**Supplementary materials**

**Table S1:** Biological data based on for the selection of variants investigated

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Gene name** | **Symbol** | **Gene ID (NCBI)** | **Variant** | **MAF (Luhya)** | **Location of variant in the gene** | **Function of the Variant** | **Citation** |
| Serotonin transporter | 5-HTT | 6532 | rs*25531* | 0.29 | Chr17: 28,564,346 | Regulates gene expression | (Voyiaziakis *et al*., 2011) |
| STin2.VNTRs | 0.27 | Chr5: 1-180,915,260 | Regulates gene expression |  |
| Tryptophan hydroxylase 2 | TPH2 | 121278 | rs*4570625* | 0.35 | Chr12: 72,331,923 | Associated with MDD | (Gao *et al*., 2012) |
| rs*1843809* | 0.40 | Chr12: 72,348,698 | Associated with MDD | (Zill *et al*., 2004) |
| rs*1386494* | 0.23 | Chr12:72,352,543 | Associated with MDD | (Zill *et al*., 2004) |
| rs*34517220* | 0.53 | Chr12:72,395,229 | Associated with reduction in depressive symptoms in patients treated with fluoxetine | (Gassó *et al.*, 2017) |

**Figure S1**

LD plot showing linkage disequilibrium (LD) for *SLC6A4* 5*-HTTLPR*, rs25531 and *STin2* VNTR



Linkage disequilibrium map of *SLC6A4*. D’ values are depicted in the diamonds with darker colors depicting stronger LD. The LD map was created using the default Gabriel LD (Gabriel *et al*., 2002), implemented in Haploview, version 4.2 (Barrett, 2009). 1 = rs25531, 2 = *5-HTTLPR*, 3 = *STin2* VNTR. *5-HTTLPR* and rs25531 were in LD. Location = 5’ to 3’ on chromosome 17.

**Figure S2**



Linkage disequilibrium map of *TPH2*. D’ values are depicted in the diamonds with darker colors depicting stronger LD. The LD map was created using the default Gabriel LD

(Gabriel *et al*., 2002), implemented in Haploview, version 4.2 (Barrett, 2009). 1 = rs4570625, 2 = rs1843809 and 3 = rs34517220. None of the SNPs were in LD. Location = 5’ to 3’ strand on chromosome 12.

**Table S2**: Logistic regression analysis for the interaction of acute stress on selected serotonin transporter gene and tryptophan hydroxylase 2 gene polymorphisms on IMDs

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Model** | **Variable** | **Odds ratio** | **P>|Z|** | **95% CI** | **P-value** |
| Excluding any polymorphism | Mild acute stress | Reference |  |  | 0.046ƒ |
| Moderate acute stress | 1.22 | 0.282 | 0.848 - 1.761 |
| Severe acute stress | 1.92 | 0.001 | 1.327 – 2.785 |
| Including rs1386494 | **Acute stress\*rs1386494** |
|  | Moderate AS\**GA* | 1.17 | 0.889 | 0.125 – 11.004 | 0.786ƒ |
|  | Moderate AS\**GG* | 1.88 | 0.574 | 0.208 – 17.067 |
|  |  |  |  |  |
|  | Severe AS\**GA* | 0.73 | 0.808 | 0.056 – 9.508 |
|  | Severe AS\**GG* | 0.94 | 0.963 | 0.074 – 11.990 |
| Including rs1843809 | **Acute stress\*rs1843809** |  |  |  |  |
|  | Moderate AS\**TG* | 1.93 | 0.174 | 0.750 – 4.951 | 0.198ƒ |
|  | Moderate AS\**TT* | 3.07 | 0.031 | 1.110 – 8.490 |  |
|  |  |  |  |  |  |
|  | Severe AS\**TG* | 0.99 | 0.988 | 0.359 – 2.743 |  |
|  | Severe AS\**TT* | 1.89 | 0.253 | 0.635 – 5.634 |  |
| Including rs34517220 | **Acute stress\*rs34517220** |  |  |  |  |
|  | Moderate AS\**GA* | 1.31 | 0.544 | 0.544 – 3.177 | 0.927ƒ  |
|  | Moderate AS\**GG* | 1.48 | 0.459 | 0.527 – 4.138 |  |
|  |  |  |  |  |  |
|  | Severe AS\**GA* | 1.37 | 0.491 | 0.557 – 3.378 |  |
|  | Severe AS\**GG* | 1.23 | 0.685 | 0.446 – 3.419 |  |
| Including rs4570625 | **Acute stress\*rs4570625** |  |  |  |  |
|  | Moderate AS\**TG* | 2.26 | 0.073 | 0.926 – 5.532 | 0.390ƒ  |
|  | Moderate AS\**TT* | 2.41 | 0.085 | 0.886 – 6.568 |  |
|  |  |  |  |  |  |
|  | Severe AS\**TG* | 1.35 | 0.507 | 0.554 – 3.299 |  |
|  | Severe AS\**TT* | 1.21 | 0.719 | 0.423 – 3.480 |  |
| Including rs25531 | **Acute stress\*rs25531** |  |  |  |  |
|  | Moderate AS\**2* | 1.88 | 0.117 | 0.853 – 4.153 | 0.487ƒ |
|  | Moderate AS\*3 | 0.77 | 0.815 | 0.082 – 7.172 |  |
|  |  |  |  |  |  |
|  | Severe AS\**2* | 1.46 | 0.362 | 0.647 – 3.298 |  |
|  | Severe AS\**3* | 0.43 | 0.404 | 0.058 – 3.418 |  |
| Including *5-HTTLPR* | **Acute stress\**5-HTTLPR*** |  |  |  |  |
|  | Moderate AS\**LS* | 1.47 | 0.346 | 0.662 – 3.246 | 0.463ƒ |
|  | Moderate AS\**SS* | 3.08 | 0.269 | 0.419 – 22.654 |  |
|  |  |  |  |  |  |
|  | Severe AS\**LS* | 1.31 | 0.521 | 0.577 – 2.958 |  |
|  | Severe AS\**SS* | 4.15 | 0.133 | 0.647 – 26.574 |  |
| Including *STin2.*VNTR | **Acute stress\**STin2.*VNTR** |  |  |  |  |
|  | Moderate AS\**10/12* | 1.79 | 0.432 | 0.419 – 7.625 | 0.203ƒ |
|  | Moderate AS\**12/12* | 1.76 | 0.429 | 0.434 – 7140 |  |
|  |  |  |  |  |  |
|  | Severe AS\**10/12* | 0.53 | 0.429 | 0.106 – 2.592 |  |
|  | Severe AS\**12/12* | 1.14 | 0.868 | 0.239 – 5.450 |  |

AS = acute stress, \* = interaction, ƒ = p-value for the likelihood-ratio test of interaction between acute stress and the selected polymorphism on IMDs.