

Circulation

JOURNAL OF THE AMERICAN HEART ASSOCIATION



Heart Malformation. What Are the Chances It Could Happen Again?

Joseph T.C. Shieh and Deepak Srivastava

Circulation published online Jul 13, 2009;

DOI: 10.1161/CIRCULATIONAHA.109.878637

Circulation is published by the American Heart Association, 7272 Greenville Avenue, Dallas, TX 75214

Copyright © 2009 American Heart Association. All rights reserved. Print ISSN: 0009-7322. Online ISSN: 1524-4539

The online version of this article, along with updated information and services, is located on the World Wide Web at:

<http://circ.ahajournals.org>

Subscriptions: Information about subscribing to *Circulation* is online at
<http://circ.ahajournals.org/subscriptions/>

Permissions: Permissions & Rights Desk, Lippincott Williams & Wilkins, a division of Wolters Kluwer Health, 351 West Camden Street, Baltimore, MD 21202-2436. Phone: 410-528-4050. Fax: 410-528-8550. E-mail:
journalpermissions@lww.com

Reprints: Information about reprints can be found online at
<http://www.lww.com/reprints>

Heart Malformation What Are the Chances It Could Happen Again?

Joseph T.C. Shieh, MD, PhD; Deepak Srivastava, MD

Congenital heart disease (CHD) is the most common human birth defect worldwide,¹ taking a tremendous toll on affected families, caregivers, and healthcare systems. Approximately 40 000 children are born each year in the United States with a heart malformation, and at least another 40 000 are born annually with subclinical malformations that result in heart disease later in adulthood. Significant advances in cardiac care and surgery have lowered mortality, and there are now >1 million survivors of CHD in the United States. As a result, the economic effects of CHD are substantial, particularly when lifetime costs of management are considered.

Article see p 295

As an increasing proportion of the CHD population reaches reproductive age, questions of the genetic contribution to disease and risk of transmission have become paramount. Such individuals also often suffer age-dependent complications in heart function that may be related to the initial developmental and/or genetic insult that resulted in the CHD. Although their causes remain generally unknown, most CHDs are thought to have a multifactorial origin with an interplay of genetic and environmental effects.² However, the relative contributions of genes and the environment have been difficult to discern. In this issue of *Circulation*, Øyen et al³ use a uniquely sized and annotated population to estimate recurrence risk for specific CHDs in families and thereby indirectly assess the role of genetic inheritance in CHD.

A number of studies have attempted to quantify the risks conferred by a family history of CHD, demographic qualities, or environmental exposures.^{4,5} Gestational insults such as rubella infection and gestational diabetes can predispose to CHD, as can exposure to ethanol and other teratogens like retinoic acid.^{4,6} Although the incidence of CHD is higher in the setting of these exposures, most fetuses remain unaffected, suggesting that only a subpopulation may be at risk. In contrast, several syndromic and familial cases of CHD are caused by rare single-gene mutations that have major effects, sometimes with 100% penetrance.⁷⁻⁹ Thus, the more common forms of CHD that appear to be sporadic may, in fact, be

caused by inherited genetic variants that modestly affect protein expression or function and manifest as disease only when combined with additional genetic, epigenetic, environmental, or hemodynamic insults (Figure 1). However, experimental evidence for this theory remains elusive.

Øyen et al address the epidemiological aspect of this theory by examining familial aggregation of CHD using an unusually large and well-defined Danish population that has been annotated in multiple registries.³ The authors used a population-based design that uniquely captured all residents of Denmark (>1.7 million) over a 28-year period. They identified ≈18 000 individuals with CHD and capitalized on the Danish Family Relations Database to link affected individuals with first-, second-, and third-degree relatives. Disease information for relatives also was available in the database and allowed phenotype-based development of pedigrees. Using this population, the authors estimated the contribution of a family history of CHD to an individual's risk of CHD, and they estimated the population risk conferred by such family histories.

They found the relative risk of recurrence for all types of CHD to be ≈3 when a first-degree relative had CHD. This relative risk diminished when the family history of CHD was in only second- and third-degree relatives. These findings are consistent with the commonly used empirical risks provided to families faced with a potential recurrence of CHD. Even after the authors accounted for cases with known chromosome abnormalities or other congenital anomalies, the increased relative risks of recurrence persisted. Therefore, their findings might be applicable to the most common scenario in which CHD is an isolated finding. Furthermore, the authors analyzed the relative risk of recurrence of disease in unlike-sex twin pairings (presumably dizygotic twins), and this estimate was similar to the relative risk found in those individuals with affected first-degree relatives. Interestingly, same-sex twins, which likely include some monozygotic twins, demonstrated an ≈3-fold higher relative risk of recurrence than unlike-sex twins. These data strongly suggest a genetic component to "sporadic" congenital heart disease (Figure 1).

Interestingly, when the authors analyzed recurrence of the same type of CHD within families, the relative risk of recurrence was significantly higher for certain malformations. For example, heterotaxy, atrioventricular septal defect, and left and right ventricular outflow tract obstructive lesions had particularly higher relative risks of recurrence, with heterotaxy having a relative risk of ≈80. Although the numbers available for analysis were inevitably smaller than when CHD was analyzed as a collective group, the large initial size of this population still provides compelling evidence for a

The opinions expressed in this article are not necessarily those of the editors or of the American Heart Association.

From the Gladstone Institute of Cardiovascular Disease (J.S., D.S.) and Division of Medical Genetics (J.S.) and Departments of Pediatrics and Biochemistry and Biophysics (D.S.), University of California, San Francisco.

Correspondence to Deepak Srivastava, MD, Gladstone Institute of Cardiovascular Disease, 1650 Owens St, San Francisco, CA 94158. E-mail dsrivastava@gladstone.ucsf.edu

(*Circulation*. 2009;120:269-271.)

© 2009 American Heart Association, Inc.

Circulation is available at <http://circ.ahajournals.org>
DOI: 10.1161/CIRCULATIONAHA.109.878637

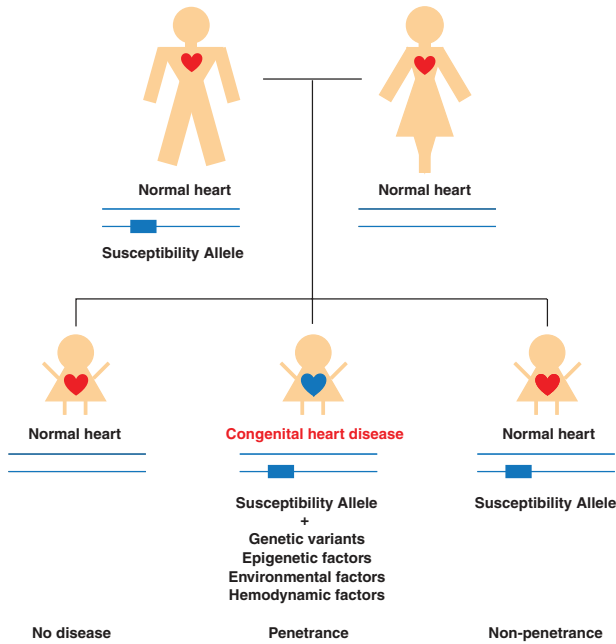


Figure 1. Multifactorial origin of CHD. A parent may harbor a genetic predisposition to disease (susceptibility allele) and transmit this genetic risk to offspring. However, this would result in CHD only in conjunction with variants in other genetic loci or with epigenetic factors, resulting in disease penetrance. The susceptibility allele alone may not be sufficient to cause disease in offspring (nonpenetrance), but the individual would still be at risk for vertical transmission of increased risk.

strong genetic effect on many forms of CHD. These findings are similar to the high incidence of aortic valve disease found in first-degree relatives of individuals with aortic valve atresia associated with hypoplastic left heart syndrome.^{10,11} It is intriguing to consider that the high relative risk of recurrence for lesions such as heterotaxy or aortic valve disease may reflect the presence of inherited variants of genes already implicated in autosomal-dominant disease that have more modest functional effects resulting in incomplete penetrance.^{8,12}

Despite these interesting findings, the study by Øyen et al found that the contribution of CHD family history to the overall prevalence of CHD was only $\approx 2\%$ to 4% , suggesting that most of the cases of CHD in the population did not have a family history of disease. This observation suggests that predisposition to disease involves multiple factors, including different genetic loci, epigenetic factors (eg, DNA methylation or histone modifications that affect gene expression; Figure 2), environmental influences, subtle hemodynamic factors during cardiac development, or a combination of these factors. In this scenario, a potential disease-susceptibility

allele could lead to disease penetrance or nonpenetrance (Figure 1), depending on the size of the effect of the susceptibility allele and the presence of “second hits” that modify the phenotype.

Given these findings from Øyen et al and related studies,^{11,13} where should we direct our efforts to better understand and combat cardiac birth defects? This study emphasizes the growing need to understand cardiac phenotypes that may have multifactorial origins so that we can direct efforts toward prevention and, eventually, novel therapies. Family-based genetic mapping studies and population-based association studies will play important roles in elucidating the rare and common genetic variants that predispose to CHD. Such studies are becoming increasingly feasible with rapidly evolving genome-wide technologies that can survey the genome for potential genetic changes. For example, high-density SNP detection with microarrays and, more recently, next-generation deep sequencing for whole exome analyses are tremendously powerful tools to detect human genetic variation. However, the ability to associate genetic changes with disease involves complex bioinformatics analyses that will need to be developed as the compendium of human genetic variation is discovered. In addition, a rate-limiting step will likely be access to sufficient numbers of patients with similar heart defects for association studies. This effort will require nationwide biobanks with high-quality phenotypic information.

Despite the current and future advances in genetic discovery in cardiac disease, there will undoubtedly be further complexities that underlie sporadic and familial disease. For example, noncoding regions of the genome have traditionally been understudied or overlooked altogether, and these and other regions of the genome need to be effectively interrogated to identify small noncoding RNAs (eg, microRNAs; see Figure 2), introns, and novel sequences potentially associated with disease.^{14,15} Furthermore, as the genetic bases of CHDs are elucidated, our understanding of environmental contributions and fetal hemodynamics to disease predisposition needs to grow substantially.

What does this mean practically for a family dealing with a child suffering from CHD? Currently, there is often no clear explanation of causality for the family. In fact, CHD, as with many other conditions, appears to fall into the conundrum of probabilistic causality.¹⁶ That is, it cannot be assumed that the purported “cause” (be it genetic or environmental) is always related to the expected “effect.” Given this uncertainty, when dealing with potential future pregnancies for a family already affected by disease, the current status of the field promotes

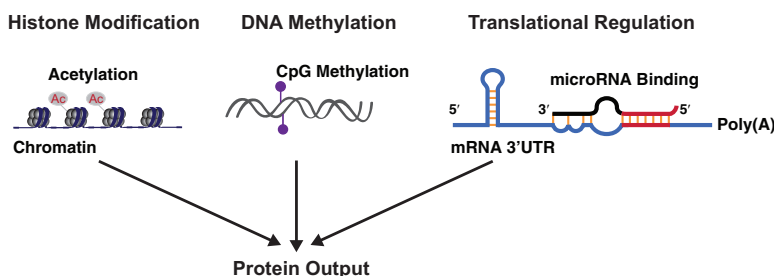


Figure 2. Epigenetic regulation of gene expression. In addition to genetic variation affecting gene expression, cellular levels of proteins can be regulated by many nongenetic mechanisms, including histone modifications (eg, acetylation) affecting chromatin structure, DNA methylation of CpG residues affecting transcription, or microRNA interaction with mRNA targets leading to translational regulation.

the use of the empirical recurrence risks to provide further information. The challenge that lies ahead is to provide better insight into the likelihood of disease. Identification of the predisposing genetic variants may lead to approaches involving modification of the environmental factors that might be able to lower penetrance even in the presence of susceptibility allele. We hope that studies such as those by Øyen et al can translate into further research from the field toward more precise testing for disease, sensitive and universal prenatal screening, and improved genetic counseling. For the sake of families faced with recurrent disease and for those that will encounter their first birth defect, it is incumbent on the field to engage in a focused effort to determine the underlying cause of the high recurrence risk reported here for subtypes of CHD and to ultimately identify effective preventive measures.

Sources of Funding

Dr Shieh is supported by National Institutes of Health grant K08 HL092970. Dr Srivastava is supported by grants from the National Heart, Lung, and Blood Institute/National Institutes of Health and the California Institute for Regenerative Medicine.

Disclosures

None.

References

- Christianson A, Howson CP, Modell B. *Global Report on Birth Defects: The Hidden Toll of Dying and Disabled Children*. White Plains, NY: March of Dimes Birth Defects Foundation; 2006.
- Nora JJ. Multifactorial inheritance hypothesis for the etiology of congenital heart diseases: the genetic-environmental interaction. *Circulation*. 1968;38:604–617.
- Øyen N, Poulsen G, Boyd HA, Wohlfahrt J, Jensen PKA, Melbye M. Recurrence of congenital heart defects in families. *Circulation*. 2009;120:295–301.
- Malik S, Cleves MA, Honein MA, Romitti PA, Botto LD, Yang S, Hobbs CA. Maternal smoking and congenital heart defects. *Pediatrics*. 2008;121:e810–e816.
- Burn J, Brennan P, Little J, Holloway S, Coffey R, Somerville J, Dennis NR, Allan L, Arnold R, Deanfield JE, Godman M, Houston A, Keeton B, Oakley C, Scott O, Silove E, Wilkinson J, Pembrey M, Hunter AS. Recurrence risks in offspring of adults with major heart defects: results from first cohort of British collaborative study. *Lancet*. 1998;351:311–316.
- Lammer EJ, Chen DT, Hoar RM, Agnish ND, Benke PJ, Braun JT, Curry CJ, Fernhoff PM, Grix AW Jr, Lott IT. Retinoic acid embryopathy. *N Engl J Med*. 1985;313:837–841.
- Garg V, Kathirya IS, Barnes R, Schluterman MK, King IN, Butler CA, Rothrock CR, Eapen RS, Hirayama-Yamada K, Joo K, Matsuoka R, Cohen JC, Srivastava D. GATA4 mutations cause human congenital heart defects and reveal an interaction with TBX5. *Nature*. 2003;424:443–447.
- Garg V, Muth AN, Ransom JF, Schluterman MK, Barnes R, King IN, Grossfeld PD, Srivastava D. Mutations in *NOTCH1* cause aortic valve disease. *Nature*. 2005;437:270–274.
- Pierpont ME, Basson CT, Benson DW Jr, Gelb BD, Giglia TM, Goldmuntz E, McGee G, Sable CA, Srivastava D, Webb CL. Genetic basis for congenital heart defects: current knowledge: a scientific statement from the American Heart Association Congenital Cardiac Defects Committee, Council on Cardiovascular Disease in the Young: endorsed by the American Academy of Pediatrics. *Circulation*. 2007;115:3015–3038.
- Lewin MB, McBride KL, Pignatelli R, Fernbach S, Combes A, Menesses A, Lam W, Bezold LI, Kaplan N, Towbin JA, Belmont JW. Echocardiographic evaluation of asymptomatic parental and sibling cardiovascular anomalies associated with congenital left ventricular outflow tract lesions. *Pediatrics*. 2004;114:691–696.
- McBride KL, Pignatelli R, Lewin M, Ho T, Fernbach S, Menesses A, Lam W, Leal SM, Kaplan N, Schliekelman P, Towbin JA, Belmont JW. Inheritance analysis of congenital left ventricular outflow tract obstruction malformations: segregation, multiplex relative risk, and heritability. *Am J Med Genet A*. 2005;134A:180–186.
- Gebbia M, Ferrero GB, Pilia G, Bassi MT, Aylsworth A, Penman-Splitt M, Bird LM, Bamforth JS, Burn J, Schlessinger D, Nelson DL, Casey B. X-linked situs abnormalities result from mutations in *ZIC3*. *Nat Genet*. 1997;17:305–308.
- Boughman JA, Berg KA, Astemborski JA, Clark EB, McCarter RJ, Rubin JD, Ferencz C. Familial risks of congenital heart defect assessed in a population-based epidemiologic study. *Am J Med Genet*. 1987;26:839–849.
- Zhao Y, Srivastava D. A developmental view of microRNA function. *Trends Biochem. Sci*. 2007;32:189–197.
- Kleinjan DA, van Heyningen V. Long-range control of gene expression: emerging mechanisms and disruption in disease. *Am J Hum Genet*. 2005;76:8–32.
- Page GP, George V, Go RC, Page PZ, Allison DB. “Are we there yet?” Deciding when one has demonstrated specific genetic causation in complex diseases and quantitative traits. *Am J Hum Genet*. 2003;73:711–719.

KEY WORDS: Editorials ■ epigenesis, genetic ■ genetics ■ heart defects, congenital