

CARDIOVASCULAR GENETICS FOR PHYSICIANS

CARDIOVASCULAR GENETICS FOR PHYSICIANS IS NO LONGER A NICHE FIELD BUT A CRITICAL COMPONENT OF MODERN CARDIOLOGY PRACTICE, OFFERING UNPRECEDENTED INSIGHTS INTO DISEASE PREDICTION, DIAGNOSIS, AND MANAGEMENT. AS OUR UNDERSTANDING OF THE HUMAN GENOME DEEPENS, PHYSICIANS ARE INCREASINGLY EQUIPPED TO LEVERAGE GENETIC INFORMATION TO PERSONALIZE PATIENT CARE, IDENTIFY AT-RISK INDIVIDUALS, AND IMPLEMENT TARGETED THERAPEUTIC STRATEGIES FOR A WIDE SPECTRUM OF CARDIOVASCULAR CONDITIONS. THIS COMPREHENSIVE ARTICLE DELVES INTO THE FUNDAMENTAL PRINCIPLES OF CARDIOVASCULAR GENETICS, ITS CLINICAL APPLICATIONS, EMERGING TRENDS, AND THE ESSENTIAL KNOWLEDGE PHYSICIANS NEED TO NAVIGATE THIS RAPIDLY EVOLVING LANDSCAPE. WE WILL EXPLORE THE GENETIC BASIS OF COMMON AND RARE CARDIOVASCULAR DISEASES, THE INTERPRETATION OF GENETIC TESTING, AND THE ETHICAL CONSIDERATIONS SURROUNDING GENETIC COUNSELING AND PRECISION MEDICINE IN CARDIOLOGY.

TABLE OF CONTENTS

INTRODUCTION TO CARDIOVASCULAR GENETICS
THE GENETIC ARCHITECTURE OF CARDIOVASCULAR DISEASE
KEY CARDIOVASCULAR GENETIC CONDITIONS
GENETIC TESTING IN CARDIOLOGY
INTERPRETING GENETIC TEST RESULTS
CLINICAL APPLICATIONS AND PRECISION MEDICINE
ETHICAL AND PRACTICAL CONSIDERATIONS
FUTURE DIRECTIONS IN CARDIOVASCULAR GENETICS
FREQUENTLY ASKED QUESTIONS

UNDERSTANDING THE FUNDAMENTALS OF CARDIOVASCULAR GENETICS

CARDIOVASCULAR GENETICS EXAMINES THE ROLE OF INHERITED FACTORS IN THE DEVELOPMENT AND PROGRESSION OF HEART AND BLOOD VESSEL DISEASES. WHILE LIFESTYLE AND ENVIRONMENTAL FACTORS PLAY SIGNIFICANT ROLES, A SUBSTANTIAL PROPORTION OF CARDIOVASCULAR RISK IS ATTRIBUTABLE TO GENETIC PREDISPOSITIONS. UNDERSTANDING THESE GENETIC UNDERPINNINGS ALLOWS PHYSICIANS TO MOVE BEYOND BROAD RISK FACTOR MANAGEMENT TOWARDS INDIVIDUALIZED RISK ASSESSMENT AND PREVENTION STRATEGIES.

THE HUMAN GENOME AND CARDIOVASCULAR HEALTH

THE HUMAN GENOME, COMPRISING APPROXIMATELY 20,000-25,000 GENES, PROVIDES THE BLUEPRINT FOR ALL CELLULAR FUNCTIONS, INCLUDING THOSE OF THE CARDIOVASCULAR SYSTEM. VARIATIONS WITHIN THESE GENES, KNOWN AS GENETIC POLYMORPHISMS OR MUTATIONS, CAN ALTER THE STRUCTURE, FUNCTION, OR REGULATION OF CARDIAC PROTEINS, ION CHANNELS, RECEPTORS, OR STRUCTURAL COMPONENTS, THEREBY INFLUENCING AN INDIVIDUAL'S SUSCEPTIBILITY TO CARDIOVASCULAR DISEASE. THESE GENETIC VARIATIONS CAN BE INHERITED FROM EITHER PARENT, FOLLOWING MENDELIAN INHERITANCE PATTERNS FOR MONOGENIC DISORDERS OR EXHIBITING COMPLEX INHERITANCE FOR MULTIFACTORIAL CONDITIONS.

MONOGENIC VS. MULTIFACTORIAL CARDIOVASCULAR DISEASES

CARDIOVASCULAR DISEASES CAN BROADLY BE CATEGORIZED INTO THOSE PRIMARILY CAUSED BY A SINGLE GENE DEFECT (MONOGENIC) AND THOSE INFLUENCED BY MULTIPLE GENES IN INTERACTION WITH ENVIRONMENTAL FACTORS (MULTIFACTORIAL). MONOGENIC DISORDERS, SUCH AS HYPERTROPHIC CARDIOMYOPATHY OR LONG QT SYNDROME, OFTEN PRESENT WITH A HIGH PENETRANCE, MEANING INDIVIDUALS CARRYING THE CAUSATIVE MUTATION HAVE A VERY HIGH PROBABILITY OF DEVELOPING THE DISEASE. MULTIFACTORIAL DISEASES, LIKE CORONARY ARTERY DISEASE OR HYPERTENSION, ARE INFLUENCED BY NUMEROUS GENETIC VARIANTS, EACH CONFERRING A SMALL INCREASE IN RISK, WHICH THEN INTERACT WITH LIFESTYLE CHOICES (DIET, EXERCISE, SMOKING) AND OTHER ENVIRONMENTAL EXPOSURES TO DETERMINE AN INDIVIDUAL'S OVERALL DISEASE RISK.

DIFFERENTIATING THESE IS CRUCIAL FOR APPROPRIATE GENETIC TESTING AND COUNSELING.

THE GENETIC ARCHITECTURE OF CARDIOVASCULAR DISEASE

THE GENETIC BASIS OF CARDIOVASCULAR DISEASE IS COMPLEX, INVOLVING BOTH RARE, HIGH-IMPACT VARIANTS AND COMMON, LOW-IMPACT VARIANTS. ADVANCES IN GENOMIC TECHNOLOGIES, SUCH AS NEXT-GENERATION SEQUENCING (NGS), HAVE REVOLUTIONIZED OUR ABILITY TO IDENTIFY THESE GENETIC CONTRIBUTORS.

IDENTIFYING DISEASE-ASSOCIATED GENES

RESEARCH UTILIZING GENOME-WIDE ASSOCIATION STUDIES (GWAS) AND WHOLE-EXOME/GENOME SEQUENCING HAS IDENTIFIED HUNDREDS OF GENETIC LOCI AND THOUSANDS OF VARIANTS ASSOCIATED WITH VARIOUS CARDIOVASCULAR CONDITIONS. THESE GENES ENCODE PROTEINS INVOLVED IN CRITICAL PATHWAYS SUCH AS LIPID METABOLISM, INFLAMMATION, VASCULAR HOMEOSTASIS, CARDIAC DEVELOPMENT, AND ELECTRICAL IMPULSE GENERATION. FOR INSTANCE, VARIANTS IN GENES LIKE APOE, LDLR, AND PCSK9 ARE STRONGLY LINKED TO DYSLIPIDEMIA AND PREMATURE CORONARY ARTERY DISEASE.

THE ROLE OF VARIANT FREQUENCY AND EFFECT SIZE

UNDERSTANDING THE GENETIC ARCHITECTURE ALSO INVOLVES APPRECIATING THE INTERPLAY BETWEEN VARIANT FREQUENCY IN THE POPULATION AND ITS EFFECT SIZE ON DISEASE RISK. RARE VARIANTS WITH LARGE EFFECT SIZES ARE OFTEN RESPONSIBLE FOR MONOGENIC FORMS OF CARDIOVASCULAR DISEASE, LEADING TO MENDELIAN INHERITANCE PATTERNS. CONVERSELY, COMMON VARIANTS WITH SMALL EFFECT SIZES CONTRIBUTE TO THE POLYGENIC RISK FOR MORE PREVALENT MULTIFACTORIAL CONDITIONS. PHYSICIANS MUST CONSIDER BOTH TYPES OF GENETIC INFLUENCES WHEN ASSESSING A PATIENT'S CARDIOVASCULAR RISK PROFILE.

KEY CARDIOVASCULAR GENETIC CONDITIONS

A GROWING NUMBER OF CARDIOVASCULAR CONDITIONS ARE RECOGNIZED TO HAVE A SIGNIFICANT GENETIC COMPONENT, IMPACTING A WIDE RANGE OF CARDIAC FUNCTIONS AND STRUCTURES.

INHERITED CARDIOMYOPATHIES

THESE ARE A GROUP OF DISEASES THAT AFFECT THE HEART MUSCLE ITSELF. HYPERTROPHIC CARDIOMYOPATHY (HCM) IS THE MOST COMMON INHERITED CARDIAC DISEASE, OFTEN CAUSED BY MUTATIONS IN SARCOMERIC PROTEIN GENES. DILATED CARDIOMYOPATHY (DCM) CAN ALSO HAVE A STRONG GENETIC BASIS, WITH MUTATIONS FOUND IN GENES RESPONSIBLE FOR CYTOSKELETAL PROTEINS, ION CHANNELS, AND NUCLEAR LAMINA. ARRHYTHMOGENIC RIGHT VENTRICULAR CARDIOMYOPATHY (ARVC) IS CHARACTERIZED BY FATTY AND FIBROUS REPLACEMENT OF THE RIGHT VENTRICULAR MYOCARDIUM, FREQUENTLY LINKED TO MUTATIONS IN GENES ENCODING DESMOSOMAL PROTEINS.

INHERITED ARRHYTHMIA SYNDROMES

THESE CONDITIONS PREDISPOSE INDIVIDUALS TO LIFE-THREATENING ARRHYTHMIAS. LONG QT SYNDROME (LQTS) IS CHARACTERIZED BY PROLONGED QT INTERVAL ON THE ELECTROCARDIOGRAM AND AN INCREASED RISK OF TORSADES DE POINTES.

BRUGADA SYNDROME, ASSOCIATED WITH CHARACTERISTIC ECG CHANGES, INCREASES THE RISK OF VENTRICULAR FIBRILLATION. CATECHOLAMINERGIC POLYMORPHIC VENTRICULAR TACHYCARDIA (CPVT) CAUSES VENTRICULAR ARRHYTHMIAS TRIGGERED BY ADRENERGIC STIMULATION.

AORTIC ANEURYSM AND DISSECTION SYNDROMES

GENETIC FACTORS SIGNIFICANTLY CONTRIBUTE TO THE RISK OF THORACIC AORTIC ANEURYSMS AND DISSECTIONS. MARFAN SYNDROME, EHLERS-DANLOS SYNDROME (VASCULAR TYPE), AND LOEYS-DIETZ SYNDROME ARE CONNECTIVE TISSUE DISORDERS THAT WEAKEN THE AORTIC WALL, PREDISPOSING INDIVIDUALS TO AORTIC DILATATION AND RUPTURE. ISOLATED FAMILIAL THORACIC AORTIC ANEURYSM AND DISSECTION (FTAAD) IS ALSO LINKED TO MUTATIONS IN GENES INVOLVED IN THE TGF- β SIGNALING PATHWAY.

FAMILIAL HYPERCHOLESTEROLEMIA (FH)

FH IS AN AUTOSOMAL DOMINANT DISORDER CHARACTERIZED BY EXTREMELY HIGH LEVELS OF LOW-DENSITY LIPOPROTEIN CHOLESTEROL (LDL-C) FROM BIRTH, LEADING TO PREMATURE ATHEROSCLEROTIC CARDIOVASCULAR DISEASE. MUTATIONS IN THE LDLR, APOB, PCSK9, AND LDLRAP1 GENES ARE THE PRIMARY CAUSES OF FH. EARLY DIAGNOSIS AND AGGRESSIVE LIPID-LOWERING THERAPY ARE CRUCIAL TO PREVENT EARLY HEART ATTACKS AND STROKES.

GENETIC TESTING IN CARDIOLOGY

GENETIC TESTING HAS BECOME AN INVALUABLE TOOL FOR DIAGNOSING, RISK STRATIFYING, AND GUIDING MANAGEMENT IN CARDIOVASCULAR MEDICINE.

INDICATIONS FOR GENETIC TESTING

PHYSICIANS SHOULD CONSIDER GENETIC TESTING IN PATIENTS WITH A PERSONAL OR FAMILY HISTORY SUGGESTIVE OF INHERITED CARDIOVASCULAR DISEASE, INCLUDING EARLY-ONSET CORONARY ARTERY DISEASE, UNEXPLAINED SYNCOPE, A FAMILY HISTORY OF SUDDEN CARDIAC DEATH, OR A KNOWN PATHOGENIC VARIANT IN A RELATIVE. TESTING CAN CONFIRM A DIAGNOSIS, INFORM PROGNOSIS, FACILITATE CASCADE SCREENING OF AT-RISK RELATIVES, AND GUIDE THERAPEUTIC DECISIONS.

TYPES OF GENETIC TESTS

- **SINGLE GENE TESTING:** PERFORMED WHEN A SPECIFIC GENETIC DISORDER IS HIGHLY SUSPECTED.
- **GENE PANEL TESTING:** ANALYZES MULTIPLE GENES KNOWN TO BE ASSOCIATED WITH A PARTICULAR PHENOTYPE (E.G., A CARDIOMYOPATHY PANEL OR ARRHYTHMIA PANEL). THIS IS OFTEN THE PREFERRED APPROACH FOR COMPLEX CONDITIONS.
- **WHOLE EXOME SEQUENCING (WES):** SEQUENCES THE PROTEIN-CODING REGIONS OF THE GENOME.
- **WHOLE GENOME SEQUENCING (WGS):** SEQUENCES THE ENTIRE GENOME, INCLUDING NON-CODING REGIONS.

THE CHOICE OF TEST DEPENDS ON THE CLINICAL PRESENTATION, FAMILY HISTORY, AND THE DIAGNOSTIC YIELD DESIRED.

INTERPRETING GENETIC TEST RESULTS

INTERPRETING GENETIC TEST RESULTS REQUIRES A MULTIDISCIPLINARY APPROACH, INVOLVING GENETICISTS, GENETIC COUNSELORS, AND THE REFERRING PHYSICIAN.

VARIANT CLASSIFICATION

GENETIC VARIANTS ARE CLASSIFIED INTO FIVE CATEGORIES BASED ON THEIR PATHOGENICITY: PATHOGENIC, LIKELY PATHOGENIC, UNCERTAIN SIGNIFICANCE (VUS), LIKELY BENIGN, AND BENIGN. A PATHOGENIC OR LIKELY PATHOGENIC VARIANT IS CONSIDERED THE CAUSE OF THE DISEASE. A VUS IS A VARIANT FOR WHICH THERE IS INSUFFICIENT EVIDENCE TO DETERMINE ITS PATHOGENICITY, AND IT CANNOT BE USED FOR CLINICAL DECISION-MAKING UNTIL RECLASSIFIED.

CLINICAL CORRELATION AND CASCADE SCREENING

IT IS CRUCIAL TO CORRELATE GENETIC FINDINGS WITH THE PATIENT'S CLINICAL PHENOTYPE AND FAMILY HISTORY. A PATHOGENIC VARIANT IDENTIFIED IN A PATIENT WITH A CONSISTENT CLINICAL PRESENTATION HAS HIGH DIAGNOSTIC UTILITY. ONCE A PATHOGENIC VARIANT IS IDENTIFIED IN AN INDIVIDUAL, CASCADE SCREENING OF AT-RISK FAMILY MEMBERS IS RECOMMENDED. THIS INVOLVES TESTING FIRST-DEGREE RELATIVES FOR THE SPECIFIC IDENTIFIED VARIANT, WHICH IS MORE EFFICIENT AND COST-EFFECTIVE THAN BROAD GENETIC TESTING.

CLINICAL APPLICATIONS AND PRECISION MEDICINE

CARDIOVASCULAR GENETICS IS DRIVING THE SHIFT TOWARDS PRECISION MEDICINE, ENABLING TAILORED APPROACHES TO PREVENTION AND TREATMENT.

PERSONALIZED RISK STRATIFICATION

GENETIC TESTING CAN REFINE CARDIOVASCULAR RISK ASSESSMENT BEYOND TRADITIONAL RISK FACTORS. FOR EXAMPLE, IDENTIFYING A PATHOGENIC VARIANT FOR FAMILIAL HYPERCHOLESTEROLEMIA ALLOWS FOR AGGRESSIVE LIPID MANAGEMENT FROM AN EARLY AGE, SIGNIFICANTLY REDUCING THE LIFETIME RISK OF ATHEROSCLEROTIC EVENTS. POLYGENIC RISK SCORES, DERIVED FROM COMMON GENETIC VARIANTS, ARE EMERGING AS A TOOL TO FURTHER STRATIFY RISK FOR COMMON CONDITIONS LIKE CORONARY ARTERY DISEASE.

PHARMACOGENOMICS IN CARDIOLOGY

PHARMACOGENOMICS, THE STUDY OF HOW GENES AFFECT A PERSON'S RESPONSE TO DRUGS, IS INCREASINGLY RELEVANT IN CARDIOLOGY. FOR INSTANCE, GENETIC VARIATIONS IN CYP2C19 CAN AFFECT THE METABOLISM AND EFFICACY OF CLOPIDOGREL, AN ANTIPLATELET MEDICATION. UNDERSTANDING THESE GENETIC PREDISPOSITIONS CAN HELP PHYSICIANS SELECT THE MOST EFFECTIVE AND SAFEST DRUG THERAPY FOR INDIVIDUAL PATIENTS, MINIMIZING ADVERSE DRUG REACTIONS AND OPTIMIZING TREATMENT OUTCOMES.

ETHICAL AND PRACTICAL CONSIDERATIONS

THE INTEGRATION OF CARDIOVASCULAR GENETICS INTO CLINICAL PRACTICE NECESSITATES CAREFUL CONSIDERATION OF ETHICAL, LEGAL, AND SOCIAL IMPLICATIONS (ELSI).

GENETIC COUNSELING AND INFORMED CONSENT

BEFORE ORDERING GENETIC TESTING, PHYSICIANS MUST ENSURE PATIENTS UNDERSTAND THE POTENTIAL BENEFITS, RISKS, AND LIMITATIONS OF THE TEST, AS WELL AS THE IMPLICATIONS OF THE RESULTS FOR THEMSELVES AND THEIR FAMILY MEMBERS. COMPREHENSIVE GENETIC COUNSELING, IDEALLY PROVIDED BY A GENETIC COUNSELOR, IS ESSENTIAL FOR OBTAINING INFORMED CONSENT AND FOR DISCUSSING THE PSYCHOSOCIAL IMPACT OF GENETIC FINDINGS. THIS INCLUDES DISCUSSING THE POSSIBILITY OF INCIDENTAL FINDINGS AND THE IMPLICATIONS FOR GENETIC PRIVACY.

DATA PRIVACY AND GENETIC DISCRIMINATION

PHYSICIANS MUST BE AWARE OF LEGAL PROTECTIONS SUCH AS THE GENETIC INFORMATION NONDISCRIMINATION ACT (GINA) IN THE UNITED STATES, WHICH PROHIBITS HEALTH INSURERS AND EMPLOYERS FROM DISCRIMINATING BASED ON GENETIC INFORMATION. HOWEVER, CONCERNS ABOUT POTENTIAL MISUSE OF GENETIC DATA AND ENSURING ROBUST PRIVACY SAFEGUARDS REMAIN PARAMOUNT. PROPER STORAGE AND HANDLING OF GENETIC INFORMATION ARE CRITICAL.

FUTURE DIRECTIONS IN CARDIOVASCULAR GENETICS

THE FIELD OF CARDIOVASCULAR GENETICS IS DYNAMIC, WITH ONGOING RESEARCH POISED TO FURTHER TRANSFORM CARDIOLOGY.

ADVANCEMENTS IN GENE EDITING AND THERAPY

EMERGING TECHNOLOGIES LIKE CRISPR-CAS9 GENE EDITING HOLD PROMISE FOR CORRECTING DISEASE-CAUSING GENETIC MUTATIONS DIRECTLY. WHILE STILL LARGELY IN THE EXPERIMENTAL STAGES FOR CARDIOVASCULAR DISEASES, THESE APPROACHES COULD OFFER DEFINITIVE CURES FOR CERTAIN INHERITED CONDITIONS IN THE FUTURE. GENE THERAPY, DELIVERING FUNCTIONAL GENE COPIES OR SILENCING DISEASE-CAUSING GENES, IS ALSO AN AREA OF ACTIVE INVESTIGATION.

INTEGRATION OF MULTI-OMICS DATA

FUTURE CARDIOVASCULAR PRECISION MEDICINE WILL LIKELY INVOLVE INTEGRATING NOT JUST GENETIC DATA (GENOMICS) BUT ALSO DATA FROM OTHER 'OMICS' LAYERS, SUCH AS TRANSCRIPTOMICS (GENE EXPRESSION), PROTEOMICS (PROTEINS), AND METABOLOMICS (METABOLITES). THIS MULTI-OMICS APPROACH WILL PROVIDE A MORE HOLISTIC UNDERSTANDING OF DISEASE PATHOGENESIS AND ENABLE MORE PRECISE IDENTIFICATION OF THERAPEUTIC TARGETS AND BIOMARKERS FOR RISK PREDICTION AND TREATMENT RESPONSE.

Q: WHAT IS THE PRIMARY BENEFIT OF INCORPORATING CARDIOVASCULAR GENETICS INTO A PHYSICIAN'S PRACTICE?

A: THE PRIMARY BENEFIT IS THE ABILITY TO PERSONALIZE PATIENT CARE BY IDENTIFYING GENETIC PREDISPOSITIONS TO CARDIOVASCULAR DISEASES, ENABLING EARLIER AND MORE TARGETED PREVENTION, DIAGNOSIS, AND TREATMENT STRATEGIES BEYOND TRADITIONAL RISK FACTOR ASSESSMENT.

Q: HOW DOES GENETIC TESTING HELP IN DIAGNOSING INHERITED CARDIOMYOPATHIES?

A: GENETIC TESTING CAN CONFIRM A DIAGNOSIS OF INHERITED CARDIOMYOPATHIES BY IDENTIFYING SPECIFIC PATHOGENIC VARIANTS IN GENES RESPONSIBLE FOR CARDIAC MUSCLE STRUCTURE AND FUNCTION, WHICH AIDS IN DIFFERENTIATING FROM ACQUIRED CAUSES AND GUIDES MANAGEMENT FOR THE PATIENT AND THEIR RELATIVES.

Q: WHAT IS MEANT BY "CASCADE SCREENING" IN CARDIOVASCULAR GENETICS?

A: CASCADE SCREENING IS THE PROCESS OF TESTING FIRST-DEGREE RELATIVES OF AN INDIVIDUAL FOUND TO HAVE A PATHOGENIC GENETIC VARIANT FOR THAT SPECIFIC VARIANT. IT'S A HIGHLY EFFICIENT METHOD FOR IDENTIFYING OTHER AT-RISK FAMILY MEMBERS IN A COST-EFFECTIVE MANNER.

Q: HOW DO PHARMACOGENOMIC INSIGHTS INFLUENCE PRESCRIBING ANTIPLATELET THERAPY LIKE CLOPIDOGREL?

A: PHARMACOGENOMIC TESTING CAN IDENTIFY VARIATIONS IN GENES LIKE CYP2C19, WHICH AFFECTS HOW PATIENTS METABOLIZE CLOPIDOGREL. THIS KNOWLEDGE HELPS PHYSICIANS PREDICT WHETHER A PATIENT WILL BE A POOR, INTERMEDIATE, OR RAPID METABOLIZER, ALLOWING FOR SELECTION OF THE MOST EFFECTIVE ANTIPLATELET REGIMEN AND AVOIDANCE OF SUBOPTIMAL TREATMENT OR INCREASED BLEEDING RISK.

Q: WHAT IS A "VARIANT OF UNCERTAIN SIGNIFICANCE" (VUS) AND WHY IS IT IMPORTANT FOR PHYSICIANS TO UNDERSTAND?

A: A VUS IS A GENETIC ALTERATION FOR WHICH THERE IS NOT ENOUGH SCIENTIFIC EVIDENCE TO DEFINITELY CLASSIFY IT AS PATHOGENIC OR BENIGN. IT'S IMPORTANT FOR PHYSICIANS TO UNDERSTAND THAT A VUS CANNOT BE USED FOR CLINICAL DECISION-MAKING UNTIL FURTHER RESEARCH LEADS TO ITS RECLASSIFICATION, PREVENTING PREMATURE OR INCORRECT INTERVENTIONS.

Q: WHAT ARE THE ETHICAL CONSIDERATIONS PHYSICIANS MUST ADDRESS BEFORE ORDERING GENETIC TESTS FOR CARDIOVASCULAR CONDITIONS?

A: PHYSICIANS MUST ENSURE COMPREHENSIVE INFORMED CONSENT, WHICH INCLUDES EXPLAINING THE POTENTIAL BENEFITS, LIMITATIONS, AND IMPLICATIONS OF TEST RESULTS FOR THE PATIENT AND THEIR FAMILY. THEY MUST ALSO ADDRESS PRIVACY CONCERNS, THE POSSIBILITY OF INCIDENTAL FINDINGS, AND THE POTENTIAL FOR GENETIC DISCRIMINATION.

Q: CAN GENETIC TESTING PREDICT THE EXACT AGE A PATIENT WILL DEVELOP A CARDIOVASCULAR DISEASE?

A: GENERALLY, GENETIC TESTING DOES NOT PREDICT THE EXACT AGE OF DISEASE ONSET. WHILE IT CAN IDENTIFY INDIVIDUALS AT HIGHER RISK OR WITH A PREDISPOSITION TO CERTAIN CONDITIONS, THE MANIFESTATION OF DISEASE IS OFTEN INFLUENCED BY A COMPLEX INTERPLAY OF GENETIC, ENVIRONMENTAL, AND LIFESTYLE FACTORS.

Q: WHAT IS THE ROLE OF POLYGENIC RISK SCORES IN CARDIOVASCULAR GENETICS?

A: POLYGENIC RISK SCORES (PRS) ARE DERIVED FROM THE COMBINED EFFECT OF MANY COMMON GENETIC VARIANTS, EACH WITH A SMALL EFFECT, TO ESTIMATE AN INDIVIDUAL'S OVERALL GENETIC PREDISPOSITION TO COMMON COMPLEX DISEASES LIKE CORONARY ARTERY DISEASE. THEY ARE EMERGING AS A TOOL TO REFINE RISK STRATIFICATION.

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