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EDITORIAL COMMENT

A large-scale biobank and more genome-wide association studies of cardiovascular disease are needed in Portugal

Um biobanco em grande escala e mais estudos de associação do genoma das doenças cardiovasculares são necessários em Portugal

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Nearly 20 years ago, following the completion of the Human Genome Project and advances in high-throughput genotyping technologies, the first genome-wide association studies (GWAS) were published.[1] GWAS identify associations between genetic variants (single nucleotide polymorphisms [SNPs]) and phenotypical traits using an agnostic approach and became more common with the development of SNP arrays.

Among their many potential applications, GWAS findings help (i) discover potential drug targets,[2] (ii) develop or improve risk prediction models,[3,4] and (iii) refine population sub-phenotyping, enabling the paradigm of personalized medicine and the tailoring of prevention and treatment based on genetic risk.[5]

Progress in the field has been exponential, driven by a dramatic reduction in the cost of genotyping using high-density SNP arrays over the past 20 years, now priced at less than €50 per sample. Additionally, the power of discovery has significantly increased as studies have expanded beyond small cohorts to include large international consortia and nation-scale biobanks.[6]

Genome-wide association studies of Portuguese cohorts are scarce[7] and there is reduced collaboration in international consortia. Despite this, the GENEs in MAdeira and CORonary Disease (GENEMACOR) study is a solid example of a national cohort assessing the impact of genetic variants in cardiovascular outcomes. This cohort has provided invaluable landmark contributions to the cardiovascular field.[8,9] In this issue of the Portuguese Journal of Cardiology, Sá et al. assessed a cohort of 1284 asymptomatic GENEMACOR participants without coronary artery disease using the coronary artery calcium score. The authors determined which of the 33 assessed genetic variants were independently associated with coronary artery calcification: *PHACTR1 rs1332844*, a downstream regulator of the endothelin-1 gene, *CDKN2B-AS1 rs4977574*, an epigenetic regulator, and *MTHFD1L rs6922269*, involved in de novo thymidylate biosynthesis, were the identified candidates.[10]

More cohorts with biological samples for GWAS should be established nationally. The creation of a large-scale Portuguese biobank should be a number one priority for health research in the coming years. GWAS have predominantly focused on individuals of European descent, resulting in

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significant disparities in genetic research, and potential issues regarding generalizability of the findings. Therefore, it is important that individuals with African and South American ancestry are well-represented in this project. This is of paramount importance for advancing our understanding not only of coronary artery disease, heart failure, and atrial fibrillation, but also of often-overlooked rheumatic heart disease, which still causes 345 000 deaths annually. Insights from the East London Genes & Health cohort,[11] which addresses the underrepresentation of South Asian individuals in genetic research and explores potential contributors to the increased cardiometabolic risk in this population, will be valuable.

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Conflicts of interest

None declared.

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