tomography (PET) imaging using the tracer [\$^{11}\$C]DASB is a sensitive and noninvasive technique for measuring brain serotonin transporter (5-HTT) levels in vivo\$^{1}\$. Previously, Cannon et al. found that 5-HTT levels were increased in thalamus, striatum, insular and cingulate cortices in unmedicated, depressed subjects with major depressive disorder\$^{2}\$ or bipolar disorder\$^{3}\$. To explore this potential biomarker for mood disorders, we undertook a proof-of-principle genome-wide association study.

5-HTT levels, measured as [\$^{11}\$C]DASB binding potential (BP\$\_{ND}), were assessed in six brain regions-of-interest (ROIs). Healthy (n=22) and unmedicated participants diagnosed with bipolar disorder (n=16) or major depressive disorder (n=17), aged 18 to 48 years (Mean  $\pm$  SD, 34  $\pm$  9 yr) underwent PET scanning with [\$^{11}\$C]DASB. Subject ascertainment, PET scanning, and analysis were described previously\$^{2-3}\$. DNA was extracted from peripheral blood and genotyped on the Illumina Human-1 SNP array. Genotypes were called with

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BeadStudio v3.0. Data were filtered for minor allele frequencies < 1%, missing genotype rates > 8%, Hardy-Weinberg Equilibrium p-values <0.05, gender mismatch, and hidden relatedness. A total of 93,427 SNPs passed all quality control filters for all of the ROIs tested. Association analysis was performed by linear regression in PLINK $^4$  (v1.02), with 3 covariates to control for ancestry. Genomic Control lambda values were all <1.05, indicating good control of confounding factors

Overall, 5 SNPs representing 5 different genes met our FDR<0.1 criterion for being declared of interest: rs6741892 in GALM, rs390704 near FRY, rs7161217 near TTLL5, rs583241 near CPLX4, and rs7095106 near CASC2. The strongest association was between thalamic [ $^{11}$ C]DASB-BP $_{ND}$  and a coding SNP in the gene GALM (rs6741892, p=4.67×10 $^{-8}$ ; FDR=0.004). This result meets the threshold of genome-wide significance under typical frequentist assumptions, but not if corrected for 6 ROIs. rs6741892 accounted for about 50% of the variance in [ $^{11}$ C]DASB-BP $_{ND}$  in thalamus. Carriers of the "TT" genotype showed the highest [ $^{11}$ C]DASB-BP $_{ND}$ .

Since the T-allele frequency differed by self-reported ancestry (10/13 in African-Americans, 3/13 in whites, and 0/7 in Hispanics), we also performed the analysis within each ancestry group, then combined the p-values by meta-analysis (META 5.3, http://userpage.fuberlin.de/~health/meta\_e.htm), with similar results. We further confirmed this finding in a voxel-based analysis (Fig 1).

Nominally-significant associations were also observed between rs6741892 and [ $^{11}$ C]DASB-BP<sub>ND</sub> in dorsal cingulate cortex (DCC; p=4.03×10<sup>-2</sup>) and insula (p=1.14×10<sup>-3</sup>). No SNPs near the gene encoding the 5-HTT (SLC6A4) showed significant association in this sample, consistent with one prior study<sup>5</sup>, but we may have missed a true association due to lack of power. Rs6741892 was also individually genotyped using a modification of the 5' nuclease (Taqman) assay, with similar results.

Consistent with our prior findings<sup>2</sup>-<sup>3</sup>, we found a significant main effect of diagnosis on [ $^{11}$ C]DASB-BP<sub>ND</sub> measured in thalamus (F (2, 52) =7.07, p<0.002) due to significantly higher thalamic [ $^{11}$ C]DASB-BP<sub>ND</sub> in participants with mood disorders. However, the overall association results were not dependent on diagnosis: rs6741892 was also associated with [ $^{11}$ C]DASB-BP<sub>ND</sub> in healthy participants.

Supportive evidence of association with rs6741892 was obtained from an independent replication sample of 51 European-ancestry subjects (16 females aged  $43\pm20$  yr, 35 males aged  $34\pm18$  yr) ascertained in Denmark, using TaqMan. Imaging and analysis were as described<sup>6</sup>. Significant associations were observed between rs6741892 and [ $^{11}$ C]DASB-BP<sub>ND</sub> in DCC (p= $3.5\times10^{-3}$ ) and insula (p= $4.9\times10^{-3}$ ), but not in thalamus, although [ $^{11}$ C]DASB-BP<sub>ND</sub> is highly correlated across subcortical structures<sup>7</sup>. Combined analysis with META 5.3 supported association between rs6741892 and [ $^{11}$ C]DASB-BP<sub>ND</sub> in all 3 regions of interest (DCC, p= $9.18\times10^{-4}$ ; insula, p= $3.25\times10^{-5}$ ; and thalamus, p= $4.6\times10^{-6}$ ).

*GALM* encodes galactose mutarotase, which catalyzes the conversion of beta-D-galactose to alpha-D-galactose<sup>8</sup>, important in carbohydrate metabolism and the production of complex oligosaccharides. Galactose mutarotase might affect regional neurophysiology, leading to

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local increases in serotonin release and in membrane trafficking of 5-HTT $^9$ , thereby increasing [ $^{11}$ C]DASB-BP $_{ND}$ . Galactose mutarotase may also play a role in N-glycosylation, which is important for surface expression of 5-HTT $^{10}$ .

To our knowledge, this is the first genome-wide association study of brain 5-HTT. These preliminary results suggest that neuroimaging phenotypes could represent informative targets for a GWAS, even in relatively small samples. Further studies are needed to confirm these findings and determine the underlying biological mechanisms.

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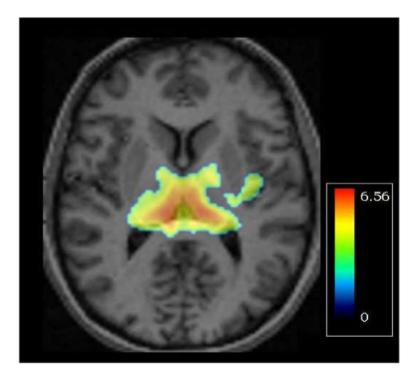


Figure 1. Map of t-values from voxel-wise analysis of rs6741892, overlaid on a sample axial MRI slice at the level of the medial thalamus (z=6 mm). Bilaterally, T-allele carriers (n=13) have greater serotonin-transporter binding potential than AA homozygotes (n=42). The color bar indicates the range of t-values displayed (max t = 6.56, df=53, p=2.3  $\times$  10<sup>-8</sup>).