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ARTYKUŁ ORYGINALNY / *ORIGINAL ARTICLE*

Association of genetic variation in the natriuretic peptide system and left ventricular mass and blood pressure in newborns

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Abstract

Background: The natriuretic peptides play a key role in the modulation of left ventricular mass (LVM) and blood pressure (BP). We hypothesised that *NPPA* (natriuretic peptide precursor A gene), *NPPB* (natriuretic peptide precursor B gene), and *NPPC* (natriuretic peptide precursor C gene) are candidate genes possibly involved in the development or modulation of LVM at early life.

Aim: To assess the relationship between *NPPA*, *NPPB*, and *NPPC* gene polymorphisms with LVM and BP in newborns.

Methods: A total of 206 healthy newborns were studied by two-dimensional M-mode echocardiography. The polymorphisms *NPPA* rs5065, *NPPB* rs198389, and *NPPC* rs5268 were characterised.

Results: Newborns carrying the C allele of the *NPPB* polymorphism had significantly lower LVM/body surface area (BSA) and LVM/body weight (BW) values when compared with newborns' homozygotes for the T allele (41.76 g/m^2 vs. 48.31 g/m^2, $p_{adjusted} = 0.044$ and 2.78 g/kg vs. 3.26 g/kg, $p_{adjusted} = 0.031$, respectively). An association was observed between *NPPA* genotype and systolic BP, diastolic BP, and mean arterial pressure ≥ 90th percentile ($p = 0.029$, $p = 0.0048$, $p = 0.004$, respectively). Also an association was observed for systolic BP ≥ 90th percentile for *NPPB* ($p = 0.016$).

Conclusions: The present study shows that the *NPPB* gene polymorphism is associated with modulation of LVM in newborns. The *NPPA* and *NPPB* gene polymorphisms are associated with BP.

Key words: left ventricular mass, gene polymorphism, natriuretic peptides, blood pressure

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INTRODUCTION

Left ventricular hypertrophy is a risk factor for cardiovascular events [1]. Left ventricular mass (LVM) is influenced by factors including blood pressure (BP), age, gender, obesity, and/or dietary habits. However, genetic factors play an important role in modulating LVM in humans. Identification of genes involved in the modulation of LVM could contribute to an understanding of the etiopathogenesis of left ventricular hypertrophy development.

The natriuretic peptide (NP) family consisting of the three NPs, the genes encoding A-type natriuretic peptide (ANP), B-type natriuretic peptide (BNP), and C-type natriuretic peptide (CNP), are named from NP precursors A, B, and C, i.e. *NPPA* (natriuretic peptide precursor A gene), *NPPB* (natriuretic peptide precursor B gene), and *NPPC* (natriuretic peptide precursor C gene), respectively. The actions of the NP include vasodilatation, natriuresis, suppression of the rennin–angiotensin system (RAS), and inhibition of both cardiomyocyte hyper-

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trophy and cardiac fibroblast activation [2]. NP indicates the impact on the development of cardiovascular diseases [3, 4]. Published papers have shown that BNP is a good marker in identifying heart failure and left ventricular dysfunction in children [5]. However, the measurements NP are not generally part of the routine testing performed in children with cardiac disease because relatively little is known about their function and accuracy as a diagnostic test in children [6]. Furthermore, it should be emphasised that BNP levels were higher in the umbilical artery from birth and not related to maternal levels [7].

The NP might also be important during development. This hypothesis has been based on the findings that NP can act as a modulator of growth in cells of the heart. Experimental studies exhibit dynamic expression of cardiac NP during cardiogenesis (modulating growth of vascular cells, fibroblast proliferation, collagen production) and BP regulation in foetal life [8, 9]. Polymorphisms of the gene through variation of the concentration of the peptide or modification its structure can influence the pathogenesis of cardiovascular diseases. Recently Newton-Cheh et al. [10] reported that genetic variants of *NPPA* and *NPPB* genes are associated with increased circulating levels of BNP and ANP.

Therefore, we hypothesised that *NPPA, NPPB*, and *NPPC* are candidate genes possibly involved in the development or modulation of LVM in foetal life. In this study we evaluated the effects of the T2238C *NPPA* (rs5065), T(-381)C *NPPB* (rs198389), and G2628A *NPPC* (rs5268) gene polymorphisms in the development of LVM and regulation of BP in Polish newborns.

METHODS

Study subjects

The population included 206 healthy newborns born after the end of the 37th week of gestation (37 to 40 weeks). The mothers in this study were healthy without any complications. Body surface area (BSA) was calculated using the following equation: BSA = (BL [cm] × BW [kg]/3600)$^{1/2}$, where BL is body length and BW is body weight [11].

Echocardiographic and blood pressure measurements

Echocardiographic and BP measurements in neonates were made on the 3rd day after delivery. Two-dimensional M-mode echocardiography was performed using an Acuson Sequoia 512 unit (USA) equipped with a 2–4 MHz imaging transducer. Measurement techniques were consistent with the American Society of Echocardiography conventions. The LVM were calculated from the echocardiographic left ventricular dimension measurements using the Penn convention with the equation modified by Huwez et al. [12].

To standardise the LVM, it was indexed with respect to BL (LVM/BL), BW (LVM/BW), and BSA (LVM/BSA), respectively. A Diascope oscillometer (Artema) was used to determine systolic BP (SBP) and diastolic BP (DBP), and one of the investigators performed all of the BP measurements using a standardised protocol.

Genetic analysis

Genomic DNA from cord blood was isolated using the QIAamp Blood DNA Mini Kit (QIAGEN, Germany). For the analysis of the C(-381)T *NPPB* (rs198389) and the C(-381 T *NPPB* (rs198389) gene polymorphisms, a polymerase chain reaction/restriction fragment length polymorphism (PCR/RFLP) method was designed. For the analysis of the T2238C *NPPA* (rs5065) gene polymorphism, the following primer pairs were used: forward 5′-gCCggggCTgTTTTCgCTgTgAgT-3′ and reverse 5′-CggAggCTgCTgCTgCTTCTg-3′. The *NPPA* amplicons were subsequently digested with the enzyme *ScaI* enzyme (MBI Fermentas, Vilnius, Lithuania). DNA fragments that contained the C(-381)T *NPPB* (rs198389) gene polymorphism were amplified using PCR with forward 5′-gCCggggCTgTTTTCgCTgTgAgT-3′ and reverse 5′-CggAggCTgCTgCTgCTTCTg-3′ primers. The reaction was run with the addition of betaine (20% of the final volume). Afterwards the amplicons were purified with Gene Elute PCR Clean Up Kit (Sigma Aldrich) and PCR-RFLP with the *EcoRII* restriction enzyme was performed. For analysis of the G2628A *NPPC* (rs5268) gene, PCR with forward 5′-gCTgAGCCgTTTCTgACCTT-3′ and reverse 5′-ATgAGCggCCTgggATGTTAgT-3′ primers were used. The amplification was run with the addition of Dimethyl sulfoxidate PCR reagent (10% of the final volume) and the amplicons were subsequently digested with *Taq* restriction enzyme (MBI Fermentas, Vilnius, Lithuania).

Statistical analysis

The divergence of *NPPA, NPPB*, and *NPPC* genotype frequencies from Hardy-Weinberg equilibrium was assessed using χ^2 tests, and the distribution of each quantitative variable was tested for skewness. Quantitative data were presented as means ± standard deviation and analysed either by Student`s *t*-test or by one-way ANOVA. LVM index (LVMI) was tested for association with genotype in multivariate analysis (ANCOVA) in order to adjust for possible confounding factors: neonatal (gestational age, gender, APGAR at 3 min) and maternal (age, body mass index [BMI] at beginning and end of the pregnancy, smoking status, and hypertension status). Dominant, recessive, and additive modes of inheritance were tested. Statistical significance was defined as $p < 0.05$. All data were analysed with STATISTICA software (data analysis software system, version 8.0, StatSoft, Inc. 2007, www.statsoft.com).

RESULTS

The characteristics of the newborn cohort (n = 206) are shown in Table 1. The distribution of these characteristics in our cohort approached normality (skewness < 2 for all variables). There were no significant differences in *NPPA* rs5065,

Table 1. Clinical and echocardiographic characteristics of the newborns with regard to gender

	Total	Males	Females	P
N (%)	206 (100%)	114 (55.3%)	92 (44.7%)	
Gender (male/female)	114/92			
BL [m]	0.56 ± 0.03	0.56 ± 0.03	0.55 ± 0.03	0.106
BW [kg]	3.47 ± 0.45	3.56 ± 0.47	3.36 ± 0.38	0.0009
BSA [m^2]	0.23 ± 0.02	0.24 ± 0.02	0.23 ± 0.02	0.002
SBP [mm Hg] n=210	69.07 ± 9.02	69.21 ± 9.89	68.88 ± 7.87	0.796
DBP [mm Hg] n=210	40.03 ± 7.84	39.91 ± 8.09	40.18 ± 7.57	0.806
MAP [mm Hg] n=210	51.89 ± 7.63	51.80 ± 7.96	51.60 ± 7.25	0.854
LVDd [mm]	18.58 ± 1.62	18.68 ± 1.66	18.46 ± 1.57	0.339
LVDs [mm]	11.83 ± 1.38	11.71 ± 1.42	11.98 ± 1.32	0.170
IVS [mm]	3.73 ± 0.67	3.77 ± 0.63	3.69 ± 0.71	0.380
LVPW [mm]	2.76 ± 0.69	2.81 ± 0.68	2.71 ± 0.69	0.318
LVM [g]*	9.89 ± 2.84	10.15 ± 2.89	9.58 ± 2.76	0.153
LVV [mL]*	10.70 ± 2.47	10.85 ± 2.53	10.51 ± 2.41	0.337
LVM/BL [g/m]*	17.71 ± 4.83	18.05 ± 4.79	17.30 ± 4.88	0.271/0.269*
LVM/BW [g/kg]*	2.86 ± 0.79	2.86 ± 0.79	2.86 ± 0.79	0.996/0.998*
LVM/BSA [g/m^2]*	42.67 ± 11.51	43.07 ± 11.43	42.17 ± 11.64	0.580/0.579*

*Adjusted for systolic blood pressure (SBP); DPB — diastolic blood pressure; BL — body length; BW — body weight; BSA — body surface area; MAP — mean arterial pressure; LVDd — left ventricular internal diameter diastolic; LVDs — left ventricular internal diameter systolic; IVS — thickness of interventricular septum; LVPW — left ventricular posterior wall; LVM — left ventricular mass; LVV — left ventricular volume

NPPB rs198389, and *NPPC* rs5268 genotypes or allele distributions between boys and girls, and the genotype distributions conformed to the expected Hardy-Weinberg equilibria (Table 1).

LVMI were tested for association with genotype in multivariate analysis (ANCOVA) in order to adjust for possible confounding factors. After adjusting for neonatal (gestational age, gender, APGAR at 3 min) and maternal (age, BMI at beginning and end of the pregnancy, smoking status, and hypertension status) parameters, we revealed a significant association between LVMIs (LVM/BSA and LVM/BW) and the *NPPB* polymorphism. The carriers of the C allele of the *NPPB* polymorphism had significantly lower LVM/BSA and LVM/BW values when compared with newborns homozygous for the T allele (41.76 g/m^2 vs. 48.31 g/m^2, $p_{adjusted}$ = 0.044 and 2.78 g/kg vs. 3.26 g/kg, $p_{adjusted}$ = 0.031, respectively) (Fig. 1).

There was no independent association between *NPPA, NPPC* genetic variation, and LVMI in newborns. The frequency of homozygous TT *NPPA* gene was low (only 3 homozygous), and therefore no effect of the TT homozygous *NPPA* gene on the LVM in this study was considered. Owing to the low number of CC homozygotes for the *NPPA* polymorphism, only the dominant mode was considered (date not shown).

An association was observed between *NPPA* genotype and SBP, DBP, and mean arterial pressure (MAP) ≥ 90th percentile (p = 0.029, p = 0.0048, p = 0.004, respectively). The frequency of newborns with SBP ≥ 90th percentile was greater in the carriers of C allele (CC+TC vs. TT, p = 0.013),

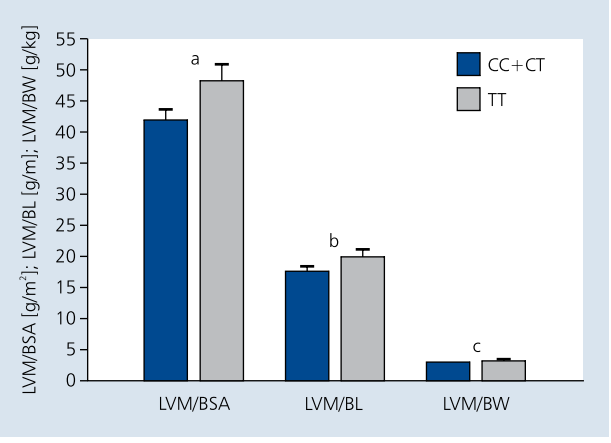

Figure 1. Left ventricular mass indexes according to B-type natriuretic peptide (*BNP*) genotype. Mean and standard error of mean are shown; [a]p = 0.044; [b]p = 0.080; [c]p = 0.031; [a, b, c]CC+CT vs. TT; BSA — body surface area; BL — body length; BW — body weight

while the frequencies of newborns of DBP ≥ 90th percentile, MAP ≥ 90th percentile were greater in the homozygotes CC (p = 0.001 and p = 0.002, respectively). An association of SBP ≥ 90th percentile for *NPPB* (p = 0.016) was additionally observed. The homozygotes CC exhibited higher frequency of SBP ≥ 90th percentile, compared to the carriers of T allele (23% vs. 7%, p = 0.004). The *NPPC* gene variant was

Table 2. Overview of results depending on foetal genotypes

	NPPA			*NPPB*				*NPPC*			
	TT (n = 143)	CC+TC (n = 63)	P	TC (n = 109)	TT (n = 62)	CC (n = 35)	P	AA (n = 85)	GA (n = 90)	GG (n = 31)	P
Gestational age [weeks]	39.3 ± 1.0	39.3 ± 1.0	0.754	39.4 ± 1.0	39.3 ± 0.9	39.3 ± 1.1	0.758	39.3 ± 1.1	39.4 ± 0.9	39.2 ± 1.0	0.666
Gender (female/male)	6/81 (43.4/56.6)	30/33 (47.6/52.4)	0.571	50/95 (45.9/54.1)	24/38 (38.7/61.3)	18/17 (51.4/48.6)	0.449	40/45 (47.1/52.9)	38/52 (42.2/57.8)	14/17 (45.2/54.8)	0.812
Birth weight [kg]	3.5 ± 0.43	3.51 ± 0.47	0.356	3.46 ± 0.46	3.48 ± 0.44	3.50 ± 0.44	0.899	3.44 ± 0.39	3.49 ± 0.48	3.50 ± 0.50	0.661
Neonatal body length [cm]	55.80 ± 3.08	55.62 ± 2.86	0.685	55.85 ± 2.98	55.82 ± 3.27	55.29 ± 2.65	0.610	55.67 ± 3.06	55.80 ± 2.94	55.81 ± 3.18	0.954
Neonatal head circumference [cm]	33.69 ± 1.42	34.26 ± 1.02	0.969	33.63 ± 1.36	34.29 ± 1.25	33.85 ± 1.33	0.193	33.80 ± 1.48	33.75 ± 1.16	34.39 ± 1.45	0.439
APGAR 3 min	9.57 ± 1.07	9.59 ± 0.96	0.895	9.55 ± 0.96	9.55 ± 1.29	9.69 ± 0.76	0.780	9.67 ± 1.02	9.54 ± 1.01	9.39 ± 1.17	0.404
SBP [mm Hg]	68.24 ± 8.57	68.24 ± 8.57	0.488	67.53 ± 9.10	69.97 ± 8.40	72.18 ± 9.06	0.018	70.37 ± 9.08	69.03 ± 9.19	65.59 ± 7.56	0.040
SBP ≥ 90 percentile	9 (6.3%)	11 (17.5%)	0.013	8 (7.4%)	4 (6.5%)	8 (22.9%)	0.016	10 (11.8%)	9 (10.1%)	1 (3.23%)	0.386
SBP ≥ 75 percentile	32 (22.5%)	20 (31.8%)	0.162	21 (19.4%)	19 (30.7%)	12 (34.3%)	0.112	23 (27.1%)	25 (28.1%)	4 (12.9%)	0.221
DBP [mm Hg]	40.25 ± 7.60	39.53 ± 8.41	0.547	39.09 ± 7.76	40.31 ± 7.77	42.44 ± 7.90	0.084	41.36 ± 8.44	39.55 ± 7.76	37.75 ± 5.60	0.067
DBP ≥ 90 percentile	14 (9.9%)	7 (11.1%)	0.785	9 (8.3%)	7 (11.3%)	5 (14.3%)	0.570	12 (14.1%)	9 (10.1%)	0 (0%)	0.085
DBP ≥ 75 percentile	37 (26.1%)	14 (22.2%)	0.558	25 (23.2%)	14 (22.6%)	12 (34.3%)	0.367	26 (30.6%)	21 (23.6%)	4 (12.9%)	0.139
MAP [mm Hg]	40.25 ± 7.60	51.29 ± 7.41	0.615	50.45 ± 7.26	52.59 ± 7.42	55.07 ± 8.14	0.005	52.90 ± 7.69	51.57 ± 7.97	50.01 ± 6.07	0.169
MAP ≥ 90 percentile	12 (8.5%)	10 (15.9%)	0.113	9 (8.3%)	6 (9.7%)	7 (20.0%)	0.145	11 (12.9%)	10 (11.2%)	1 (3.2%)	0.320
MAP ≥ 75 percentile	37 (26.1%)	12 (19.1%)	0.278	19 (17.6%)	15 (24.2%)	15 (42.9%)	0.010	27 (31.8%)	19 (21.4%)	3 (9.7%)	0.036
Maternal age [years]	28.27 ± 5.23	28.11 ± 5.77	0.850	28.01 ± 4.77	28.77 ± 6.05	27.86 ± 5.99	0.618	27.24 ± 4.88	28.61 ± 5.89	29.77 ± 4.77	0.051
Smoking habits OR History during pregnancy	17 (11.9%)	4 (6.4%)	0.226	5 (4.6%)	10 (16.1%)	6 (17.1%)	0.019	5 (5.9%)	9 (10.0%)	7 (22.6%)	0.031
Hypertension OR History during pregnancy OR History of hypertension	12 (8.4%)	5 (7.9%)	0.913	7 (6.4%)	6 (9.7%)	4 (11.4%)	0.573	5 (5.9%)	7 (7.8%)	5 (16.1%)	0.202
BMI [kg/m^2] at beginning of pregnancy	22.11 ± 3.61	22.11 ± 3.61	0.672	22.02 ± 3.18	22.50 ± 3.77	22.09 ± 4.45	0.693	22.03 ± 4.23	22.34 ± 3.06	21.23 ± 3.01	0.288
BMI [kg/m^2] at the end of pregnancy	27.44 ± 4.03	22.11 ± 3.61	0.268	27.15 ± 3.63	28.23 ± 4.43	28.77 ± 3.96	0.057	27.76 ± 4.49	27.94 ± 3.39	27.18 ± 4.15	0.660
Parity	1.5 ± 0.9	1.6 ± 0.9	0.306	1.4 ± 0.8	1.8 ± 1.0	1.5 ± 0.9	0.014	1.5 ± 0.8	1.4 ± 0.8	1.9 ± 1.2	0.026

Observation data of the study population according to *NPPA*, *NPPB* and *NPPC* genotype. Tested for significant differences with one-way ANOVA; χ^2/Fisher's exact test (SBP ≥ 90 percentile, SBP ≥ 75 percentile, DBP ≥ 90 percentile, DBP ≥ 75 percentile, MAP ≥ 90 percentile, MAP ≥ 75 percentile); *NPPA* — natriuretic peptide precursor A gene; *NPPB* — natriuretic peptide precursor B gene; *NPPC* — natriuretic peptide precursor C gene; SBP — systolic blood pressure; DBP — diastolic blood pressure; MAP — mean arterial pressure; BMI — body mass index

unrelated to BP in newborns. Additionally, *NPPB* and *NPPC* polymorphisms were significantly correlated with maternal history of smoking habits and *NPPA, NPPB*, and *NPPC* genotypes were significantly correlated with parity (Table 2).

DISCUSSION

The present study demonstrates an association between *NPPA*, *NPPB*, and *NPPC* gene polymorphisms and LVM and BP in newborns. It is known that the role of genetic factors in the development or heart parameters may be particularly relevant. Recently we presented a study in which is was suggested that RAS or bone morphogenetic protein (*BMP4*) and bone morphogenetic protein type 1 receptor (*BMPR1A*) and calmodulin (*CALM2*) genetic variation may partially account for subtle variations in LVM or heart parameters in newborns, when external environmental factors have not yet had a marked impact [13, 14].

The present study demonstrates a significant association between variants of *NPPB* and a decrease in LVMIs in newborns. We used the suggested methods of determining the LVM in relation to BSA, BL, and BW to accurately transform and index the determined LVM. In carriers of the C allele of the *NPPB* gene, we observed a significant decrease in LVM/BSA and LVM/BW. This finding may be connected with varying levels of NP plasma concentrations. The T(-381)C rs198389 is located in the promoter region of *NPPB*. A previous study has demonstrated that the rs198389 C allele may be associated with higher BNP promoter activity [15], and that the rs198389 is correlated with levels of plasma BNP. As Lanfear [4] suggested, the *NPPB* promoter variants are the key source of inter-individual variation in BNP levels and may also impact the clinical interpretation of BNP testing. NP levels were not measured in the present study, which is its main limitation.

In the current study we investigated healthy newborns born full term, when external environmental factors had not yet had a marked impact and the influence of genes on LVM could be expressed. The strength of our study is determined by the well-documented cohort of healthy newborns born full term without coexisting heart defects. It is known that BNP is an important biomarker in cardiology in adults, and it is correlated with poor ventricular function. Genetic variation in the *NPPB* has potential implication in the BNP pathway and is associated with alterations in BNP levels. We hypothesised that genetic variation in the NP system may also cause minor changes in the development or modulation of LVM in healthy newborns. Our data on the genetic variability in *NPPB* shows the possible importance in the subtle modulating of LVM in foetal life and in the first days of life in healthy newborns. La Pointe [16] expressed a theory that BNP may work more as an autocrine/paracrine inhibitor of cell growth in the heart, while ANP is potent diuretic vasorelaxant hormone. Some studies indicate that BNP inhibits growth of vascular cells, as well as fibroblast proliferation and collagen production. We continue observing our population and we are considering conducting a follow-up, which will show in later years whether the variation of *NPPB* has a predisposition to modulate LVM and several echocardiographic variables. However, our results require confirmation in further independent large studies**.**

Another finding in our study is the influence of genetic variation of the *NPPA* and *NPPB* on the BP. *NPPA* rs5065, which introduces the stop codon and extends ANP by two amino acids, is located in the 3'UTR. Most of the mechanisms that this regulation affects are trough vascular volume (mainly natriuresis) and tone, resulting in lower BP [17]. In addition, the NP system has haemodynamic effects via antagonisation of the RAS and the adrenergic system, which also contribute to lowering of BP and vascular tone [4]. Genetic variation in the NP system is well documented. For blood, BNP levels have been shown to be heritable, supporting the notion that genetic variation in the system impacts its function [18]. However, the observed association with hypertension may be explained not only by increased levels of NP, but also by an increase in ANP receptor binding or activity in individuals carrying the rs5065 C allele. It is worth mentioning that the predominant phenotypes of *NPPA* and *NPR1* (natriuretic peptide receptor type 1) knockout mice are arterial hypertension and myocardial hypertrophy [19]. In the current study an association was observed between *NPPA* rs5065 and SBP, DBP, and MAP $\geq 90^{th}$ percentile, and also for *NPPB* rs198389 and SBP $\geq 90^{th}$ percentile. In addition to its role in cardiovascular homeostasis in adults, the NP might also be important during development. In newborns this may not only be related to different levels of plasma concentrations of NP associated with different genetic variants, but also to diminished water and electrolyte distribution in the perinatal period. Therefore, these results should be interpreted with caution. Interestingly, Hammerer-Lerchel et al. [20] showed that umbilical cord N-terminal-proBNP levels were higher than maternal levels. The reason for this neonatal surge is not clear. Our suggested hypothesis is that genetic variation of *NPPA* and *NPPB* may be partly involved in modulating the levels of NP as early as in foetal life.

CONCLUSIONS

In conclusion, LVM is a continuous trait influenced by interaction between genetic, environmental, and lifestyle factors. The present study shows an association between *NPPB* gene polymorphism and LVM in newborns. Our data confirm a role of *NPPB* in LVM development in newborns and provide the first evidence suggesting that the *NPPB* polymorphism might be considered as one of the factors important in the development and/or modulation of LVM in foetal life. Additionally, an association between *NPPA*, *NPPB*, and BP was found. Further studies are needed to define the role of genetic variation in the NP system in the development or modulation of LVM and BP in newborns.

Conflict of interest: *none declared*

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Analiza związku polimorfizmów genów kodujących peptydy natriuretyczne z masą lewej komory i ciśnieniem tętniczym u noworodków

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Streszczenie

Wstęp: Peptydy natriuretyczne odgrywają kluczową rolę w modulacji masy lewej komory mięśnia sercowego (LVM) i ciśnienia tętniczego (BP). Geny *NPPA* (gen kodujący typ A peptydu natriuretycznego), *NPPB* (gen kodujący typ B peptydu natriuretycznego), *NPPC* (gen kodujący typ C peptydu natriuretycznego) mogą być potencjalnie zaangażowane w rozwój i/lub modulowanie LVM i BP już na wczesnych etapach życia.

Cel: Celem niniejszej pracy była ocena związku między polimorfizmem genów *NPPA*, *NPPB, NPPC* i LVM oraz BP u noworodków.

Metody: Za pomocą dwuwymiarowej echokardiografii M-*mode* przebadano 206 zdrowych noworodków. Przeprowadzono oznaczenia polimorfizmów genów *NPPA* rs5065, *NPPB* rs198389, *NPPC* rs5268.

Wyniki: Noworodki będące nosicielami przynajmniej jednego allelu C genu *NPPB* charakteryzowały się istotnie niższymi wartościami wskaźnika LVM/powierzchni ciała (BSA) i LVM/masy ciała (BW) w porównaniu z noworodkami będącymi homozygotami TT (odpowiednio 41,76 g/m^2 *vs*. 48,31 g/m^2, $p_{adjusted}$ = 0,044 i 2,78 g/kg *vs*. 3,26 g/kg, $p_{adjusted}$ = 0,031). Wykazano korelację między genotypem *NPPA* a ciśnieniem skurczowym, rozkurczowym i średnim ≥ 90. percentyla (odpowiednio p = 0.029; p = 0.0048; p = 0.004). Ponadto zaobserwowano związek z ciśnieniem skurczowym ≥ 90. percentyla dla *NPPB* (p = 0,016).

Wnioski: Niniejsze badanie potwierdza, że polimorfizm genu *NPPB* wiąże się z modulowaniem LVM u noworodków. Polimorfizmy genów *NPPA*, *NPPB* są związane z potencjalną regulacją ciśnienia tętniczego.

Słowa kluczowe: masa lewej komory, polimorfizm, peptydy natriuretyczne, ciśnienie tętnicze

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