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CardioGuardian: A Cell-free RNA Method to Assess Inherited Cardiovascular Disease Risk

Stanford scientists have developed ***CardioGuardian***, a method that uses cell-free RNA from a routine blood draw to estimate an individual's inherited risk of cardiovascular disease, capturing heritable risk that conventional DNA-based approaches miss.

Genome-wide association studies have made it possible to estimate disease risk by reading inherited single nucleotide polymorphisms (SNPs) in a patient's DNA. For cardiovascular disease, however, this approach captures only a small fraction of heritable risk, roughly 6 to 10 percent, and it performs poorly in the many populations that remain underrepresented in genomic reference data. This leaves a large portion of inherited cardiovascular risk invisible to standard testing and limits equitable use across diverse patient groups.

CardioGuardian takes a different approach by measuring gene expression rather than DNA sequence. The method builds on the observation that cell-free RNA circulating in blood is enriched for tissue-specific genes, including those highly expressed by coronary arteries. Using a curated set of genes known to be regulated by inherited genetic loci, CardioGuardian reads the cell-free RNA phenotype to identify individuals with a family history of cardiovascular disease. Because it captures a downstream expression signal rather than relying on specific inherited variants, the assay is noninvasive and has the potential to explain more of the heritability of cardiovascular disease while remaining broadly applicable across populations that current SNP-based tests serve poorly. The same framework may extend to inherited risk assessment for other diseases.

Stage of Development
Proof of Concept

Applications

- Noninvasive blood-based test for estimating inherited cardiovascular disease risk
- Risk profiling for diverse and historically underprofiled populations where SNP-based tests underperform
- Extension of the cell-free RNA framework to inherited risk assessment for other diseases
- Research tool for studying the relationship between inherited genetic loci and circulating gene expression

Advantages

- Measures a gene expression phenotype rather than relying on SNPs present in the patient
- Captures inherited cardiovascular risk beyond the 6 to 10 percent explained by SNP-based approaches
- Noninvasive, requiring only a routine blood draw
- Broadly applicable across diverse populations, including those underrepresented in genomic databases
- Adaptable to existing RNA sequencing workflows for straightforward commercial development

Innovators

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