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Understanding Genetics and Pediatric Cardiac Health

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Purpose Congenital heart defects (CHD) continue to be the most prevalent birth defect that occurs worldwide in approximately 6–8 of every 1,000 live births. High rates of morbidity and mortality in infants, children, and adults living with CHD place a growing need for health care professionals (HCPs) to better understand potentially modifiable genetic and environmental influences. This paper will present examples of research and governmental initiatives that support genetics education and research and a review of known genetic factors associated with CHD development.
Organizing Construct: A review of the known genetic factors on risk for CHD formation in infants will be provided to help health care professionals gain a greater understanding of the genetic influences on pediatric cardiac health.
Conclusions: There are known genetic pathways and risk factors that contribute to development of CHD. This paper is a primer for nurses and HCPs providing information of the genetics and inheritance patterns of CHD to be useful in daily clinical practice.
Clinical Relevance: Nurses work in multiple communities where they are uniquely positioned to educate and provide information about research and current models of care with families affected by CHD. Nurses and HCPs who better understand genetic risk factors associated with CHD development can more promptly refer and offer treatment for these children and families thus providing individuals of childbearing age with the necessary resources and information about risk factors.

CONGENITAL HEART DEFECTS (chd) are the most prevalent birth defect in the world and occur in approximately 6–8 of every 1,000 live births (Hoffman & Kaplan, 2002). It is important to identify potential etiological factors of CHD as it is one of the leading causes of infant morbidity and mortality. Only 10–15% of the etiologies for CHD are understood or known. In 2001 the National Heart, Lung, and Blood Institute (NHLBI) convened a task force in Pediatric Cardiovascular Disease to identify research priorities, and scientific opportunities (NHLBI, 2002). This task force acknowledged the significant public health problems associated with the financial costs and emotional drain on children and adults affected by CHD. It was estimated that a lifetime cost for children in the U.S. with complex CHD can be in excess of $1.2 billion (CDC, 2010). In 2004 it was estimated that hospital care for all patients with CHD, children and adults, exceeded $2.6 billion (AHA, 2009). From this knowledge and experience, research priorities were identified from supporting basic science studies of the heart and blood vessel

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formation, including cardiovascular genetics and genomics to transitional research for the enhancement of clinical care.

In 2012 the American Heart Association (AHA) publically recognized the impact of genetics in diagnosing and directing treatment of cardiovascular disease (Ashley et al., 2012). The AHA published a policy statement and recommendations that prompt clinicians to better understand and incorporate genetic technology and modalities into the care of children and adults with cardiovascular disease or increased risk of CHD. The policy statement (Ashley et al., 2012) incorporated all aspects of genetic material and testing in patients, legal and ethical considerations, and discussed the necessity of education among all healthcare professionals.

Technology to identify genetic markers specific to heart disease continues to evolve and is an innovative part of research and clinical care. Thus, greater knowledge of genetics is required of nurses who care for individuals with or with increased risk of CHD and all nurses of varying degrees and practices (Jenkins & Calzone, 2007). This article provides an overview of basic genetics, fetal heart development, modes of inheritance and implications for nursing research and clinical care. This document will serve as a primer for nurses who care for women of childbearing age, in order to provide them with information about genetic factors that are associated with an increased risk of CHD. Table 1 provides a glossary of genetic terms discussed throughout the article.

Table 1 Definition of terms.

Term	Definition
Allele	Alternate forms of the same gene
Chromosome	Thread-like molecular materials of DNA and proteins that contain genes
Deletion	Absence of segment of a chromosome
Dominant	Character is manifested in a heterozygous person
Epigenetic	Heritable (from mother cell to daughter cell, or sometimes from parent to child), but is not produced by a change in DNA sequence.
Genotype	List of alleles present at one or a number of loci
Heterogeneous	Diverse in character or content
Heterozygous	Both alleles are at the locus are the same
Homozygous	Both alleles are at the locus are different
Locus (plural-loci)	Unique chromosomal location defining the position of an individual gene or DNA sequence.
Mosaicism	2 or more populations of cells with different genetic or chromosomal constitutions
Mutation	1) Event which changes the DNA sequence 2) DNA sequence change that occurred a long time ago
Penetrance	The frequency with which a genotype manifests itself in a given phenotype
Phenotype	The observable characteristics of a cell or organism, including the result of any test that is not a direct test of the genotype.
Recessive	Character is not manifested in a heterozygous person
Trait	A characteristic or phenotype.
Transcription factors	DNA-binding proteins that promote transcription of genes
Translocation	Whole chromosome or segment of a chromosome becomes attached or interchanged with another segment or whole chromosome.
Variable expression	Variable extent or intensity of the phenotype signs among people with a given phenotype.

Strachan & Read, 2011.

The Basic Building Blocks of Life

During the last two decades, scientists' ability to map the human genome has evolved and the complex molecular processes sustaining daily life continues to be critically studied. As a central concept of molecular biology, the Central Dogma of Molecular Biology describes the one-way directional flow of genetic information; deoxyribonucleic acid (DNA) produces ribonucleic acid (RNA) which then produces proteins (Strachan & Read, 2011). Although there are many complex processes and components to the creation of genetic material, scientists noted that these essential processes are needed by all cellular organisms to sustain life. Over the last several years, scientists have appreciated that these processes and DNA are not the only factors responsible for expressing our genetic makeup, but include more complex interactions between various environmental, prenatal, and chemical exposures throughout an individuals' life. During this rapid evolution of molecular genetics, a new area of study called epigenetics has developed to promote knowledge generation of the influences the environment has on our genetic makeup.

Epigenetics is a rapidly evolving field of study that focuses on the interactions and factors that influence chemical changes that switch parts of the genome off and on. This field of study facilitates and provides an explanation of the effect the environment has on gene expression. There are multiple mechanisms occurring within the cells that either silence or activate specific genes thus causing a cascade of events, which eventually change the expression of the genetic material (Kim, Ryan, Marshboom, & Archer, 2011).

Epigenetic changes appear to be influenced by environmental conditions that can include famine, chemicals, and diet in which these exposures induce changes which may be passed to children and grandchildren (Perera & Herbstman, 2011). Exposures to environmental disasters, chemical spills, or other naturally occurring events that disrupt the current conditions or environment over time may provide an explanation for the increase in specific phenotypes that