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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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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]

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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.

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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.