

Appendix S1. PRISMA checklist

Appendix S2. Search strategy

Table S3. Criteria used to define essential hypertension across studies.

Table S4. Gene methylation in candidate gene approach and blood pressure

Appendix S1. PRISMA checklist

Section/topic	#	Checklist item	Reported on page #
TITLE			
Title	1	Identify the report as a systematic review, meta-analysis, or both.	1
ABSTRACT			
Structured summary	2	Provide a structured summary including, as applicable: background; objectives; data sources; study eligibility criteria, participants, and interventions; study appraisal and synthesis methods; results; limitations; conclusions and implications of key findings; systematic review registration number.	2
INTRODUCTION			
Rationale	3	Describe the rationale for the review in the context of what is already known.	3
Objectives	4	Provide an explicit statement of questions being addressed with reference to participants, interventions, comparisons, outcomes, and study design (PICOS).	4
METHODS			
Protocol and registration	5	Indicate if a review protocol exists, if and where it can be accessed (e.g., Web address), and, if available, provide registration information including registration number.	4
Eligibility criteria	6	Specify study characteristics (e.g., PICOS, length of follow-up) and report characteristics (e.g., years considered, language, publication status) used as criteria for eligibility, giving rationale.	5
Information sources	7	Describe all information sources (e.g., databases with dates of coverage, contact with study authors to identify additional studies) in the search and date last searched.	4
Search	8	Present full electronic search strategy for at least one database, including any limits used, such that it could be repeated.	4, Appendix S2
Study selection	9	State the process for selecting studies (i.e., screening, eligibility, included in systematic review, and, if applicable, included in the meta-analysis).	5
Data collection process	10	Describe method of data extraction from reports (e.g., piloted forms, independently, in duplicate) and any processes for obtaining and confirming data from investigators.	5
Data items	11	List and define all variables for which data were sought (e.g., PICOS, funding sources) and any assumptions and simplifications made.	5

Risk of bias in individual studies	12	Describe methods used for assessing risk of bias of individual studies (including specification of whether this was done at the study or outcome level), and how this information is to be used in any data synthesis.	6
Summary measures	13	State the principal summary measures (e.g., risk ratio, difference in means).	NA*
Synthesis of results	14	Describe the methods of handling data and combining results of studies, if done, including measures of consistency (e.g., I ²) for each meta-analysis.	NA*
Risk of bias across studies	15	Specify any assessment of risk of bias that may affect the cumulative evidence (e.g., publication bias, selective reporting within studies).	NA*
Additional analyses	16	Describe methods of additional analyses (e.g., sensitivity or subgroup analyses, meta-regression), if done, indicating which were pre-specified.	NA*
RESULTS			
Study selection	17	Give numbers of studies screened, assessed for eligibility, and included in the review, with reasons for exclusions at each stage, ideally with a flow diagram.	6, Fig 1
Study characteristics	18	For each study, present characteristics for which data were extracted (e.g., study size, PICOS, follow-up period) and provide the citations.	Tables 1-3
Risk of bias within studies	19	Present data on risk of bias of each study and, if available, any outcome level assessment (see item 12).	7, Tables 1-3
Results of individual studies	20	For all outcomes considered (benefits or harms), present, for each study: (a) simple summary data for each intervention group (b) effect estimates and confidence intervals, ideally with a forest plot.	NA*
Synthesis of results	21	Present results of each meta-analysis done, including confidence intervals and measures of consistency.	NA*
Risk of bias across studies	22	Present results of any assessment of risk of bias across studies (see item 15).	NA*
Additional analysis	23	Give results of additional analyses, if done (e.g., sensitivity or subgroup analyses, meta-regression [see item 16]).	NA*
DISCUSSION			
Summary of evidence	24	Summarize the main findings including the strength of evidence for each main outcome; consider their relevance to key groups (e.g., healthcare providers, users, and policy makers).	8-11
Limitations	25	Discuss limitations at study and outcome level (e.g., risk of bias), and at review-level (e.g., incomplete retrieval of identified research, reporting bias).	16-17
Conclusions	26	Provide a general interpretation of the results in the context of other evidence, and implications for future research.	17
FUNDING			
Funding	27	Describe sources of funding for the systematic review and other support (e.g., supply of data); role of funders for the systematic review.	1

*NA: not applicable

Appendix S2. Search strategy

embase.com

(epigenetics/exp OR 'DNA methylation'/exp OR 'histone modification'/exp OR 's adenosylmethionine'/exp OR 'CpG island'/exp OR (((histone* OR dna OR 'long interspersed') NEAR/3 (acetyl* OR demethylat* OR methylat* OR phosphorylat* OR ubiquitinat* OR modif*)) OR 's adenosylmethionine' OR cpg OR epigenetic* OR epigenomic*):ab,ti) AND ('abnormal blood pressure'/exp OR 'blood pressure'/exp OR (hypertensi* OR hypotensi* OR 'blood pressure*'):ab,ti) NOT ([animals]/lim NOT [humans]/lim) NOT ([Conference Abstract]/lim OR [Letter]/lim OR [Note]/lim OR [Editorial]/lim)

Medline (Ovid)

(Epigenomics/ OR DNA methylation/ OR S-Adenosylmethionine/ OR CpG Islands/ OR (((histone* OR dna OR long interspersed) ADJ3 (acetyl* OR demethylat* OR methylat* OR phosphorylat* OR ubiquitinat* OR modif*)) OR s adenosylmethionine OR cpg OR epigenetic* OR epigenomic*).ab,ti.) AND (exp Hypertension/ OR exp Hypotension/ OR exp blood pressure/ OR (hypertensi* OR hypotensi* OR blood pressure*).ab,ti.) NOT (exp animals/ NOT humans/) NOT (letter OR news OR comment OR editorial OR congresses OR abstracts).pt.

Cochrane

(((((histone* OR dna OR 'long interspersed') NEAR/3 (acetyl* OR demethylat* OR methylat* OR phosphorylat* OR ubiquitinat* OR modif*)) OR 's adenosylmethionine' OR cpg OR epigenetic* OR epigenomic*):ab,ti) AND ((hypertensi* OR hypotensi* OR 'blood pressure*'):ab,ti)

Web-of-science

TS=(((((((histone* OR dna OR "long interspersed") NEAR/2 (acetyl* OR demethylat* OR methylat* OR phosphorylat* OR ubiquitinat* OR modif*)) OR "s adenosylmethionine" OR cpg OR epigenetic* OR epigenomic*)) AND ((hypertensi* OR hypotensi* OR "blood pressure*"))) NOT ((animal* OR rat OR rats OR mouse OR mice OR murine OR dog OR dogs OR canine OR cat OR cats OR feline) NOT (human* OR patient* OR man OR men OR woman OR women))) AND DT=(Article)

Google scholar

"histone|dna methylation|modification"|epigenetics hypertension|hypotension|"blood pressure"

Table S3. Criteria used to define essential hypertension across studies.

SBP cut-off	DBP cut-off	Additional criteria	Study author
≥130	≥85	And/or medication therapy for the treatment of hypertension.	Luttmer et al., 2013
>140 *	>90*	Had received antihypertensive medications for more than three months, self-report or physician-report of the diagnosis.*	Zhang et al.,2013 ; Fan et al.,2015 (“Aberrant methylation...”); Fan et al.,2015 (“Association of...”); Mao et al., 2016; Bayoumy et al.,2017, Lin et al.,2017 ; Mao et al.,2017 ; Meng et al.,2017 ; Bao et al.,2018 ; Jin et al.,2018 ; Xu et al.,2018
≥140	≥90	None	Smolarek et al.,2010
≥140	≥90	Or: age, sex, and height adjusted SBP ≥95th percentile	Wang et al.,2013
≥160	≥95	And/or medication therapy for the treatment of hypertension.	Baccarelli et al.,2010
≥160	≥100	And/or medication therapy for the treatment of hypertension.	Kato et al.,2015
Not described**	Not described**	None	Boström et al.,2016
Not described	Not described	History of hypertension	Peng et al.,2014

* Definition from the European Society of Hypertension-European Society of Cardiology Guidelines, 2003.

**Information about diagnosis provided by researcher.

Table S4. Gene methylation in candidate gene approach and blood pressure

Outcome	Sample	Hypomethylated genes	Hypermethylated genes	Null association
SBP	WB	<i>TLR4</i>		<i>F3, GCR, ICAM-1</i>
	PBL	<i>ACE promoter</i>		
	VAT		<i>ADRB3</i>	
	PBMC	<i>NFKB1</i>		<i>PPARγ, SLC19A1, IL-6,</i>
DBP	WB	<i>TLR4, IFNγ</i>	<i>TRL2, iNOS,</i>	<i>F3, GCR, ICAM-1</i>
	VAT		<i>ADRB3</i>	
	PBMC	<i>NFKB1</i>		<i>PPARγ, SLC19A1, IL-6,</i>
Hypertension	WB	<i>ADD1</i>		
	PB	<i>ADD1, ADD1 promoter, GCK, AGTR1, IL-6, NET promoter, Mfn2, IFNγ promoter</i>	<i>MTHFD1 promoter</i>	<i>ABCG1, GALNT2, HMGCR</i>
	Saliva	<i>AGTR1</i>		

SBP: systolic blood pressure; WB: whole blood; PBL: peripheral blood leukocytes; VAT: visceral fat tissue; PBMC: peripheral blood mononuclear cells; DBP: diastolic blood pressure; PB: peripheral blood.