# Framingham Heart Study, The Legacy and health education implications in the age of genomic medicine

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Abstract: This study reviewed the legacy derived from the Framingham heart disease study (FHS). The investigator argues that the associated benefits from the FHS transcends medical and epidemiological sciences. In fact, several inklings from FHS have informed the initiation of many similar but un-identical studies not only in the United Sates but in many nations worldwide. The milestones were listed and there are many other serendipitous benefits from FHS including the development of various non-invasive medical devices used today to reduce the inadvertent occurrence of iatrogenic diseases and death. The role of genetics and genomics were described, emphasizing the relevance of physicians and behavioral scientists to reduce the barrier in their practice of clinical interventions in the management of cardiovascular disease so as to reduce the loss of human lives and the economic burden of heart disease nationwide. [Researcher. 2010;2(6):33-43]. (ISSN: 1553-9865).

## Introduction

The Framingham heart study (FHS) and the associated legacy transcends medical and epidemiologic sciences. The ramification of Framingham cardiovascular study which was initiated in 1948 has implications which link clinical, social and behavioral sciences. Besides, it is just an inkling of the multifarious, serendipitous benefits which have been reported by medical scientists and journalists. As a Tuft Medical school faculty in 1990-1991, a visit to Framingham revealed suitability of this community for a landmark prospective epidemiological investigation. Owing to the dearth of information about the medical, medical engineering, and other studies informed by Framingham methodology, the study described here was designed to:

Outline the conceptual framework of Framingham study from the outset in 1948,

Explore the serendipitous benefits of Framingham regarding development of medical technology aimed at reducing the clinical risks associated with invasive procedure,

Explore the adoption of Framingham's methodology in designing similar but un-identical studies

Explore the application of Framingham's techniques in the training of medical, public health and other behavioral students, and provide a succinct analysis of the health education implications of cardiovascular disease in the age of genomic medicine.

## Nature of Cardiovascular Diseases

The American Heart Association has categorized the six forms of cardiovascular diseases to include coronary heart disease, hypertension, stroke, congenital heart diseases, rheumatic heart disease, and congestive heart failure. A patient may suffer from one of these diseases or encounter a combination of these problems. In the 1900, cardiovascular disease was not the leading cause of death in the United States; instead pneumonia was the leading cause of death. However, the excessive consumption of food items that are extremely rich in lipids, the habitual use of tobacco and alcohol and exposure to stressful lifestyle created the upsurge of death associated with cardiovascular diseases. Since 1940, cardiovascular disease became the leading cause of death not only in the United States but also in most of the developed nations (American Heart Association, 2003).

The impetus for Framingham study which was initiated in 1948 was to investigate the epidemic of coronary disease in the United States and successfully

characterize the risk factors associated with this lethal disease. In 1948, the Framingham Heart study, under the direction of the present National Heart, Lung and Blood Institute (NHLBI), embarked on a very expensive and ambitious epidemiological project which changed our understanding of cardiovascular health problem. Since 1971, this landmark study is now conducted in collaboration with the Boston University. As confirmed by Kannel (2010), the study utilized the prospective epidemiological design, and insights were provided about prevalence, incidence, full clinical spectrum in terms of attrition rates, and the predisposing factors. The recognized risk factors, then which were associated with coronary disease in United States were stroke, peripheral artery diseases and heart failure. The research team dispelled clinical misconception about isolated systolic hypertension, left ventricular hypertrophy, dyslipidemia, atrial fibrillation and glucose intolerance. But they emphasized that statistical mean values for blood lipids, blood pressure, body weight, glucose and fibrinogen were observed to be dangerously suboptimal and had strong association to the onset of cardiovascular disease (Futherman and Lemberg, 2000).

However, the mean values of blood lipids, blood pressure, body weight, glucose and fibrinogen in the legacy cohort were demonstrated to be dangerously suboptimal and had a continuous graded association to cardiovascular disease without critical values (Femin, et al, 2008; Smith et al,2009; McCarthy et al, 2008; German et al, 2003).

Quantitatively, the total high density lipoproteins (HDL)-cholesterol ratio was shown to be the most critical lipid profile predicting coronary disease. Besides, low density lipoproteins (LDL) was shown to be correlated with homocysteine factor, indicating insulin resistance and small dense LDL was demonstrated to be associated with excess coronary artery disease.

A plethora of studies conducted at Framingham on cardiovascular disease revealed the following risk factors such as age, stress, obesity, high cholesterol levels, and high levels of low density lipoproteins, high blood pressure, high sodium intake, over-enlarged heart, smoking, diabetes, sedentary lifestyle, or physical inactivity, cytomegalovirus and type-A personality.

The documented overarching objective of FHS was to identify common characteristics which contributed to CVD. As a prospective epidemiological study, subjects who had not previously experienced detectable signs and symptoms of CVD were recruited for the study and followed over a long period of time. This group was described as the Legacy cohort and this group was made up of 5209 men and women between the ages of 30 and 62.

These subjects were provided free comprehensive physical examination and a battery of questionnaire was used to elicit their pertinent demographic data, including various anthropometric measurements. Since 1948, the legacy group and other two cohorts continue to return to the study every two years for their comprehensive medical history taking and physical examination. The involvement of these three groups of participants with intra-familial relationships provided the inkling about possible genetic association regarding the onset of some forms of cardiovascular disease even before the initiation of the human genome sequencing which was accomplished by April 2003. In global epidemiologic study of cardiovascular disease, the FHS has become the international pioneer in exemplifying the application of sound, prospective epidemiological design with the possibility of generating yet unidentifiable innovative incidence data to enhance the management of heart disease (Almasy et al, 2010).

In 1971, the FHS enrolled a second generation made of 5124 who are children of the legacy cohort. The second group received similar detailed medical examinations and other anthropometric assessment and clinical laboratory tests. In recent times, the third generation that is, the grandchildren of the legacy group, which make-up 3500 males and females, are being recruited and examined to provide the necessary data not only to establish genetic linkages but to enable clinicians to have succinct knowledge for the management of heart disease which is the leading cause of death in the developed nations.

In fact, since 1900 in assessing risk factors associated with CVD, very little was known about the genetic basis of heart-related diseases. Instead, most cardiologists suspected intra-familial relationship but not a direct Mendelian pattern in the onset of CVD. However, as a serendipitous benefit from FHS, the current enrollment of three cohorts who have an established genetic affiliation with 1.-the legacy group, 2.children of the legacy cohort and 3. the grandchildren of the original cohort; this epidemiological design has provided the much needed foundation for the human genome study of complex diseases. It also creates the probability for the international scientific community to understand those sequenced genes which code for cardiovascular diseases.

Between 1970 and up to 2000, before the accomplishment of the human genome sequencing by April, 2003, through the collaboration of physicians, bio-medical engineers, venture capitalist, and entrepreneurs, various non-invasive medical devices were developed to reduce the risk of invasive procedures and medical errors. Dr. Barbara Starfield, a distinguish professor in the Department of Health Policy, Management and Pediatrics, Johns Hopkins University School of Public Health and Medicine (Baltimore, MD) has emphasized that 20,000 deaths are recorded each year due to medical errors (Starfield, 2010) .

The non-invasive medical equipment include electrocardiogram, nuclear stress test (EKG), echocardiogram (ECHO), positron emission tomography (PET) and computer tomography and magnetic resonance imaging (MRI). In addition to these monumental medical breakthroughs, the prominent milestones of FHS are summarized in Table 1.

## 1 Computed tomography (CT)
CT scan is the test which combines instantaneous x-ray scanning with multiple computed tomography to produce detailed images of the heart arteries without surgery. Pictures of the heart are taken by rotating a camera called detector around human body. The patient lies on a specially designed narrow bed which is comfortably moved through the camera's area of focus.

## 2 Nuclear Cardiology stress test
Physicians inject a radioactive substance into the blood of CVD patient and use gamma x-ray camera to visualize the movement of blood through the heart. This non-invasive procedure is able to detect the movement of blood through the heart. The test can reveal how the heart is functioning in keeping itself saturated with oxygen rich blood; this test is conducted twice to confirm cardiac performance at rest and under severe stress

## 3 Cardiovascular magnetic resonance imaging (Cardiovascular MRI).
This medical technique utilizes powerful magnets to create a field that sets the nuclei of atoms in heart cell vibrating. The oscillating atoms emit radio signals which are converted by computer into either stationary or moving 3-D images. This noninvasive procedure which visualizes the heart and the vascular structures and functions without exposing patients to radiation and iodinated contrast dye is widely used across the nation.

## 4 Echocardiogram
Also called trans-thoracic echocardiogram (TTE)
Harmless ultrasound waves which are quite similar to the ones used in taking sonograms of a fetus are aimed at the chest and bounces off the heart's walls and valves. A computer performs analysis of these rebounding waves and precisely calculates the size and movement of the structure of the heart. Again, physicians usually performs two echogram of the heart, one at rest and the other under stress.

## 5 Electrocardiogram (EKG)
This medical device simply scans and records the electrical impulses which regulate one's heart's pumping action. When there are deviations from normal rhythm pattern; such irregularities are symptomatic of the probability of damaged heart tissue and impeded blood flow.

## 6 Positron emission tomography (PET) and CT
This non-invasive procedure provides structural and functional information about the heart in one scanning bout. Physicians use CT to locate specific narrowed regions along the arteries; and PET is efficiently used to locate portions of the heart muscles that are deprived of blood flow.

Sources: G.E. Healthcare Siemens. Time graphic by Lon Tweeten and Kristina Dell. Time September 5, 2005 pp 59-71.

## Table 1. Milestones and accomplishments from Framingham Heart Study
- 1948 Initiation of FHS
- 1956 Findings on progression of rheumatic heart disease reported
- 1959 Factors detected to increase the likelihood of heart disease; some heart attack discovered to be silent; specifically without pain
- 1960 Cigarette smoking found to increase the risk of heart disease; in spite of the vigorous counter claim of the major tobacco industries to debunk scientific evidence
- 1961 Cholesterol level, blood pressure and electrocardiogram abnormalities found to increase the risk of heart disease.
- 1965 First FHS published peer-reviewed study on stroke.
- 1967 Physical activity discovered to reduce the risk of heart disease and obesity to increase the risk of heart disease.
- 1970 High blood pressure to increase the risk of stroke
- 1974 Overview of diabetes and its complications

- 1976 Menopause found to increase the risk of heart disease
- 1977 Effects of triglycerides and LDL and HDL cholesterol described
- 1978 Psychological factors found to affect heart disease Atrial fibrillation (condition in which the heart beats irregularly) found to increase the risk of stroke
- 1981 Filter cigarettes found to give no protection against coronary heart disease
- 1983 Reports on mitral valve prolapse (which causes a backward leak between heart chambers)
- 1986 First report on dementia
- 1987 High blood cholesterol levels found to correlate directly with risk of death in young men Fibrinogen (allows blood to clot more easily) found to increase the risk of heart disease Estrogen replacement therapy found to reduce risk of hip fractures in post-menopausal women
- 1988 High levels of HDL cholesterol found to reduce risk of death
- Type "A" behavior associated with heart disease
- Isolated systolic hypertension found to increase risk of heart disease
- Cigarette smoking found to increase risk of stroke
- 1994 Enlarged left ventricle (one of two lower chambers of the heart) shown to increase the risk of stroke Lipoprotein

- Low-density lipoprotein Found as possible risk factor for heart disease
- Risk factors for atrial fibrillation described A poliprotein E found as possible risk factor for heart disease
- 1995 First Framingham report on diastolic heart failure
- Start of the OMNI Study of Minorities
- 1996 Progression from hypertension to heart failure described
- 1997 Report on the cumulative effects of smoking and high cholesterol on the risk for atherosclerosis
- Investigation of the impact of an enlarged ventricle and risk for heart failure in asymptomatic individuals
- 2000-till now over 1000 peer-reviewed publications reported from FHS.

Epidemiologic benefits from FHS

The classical prospective epidemiological design, was for the first time, tested on a large scale and practicalised to yield incidence data with pertinent clinical applications worldwide.

To illustrate, a similar or a glimpse of the FHS design is presented in Table 2.

Table 2. The Framework of Cohort Epidemiological Study(FHS)

| Etiologic traits | | | Total |
|---|---|---|---|
| | | Did not develop CVD | |
| Or Exposure | Developed CVD | | |
| Present(Exposure) | a | b | a+b |
| Absent(Not exposed | c | d | c+d |
| Total | | | a+b+c+d |

The incidence rate among those exposed to risk factors (e.g. tobacco use, high lipid intake, excessive use of table salt, obesity, stressful lifestyle, over 40year of age) can be computed as follows:

$$\frac{A}{A+B}$$

The incidence rate for the unexposed that is those who engage in exercise and the abstainers from tobacco, alcohol, lipids, and users of low sodium diet is computed as

C

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C+D

The research question is whether the incidence rate for the exposed group is greater than the incidence rate for the unexposed group. If the incidence for the exposed group is higher than the incidence for the unexposed group, an association can be inferred between risks factors and the subsequent development of cardiovascular disease. However, there are a few pathogmonomic variables as age, intra-familial traits and inherited gene chromosomes. This hunch was ingeniously anticipated in FHS, therefore the research team created three viable cohorts, where a significant proportion had genetic linkages (1). The legacy group, (2). Their children and (3). Their grandchildren)

The relative risk which is used to measure the strength of association is computed as follows:

=                Incidence   rate of CVD in the exposed group

     --------------------------------------------------------------------------
                    Incidence rate of CVD in the unexposed group

The research question is whether the incidence rate is greater for those exposed than those that were unexposed. Hypothetically, if the incidence of CVD among smokers was 6per 1000, for non-smokers, it will be 1 per 1000; then the relative risk for CVD for smokers compared to the non-smokers would be

RR   =      6/1000

           ------------- = 6.0

        I/1000

This basic epidemiological computation reveals that cigarette smokers are six times as likely to develop CVD compared to non-smokers. Basic chi-square test can be used to establish the association between smoking and the onset of CVD.  However, association does not establish clear cut indictment of etiological agents. But in FHS, autopsy examination of deceased subjects were examined to confirm the association of specific risk factors and death due to associated web of causation, namely age, tobacco and  obesity. In the same vein, in an effort to screen for risk factors for cardiovascular disease, the epidemiological gold standard for such screening in a 2 by 2 format is illustrated below (Table 3):

Table 3. Screening for Risk factors for cardiovascular disease

| Technology Sphygmomanother | Abnormal Values BP Values> 140/100 | Normal Values BP<, =120/80 | Total |
|---|---|---|---|
| + | A=100 True Positive | B=50 False Positive | A+B=150 |
| - | C=50 False Negative | D=300 True Negative | C+D=350 |
| Total | A+C= 150 | B+D=350 | A+B+C+D=500 |

Sensitivity= A
         ---------X 100 = 66.7%
         A+C

Specificity= D

$$\frac{D}{B+D} \times 100 = 85.7\%$$

Positive Predictive Index = A

$$\frac{A}{A+B} \times 100 = 66.7\%$$

Negative Predictive Index= D

$$\frac{D}{C+D} \times 100 = 85.7\%$$

Efficiency of the test = A+D

$$\frac{A+D}{A+B+C+D} \times 100 = 80\%$$

Prevalence of the disease = A+C

$$\frac{A+C}{A+B+C+D} \times 100 = 30\%$$

Lessons from the FHS study have been used to guide many similar but un-identical prospective epidemiological studies which include: 1. The Bogalusa heart study in children, 2. The Tecumseh Michigan community health study, and the recently developed, 3. National children study. The first two studies which utilized prospective epidemiologic approach have not reported the involvement of the services of geneticists in their study.

However, in the National children's study, which is a multi-year prospective research study designed to examine the effects of environmental influences on the health and development of more than 100,000 children across the United States, following them from birth until the age of 21. The method advocated by our team to implement and monitor this elaborate and expensive study was the prospective epidemiological techniques; employing the lessons of Framingham to guide the trajectory of the study. This project involves five federal agencies such as the National Institute of Child Health and Human Development and the National Institute of Environmental Health Sciences of the National Institutes of Health and the Centers for Diseases and Prevention, The United States Environmental Protection Agency, and the U.S. Department of Education. The two cardinal objectives were (1) to plan, develop, and implement a prospective cohort study, from birth to adulthood, to evaluate the effects of both chronic and intermittent exposures on child health and human development; and (2) investigate basic mechanisms of developmental disorders and environmental factors, both risk and protective, that influence health and developmental processes. This NCH study is currently being implemented in 41Vaguard sites across the nation (National Institute of Child Health and Human Development, National Children Study, 2010).

In multiple academic programs across the United States, most health-oriented disciplines such as medical institutions, the school of public health, nutrition education, nursing and even clinical pharmacology, the FHS is used to hone the skills of students about the significance and limitations of the prospective epidemiological design.

The FHS and genetic linkages to Cardiovascular disease

Even before the human genome sequencing conducted by the National Institutes of Health and the U.S. Department of Energy, the FHS team had proposed the possible genetic linkage of participants and the onset of CVD as far back as 1971. The role of genetic linkages to CVD was designed to investigate whether there were any association between genetically related project participants and the onset of CVD by studying the 5124 off springs, including spouses from the original group. A third generation of participants has been included. They now involved 3,500 grandchildren of the original cohort (Murabito et al, 2007).

Since the original FHS group was previously restricted to the predominant Caucasians in Framingham community, due to the differences in single nucleotide polymorphism and their unique

haplotype characteristics, the questions of its applicability to other ethnic groups was criticized. Now, the Framingham Omni study was recently initiated involving 500 of the Framingham's minority members. Using the same instrument, the study participants are given free but extensive medical examination every two to four years. The tests include: medical history, a blood test, a bone scan, an echocardiogram, an eye examination and various anthropometric measurements.

Although the current state of CVD treatment remains complex, the on-going research in genomic epidemiology could, with time enlighten medical clinicians and cardiologists about how best to manage CVD using information from genetics and genomic sciences. However, the documented clear cut cases of genetic linkage to CVD include both Mendelian and multi-factorial patterns of inheritance. For example, there are the single gene mutations which affect individuals of all ethnic groups and this dysfunction culminates in premature cardiovascular morbidity and death. The Brugada syndrome which manifests as sudden death while asleep is due to autosomal dominant 3p21 SCN5A. Genetic mutations have been characterized regarding cardiac specific homeobox NKX2.5 and TGFBR2 in congenital malformation of atria and ventricular septation. Gene defect has been associated with junctional heart muscles cells which lead to myocardial dysfunction or cardiomyopathy (Smith, et al, 2000).

McPherson et al (2009) have used the genome wide association scanning to identify a 58-kilobase interval on chromosome 9P21 which was previously linked with CHD in six independent samples from more than 23,000 participants. In these data from four Caucasian populations which were used to identify specific intervals near the CDKN2A and CDKN29 genes; these genes were not associated with known risk factors such as plasma lipoproteins, hypertension, or diabetes.

Damani and Topol (2009) have substantiated the application of high-throughput genotyping technology which facilitated scanning of the genome with greater statistical power to detect susceptibility alleles for atrial fibrillation and the identification of a region on 4q25.

Regarding congenital heart disease gene in chromosome3P25, the critical region was reduced to an interval between D3S1263 and D3S3594. The candidate agents such as 3P25 CHD gene, PMCA2 (ATP2B2), and fibulin2, TIMP4 andSec13R were reported to map outside the target interval. The largest

study ever completed of genetic factors associated with heart attacks, identified nine genetic regions out which three had not been previously characterized(Danami and Topol, 2009).. A team of scientists assessed the SNP of 26,000 subjects from ten countries, using the international Haplotyping Map, a comprehensive map of SNPs across the genome. The other technology used included the genotyping arrays and gene chip developed by Altshuler's group (Altshuler, Daly, and Lander, 2008; Frazier, 2005).

Their investigation revealed significant association in nine genetic regions with heart attack-associated risks. The known chromosomal variant isolated by this group is a gene called PGSK9 which was originally reported by Kathresan (2009). Medical scientists, cardiologists and other clinicians now believe that since an effective intervention currently exist for the management of heart attack, new patients at a higher genetic risk may benefit from earlier treatment modality.

Recently, an international team of researchers (Altshuler, et al, 2008) has successfully identified new gene variants associated with an increased risk of myocardial infarction (MI). The new genes they identified were detected after having studied a million genetic biomarkers in 1,200MI patients. From their healthy counterparts, the genes for MI were found to be located on chromosome 3 and 12. Scientists now suspect one of the genes, the MRSA gene, as playing significant role in the onset of cardiovascular disease. Also, a second gene described as HNF1A was described to be closely associated with cholesterol metabolism (Altshuler et al, 2008).

At present, the Genome Wide Association study has only revealed some inkling about specific chromosomes and specific alleles which are associated with CVD. However, there over 1400 genes associated with 1200 Mendelian traits and only about 10 to 15 of them are the etiologic genetic variants for complex diseases (McMarthy et al, 2008). Epidemiologists are interested in testing for the authenticity of some of these clinical tests by determining the specificity, sensitivity, positive and negative predictive indices and efficiency of these genetic tests. In an investigation reported by Smith et al (2009) using the genome-wide association study, they replicated common genetic variants on chromosome 9p21 to confer risk of coronary heart disease. They also hypothesized the association of these SNPs with ischemic stroke, because previous studies claimed overlapping heritability of myocardial infarction and ischemic stroke principally due to a

common atherosclerotic pathogenesis. The caveat about the genetics of ischemic stroke is a field that has been long plagued by non-replication of reported findings, accentuating the equivocal results of complex traits (Frazier et al, 2005).

Health education implications of CVD in the age of genomic medicine

Cardiovascular disease is principally due to atherosclerosis or hardening of the arteries and it is very lethal. It accounts for over 40% mortality in the United States, killing about 950,000 Americans yearly ( American Heart Association [AHA],2003). By 2003, 1.1 million Americans will have experienced recurrent coronary attack and over 45% of them will die. The age-adjusted death rate by 2000 from CVD was 186.9 per 100,000 per total population. The total cost of this deadly disease increased beyond the $300 billion dollar mark over the past three years. The American Heart Association estimated the total cost of the disease to be 298.2 billion for the year 2003(AHA,2002, 2003).]. In view of the human lives lost to CVD, and the economic burden to society, it is imperative that medical scientists, physicians, epidemiologists, health educators and nurses must eliminate the barriers among their disciplines in the treatment and management of this lethal disease

Also, medical scientists, educators and nurses must be retrained to appreciate the role of genetics and genomics in clinical medicine. Although educators are adept in recommending multi-disciplinary approach for the prevention of CVD, currently, with the existing innovative of non-invasive medical devices, health educators must be willing to refer their clients for a comprehensive check-up using the innovative devices listed in Table 1.

Although health education programs focus on prescriptive exercise, stress management techniques and multiple cardiovascular risk reduction, these behavioral programs are insufficient in the age of genomic science. The routine onset of CVD which have genetic etiology cannot be eliminated just through routine exercise. There are pathogmonomic variables in the onset of CVD, we suspect age, and specific gene variants, chromosome 1q21.1, chromosome 9p21 for CHD which exercise and nutrition education cannot extirpate.

However, advances in the use of MRI as a non-invasive medical technique have astonished physicians particularly cardiologists with the clarity of details about the internal workings of the heart. This medical breakthrough enables the patient to receive

the best treatment most suitable for their nagging health problem. Similarly, CT scan being 90% accurate enables a physician to rule out completely coronary artery disease even when a patient is experiencing chest pain due to muscle spasm or excessive acid secretion (Green et al, 2000). The application of the medical devices listed in Table 1 to facilitate the clinical assessment of CVD problems of patients can assist physicians in preventing the imminent onset of myocardial infarction, coronary artery disease, atria fibrillation and other internal problems associated with CVD.

In the genomic age, precision medicine which was described by Dr. Elias Zerhouni (2010), the former director of the National Institutes of Health (NIH), is the innovative medicine which must anticipate and interrupt the disease process, thereby preventing the patient from being overwhelmed by the actual disease burden. This innovative medical paradigm is now characterized as P4 medicine and it is defined as: (1) predictive approach as the development of probabilistic health projection for a person based on their DNA, or sequenced chromosome, and protein expression. (2) Preventive medicine is the creation of interventions or therapeutic that will prevent a disease that an individual is assessed to have a high probability of developing. Regarding CVD, counseling of young adults which involve the requisite health behaviors particularly about the avoidance of tobacco, and the ingestion of food items that are rich in lipids and high salt content so as to avoid CVD is very important.. Although age is a pathogmonomic risk factor, exercise and compliance with adequate health habits can be play significant protective against many heart-problems. (3) Personalized medicine refers to treating individuals based on their unique human genetic variations. For example, what are their sequenced DNA and haplotype characteristics? Does the patient have inherited chromosomes that place such a patient at risk? (4) Participatory medicine implies a patient's active, informed involvement in their medical choices, treatment, and acting in partnership with their health care providers. A patient must be health-educated enough to inform a physician if the parents died from cardiovascular disease, such as heart failure, coronary disease or myocardial infarction (Institute of System Medicine, 2010).

Many technological sequencing devices relevant to CVD have been developed in recent times. Some of the developed medical technologies used to enhance personalized medical care were the 454 life sequencers manufactured by Roche Diagnostics

(Brandford, CT), chromatography and electrophoresis, gene amplification, capillary analysis, polymerase chain reaction tests and microarray sequencing. These state-of-the-science approaches and bioinformatics technologies have the potential to provide significant insights into disease manifestation in individual patients and clinical differences at the molecular level. Such knowledge will enable the physician to tailor treatment to the precise needs of patients.

A comprehensive list of the state of the art technologies required to improve the dissemination of personalized health care services were compiled by Ebomoyi and Srinivasan (2008).

In the era of genomic medicine, the key benefits of predictive, preventive, personalized and participatory interventions to the patient include new abilities to:

- Detect disease at an earlier stage, when it is easier and less expensive to treat effectively
- Stratify patients into groups that enable the selections of optimal therapy
- Reduce adverse drug reactions by more effective early assessment of individual drug responses
- Improve the selection of new biochemical targets for drug discovery
- Reduce the time, cost, and failure rate of clinical trials for new therapies
- Shift the emphasis in medicine from reaction to prevention and from disease to wellness.

With the availability of cutting edge biotechnology and genomic science, it is prudent to predict that genetic variation within the human genome can be characterized and genotyped for many ethnic groups. Through the use of molecular techniques, and genomic techniques scientists expect to detect increasing number of genetic diseases. Therefore, there is the urgent need to train more scientist with the capabilities to provided the relevant genomic. James Watson, (2004), the first director of NIH genomic center was the first biologist to advocate the relevance of the ethical, legal, and social issues about advances in genomic technology. Today, United States Department of Energy (2004; USDoE, 2010; USDoE, 2003), Genome programs have become vociferous about adhering to stringent and sanctimonious principles while screening for genetic diseases. Collectively, their resolutions enforced:

- Maintaining privacy and confidentiality of genetic information. Adoption of fairness in the use of genetic information by insurance companies, employers, court, schools, the military, adoption agencies and health associations among others. Avoidance of social stigmatization status and discrimination against an individual due to a person's genetic differences.
- Ensuring that researchers seek adequate and informed consent while working with expectant mothers, and patients with specific genetic defects. Education of physicians, other clinicians, health service providers about clients identities with genetic conditions and the general public about the capabilities, limitations and social risks associated with certain disorders and the implementation of standards and quality control measure at all laboratories and counseling centers. Use of experienced geneticists and other clinicians to explain the uncertainties associated with genetic tests for susceptibility, particularly for multi-factorial complex diseases such as heart disease, diabetes and Alzheimer's disease.
- Ensuring that there is fairness in access to advanced genomic technology and other pertinent philosophical and conceptual leanings of clients.

certificate in epidemiological science from the National Institutes of Health, Bethesda, MD; and a Ph.D. in community health and statistics from the University of Illinois, at Urbana-Champaign, Illinois. Dr Ebomoyi previously held a faculty appointment at Tuft University Medical School in the early nineties and he taught epidemiology and biostatistics. Currently he holds a full professorial appointment in the Department of Health Studies, College of Health sciences, at the Chicago State University, Chicago Illinois.

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