VAL66MET POLYMORFISMUS GENU PRO BDNF NELZE V ČESKÉ POPULACI SPOJOVAT S DIAGNÓZOU INFARKTU MYOKARDU

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Introduction

Brain-derived neurotrophic factor (BDNF) has been implicated in the pathogenesis of coronary artery disease (CAD).

Recently, human *BDNF* Val66Met polymorphism has been associated with CAD in Chinese population [1] and this growth factor has been implicated as a plausible player in regulation of neuro-hormonal processes in patients with cardiovascular disease [2].

[1] Jiang H et al. BDNF Val66Met polymorphism is associated with unstable angina. *Clin Chim Acta* 2009; 400:3-7
[2] Erasmus RT. The brain and heart: Dancing in unison? *Clin Chim Acta* 2009; 400:1-2

Rationale and Aim

To further explore a possible role of this ***BDNF* polymorphism as a genetic modifier in CAD** we have investigated its association with **myocardial infarction** in the Czech population.

Patients and Methods

Study subjects: A total of 397 unrelated individuals were enrolled into the study: 217 Czech patients from Olomouc area [age, median (range): 53 (25-79); males/females: 185/32] and 180 Czech healthy individuals [age, median (range): 29 (18-64); males/females: 95/85] serving as control population.

Diagnostic criteria for myocardial infarction (MI) were compatible with those recommended by an international consensus. Informed consent was obtained from all patients and controls.

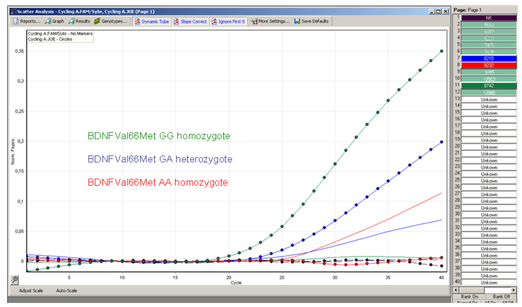
Genotyping for *BDNF* Val66Met ***rs6265*** G / A polymorphism was performed using qRT-PCR with "TaqMan" probes (Applied Biosystems, Assay ID C_11592758_10, **Fig. 1**).

The genotyping results were verified using the independent technique (PCR-SSP) with the primers as follows:
5´ GGCTGACACTTTCGAACACG with 5´ GTTACCCACTCACTAATACTG for 66Val allele and
5´ GGCTGACACTTTCGAACACA with 5´ GTTACCCACTCACTAATACTG for 66Met allele.

Statistical analysis: Consistency of the distribution of *BDNF* Val66Met genotypes with Hardy-Weinberg expectation was verified by the "χ2 goodness-of-fit" test, comparisons of the frequencies of *BDNF Val66Met* variants in the studied groups was performed by χ2 test.

Results

Figure 1: Genotyping of SNP BDNF rs6265 by qRT-PCR – interpretation



The distribution of *BDNF* Val66Met genotypes complied to Hardy-Weinberg equilibrium in MI patients and control subjects (p> 0.05)

Genotype and allele frequencies of the *BDNF* Val66Met polymorphism did not differ between the patients and control subjects (p> 0.05, **Tab. 1**). Two investigated groups also did not differ in carriage rates (phenotype frequencies) of the *BDNF* Val66Met polymorphism.

Similarly, no association with MI was found when male/female MI patients were compared with control subjects separately **(Tab. 2)**

Table 1: Distribution of *BDNF* Val66Met polymorphism in MI patients and controls

BDNF rs6265 G/A (Val66Met)		Czech population	
		MI	Controls
		(N=217)	(N=180)
Genotypes	GG	149(0.687)	127(0.706)
	GA	59(0.272)	44(0.244)
	AA*	9(0.041)	9(0.050)
Alleles	G	357(0.823)	298(0.828)
	A†	77(0.177)	62(0.172)
Carriers	A‡	68(0.313)	53(0.294)

Table 2: Distribution of *BDNF* Val66Met polymorphism in MI patients and controls by gender

BDNF rs6265 G/A (Val66Met)		Czech population			
		MI		Controls	
		(N=217)		(N=180)	
		Male	Female	Male	Female
Genotypes	GG	125(0.676)	24(0.75)	69(0.726)	58(0.682)
	GA	54(0.292)	5(0.156)	21(0.221)	23(0.271)
	AA*	6(0.032)	3(0.094)	5(0.053)	4(0.047)
Alleles	G	304(0.822)	53(0.828)	159(0.837)	139(0.181)
	A†	66(0.178)	11(0.172)	31(0.163)	31(0.182)
Carriers	A‡	60(0.324)	8(0.25)	26(0.274)	27(0.318)

Conclusion

The BDNF Val66Met polymorphism is not associated with myocardial infarction in Czech population.

We could not, therefore, replicate the observation from China [1], which suggested that *BDNF* Met/Met genotype is a genetic modifier in CAD.

Investigations in further centres and/or populations [2] are, therefore, necessary to obtain more information on possible role of BDNF genetic variability in coronary artery disease.

[1] Jiang H et al. *Clin Chim Acta* 2009; 400:3-7;
[2] Little J et al. Strengthening the reporting of genetic association studies (STREGA): an extension of the STROBE Statement. *Hum Genet* 2009, 125:131-51.

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