Central Asian Journal of Medical Sciences
CAJMS

Editorial

Cent Asian J Med Sci. 2019 Dec;5(4):245-246. https://doi.org/10.24079/CAJMS.2019.12.001

Increased Resting Heart Rate and Genetic Variability

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Increased resting heart rate is associated with various cardiovascular events and diseases, such as atherosclerotic lesions in the coronary arteries, atrial fibrillation, acute myocardial infarction, and hypertension [1]. These associations have been shown not only in patients with cardiovascular diseases but also in the general population [2]. It has been reported that an increased resting HR is an independent risk factor for cardiovascular mortality, including sudden cardiac death and total mortality even after adjusting for other potential risk factors [3]. However, the association between increased resting heart rate and both cardiovascular diseases and mortality has been shown in a large number of studies. However, their molecular mechanism is still not well understood.

The heart rate is a complex trait influenced by multiple genetic and environmental factors and their interactions. Several environmental risk factors for increased heart rate are already known, and the heritability of heart rate has been estimated up to 32-63 %, which could result from common or rare genetic variants [4,5]. Although heritable factors play an extensive role in regulating heart rate, evidence about its specific genetic determinants is still limited, even though it may provide additional insight into the pathophysiology of cardiac function and help explain the molecular mechanisms and genetic basis for disorders associated with its regulation.

Much effort has been devoted to mapping the genes that are associated with heart rate regulation, including linkage and genome-wide linkage studies as well as candidate-gene approaches; however, the results have been inconsistent. In recent years, genome-wide association studies [6] have been a successful strategy for identifying highly compelling candidate genes that influence common human traits, including those for various electrocardiogram parameters such as PR, QT and RR intervals [7-11]. The hope is that through a better understanding of genetic factors impacting resting heart rate, patients can be better advised regarding their risks for sudden cardiac death, and perhaps someday gene-based treatments may be offered.

References

1. Fox KM, Ferrari R. Heart rate: A forgotten link in coronary artery disease? Nat Rev Cardiol 2011; 8: 369-79.
2. Cooney MT, Vartiainen E, Laatikainen T, Juolevi A, Dudina A, Graham IM. Elevated resting heart rate is an independent risk factor for cardiovascular disease in healthy men and women. Am Heart J 2010;159: 612-9.
3. Kristal-Boneh E, Silber H, Harari G, Froom P. The association of resting heart rate with cardiovascular, cancer and all-cause mortality. Eight year follow-up of 3527 male israeli employees (the cordis study). Eur Heart J 2000; 21: 116-24.
4. Osztovits J, Horvath T, Littvay L, Steinbach R, Jermendy A, Tarnoki A, et al. Effects of genetic vs. Environmental factors on cardiovascular autonomic function: A twin study. Diabet Med 2011; 28: 1241-8.
5. Gombojav B, Park H, Kim JI, Ju YS, Sung J, Cho SI, et al. Heritability and linkage study on heart rates in a mongolian population. Exp Mol Med 2008; 40: 558-64.
6. Hirschhorn JN, Daly MJ. Genome-wide association studies for common diseases and complex traits. Nat Rev Genet 2005; 6: 95-108.
7. Den HM, Eijgelsheim M, Esko T, Brundel BJ, Peal DS, Evans DM, et al. Identification of heart rate-associated loci and their effects on cardiac conduction and rhythm disorders. Nat Genet 2013; 45: 621-31.
8. Holm H, Gudbjartsson DF, Arnar DO, Thorleifsson G, Thorgeirsson G, Stefansdottir H, et al. Several common variants modulate heart rate, pr interval and qrs duration. Nat Genet 2010; 42: 117-22.
9. Marroni F, Pfeufer A, Aulchenko YS, Franklin CS, Isaacs A, Pichler I, et al. A genome-wide association scan of rr and qt interval duration in 3 european genetically isolated populations: The eurospan project. Circ Cardiovasc Genet 2009; 2: 322-8.
10. Eijgelsheim M, Newton-Cheh C, Sotoodehnia N, De Bakker PI, Muller M, Morrison AC, et al. Genome-wide association analysis identifies multiple loci related to resting heart rate. Hum Mol Genet 2010; 19: 3885-94.
11. Sung J, Cho SI, Lee K, Ha M, Choi EY, Choi JS, et al. Healthy twin: A twin-family study of korea protocols and current status. Twin Res Hum Genet 2006; 9: 844-8.