Data in Brief 4 (2015) 529–533

Contents lists available at ScienceDirect

Data in Brief

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Data Article

# Data in support of association study of the brain-derived neurotrophic factor gene SNPs and completed suicide in the Slovenian sample

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ARTICLE INFO

*Article history:*
Received 8 July 2015
Received in revised form
15 July 2015
Accepted 15 July 2015
Available online 22 July 2015

*Keywords:*
Genotypes
Logistic regression
Inheritance models
Haplotypes
Sliding window procedure

ABSTRACT

This data article provides the data generated from additional analyses of a genetic association study, where 7 single nucleotide polymorphisms (SNPs) near/within the brain-derived neurotrophic factor (*BDNF*) gene were investigated for an association with completed suicide in Slavic population (Ropret et al., 2015) [1]. One SNP was excluded from the present analyses due to insufficient genotyping rate (rs1491850) and the remaining 6 SNPs (rs7124442, rs10767664, rs962369, rs12273363, rs908867, rs1491851) were analyzed to gain deeper insight into the possible role of these SNPs in the studied phenotype. We present data on logistic regression analyses of: (a) genotypes under four inheritance models, and (b) haplotypes using 2-, 3- and 4-adjacent SNPs sliding window procedure. In both analyses adjustments for potential confounders (age, gender and alcohol dependence syndrome status) were executed. Data may serve as a reference for comparison of the populations with either low or very high suicide rates. The raw genotyping data that could be used in case meta-analyses should be performed may be provided upon request.[1]


DOI of original article: http://dx.doi.org/10.1016/j.neulet.2015.06.027
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[1] The corresponding author will notify the co-authors of this Data article whenever request for the raw genotyping data file occurs.

http://dx.doi.org/10.1016/j.dib.2015.07.015

## Specifications Table

| | |
|---|---|
| Subject area | *Biology* |
| More specific subject area | *Neurobiology of psychiatric disorders, particularly completed suicide* |
| Type of data | *Tables* |
| How data was acquired | *Software for genetic analysis PLINK v1.07* [2] |
| Data format | *Analyzed* |
| Experimental factors | *Genotyping of controls and suicide completers* [1] |
| Experimental features | *In-depth analysis of genotype and haplotype data, using PLINK v1.07* |
| Data source location | *Ljubljana, Slovenia, EU* |
| Data accessibility | *All the data are supplied within this article* (*raw genotyping data may be provided upon request*) |

## Value of the data

- Data presented here may be useful as an incentive for analyses of the SNPs rs7124442, rs10767664, rs962369, rs12273363 and rs908867, especially haplotypes consisting of two to five of these SNPs in larger samples from different populations with high suicide rates and also for comparative analyses of populations with high and low suicide rates.

**Table 1**
Logistic regression analysis of the SNPs in the *BDNF* gene between controls and suicide completers, adjusted by age, gender and alcohol dependence syndrome status.

| SNP | Model | | OR | 95% CI | *p*[a] |
|---|---|---|---|---|---|
| rs7124442 | Geno_2df[b] | **TT** *vs.* CT *vs.* CC | N/A | N/A | 0.313 |
| | ADD[c] | 2 CC+CT *vs.* **TT** | 1.234 | 0.939–1.623 | 0.131 |
| | Dominant[d] | **TT** *vs.* CT+CC | 1.106 | 0.821–1.489 | 0.508 |
| | Recessive[e] | **TT**+CT *vs.* CC | 1.513 | 0.887–2.579 | 1.128 |
| rs10767664 | Geno_2df | **AA** *vs.* TA *vs.* TT | N/A | N/A | 0.161 |
| | ADD | 2 TT+TA *vs.* **AA** | 1.296 | 0.954–1.761 | 0.097 |
| | Dominant | **AA** *vs.* TA+TT | 1.287 | 0.955–1.736 | 0.098 |
| | Recessive | **AA**+TA *vs.* TT | 1.559 | 0.854–2.847 | 0.148 |
| rs962369 | Geno_2df | **TT** *vs.* CT *vs.* CC | N/A | N/A | 0.813 |
| | ADD | 2 CC+CT *vs.* **TT** | 1.039 | 0.762–1.415 | 0.811 |
| | Dominant | **TT** *vs.* CT+CC | 0.940 | 0.698–1.267 | 0.686 |
| | Recessive | **TT**+CT *vs.* CC | 1.113 | 0.606–2.045 | 0.730 |
| rs12273363 | Geno_2df | **TT** *vs.* CT *vs.* CC | N/A | N/A | 0.905 |
| | ADD | 2 CC+CT *vs.* **TT** | 1.085 | 0.682–1.728 | 0.730 |
| | Dominant | **TT** *vs.* CT+CC | 0.977 | 0.706–1.352 | 0.889 |
| | Recessive | **TT**+CT *vs.* CC | 1.191 | 0.472–3.008 | 0.711 |
| rs908867 | Geno_2df | **CC** *vs.* TC *vs.* TT | N/A | N/A | 0.838 |
| | ADD | 2 TT+TC *vs.* **CC** | 0.956 | 0.464–1.970 | 0.902 |
| | Dominant | **CC** *vs.* TC+TT | 0.886 | 0.592–1.324 | 0.554 |
| | Recessive | **CC**+TC *vs.* TT | 0.930 | 0.219–3.949 | 0.922 |
| rs1491851 | Geno_2df | **CC** *vs.* TC *vs.* TT | N/A | N/A | 0.623 |
| | ADD | 2 TT+TC *vs.* **CC** | 0.994 | 0.813–1.216 | 0.953 |
| | Dominant | **CC** *vs.* TC+TT | 1.094 | 0.795–1.504 | 0.581 |
| | Recessive | **CC**+TC *vs.* TT | 0.908 | 0.642–1.284 | 0.583 |

OR: odds ratio; CI: confidence interval.

[a] *p*-values are not corrected for multiple testing (Bonferroni); **bold**: major allele homozygotes.

[b] Geno_2df (general genotypic model): major allele homozygotes *vs.* heterozygotes *vs.* minor allele homozygotes.

[c] ADD (additive model, where each copy of the minor allele alters the risk in an additive form; a combination of the minor allele homozygotes with weight 2+heterozygotes is compared to major allele homozygotes): 2× minor allele homozygotes+heterozygotes *vs.* major allele homozygotes.

[d] Dominant: major allele homozygotes *vs.* heterozygotes+minor allele homozygotes.

[e] Recessive: major allele homozygotes+heterozygotes *vs.* minor allele homozygotes.

**Table 2**
Associations between *BDNF* gene haplotypes (3′→5′, reverse strand) and completed suicide (age, gender and alcohol dependence syndrome status adjusted).

| NSNP | NHAP | SNP-first | SNP2 | SNP3 | SNP4 | SNP-last | Haplotype | Freq | OR | STAT | *P* | EMP *p* |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 2 | 4 | rs7124442 | | | | rs10767664 | CT | 0.0114 | 3.52 | 1.79 | 0.181 | 0.7516 |
| 2 | 4 | rs7124442 | | | | rs10767664 | TT | 0.241 | 1.21 | 2.41 | 0.12 | 0.587 |
| 2 | 4 | rs7124442 | | | | rs10767664 | *CA* | 0.255 | 1.1 | 0.651 | 0.42 | 0.9731 |
| 2 | 4 | rs7124442 | | | | rs10767664 | TA | 0.493 | 0.794 | 4.98 | **0.0256*** | 0.1709 |
| 2 | 3 | rs10767664 | | | | rs962369 | AC | 0.233 | 0.975 | 0.0399 | 0.842 | 1 |
| 2 | 3 | rs10767664 | | | | rs962369 | TT | 0.245 | 1.25 | 3.22 | 0.0726 | 0.4028 |
| 2 | 3 | rs10767664 | | | | rs962369 | AT | 0.514 | 0.858 | 2.14 | 0.144 | 0.6595 |
| 2 | 3 | rs962369 | | | | rs12273363 | CC | 0.151 | 1.01 | 0.0063 | 0.937 | 1 |
| 2 | 3 | rs962369 | | | | rs12273363 | CT | 0.0881 | 0.933 | 0.144 | 0.704 | 0.9997 |
| 2 | 3 | rs962369 | | | | rs12273363 | TT | 0.756 | 1.03 | 0.0667 | 0.796 | 1 |
| 2 | 3 | rs12273363 | | | | rs908867 | TT | 0.0824 | 0.9 | 0.317 | 0.573 | 0.9961 |
| 2 | 3 | rs12273363 | | | | rs908867 | CC | 0.156 | 1.01 | 0.0033 | 0.954 | 1 |
| 2 | 3 | rs12273363 | | | | rs908867 | TC | 0.762 | 1.04 | 0.102 | 0.749 | 1 |
| 3 | 4 | rs7124442 | rs10767664 | | | rs962369 | CAC | 0.226 | 0.983 | 0.018 | 0.893 | 1 |
| 3 | 4 | rs7124442 | rs10767664 | | | rs962369 | TTT | 0.24 | 1.22 | 2.57 | 0.109 | 0.5483 |
| 3 | 4 | rs7124442 | rs10767664 | | | rs962369 | CAT | 0.0297 | 2.57 | 5.79 | **0.0161*** | 0.1124 |
| 3 | 4 | rs7124442 | rs10767664 | | | rs962369 | TAT | 0.485 | 0.795 | 5.01 | **0.0252*** | 0.1689 |
| 3 | 4 | rs10767664 | rs962369 | | | rs12273363 | ACC | 0.146 | 1 | 0.000101 | 0.992 | 1 |
| 3 | 4 | rs10767664 | rs962369 | | | rs12273363 | ACT | 0.0851 | 0.918 | 0.211 | 0.646 | 0.9988 |
| 3 | 4 | rs10767664 | rs962369 | | | rs12273363 | TTT | 0.245 | 1.26 | 3.44 | 0.0637 | 0.3651 |
| 3 | 4 | rs10767664 | rs962369 | | | rs12273363 | ATT | 0.512 | 0.867 | 1.87 | 0.171 | 0.7323 |
| 3 | 3 | rs962369 | rs12273363 | | | rs908867 | CTT | 0.0815 | 0.884 | 0.433 | 0.511 | 0.9895 |
| 3 | 3 | rs962369 | rs12273363 | | | rs908867 | CCC | 0.151 | 1.02 | 0.0131 | 0.909 | 1 |
| 3 | 3 | rs962369 | rs12273363 | | | rs908867 | TTC | 0.757 | 1.03 | 0.0417 | 0.838 | 1 |
| 4 | 5 | rs7124442 | rs10767664 | rs962369 | | rs12273363 | CACC | 0.141 | 1.02 | 0.015 | 0.902 | 1 |
| 4 | 5 | rs7124442 | rs10767664 | rs962369 | | rs12273363 | CACT | 0.0853 | 0.937 | 0.124 | 0.725 | 0.9999 |
| 4 | 5 | rs7124442 | rs10767664 | rs962369 | | rs12273363 | TTTT | 0.24 | 1.22 | 2.57 | 0.109 | 0.5482 |
| 4 | 5 | rs7124442 | rs10767664 | rs962369 | | rs12273363 | CATT | 0.0297 | 2.58 | 5.84 | **0.0156*** | 0.1098 |
| 4 | 5 | rs7124442 | rs10767664 | rs962369 | | rs12273363 | TATT | 0.482 | 0.802 | 4.62 | **0.0317*** | 0.2031 |
| 4 | 4 | rs10767664 | rs962369 | rs12273363 | | rs908867 | ACTT | 0.0803 | 0.876 | 0.496 | 0.481 | 0.9865 |
| 4 | 4 | rs10767664 | rs962369 | rs12273363 | | rs908867 | ACCC | 0.147 | 1 | 2.77e-006 | 0.999 | 1 |
| 4 | 4 | rs10767664 | rs962369 | rs12273363 | | rs908867 | TTTC | 0.245 | 1.24 | 3.06 | 0.0803 | 0.4357 |
| 4 | 4 | rs10767664 | rs962369 | rs12273363 | | rs908867 | ATTC | 0.512 | 0.87 | 1.79 | 0.181 | 0.7511 |
| 5 | 5 | rs7124442 | rs10767664 | rs962369 | rs12273363 | rs908867 | CACTT | 0.0794 | 0.86 | 0.642 | 0.423 | 0.9741 |

**Table 2** (*continued*)

| NSNP | NHAP | SNP-first | SNP2 | SNP3 | SNP4 | SNP-last | Haplotype | Freq | OR | STAT | *P* | EMP *p* |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 5 | 5 | rs7124442 | rs10767664 | rs962369 | rs12273363 | rs908867 | CACCC | 0.141 | 1.01 | 0.0051 | 0.943 | 1 |
| 5 | 5 | rs7124442 | rs10767664 | rs962369 | rs12273363 | rs908867 | TTTTC | 0.24 | 1.22 | 2.52 | 0.112 | 0.5603 |
| 5 | 5 | rs7124442 | rs10767664 | rs962369 | rs12273363 | rs908867 | CATTC | 0.0302 | 2.66 | 6.19 | **0.0129*** | 0.09249 |
| 5 | 5 | rs7124442 | rs10767664 | rs962369 | rs12273363 | rs908867 | TATTC | 0.482 | 0.803 | 4.55 | **0.0328*** | 0.21 |

NSNP: number of SNPs included in haplotype; NHAP: number of common haplotypes (haplotypes with Freq $< 0.01$ were excluded from the analysis); SNP-first: SNP ID of the left-most (3′) SNP in the haplotype; SNP-last: SNP ID of the right-most (5′) SNP in the haplotype; Freq: frequency of a haplotype in the whole sample; OR: estimated odds ratio; STAT: test statistic (*T* from Wald test); *p*: asymptotic *p*-value.

* Nominal significance; EMP *p*: empirical *p*-value after 10,000 permutations correction for multiple comparisons.

- Supportive evidence to the proposed role of the SNP rs7124442 in the completed suicide phenotype [1] when in a specific allelic context (**A**/T–**T**/C–**T**/C–**C**/T) of at least two of the four SNPs (rs10767664, rs962369, rs12273363, rs908867).

## 1. Data

We provide data on additional analyses (Tables 1 and 2) of SNPs rs7124442, rs10767664, rs962369, rs12273363, rs908867 and rs1491851 for association with completed suicide phenotype, especially to highlight a proposed role of the SNP rs7124442 in the phenotype when in a specific haplotype context of two to four other SNPs (rs10767664, rs962369, rs12273363, rs908867) (Table 2). Raw genotyping data, potentially useful to conduct meta-analyses in the future, may be provided upon request.

## 2. Experimental design, materials and methods

Our study sample consisted of 775 unrelated Caucasian subjects, namely 289 controls (218 males and 71 females; mean age $51.9 \pm 18.3$ years) and 486 suicide completers (362 males and 124 females; mean age $49.2 \pm 17.8$ years). The control group was comprised of deceased persons, in which suicide as a cause of death was excluded. Criteria for positive alcohol dependence syndrome (ADS) status were met in 72 controls and in 97 suicide completers (for the details on the ADS status determination also see Materials and methods section in [1]).

Here, by means of software specifically designed for genetic analyses PLINK v1.07 [2], we performed logistic regression analyses (adjusted for covariates age, gender and ADS status) of the genotype data (raw file may be provided upon request) in order to gain more insight into the role of the studied SNPs in completed suicide phenotype [1].

First, the genotype analysis was done under four inheritance models: general genotype model (2 degrees of freedom), additive model (each copy of the minor allele alters the risk in an additive form), dominant model (a single copy of the minor allele is sufficient to modify the risk) and recessive model (two copies of the minor allele are needed to modify the risk) (Table 1). The data show no association of the studied SNPs under any of the model with completed suicide in our sample ($p > 0.05$) (Table 1).

Haplotype analysis was carried out using 2-, 3- and 4-adjacent SNPs sliding window approach implemented in PLINK v1.07 [2]. We also carried out the haplotype analysis for all 5 SNPs (rs7124442, rs10767664, rs962369, rs12273363 and rs908867) which are in strong linkage disequilibrium (also see in Ref. [1, Fig. 1]). Haplotypes with frequencies lower than 1% were excluded from the analysis and correction for multiple testing was performed by 10,000 permutations test. As shown in Table 2, none of the haplotypes showed significant association with completed suicide after 10,000 permutations correction (EMP $p > 0.05$). However, the T/C base change in the first position (rs7124442) in a specific context of common alleles (**A**/T–**T**/C–**T**/C–**C**/T) of at least two of the four SNPs rs10767664, rs962369, rs12273363 and rs908867, always resulted in at least a nominally significant $p$-value (Table 2).

## Acknowledgemets

Funding for the study was provided by the Slovenian Research Agency, Programme Grant no. P1-0390, and by a Junior Researchers Grant to SR. We would like to thank the Institute of Forensic Medicine in the Faculty of Medicine of the University of Ljubljana, Slovenia, for long term cooperation.

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