

ESPS Peer-review Report

Name of Journal: World Journal of Cardiology

ESPS Manuscript NO: 8439

Title: Elevated Blood Pressure: Is It Our Family's Fault? The Genetics of Essential Hypertension

Reviewer code: 00506252

Science editor: Gou, Su-Xin

Date sent for review: 2013-12-28 18:42

Date reviewed: 2013-12-29 17:55

CLASSIFICATION	LANGUAGE EVALUATION	RECOMMENDATION	CONCLUSION
<input checked="" type="checkbox"/> Grade A (Excellent)	<input checked="" type="checkbox"/> Grade A: Priority Publishing	Google Search:	<input checked="" type="checkbox"/> Accept
<input type="checkbox"/> Grade B (Very good)	<input type="checkbox"/> Grade B: minor language polishing	<input type="checkbox"/> Existed	<input type="checkbox"/> High priority for publication
<input type="checkbox"/> Grade C (Good)	<input type="checkbox"/> Grade C: a great deal of language polishing	<input type="checkbox"/> No records	<input type="checkbox"/> Rejection
<input type="checkbox"/> Grade D (Fair)	<input type="checkbox"/> Grade D: rejected	<input type="checkbox"/> Existed	<input type="checkbox"/> Minor revision
<input type="checkbox"/> Grade E (Poor)		<input type="checkbox"/> No records	<input type="checkbox"/> Major revision

COMMENTS TO AUTHORS

General Comments The present study appears well conducted for design and contents. Inclusion criteria and exclusion criteria are reasonable. Essential hypertension is thought to be a multifactorial disease resulted from epigenetic factors as well as genetic factors. Epigenetic factors involve environmental factors, renal function, and so on. The review reported here by Natekar A and Slavin TP, and et al. appears to be the first one with regard to genes, DNA methylation, histone modification, and miRNA. However, there are still no well-established cause-and-effect relationships for increasing blood pressure among reported factors. And, reported genes and methylation must affect the development of hypertension, but also other physiological functions unrelated to blood pressure control. These studies will elucidate which genetic and epigenetic factors can prolong life span. The referee did not find any specific comments.

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Title: Elevated Blood Pressure: Is It Our Family's Fault? The Genetics of Essential Hypertension

Reviewer code: 00031349

Science editor: Gou, Su-Xin

Date sent for review: 2013-12-28 18:42

Date reviewed: 2014-01-13 23:28

CLASSIFICATION	LANGUAGE EVALUATION	RECOMMENDATION	CONCLUSION
<input type="checkbox"/> Grade A (Excellent)	<input checked="" type="checkbox"/> Grade A: Priority Publishing	Google Search:	<input type="checkbox"/> Accept
<input checked="" type="checkbox"/> Grade B (Very good)	<input type="checkbox"/> Grade B: minor language polishing	<input type="checkbox"/> Existed	<input type="checkbox"/> High priority for publication
<input type="checkbox"/> Grade C (Good)	<input type="checkbox"/> Grade C: a great deal of language polishing	<input type="checkbox"/> No records	<input type="checkbox"/> Rejection
<input type="checkbox"/> Grade D (Fair)	<input type="checkbox"/> Grade D: rejected	<input type="checkbox"/> Existed	<input checked="" type="checkbox"/> Minor revision
<input type="checkbox"/> Grade E (Poor)		<input type="checkbox"/> No records	<input type="checkbox"/> Major revision

COMMENTS TO AUTHORS

The manuscript, entitled "Elevated blood pressure: is it our family's fault? The genetics of essential hypertension", is a meta-analysis of data found within 11 genome wide association studies (GWAS) studies, 5 methylation and 3 micro-RNA studies. This review of hypertension-associated genetic and epigenetic factors analyzes the multiple roles of the 112 genes, some histone methylations, and micro RNAs found within these studies in the pathogenesis of essential hypertension. This review is both novel and important. However, the following comments would be helpful for a full understanding of how alterations of one's genetics and epigenetics contribute to the initiation and progression of essential hypertension. 1. Please include gene names as well as their function in the tables. 2. Please analyze/ summarize the major signaling pathways that the 112 genes participate in such as vascular constriction and relaxation, inflammation pathways. These signaling pathways may drive an increase in blood pressure. 3. How do epigenetic changes alter these pathways? 4. Please point out how these studies may affect personalized medicine with respect to hypertension in the future.