

α -ADDUCIN METHYLATION AND BLOOD PRESSURE IN YOUNG ADULTS | Less is More

WAN FATEIN NABEILA WAN OMAR¹, NORLELAWATI A. TALIB², JAMALLUDIN AB. RAHMAN³, AZARISMAN SHAH MOHD SHAH⁴, ASZRIN ABDULLAH¹.

¹Dept of Basic Medical Sciences | ²Dept of Pathology and Laboratory Medicine |
³Dept of Community Medicine | ⁴Dept of Internal Medicine,
Kulliyyah of Medicine, International Islamic University Malaysia



OUTLINE



Introduction



Results and
Discussion



Literature review



Strength and
Limitation



Methods



Conclusion

INTRODUCTION

Cardiovascular risk factors	Prevalence (%)	
	Malaysia ²	Other countries ⁴
Age, years (mean/median)	58.5	65
Hypertension	65.0	52
Smoking	38.0	62
Diabetes mellitus	45.8	21
Dyslipidaemia	37.4	38
Male	78.8	70
Family history	13.2	-
Body mass index (mean (SD))	26.1 (4.3)	-

ACS
<45y in
Malaysia
Hypertension

3
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HYPERTENSION

Malaysia
>18 y

Normotension **23.9%**

Prehypertension **45.8%**

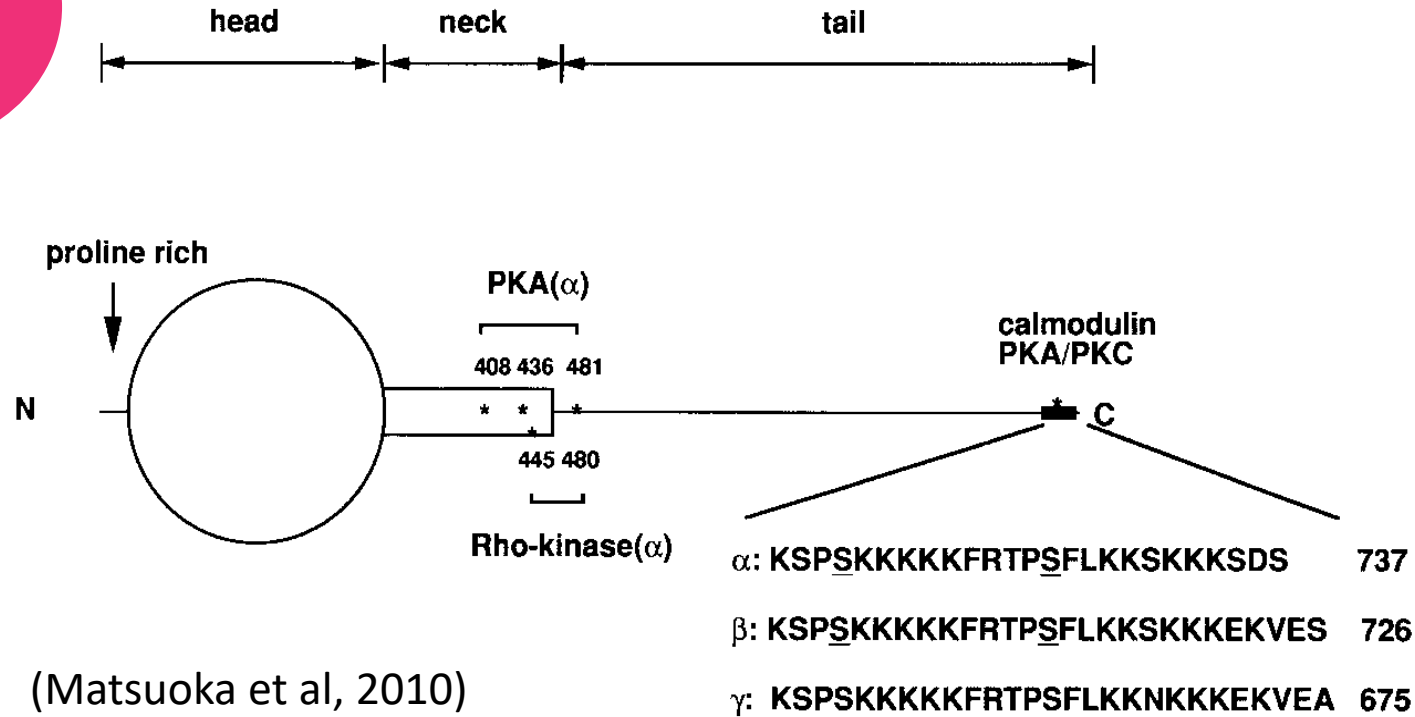
Hypertension **30.3%**

Age group (years)	Prevalence of hypertension (%) ²		Ratio unknown:known
	Known	Unknown	
18-19	0.7	6.0	8.6
20-24	1.9	7.5	3.9
25-29	2.8	10.4	3.7
30-34	3.9	12.0	3.1
35-39	5.8	18.1	3.1
40-44	11.9	20.3	1.7
45-49	15.0	23.8	1.6
50-54	23.1	26.2	1.1
55-59	29.3	26.2	0.9
60-64	37.1	27.9	0.8
65-69	39.1	28.7	0.7
70-74	50.4	25.0	0.5
≥ 75	46.1	27.3	0.6

α -ADDUCIN (ADD1)



ADD



- Adducin is a cytoskeletal protein
- Exists as α - γ and α - β heterodimers
- Tail – important interaction site with other proteins

ADD1 & ESSENTIAL HYPERTENSION



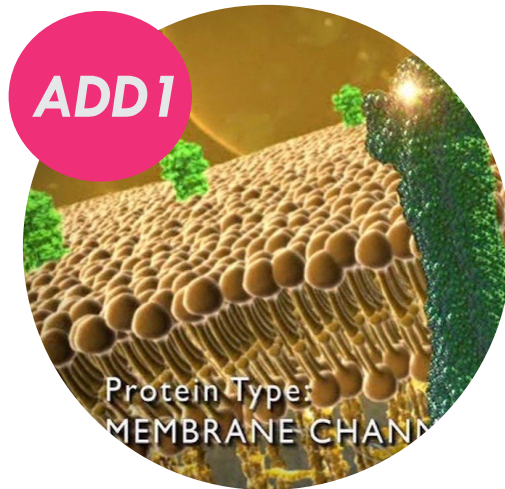
ADD1 References into Functions		References
Polymorphism	Gly460Trp polymorphism is associated with Essential Hypertension in a Caucasian population from Madeira Island.	Sousa et al. (2017)
	rs4963 polymorphism showed an increased hypertension risk.	Qu et al. (2017)
	G460T polymorphism is associated with essential hypertension.	Soualmia et al.(2016)
	The T allele is associated with essential hypertension in Asians.	Liao et al. (2016)
	No difference in Gly460Trp polymorphism between control and pediatric hypertensive group.	Kaplan et al. (2015)
	G614T polymorphism is associated with essential hypertension in Chinese patients.	Wang et al. (2015)
	rs4961 has a protective role in development of EH; interactions between alcohol consumption	Han et al. (2016)
	rs4963 polymorphism is associated with essential hypertension in the Chinese population	Zhang et al. (2013)
	G460W gene polymorphism was linked to essential hypertension	Li (2012)
	G460W polymorphism was associated with hypertension in female Japanese subjects.	Shioji et al (2010)
	G460W polymorphism as predisposition gene to hypertension among Russians, but is influenced by environmental factors.	Polonikov et al. (2012)
	Null association of G460T with hypertension in Chinese.	Niu et al. (2011)

ADD1 & ESSENTIAL HYPERTENSION



ADD1 References into Functions		References
Polymorphism	Gly460Trp polymorphism might increase the risk of hypertension in Han Chinese populations.	Liu et al. (2011)
	Genetic variation in <i>ADD1</i> alter renal function and/or vasoreactivity	Alioglu et al. (2011)
	Gly460Trp polymorphism is associated with salt-sensitivity.	Wang et al. (2010)
	460Trp allele was associated with lower levels of central systolic pressure and pulse pressure in JingNing population.	Guo et al. (2010)
	Role for the <i>ADD1</i> variants in blood pressure salt sensitivity	Kelly et al. (2010)
	rs4961 polymorphism is associated with essential hypertension	Gong et al. (2010)
	TT genotypes might be genetic susceptibility factors to hypertension accompanying renal injury.	Lu, Chen & Yu (2010)
	Gly460Trp polymorphism is significantly associated with an increased risk of coronary artery disease as well as blood pressure in Koreans	Cha et al. (2010)
	G460W polymorphism influences blood pressure when BMI and sex are taken into account	Fava et al. (2010)
	Gly460Trp polymorphism is associated with low renin hypertension.	Sugimoto et al. (2010)
Mutation	The ACE I/D, alpha-adducin Gly460Trp and aldosterone synthase -344C/T polymorphisms interact to influence SBP in Chinese.	Wang et al. (2010)
	Increased CFTR surface expression and activity in HEK (G460W) and cultured rat distal convoluted tubule cells (F316Y).	Mondini et al. (2013)

ADD1 & ESSENTIAL HYPERTENSION



SODIUM HANDLING

Sodium retention

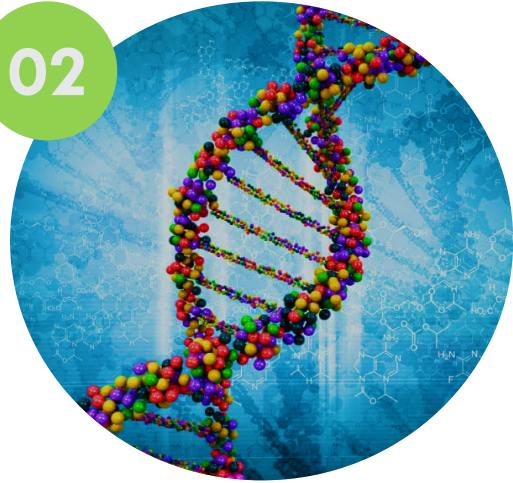
Mutated ADD variant induced constitutive reduction of the Na/K pump endocytic rate (Torielli et al., 2010).

Physiological interaction between the *ADD1* and WNK1-NEDD4L pathways influences the effects of variants in these genes on Na-related BP regulation. (Manunta, Lavery et al., 2010).

Patients with *ADD1* Trp alleles are sensitive to salt and tubular Na reabsorption remains elevated after volume expansion (Manunta, Milliard et al. 2010).

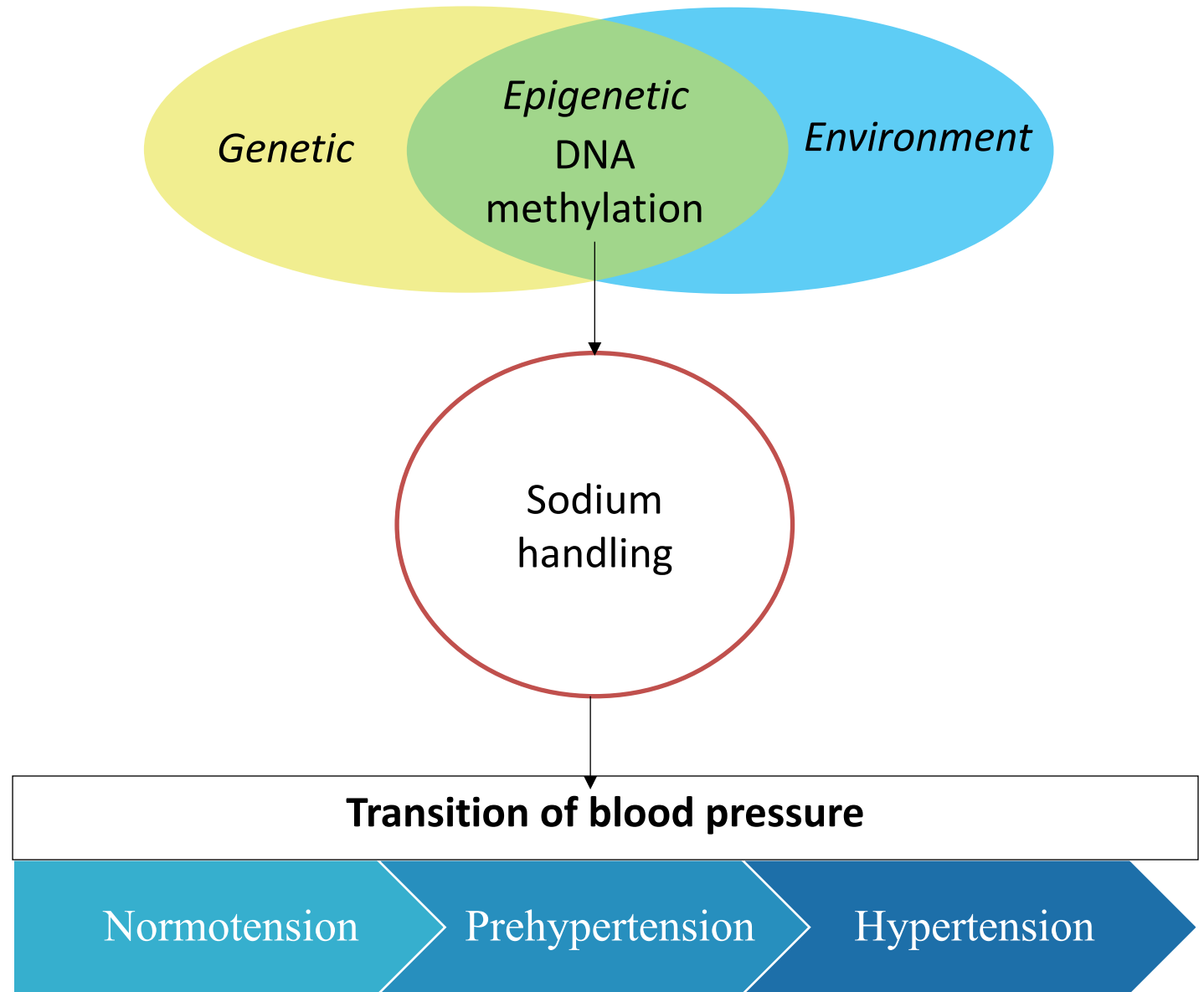
ADD1 Trp460Trp genotype is significantly associated with reduced renal plasma flow and glomerular filtration rate. (Beeks et al, 2010).

02



EPIGENETICS

Links genetic and environment



ADD1 METHYLATION IN ESSENTIAL HYPERTENSION



1

HYPOMETHYLATED

Chinese adults with essential hypertension (Zhang et al., 2013).



2

HYPOMETHYLATED

Middle-age Egyptian with essential hypertension (Bayoumy et al. 2017).



3

INTERACTION WITH ALCOHOL

Modifies EH susceptibility in Han Chinese adults (Han et al., 2015).




GAPS OF KNOWLEDGE




GAP 1

YOUNG ADULTS
Most studies:
general adults




GAP 2

METHYLATION METHODS
Incomparable
results

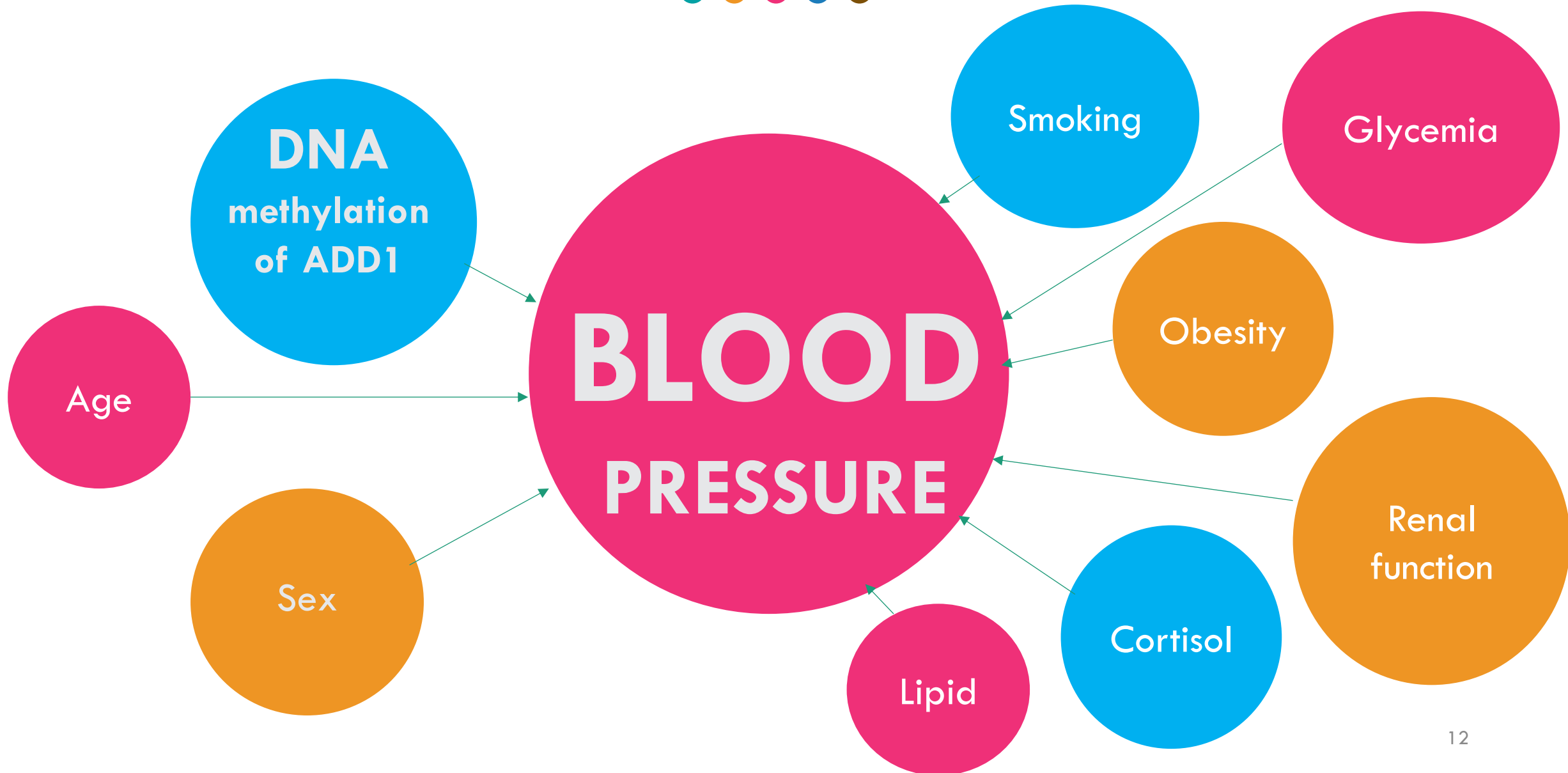


GAP 3

EFFECT ON GENE EXPRESSION
Unknown



CONCEPTUAL FRAMEWORK



RESEARCH OBJECTIVES



To investigate the association between DNA methylation of the promoter of α -adducin (*ADD1*) with blood pressure in young adults

1

To investigate the association between the level of DNA methylation of the promoter of *ADD1*, and other covariates, with blood pressure in young adults

2

To investigate the association between level of *ADD1* methylation with the gene expression level.

3

METHODOLOGY



01 ETHICAL APPROVAL

Medical Research
Ethical Committee
(NMRR-16-2572-
32869)
Institutional
Research Ethic
Committee
(IREC544)



02 RECRUITMENT

$N = 80$ for
each Nt and
Hpt group



Sample Size For Comparing Two Means

Input Data

Confidence Interval (2-sided)	95%
Power	80%
Ratio of sample size (Group 2/Group 1)	1

	Group 1	Group 2	Difference*
Mean	16	14	2
Standard deviation	4.5	4.5	
Variance	20.25	20.25	

Sample size of Group 1	80
Sample size of Group 2	80
Total sample size	160

*Difference between the means

Results from OpenEpi, Version 3, open source calculator--SSMean

Values adopted
from previous
methylation
study by Mao
et al (2017)¹⁰

M E T H O D O L O G Y

Inclusion criteria	Exclusion criteria
<ol style="list-style-type: none"> Age 18–45 years as determined by the year of birth Consented 	<ol style="list-style-type: none"> Previous or current diagnosis of hypertension and/or current use of anti-hypertensive medication History of ischemic heart disease as reported by subject History of Type 1 or 2 diabetes mellitus as reported by subject History of chronic renal failure as reported by subject or serum creatinine more than 112 mmol/L as reported by subject Current use of steroid medication or history of conditions hyper-or hypocortisolism as reported by subject including but not limited to Cushing's syndrome Female subjects who are pregnant as reported by subject Female subjects who are on hormonal contraception as reported by subject



Blood pressure class according to CPG 4 th ed ¹⁷ and JNC7 ¹⁸	Systolic blood pressure (mmHg)		Diastolic blood pressure (mmHg)
Normotension (Nt)	< 120	and	< 80
Hypertension (Hpt)	≥ 140	and/or	≥ 90

each Nt and
Hpt group

Study protocol

Sociodemographic

Weight, height,
waist circumference

Blood pressure x 3

Fasting blood

Epigenetics & genetic

Biochemical profile (accredited
lab)

ET
APP

Medical R
Ethical Co
(NMRR-16

Inst
Resea
Co
(IR

Primer design targeting
promoter region
(*ADD1*, *Alu*)

DNA isolation and
quantification

Optimisation

Bisulphite treatment

MethyLight

Data analysis.

$$\text{Gene methylation} = \text{antilog} \frac{Cq \text{ gene of interest}}{Cq \text{ Alu}}$$

ADD1 gene expression study

Nt

Hpt

5 samples with highest
ADD1 methylation

5 samples with highest
ADD1 methylation

5 samples with lowest
ADD1 methylation

5 samples with lowest
ADD1 methylation

01
ETHICAL
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RECRUI

N =
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Hpt

SSION

METHODOLOGY



01 ETHICAL APPROVAL

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03 STUDY PROTOCOL

Anthropometry,
blood pressure,
fasting blood
collection and
processing

02 RECRUITMENT

$N = 80$ for
each Nt and
Hpt group

04 METHYLATION STUDY

MethyLight

06 DATA ANALYSIS

IBM SPSS 22.0

05 GENE EXPRESSION

$N = 10$

RESULTS | Sociodemographic

Sociodemographic aspect		Blood pressure status		
		Nt	Htn	p-value
Age (years) ^Φ		31 (7)	35 (6)	<0.001 ^c
Male ^Ψ		40 (39.6)	61 (60.4)	0.001 ^a
Malay ^Ψ		78 (53.1)	69 (46.9)	0.016 ^a
Education level ^Ψ	Primary	0 (0.0)	1 (100.0)	0.006 ^b
	Secondary	12 (30.8)	27 (69.2)	
	Tertiary	68 (56.7)	52 (30.1)	
Smoking ^Ψ		13 (39.4)	20 (60.6)	0.171 ^a
Consume alcohol ^Ψ		1 (12.5)	7 (87.5)	0.030 ^b
Body mass index (kg/m ²) ^Φ		25.2 (5.6)	29.4 (5.0)	<0.001 ^c
Body mass index category ^Ψ	Underweight/Normal (<23 kg/m ²)	31 (93.9)	2 (6.1)	<0.001 ^a
	Overweight (23–27.49 kg/m ²)	28 (47.5)	31 (52.5)	
	Obese (≥27.5kg/m ²)	21 (30.9)	47 (69.1)	
Waist circumference (cm) ^Φ		84.9 (10.5)	94.5(13.3)	<0.001 ^c
	Female	83.4 (11.6)	85.8(10.0)	0.446 ^c
	Male	86.4 (9.1)	97.3(13.0)	<0.001 ^c

Note ^ΦMean(standard deviation). ^Ψn(%). ^aAnalysed using Chi-squared test, ^bAnalysed using Fisher's exact test, ^cAnalysed using student's t-test. Body mass index status is according to World Health Organisation recommendation for Asian population.

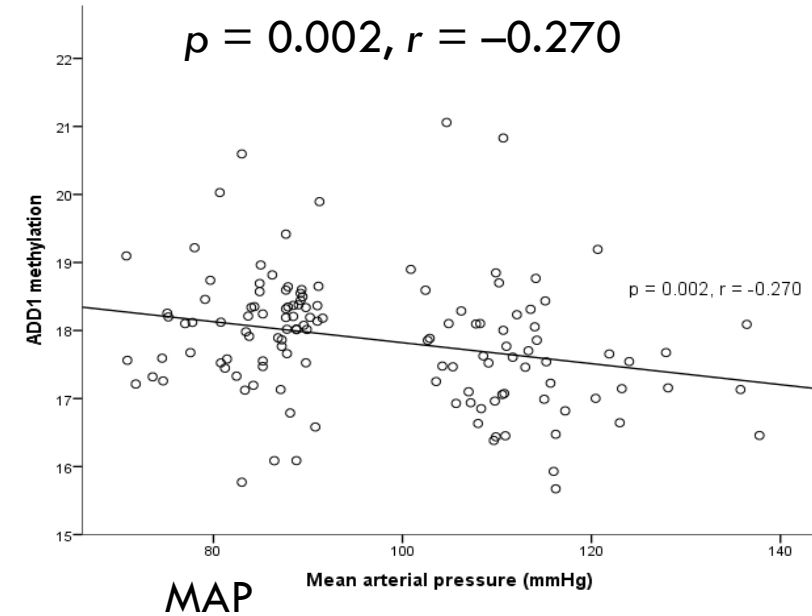
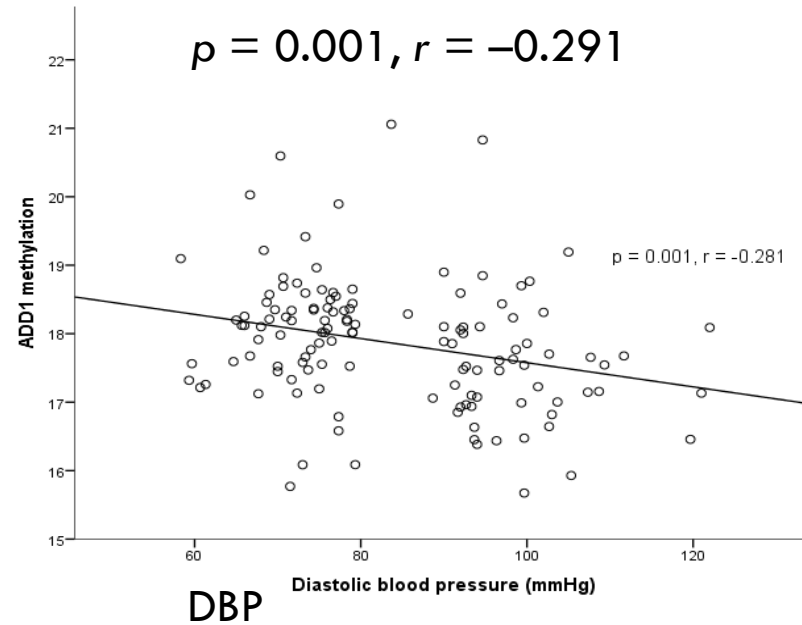
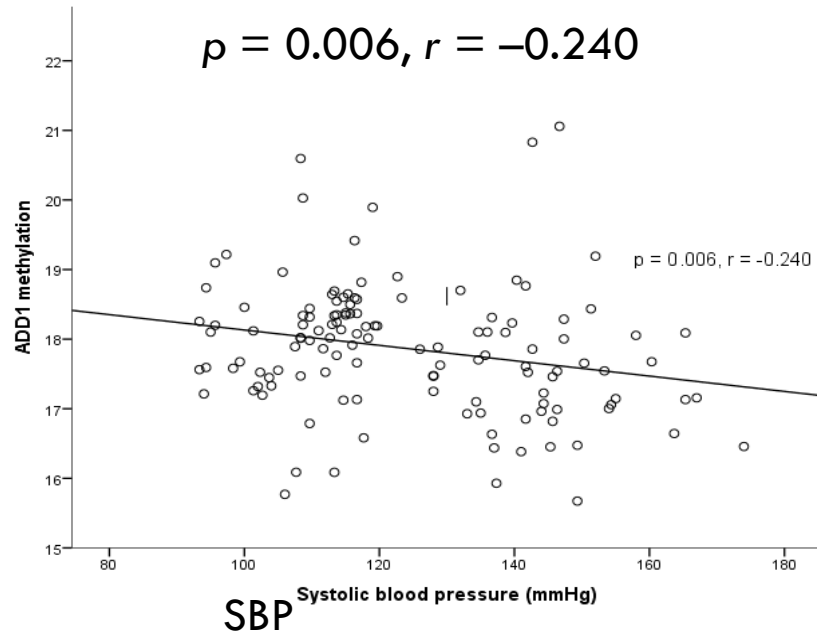
RESULTS | Biochemical



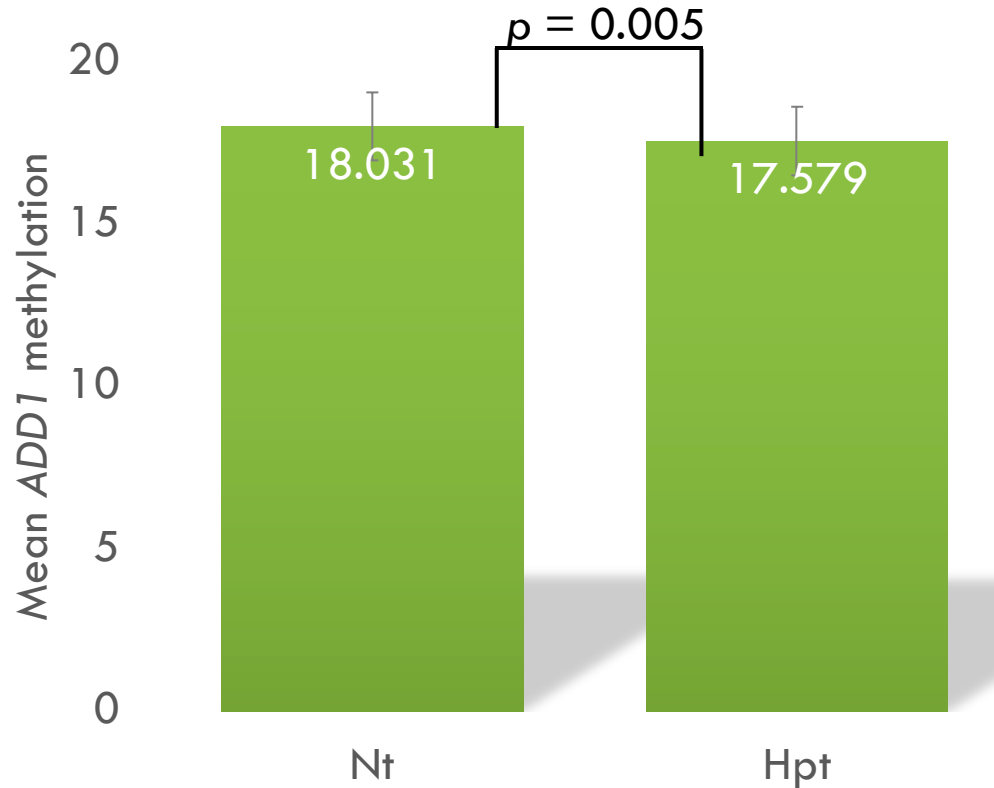
Biochemical profile	Blood pressure status		
	Nt	Htn	p-value
Creatinine ($\mu\text{mol/L}$) ^Ω	66.0 (27.0)	77.50(30.0)	0.032 ^a
Fasting blood glucose (mmol/L) ^Φ	4.8 (0.5)	5.0(0.56)	0.043 ^b
HbA1c (%) ^Φ	5.3 (0.3)	5.5(0.3)	<0.001 ^b
Total cholesterol (mmol/L) ^Φ	5.51 (0.92)	6.01(1.08)	0.002 ^b
HDL-cholesterol (mmol/L) ^Ω	1.41 (0.43)	1.21(0.34)	<0.001 ^a
LDL-cholesterol (mmol/L) ^Ω	3.43 (1.28)	3.89(1.09)	0.002 ^a
Triglycerides (mmol/L) ^Ω	0.95 (0.67)	1.68(1.04)	<0.001 ^a
TC/HDL ratio ^Ω	3.95 (1.4)	4.85(1.7)	<0.001 ^a
Cortisol (nmol/l) ^Ω	254.0 (177.0)	314.5(159.0)	0.014 ^a
hsCRP (mg/l) ^Ω	0.9 (2.1)	2.6(4.8)	<0.001 ^a

Note ^Φmean (standard deviation). ^Ω median (IQR). ^aAnalysed using Wilcoxon-Mann-Whitney test, ^bAnalysed using student's *t*-test. HbA1c glycated haemoglobin. HDL high density lipoprotein. LDL low density lipoprotein. TC/HDL ratio total cholesterol to HDL ratio, HsCRP high sensitivity C-reactive protein.

RESULTS | Association between *ADD1* methylation and blood pressure



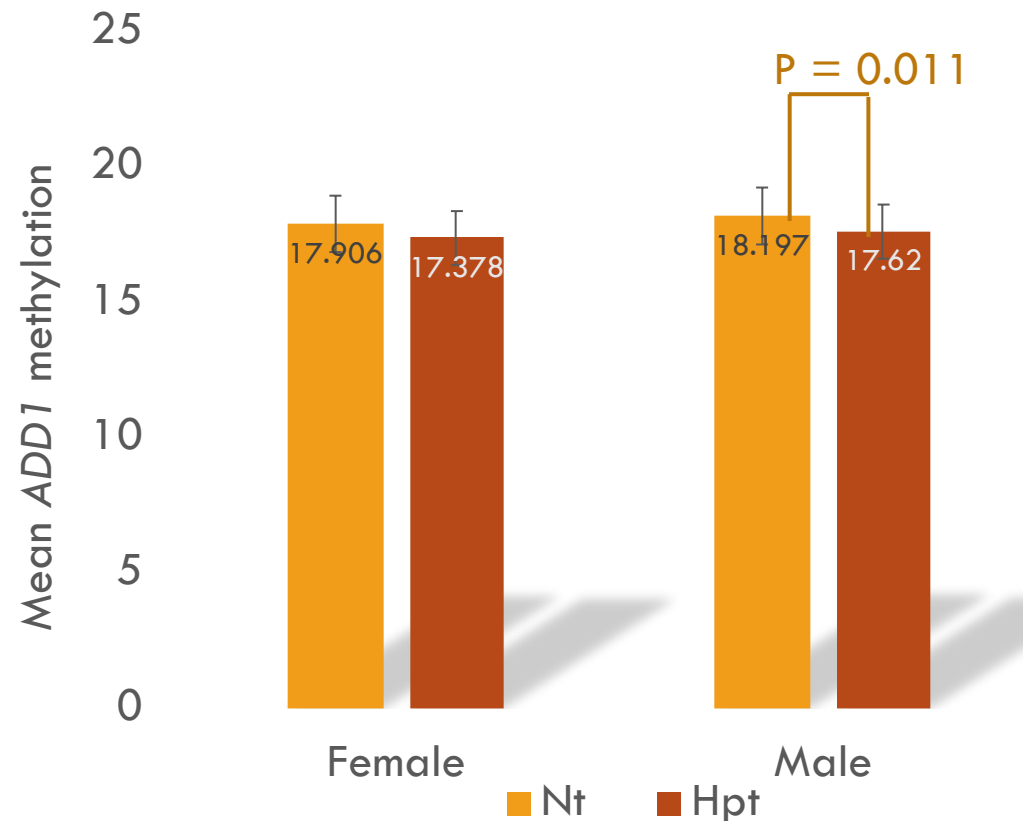
RESULTS | Association between *ADD1* methylation and blood pressure





Hpt < Nt

Error-bars indicate standard deviation. Difference in mean were analysed by student's t-test.

RESULTS | Association between *ADD1* methylation and blood pressure



Hpt  < Nt 

Error-bars indicate standard deviation. Difference in mean were analysed by student's t-test.

RESULTS | Association between *ADD1* methylation and blood pressure



Variable	Hypertension ^a			
	p	OR	95 % C.I. of OR	
			Lower	Upper
<i>ADD1</i> methylation	0.008	0.516	0.316	0.844
Age	0.006	1.110	1.031	1.194
BMI	<0.001	1.207	1.094	1.331
Creatinine	0.730	1.006	0.970	1.044
FBG	0.799	1.174	0.383	3.596
LDLC	0.316	1.326	0.764	2.304
Female ^b	0.080	0.305	0.081	1.154
Non-smoker ^c	0.708	0.795	0.240	2.633

^aCompared to normotension, ^bcompared to male, ^ccompared to current smoker.

B = coefficient, S.E. = standard error, df = degree of freedom, p = significance, OR = odd ratio, CI = confidence interval.

BMI = body mass index, FBG = fasting blood glucose, LDLC = low-density lipoprotein cholesterol.

Classification table: 80.3% correct. Nagelkerke R square, p = 0.461, Cox & Snell p = 0.344. Hosmer lemeshow 0.165

RESULTS | Association between *ADD1* methylation and blood pressure



Variable	Female, hypertension ^a				Male, hypertension ^a			
	p	OR	95 % C.I. of OR		p	OR	95 % C.I. of OR	
			Lower	Upper			Lower	Upper
<i>ADD1</i> methylation	0.803	0.866	0.280	2.683	0.024	0.509	0.282	0.916
Age	0.065	1.205	0.989	1.468	0.007	1.138	1.036	1.250
BMI	0.296	1.103	0.918	1.326	<0.001	1.317	1.131	1.533
Creatinine	0.846	1.102	0.899	1.138	0.570	1.012	0.971	1.054
FBG	0.641	1.960	0.118	32.280	0.546	0.650	0.160	2.632
LDLC	0.058	3.888	0.953	15.858	0.689	0.867	0.430	1.746
Non-smoker ^b					0.608	0.714	0.197	2.587

^aCompared to normotension, ^bcompared to current smoker.

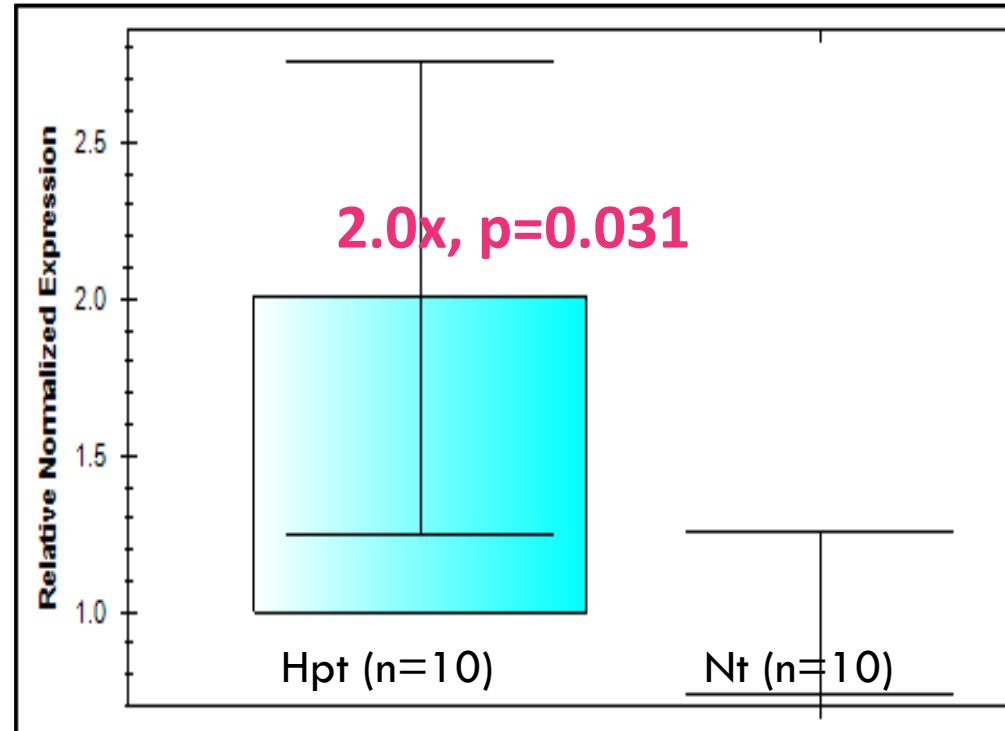
B = coefficient, S.E. = standard error, df = degree of freedom, p = significance, OR = odd ratio, CI = confidence interval.

BMI = body mass index, FBG = fasting blood glucose, LDLC = low-density lipoprotein cholesterol.

RESULTS | Association between *ADD1* methylation and gene expression



Gene
expression
of *ADD1*
normalised to *ACTB*
and *GAPDH*

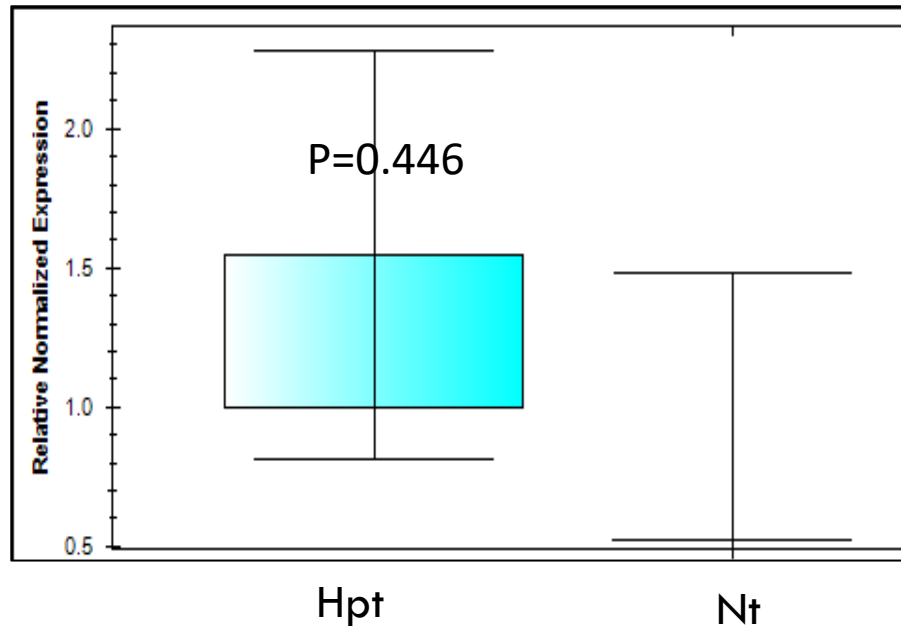


Graph was generated by CFX Manager ver 3.0 (BioRad, USA). Error bar indicates standard deviation.

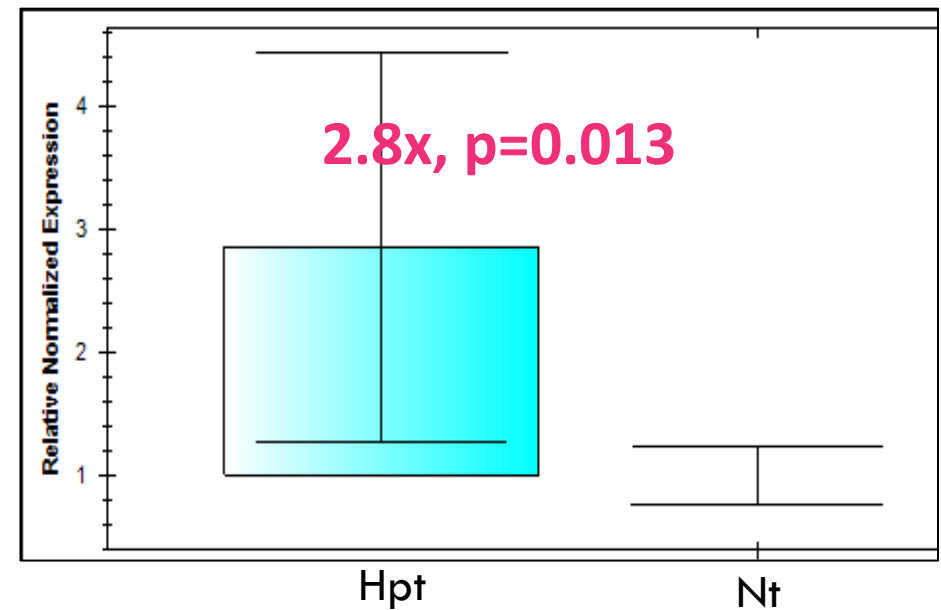
RESULTS | Association between *ADD1* methylation and gene expression



Gene expression of *ADD1* normalised to *ACTB* and *GAPDH* in **low-methylated** samples (n = 5)



Gene expression of *ADD1* normalised to *ACTB* and *GAPDH* in **high-methylated** samples (n = 5)



Expression normalised to normotension group (Nt). Graph was generated by CFX Manager ver 3.0 (BioRad, USA). Error bar indicates standard deviation.

DISCUSSION



1st
study

comparing ADD1 methylation in Hpt
young adults

Estrog

al

Findings are in
agreement with
previous studies among adults^{7,8}

expression

red
TPase
ivity

CONCLUSION



**LOWER *ADD1*
methylation**

in Hpt male young adults



**ADD1
HYPOMETHYLATION**

Predicts Hpt in male young
adults



**COMPLEX
RELATIONSHIP**

between *ADD1* methylation
and gene expression

STRENGTH



01 First in Young Adults

Previous methylation study in general adult

02 Anti-HPT naïve subjects

Eliminate anti-HPT confounding effects

03 MethyLight

Real-time, high sensitivity, quantitative

04 Gene expression study

Following methylation study

LIMITATION



01 Cross-sectional design
Cause & effect is not certain

Longitudinal study
or experimental animal study

02 Non-generalizable
Single centre study

Multi-centre study
For national data

03 ? Environment effects
on *ADD1* methylation
Sociodemographic, hormonal



Role of *ADD1*
methylation as mediator
on blood pressure



THANK YOU



fateinwanomar@iium.edu.my



Wan Fatein Nabeila Wan Omar



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