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GWAS of heart rate in 87,759 Chinese subjects highlighted its genetic correlations with cardiometabolic traits

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Background: Resting heart rate (RHR) has been associated with risks of mortality and multiple chronic diseases. Previous studies, predominantly conducted in Europeans, have reported 91 independent variants associated with RHR and its genetic correlations with several cardiometabolic traits. Studies from East Asians are lacking.
Methods: We performed a GWAS for RHR in 87,701 participants aged 30-79 years from China Kadoorie Biobank (CKB). A linear mixed model was used under an additive model. Replication was conducted in 37,251 Chinese participants from CKB and UK Biobank. We conducted LD score regression to quantify genetic correlations across RHR and 11 cardiometabolic traits.
Results: Only 50 previously reported variants were replicated in CKB (=0.025). We identified ten novel loci associated with RHR ($P<5\times10^{-8}$), of which 50 candidate genes were prioritized. RHR

showed significant genetic correlations with diastolic blood pressure (r_g=0.258, $P=5.71\times10^{-10}$), mean arterial pressure (r_g=0.225, $P=3.08\times10^{-8}$), systolic blood pressure (r_g=0.170, $P=4.92\times10^{-5}$), plasma glucose (r_g=0.197, P=0.003), total cholesterol (r_g=0.287, P=0.012), and high-density lipoprotein (r_g=0.246, P=0.030).

Conclusions: We identified ten novel loci associated with RHR in a large Asian cohort. The identified genetic correlations of RHR with blood pressure, glucose, and lipids indicate previously reported association of RHR with risk of all-cause death might be mediated via its correlations with cardiometabolic traits.

Key messages:

- Ten novel loci associated with RHR were identified in the Chinese population.
- RHR showed significant genetic correlations with blood pressure, glucose and lipids.