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Introduction to Genetics and Childhood Obesity: Relevance to Nursing Practice

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Abstract

Purpose—The aims for this article are to provide an overview of the current state of research on genetic contributions to the development of childhood obesity and to suggest genetic-focused nursing practices to prevent childhood obesity.

Organizing Constructs—Genetic epidemiology of childhood obesity, modes to identifying obesity genes, types of human obesity genes, and nursing implications are discussed.

Clinical Relevance—The successful integration of genetics into nursing practice will provide opportunities for nurses to participate fully as major agents and collaborators in the health care revolution.

Conclusions—Practicing nurses across the profession will need to become knowledgeable about genetics and take part in obesity prevention through genetic assessment of susceptibility and appropriate environmental interventions.

Keywords

genetics; obesity; nursing practice

Childhood obesity has reached epidemic proportions in the United States, becoming a major public health concern. The prevalence of obesity among children in the United States has nearly tripled over the past 25 years, rising from 5–6.5% between 1976 and 1980 to 14–18.4% between 2000 and 2004 (U.S. Department of Health and Human Services [USDHHS], 2006). Obesity in children is defined as a body mass index (BMI) at or above the 95th percentile for children of the same age and sex based on the Centers for Disease Control and Prevention (CDC) growth charts for children in the United States (Centers for Disease Control and Prevention [CDC], 2006). BMI is calculated from a child's weight and height. The CDC and the American Academy of Pediatrics (AAP) recommend the use of BMI to screen for obesity in children and teens aged 2–19 years.

Along with the rise in childhood obesity, there has been an increase in the prevalence of obesity-related diseases in youth and adults, such as elevated serum lipid and insulin concentrations, type 2 diabetes, heart disease, and hypertension (Krebs & Jacobson, 2003; Lee, 2009). Approximately 60% of overweight children between 5 and 10 years of age have at least one risk factor for cardiovascular disease, such as hypertension, dislipidemia, left ventricular hypertrophy, or atherosclerosis (Deckelbaum & Williams, 2001). Obese children

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are also predisposed to type 2 diabetes, nonalcoholic fatty liver disease or steatohepatitis, metabolic syndrome, asthma, and sleep apnea (Speiser et al., 2005). Furthermore, obese children are more likely to develop psychosocial problems such as low self-esteem, anxiety, withdrawal from peer interaction, depression, and suicide (Daniels et al., 2005; Schwimmer, Burwinkle, & Varni, 2004). These adverse consequences can be life threatening and warrant early prevention strategies.

Previous genetic studies conducted in families, adoptees, and twins have clearly shown there is a genetic contribution to obesity (Barsh, Farooqi, & O'Rahilly, 2000; Maes, Neale, & Eaves, 1997; Sorensen, Price, Stunkard, & Schulsinger, 1989; Stunkard, Harris, Pedersen, & McClearn, 1990). In addition, human genome research has led to discoveries of human obesity genes and confirmed that obesity has a genetic basis. However, that basis alone does not result in obesity without specific environmental influences (Qi & Cho, 2008).

Nurses need to become knowledgeable about the genetic component of obesity both to develop appropriate interventions for obesity prevention and to deliver competent genetic-focused nursing practices. The purpose of this article is to provide an overview of genetic contributions to childhood obesity development and its implications for nurses. The following topics are addressed: (a) genetic epidemiology of childhood obesity, (b) modes to identifying obesity genes, (c) types of human obesity genes, and (d) nursing implications. A glossary of terms related to genes and genetic influences can be found in Table 1.

Genetic Epidemiology of Childhood Obesity

Several studies involving twins, adoption, and family have shown that obesity is highly heritable (Sorensen et al., 1989; Stunkard, Sorensen, Hanis, et al., 1986; Stunkard et al., 1986). Significant obesity-related phenotypes of heritability estimation include BMI, skin-fold thickness, waist circumference, waist-to-hip ratio, body weight, and percentage fat mass (Liu, Araujo, Recker, & Deng, 2003). Twin studies suggest that the heritability estimation of fat mass is between 40% and 70% in monozygotic (identical) twins compared with 30–40% in dizygotic (fraternal) twins (Barsh et al., 2000; Stunkard et al., 1990; Stunkard, Sorensen, et al., 1986). Correlation of monozygotic twins reared apart is virtually a direct estimate of heritability. A study of 540 adults from the Danish adoption register that contained complete and detailed information on the biological parents reported a strong relationship between the BMIs of adoptees and biological parents ($p < .0001$ for mothers and $p < .02$ for fathers) and no significant relationship between the BMIs of adoptees and their adoptive parents (Stunkard, Foch et al., 1986). The Danish study also showed significant associations ($p < .01$) between the BMI of adoptees and their biological full siblings who were reared separately by the biological parents (Sorensen et al., 1989).

The risk of obesity is increased when an individual has relatives who are obese. Obesity, however, is not inherited in families in a predictable pattern like other genetic diseases, such as cystic fibrosis, but rather demonstrates a complex “polygenetic” pattern, meaning that multiple genes are involved (Lyon & Hirschhorn, 2005). Each of the obesity genes likely makes only a small contribution to different obesity-related phenotypes (BMI, waist circumference, percentage fat mass, and body weight) but collectively inherited variations play a major role in determining how an individual responds to the environmental factors of nutrition and physical activity. Genes involved in weight gain generally increase the susceptibility to fat gain in individuals who are exposed to a high-risk environment rather than directly causing obesity (Delrue & Michaud, 2004; Qi & Cho, 2008). Not all people living in developed countries with plenty of food become obese nor will all obese people experience the same health consequences. The variation in how different people respond to the same environment suggests that genes play a role in the development of obesity;

however, there is a complex interaction between genetic, environmental, and behavioral predispositions that contributes to obesity (Hinney & Hebebrand, 2008). There may also be genetic heterogeneity among age, gender, and ethnicity. Variations occur not only among diverse groups but also among individuals from the same ethnic backgrounds and among individuals within families living in the same environment.

Modes for Identifying Obesity Genes

The genetics of obesity is complicated and heterogeneous. Advances in molecular biology have improved our understanding of the genetic epidemiology of obesity and provided ways to identify obesity susceptibility genes. There are two common experimental designs used to identify obesity susceptibility genes: hypothesis-free (genome-wide association and genome-wide linkage) and hypothesis-driven (candidate gene) approaches (Bogardus, 2009; Yang, Kelly, & He, 2007).

Hypothesis-Free Approaches

Genome-wide association study (GWAS)—GWAS is a method that involves rapidly scanning markers across the complete sets of deoxyribonucleic acid (DNA), or genomes, of many people to find genetic variations associated with obesity or a particular disease (National Institutes of Health, National Human Genome Research Institute, n.d.). Human DNA consists of approximately 3 billion chemical bases (nucleotides) and more than 99% of these bases are similar in each individual. The information in DNA is stored as a code made up of four nucleotides: adenine (A), guanine (G), cytosine (C), and thymine (T). The sequence of these nucleotides contains genetic information available for building and maintaining an organism. Human genomic variability can be present in many forms, including single nucleotide polymorphisms (SNPs) and copy number variations (CNVs). A SNP (pronounced “snip”) is a small genetic change or variation occurring when a single nucleotide, such as an A, replaces one of the other three nucleotide letters—C, G, or T—within a person’s DNA sequence (National Center for Biotechnology Information [NCBI], 2002). For instance, a SNP might change the DNA sequence AAGGCTAA to ATGGCTAA. To be considered a SNP, a variation must occur in at least 1% of the population. A small variation in DNA sequence can have a major impact on the biological function of genes and gene products and on the way humans respond to disease and their environment.

GWAS is a hypothesis-free method of identifying new and unanticipated genetic variants associated with a given disease or trait. It is the most common approach used to identify susceptibility genes for common diseases, including obesity. With this approach, investigators can detect the genomic target region precisely. The first obesity GWAS was conducted by Herbert and colleagues (2006) in Framingham Heart Study participants to identify the associations between a common genetic variant (SNP) near the insulin-induced gene 2 (INSIG2) and obesity. Recently, the association between SNPs in the FTO gene (fat mass and obesity-associated gene) and increased adiposity was discovered through a GWAS involving type 2 diabetes (T2DM; Frayling et al., 2007). A cluster of SNPs in the first intron of the FTO gene also showed a strong and highly significant association with obesity-related traits in later independent GWASs (Dina et al., 2007; Scuteri et al., 2007; Tönjes et al., 2010).

An expansion of GWAS enables scientists to detect associations between CNVs and susceptibility to complex diseases, including obesity. A CNV is a DNA segment of one kilobase (kb) or larger that is present at a variable copy number in comparison with a reference genome (Redon et al., 2006). CNVs cover approximately 12% of the human genome and encompass more nucleotide content per genome than SNPs, indicating that CNVs significantly contribute to genetic diversity. However, the contribution of CNVs to

complex diseases and obesity susceptibility requires further research. GWAS promotes increased understanding of basic biological processes affecting human health, improvement in the prediction of complex diseases such as obesity and type 2 diabetes, and the promise of personalized medicine. It is a powerful experimental method for identifying genetic variants that contribute to health and disease. Advances in GWAS will enable nurses and other health professionals to provide patients with individualized information about their risks of developing obesity and to tailor prevention programs to each person's unique genetic makeup in the future.

Genome-wide linkage—Genome-wide linkage is also a hypothesis-free approach, yet it is costly and more restricted in practice than GWAS because of the family-based data requirement (Loos & Bouchard, 2008). The genome-wide linkage approach involves the probability calculation of genetic information from a series of markers in the human genome followed by testing for co-inheritance with the disease pattern in the family (Dean, 2003). Positional candidate genes can be identified by examining the regions around the peaks of linkage. The genome-wide linkage approach, generally using a 10-centimorgan (cM) marker density containing 400 microsatellite markers evenly covering the entire human genome, detects broad intervals of several megabases that might contain hundreds of susceptibility genes for diseases of interest. Both GWAS and genome-wide linkage approaches have been used to find susceptibility genes for BMI and obesity. SNPs are currently the variants of choice for both GWAS and linkage studies.

Hypothesis-Driven Approach

Candidate gene analysis—Candidate gene analysis, a hypothesis-driven experimental method, involves testing the association between obesity and a specific allele of a gene that appears to be a good candidate, such as a gene influencing the regulation of food intake (Clement & Ferre, 2003). Identification of a candidate gene can also be based on other information, such as pharmacological findings or location of a gene within a linkage region (Hinney & Hebebrand, 2008). There are two main types of candidates: functional and positional. Functional candidates are genes with products that are somehow involved in the pathogenesis of the disease. Positional candidates are genes located within specific genomic regions and identified to be genetically significant in linkage or association studies (Bell, Walley, & Froguel, 2005). The selection of candidate genes is based on the relevance of the candidate gene to the pathogenesis of the disease of interest and the functional effects of a particular gene variant (Daly & Day, 2001). Candidate gene analysis is considered to be an effective strategy for identifying genetic variants with small or modest effects that underlie susceptibility to complex diseases, including obesity.

A number of obesity candidate genes have been tested in various populations. These candidate genes were selected based on their potential functions related to energy intake, energy expenditure, and obesity-related phenotypes, including body weight, BMI, and fat mass. A total of 416 studies finding positive associations have reported 127 candidate genes. However, only 22 genes, including LEPR (leptin receptor), PPARG (peroxisome proliferator-activated receptor gamma), and MC4R (Melanocortin-4 Receptor), have been confirmed by at least five positive results (Rankinen et al., 2006). Discovery of the genes involved in the development of obesity, thereby identifying causal pathways in individuals, will guide nurses and other health care providers in identifying high-risk individuals for early intervention (Barsh et al., 2000; Rankinen et al., 2006).

Genetic Types of Human Obesity

Molecular approaches have expanded our understanding of some forms of obesity in humans. The forms of obesity described here include monogenic, syndromic, and polygenomic, or common.

Monogenic Forms of Obesity

Obesity stemming from a single, dysfunctional gene is both severe and rare in the general population (less than 1%; Farooqi & O'Rahilly, 2005). Approximately 200 cases of human obesity have been associated with a single gene mutation (Rankinen et al., 2006). Evidence shows that genes causing monogenic obesity include leptin (LEP), LEPR, pro-opiomelanocortin (POMC), MC4R, and the enzyme pro-hormone convertase-1 (PC1; Jackson et al., 1997; Krude et al., 1998; Montague et al., 1997; Vaisse et al., 1998). Mutations of these genes result in humans becoming morbidly obese through disruption of a homeostatic system regulating energy balance (O'Rahilly, Farooqi, Yeo, & Challis, 2003). Genes involved in monogenic forms are usually involved in the regulation of food intake (Clement & Ferre, 2003). Monogenic obesity may exhibit a phenotype of morbid obesity and a variety of neuroendocrine abnormalities, including hyperphagia and hypogonadism (O'Rahilly et al., 2003).

Syndromic Forms of Obesity

Most obesity syndromes are distinguished by the presence of mental retardation, dysmorphic features, and organ-specific developmental abnormalities (Delrue & Michaud, 2004). These syndromes emerge from discrete genetic defects or chromosomal abnormalities and can be either autosomal or X-linked disorders (Bell et al., 2005). The most frequent of these syndromes (1 in 25,000 births) is Prader-Willi syndrome (PWS), an autosomal-dominant disorder characterized by obesity, hyperphagia, mental retardation, short stature, muscular hypotonia, and hypogonadotropic hypogonadism (Cummings et al., 2002). PWS is usually caused by a paternally inherited deletion at the chromosomal region 15q11.2-q12 (Jiang, Tsai, Bressler, & Beaudet, 1998). It is clear that the molecular causes of syndromic obesity are more complex than those causing the monogenic form. Further studies are required to elucidate the genetic bases.

Common Forms of Obesity

The common forms of obesity found in humans are called polygenic obesity. Polygenic obesity is complex and is presumably influenced by a substantial number of genes, usually two or more (Clement, 2005). Thus, the search for genes predisposing to polygenic obesity has been challenging. Polygenic obesity is caused by the interaction of several polygenic variants and their combined interaction with environmental factors (Bell et al., 2005). Those polygenic variants presumably account for most of the genetic variation relevant in human body weight regulation (Clement, 2005). Interindividual heterogeneity is apparent and implies that the specific set of polygenes predisposing to obesity in each individual is unlikely to be similar (Mutch & Clément, 2006). Although humans all have the same genetic material, each individual's genome is slightly different. In one of every 1,200 bases of the same stretch of genome, a SNP will be different (Fullerton et al., 2000). A few of these different SNPs will alter the biologic function of a gene by either affecting the structure or altering the location or amount of the protein. Some of these functional alterations will affect susceptibility to obesity (Lohmueller, Pearce, Pike, Lander, & Hirschhorn, 2003).

Studies of polygenic obesity are currently based on the analysis of SNPs or repetition of bases (polyCAs or microsatellites) located within or near a candidate gene (Mutch & Clement, 2006). Obesity is a common disease caused by multiple factors, with genetics

playing a strong causal role. There are sequence variants present in the population that increase or decrease individuals' risk of being obese. With new molecular tools and resources, investigators can undertake well-designed studies to find common obesity genes and clarify which pathways are altered by these variations. These genes will identify origin causes of obesity and provide direction regarding how children respond to their environment and become obese.

Nursing Implications

The global epidemic of obesity in children and adults is one of the greatest challenges in public health today. The complexity of obesity origin makes the prevention and treatment of obesity especially challenging. Although unhealthy nutrition and sedentary lifestyle have been identified as primary determinants of the increase in the incidence of obesity, genetic factors are also important in determining an individual's susceptibility to obesity. The success of human genome research has provided a foundation for a new understanding of the genetic mechanisms of human obesity. Accordingly, genetics has become increasingly incorporated into everyday practice. Therefore, as members of the multidisciplinary health care team, nurses need to understand its relevance and become knowledgeable about and competent in its application to their own clinical practice. Although the science related to the genetics of obesity is complex, the nursing components of both treatment and research in this area do not go far beyond the skills that most nurses already possess. The Consensus Panel on Genetic/Genomic Nursing Competencies (2009) states, "The genetic and genomic competencies are integral to the practice of all registered nurses regardless of academic preparation, practice setting, role, or specialty." The panel lists essential competencies for registered nurses (pp.11–12). A few examples of these are

- Demonstrates an understanding of the relationship of genetics and genomics to health, prevention, screening, diagnostics, prognostics, selection of treatment, and monitoring of treatment effectiveness.
- Demonstrates ability to elicit a minimum of three-generation family health history information.
- Collects personal, health, and developmental histories that consider genetic, environmental, and genomic influences and risks.
- Conducts comprehensive health and physical assessments that incorporate knowledge about genetic, environmental, and genomic influences and risk factors.
- Critically analyzes the history and physical assessment findings for genetic, environmental, and genomic influences and risk factors.

Nurses can play a crucial role in the prevention and treatment of obesity by identifying the modifiable risk factors, evaluating individuals and their families, and collecting detailed family health histories. The family health history provides useful information for detecting an individual's risk for rare single-gene or chromosomal disorders and for other common diseases with multiple genetic and environmental contributions such as cancer, heart disease, diabetes, and obesity (U.S. Department of Health and Human Services, n.d.; Wattendorf & Hadley, 2005). Family health history should be collected at the initial patient evaluation (Lea, 2009) and be updated periodically to identify newly diagnosed diseases or developmental conditions within the family. A minimum family health history of three generations is recommended and a structured pedigree of the family health history using standardized symbols and terminology is suggested because it provides an illustration of heritable patterns within the family and throughout the generations (Consensus Panel on Genetic/Genomic Nursing Competencies, 2009). The information that needs to be carefully considered for each family member when obtaining a family health history includes current

age and ages of onset of disease; age at death and cause of death; maternal age and reproductive history such as miscarriages, stillbirths, or conditions that may increase the risk of birth defect, including gestational diabetes and phenylketonuria; developmental disabilities; chronic illnesses such as heart disease, hypertension, diabetes, cancer; ethnicity/country of origin; and genetic relatedness or consanguinity (Lea, 2002; Wattendorf & Hadley, 2005). A consanguineous family increases the probability of individuals having more genes in common, which increases the risk of inherited diseases and recurrence of common complex diseases in each family member (Lea, 2002).

As the science of genetics and obesity expands and discoveries are translated into clinical settings, practicing nurses will take part in obesity prevention through genetic assessment of susceptibility and appropriate environmental interventions involving behavioral and lifestyle modification. The following is an example of genetic-focused nursing practices for children who are overweight or at risk of being obese (Consensus Panel on Genetic/Genomic Nursing Competencies, 2009; Rowen, 2009).

1. Assess personal, medical, family, and genetic risk factors. Factors potentially contributing to obesity include (a) personal and family weight (BMI) history; (b) familial and psychosocial factors such as maternal psychopathology (Zeller & Modi, 2008); (c) personal and family endocrine abnormalities, personal and family medically related conditions such as diabetes mellitus, glucose intolerance, thyroid dysfunction, coronary heart disease, and hypertension; (d) weight perceptions and expectations; and (e) health behaviors for modifiable risk factors, such as eating habits, physical activity or exercise, and smoking.
2. Provide individuals and families with information about the basic concepts of obesity susceptibility and the methods to identify obesity susceptibility genes.
3. Provide individuals and families with information about the availability of genetic testing and treatment for monogenic and syndromic obesity.
4. Provide individuals and families with an appropriate informed consent process, including the risks, benefits, and limitations of genetic testing, to facilitate decision making.
5. Protect and maintain privacy and confidentiality related to the genetic information of individuals to the extent possible.
6. Provide health education and counseling for lifestyle changes for individuals whose genetic profiles indicate they are at increased risk for obesity.
7. Acknowledge the difficulties faced by an individual or family and provide ongoing support to individuals and families who have genetic concerns.
8. Provide referrals for further investigation when necessary.

Numerous up-to-date references are available to health care providers and the general public. Some reliable web resources are shown in Table 2.

Case Study

David, a 6-year-old Caucasian boy, comes to a pediatric unit with his mother because of his high BMI. The mother expresses her concern about her child's high BMI to a pediatric nurse. The child's BMI has increased from 16.8 (at 85th percentile) to 18.1 (at 95th percentile) in 1 year; both measures were taken by a school nurse. The mother tells the nurse that she does not want her child to be obese in his later life. The nurse reviews David's BMI and plots it on the CDC BMI growth chart. His BMI is at the 94th percentile, which falls in

the overweight category. The nurse interviews the mother about David's family medical and weight history. From the interview, the nurse learns that David's grandmother (his mother's mother) and his aunt were obese and died of diabetes. David's father and mother are overweight; his father also has hypertension. The nurse draws a family pedigree and asks more about other family members' weight and health histories (a minimum of three generations: siblings, parents and their siblings, and grandparents). The nurse asks the mother about the family's health behaviors, such as tobacco, alcohol, and drug use; nutrition; physical activity; and exercise. David's father quit smoking 7 years ago. Both father and mother drink occasionally. Nobody reports using drugs. The family usually eats together at home. The mother says that she has tried to cook healthy food as much as possible. David, however, does not like vegetables and rarely eats them. Likewise, he does not like fruits but he sometimes eats oranges and grapes. Regarding physical activity and exercise, the family usually participates in outdoor activities such as biking and playing ball only on weekends. On weekdays, David goes to school and plays computer games or watches TV after school.

David's mother also asks the nurse about genetic testing for obesity. She says that everyone in her family (mother, sister, and herself) is either overweight or obese; therefore, her family may have the "obesity genes." The nurse explains that there are three genetic types of obesity: monogenic, syndromic, and polygenic. The polygenic form of obesity, the most common form, is influenced by a substantial number of genes; and testing of genetic susceptibility to this form of obesity is not yet available. Genetic testing is only currently used to diagnose and treat monogenic and syndromic forms of obesity.

The nurse tells David's mother that an individual's risk for obesity is increased when he or she has relatives who are obese. Therefore, it would be easier for David to put on weight because his family members, particularly parents, are overweight. However, if David is active and eats healthy foods, he should be able to lower his risk for being obese. The nurse also emphasizes the potential links between obesity and diabetes and between obesity and hypertension among David's family members from their family pedigree. She tells the mother that obesity is a precursor for many health problems in later life, including diabetes, hypertension, and cardiovascular disease. These obesity-related diseases are also increasing in youth. The nurse suggests that David's eating behavior needs to be changed. David also needs to engage more in physical activity. The nurse guides the mother in creating a healthy and active family environment to promote healthy habits for David, such as increasing physical activity as a family, enrolling David in a structured activity that he enjoys, and limiting the amount of time spent watching television and playing computer games. The nurse suggests that David's mother discusses physical activity with a lifestyle modification program consultant to find appropriate physical activities for David and the family. Finally, the nurse offers to refer David to a dietitian for help in planning healthy nutrition and for reaching a healthy weight.

Conclusion

The recent developments in genetic testing for obesity susceptibility genes have had a great impact on nursing's role in the identification and management of individuals at risk for developing obesity. An increasing number of genes linked to human obesity are being identified. This knowledge will increase our understanding of the causes of obesity and the ways in which children respond to their environments and become obese. Nurses are already skilled at collecting and assessing family history information, constructing family pedigrees, and discussing behavioral and environmental factors contributing to obesity with patients and their families. They have already begun to be or will soon be faced with increasing questions about genetics from their patients; therefore, they need to become actively

involved in genetic technologies. At no time has the need been greater for nurses to become better informed about these developing technologies. They can then use this knowledge to develop nursing plans and interventions to meet the future needs of patients and families at risk for obesity.

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References

- Barsh GS, Farooqi IS, O'Rahilly S. Genetics of body-weight regulation. *Nature*. 2000; 404:644–651. [PubMed: 10766251]
- Bell CG, Walley AJ, Froguel P. The genetics of human obesity. *Nature Reviews, Genetics*. 2005; 6:221–234.
- Bogardus C. Missing heritability and GWAS utility. *Obesity*. 2009; 17:209–210. [PubMed: 19169219]
- Centers for Disease Control and Prevention. National Health and Nutrition Examination Survey. 2006. Retrieved from <http://www.cdc.gov/nchs/nhanes.htm>
- Clement K. Genetics of human obesity. *Proceedings of the Nutrition Society*. 2005; 64:133–142. [PubMed: 15960858]
- Clement K, Ferre P. Genetics and the pathophysiology of obesity. *Pediatric Research*. 2003; 53:721–725. [PubMed: 12621112]
- Consensus Panel on Genetic/Genomic Nursing Competencies. Essentials of genetic and genomic nursing: Competencies, curricula guidelines, and outcome indicators. 2nd ed. American Nurses Association; Silver Spring, MD: 2009. Retrieved from http://www.nursingworld.org/MainMenuCategories/EthicsStandards/Genetics_1.aspx
- Cummings DE, Clement K, Purnell JQ, Vaisse C, Foster KE, Frayo RS, Weigle DS. Elevated plasma ghrelin levels in Prader–Willi syndrome. *Nature Medicine*. 2002; 8:643–644.
- Daly AK, Day CP. Candidate gene case-control association studies: Advantages and potential pitfalls. *British Journal of Clinical Pharmacology*. 2001; 52:489–499. [PubMed: 11736857]
- Daniels SR, Arnett DK, Eckel RH, Gidding SS, Hayman LL, Kumanyika S, Williams CL. Overweight in children and adolescents: Pathophysiology, consequences, prevention, and treatment. *Circulation*. 2005; 111:1999–2012. [PubMed: 15837955]
- Dean M. Approaches to identify genes for complex human diseases: Lessons from Mendelian disorders. *Human Mutation*. 2003; 22:261–274. [PubMed: 12955713]
- Deckelbaum RJ, Williams CL. Childhood obesity: The health issue. *Obesity Research*. 2001; 9:S239–S243.
- Delrue MA, Michaud JL. Fat chance: Genetic syndromes with obesity. *Clinical Genetics*. 2004; 66:83–93. [PubMed: 15253756]
- Dina C, Meyre D, Gallina S, Durand E, Korner A, Jacobson P, Froguel P. Variation in FTO contributes to childhood obesity and severe adult obesity. *Nature Genetics*. 2007; 39:724–726. [PubMed: 17496892]
- Farooqi IS, O'Rahilly S. Monogenic obesity in humans. *Annual Review of Medicine*. 2005; 56:443–458.
- Frayling TM, Timpson NJ, Weedon MN, Zeggini E, Freathy RM, Lindgren CM, McCarthy MI. A common variant in the FTO gene is associated with body mass index and predisposes to childhood and adult obesity. *Science*. 2007; 316:889–894. [PubMed: 17434869]
- Fullerton SM, Clark AG, Weiss KM, Nickerson DA, Taylor SL, Stengård JH, Sing CF. Apolipoprotein E variation at the sequence haplotype level: Implications for the origin and maintenance of a major

- human polymorphism. *American Journal of Human Genetics*. 2000; 67:881–900. [PubMed: 10986041]
- Herbert A, Gerry NP, McQueen MB, Heid IM, Pfeufer A, Illig T, Christman MF. A common genetic variant is associated with adult and childhood obesity. *Science*. 2006; 312:279–283. [PubMed: 16614226]
- Hinney A, Hebebrand J. Polygenic obesity in humans. *Obesity Facts*. 2008; 1:35–42. [PubMed: 20054160]
- Jackson RS, Creemers JW, Ohagi S, Raffin-Sanson ML, Sanders L, Montague CT, O’Rahilly S. Obesity and impaired prohormone processing associated with mutations in the human prohormone convertase 1 gene. *Nature Genetics*. 1997; 16:303–306. [PubMed: 9207799]
- Jiang Y, Tsai TF, Bressler J, Beaudet AL. Imprinting in Angelman and Prader–Willi syndromes. *Current Opinion in Genetics & Development*. 1998; 8:334–342. [PubMed: 9691003]
- Krebs NF, Jacobson MS, American Academy of Pediatrics, Committee on Nutrition. Prevention of pediatric overweight and obesity. *Pediatrics*. 2003; 112:424–430. [PubMed: 12897303]
- Krude H, Biebermann H, Luck W, Horn R, Brabant G, Grüters A. Severe early-onset obesity, adrenal insufficiency and red hair pigmentation caused by POMC mutations in humans. *Nature Genetics*. 1998; 19:155–157. [PubMed: 9620771]
- Lea DH. What nurses need to know about genetics. *Dimensions of Critical Care Nursing*. 2002; 21:50–60. [PubMed: 11949469]
- Lea DH. Basic genetics and genomics: A primer for nurses. *Online Journal of Issues in Nursing*. 2009; 14 doi: 10.3912/OJIN.Vol14No02PPT01.
- Lee YS. Consequences of childhood obesity. *Annals of the Academy of Medicine*. 2009; 38:75–81.
- Liu YJ, Araujo S, Recker RR, Deng HW. Molecular and genetic mechanisms of obesity: Implications for future management. *Current Molecular Medicine*. 2003; 3:325–340. [PubMed: 12776988]
- Lohmueller KE, Pearce CL, Pike M, Lander ES, Hirschhorn JN. Metaanalysis of genetic association studies supports a contribution of common variants to susceptibility to common disease. *Nature Genetics*. 2003; 33:177–182. [PubMed: 12524541]
- Loos RJ, Bouchard C. FTO: The first gene contributing to common forms of human obesity. *Obesity Reviews*. 2008; 9:246–290. [PubMed: 18373508]
- Lyon HN, Hirschhorn JN. Genetics of common forms of obesity: A brief overview. *American Journal of Clinical Nutrition*. 2005; 82:215S–217S. [PubMed: 16002823]
- Maes HH, Neale MC, Eaves LJ. Genetic and environmental factors in relative body weight and human adiposity. *Behavior Genetics*. 1997; 27:325–351. [PubMed: 9519560]
- Montague CT, Farooqi S, Whitehead JP, Soos MA, Rau H, Wareham NJ, O’Rahilly S. Congenital leptin deficiency is associated with severe early-onset obesity in humans. *Nature*. 1997; 387:903–907. [PubMed: 9202122]
- Mutch DM, Clément K. Unraveling the genetics of human obesity. *PLoS Genetics*. 2006; 2:1956–1963.
- National Center for Biotechnology Information. [Retrieved July 15, 2009] Single nucleotide polymorphism database, (dbSNP) of nucleotide sequence variation. 2002. from the NCBI Handbook at <http://www.ncbi.nlm.nih.gov/bookshelf/br.fcgi?book=handbook&part=ch5>
- National Institutes of Health. National Human Genome Research Institute., (n.d.). Talking glossary of genetic terms. Retrieved from genome.gov at <http://www.genome.gov/glossary/?id=0>
- O’Rahilly S, Farooqi IS, Yeo GH, Challis BJ. Minireview: Human obesity—lessons from monogenic disorders. *Endocrinology*. 2003; 144:3757–3764. [PubMed: 12933645]
- Qi L, Cho YA. Gene-environment interaction and obesity. *Nutrition Reviews*. 2008; 66:684–694. [PubMed: 19019037]
- Rankinen T, Zuberi A, Chagnon YC, Weisnagel SJ, Argyropoulos G, Walts B, Bouchard C. The human obesity gene map: The 2005 update. *Obesity*. 2006; 14:529–644. [PubMed: 16741264]
- Redon R, Ishikawa SI, Fitch KR, Feuk L, Perry GH, Andrews TD, Hurles ME. Global variation in copy number in the human genome. *Nature*. 2006; 444:444–454. [PubMed: 17122850]
- Rowen L. Overview and summary: Obesity on the rise: What can nurses do? *Online Journal of Issues in Nursing*. 2009; 14 doi: 10.3912/OJIN.Vol14No1ManOS.

- Schwimmer JB, Burwinkle TM, Varni JW. Health-related quality of life of severely obese children and adolescents. *The Journal of the American Medical Association*. 2003; 289:1813–1819.
- Scuteri A, Sanna S, Chen WM, Uda M, Albai G, Strait J, Abecasis GR. Genome-wide association scan shows genetic variants in the FTO gene are associated with obesity-related traits. *PLoS Genetics*. 2007; 3:1200–1210.
- Sorensen TI, Price RA, Stunkard AJ, Schulsinger F. Genetics of obesity in adult adoptees and their biological siblings. *British Medical Journal*. 1989; 298:87–90. [PubMed: 2493303]
- Speiser PW, Rudolf MC, Anhalt H, Camacho-Hubner C, Chiarelli F, Eliakim A, Hochberg Z. Childhood obesity. *Journal of Clinical Endocrinology & Metabolism*. 2005; 90:1871–1887. [PubMed: 15598688]
- Stunkard AJ, Foch TT, Hrubec Z. A twin study of human obesity. *The Journal of the American Medical Association*. 1986; 256:51–54.
- Stunkard AJ, Harris JR, Pedersen NL, McClearn GE. The body-mass index of twins who have been reared apart. *New England Journal of Medicine*. 1990; 322:1483–1487. [PubMed: 2336075]
- Stunkard AJ, Sorensen TI, Hanis C, Teasdale TW, Chakraborty R, Schull WJ, Schulsinger F. An adoption study of human obesity. *New England Journal of Medicine*. 1986; 314:193–198. [PubMed: 3941707]
- Tönjes A, Zeggini E, Kovacs P, Böttcher Y, Schleinitz D, Dietrich K, Stumvoll M. Association of FTO variants with BMI and fat mass in the self-contained population of Sorbs in Germany. *European Journal of Human Genetics*. 2010; 18:104–110. doi: 10.1038/ejhg.2009.107. [PubMed: 19584900]
- U.S. Department of Health and Human Services., (n.d.). Surgeon General's family history initiative. Retrieved from <http://www.hhs.gov/familyhistory/>
- U.S. Department of Health and Human Services. Healthy people 2010. 2006. Retrieved from <http://www.healthypeople.gov>
- Vaisse C, Clement K, Guy GB, Froguel P. A frameshift mutation in human MC4R is associated with a dominant form of obesity. *Nature Genetics*. 1998; 20:113–114. [PubMed: 9771699]
- Wattendorf DJ, Hadley DW. Family history: The three-generation pedigree. *American Family Physician*. 2005; 72:441–448. [PubMed: 16100858]
- Yang W, Kelly T, He J. Genetic epidemiology of obesity. *Epidemiologic Reviews*. 2007; 29:49–61. [PubMed: 17566051]
- Zeller, MH.; Modi, AC. Psychosocial factors related to obesity in children and adolescents. In: Jelalian, E.; Steele, RG., editors. *Handbook of childhood and adolescent obesity*. Springer; New York, NY: 2008. p. 25-42.

Table 1

Glossary of Terms Related to Genetics and Genetic Influences

Allele:	A member of a pair or series of different forms of a gene that is located at a specific position on a specific chromosome
Autosomal:	Any of the chromosomes other than the sex-determining chromosomes (i.e., the X and Y) or the genes on these chromosomes
Autosomal dominant:	Refers to a gene on one of the 22 pairs of autosomes (non-sex chromosomes). Describes a trait or disorder in which the phenotype is expressed in those who have inherited only one copy of a particular gene mutation (heterozygotes)
Autosomal recessive:	Refers to a gene on one of the 22 pairs of autosomes (non-sex chromosomes). Describes a trait or disorder requiring the presence of two copies of a gene mutation at a particular locus in order to express observable phenotype
Centimorgan:	The unit of linkage that refers to the distance between two gene loci determined by the frequency with which recombination occurs between them. Two loci are said to be one centimorgan apart if recombination is observed between them in 1% of meioses
Chromosome:	Physical structure consisting of a large DNA molecule organized into genes and supported by proteins called chromatin
Copy number variant or polymorphism (CNV or CNP):	A structural genomic variant that results in confined copy number changes in a specific chromosomal region. If its population allele frequency is less than 1%, it is referred to as a variant; if its frequency exceeds 1%, the term <i>polymorphism</i> is used
Dizygotic twins:	Referred to as nonidentical or fraternal twins. Occurs when two fertilized eggs are implanted in the uterine wall at about the same time, within the same menstrual cycle, or in rare cases within one menstrual cycle of each other. Dizygotic twins are no more similar genetically than any siblings and develop in separate amnions with separate placenta. They may have different genders or the same gender
DNA (deoxyribonucleic acid):	The molecule that encodes the genes responsible for the structure and function of an organism and allows for transmission of genetic information from one generation to the next
Gene:	The basic unit of heredity, consisting of a segment of DNA arranged in a linear manner along a chromosome. A gene codes for a specific protein or segment of protein leading to a particular characteristic or function
Genetic predisposition (synonym: genetic susceptibility):	Increased susceptibility to a particular disease due to the presence of one or more gene mutations associated with an increased risk for the disease and/or a family history that indicates an increased risk for the disease
Genome:	The complete DNA sequence, containing all genetic information and supporting proteins, in the chromosomes of an individual or species
Heritability:	A measure of how much of the variation in a trait in a population, not in an individual, is due to genes
Intron:	Noncoding sequence of DNA removed from mature messenger RNA prior to translation
Linkage:	The tendency for genes or segments of DNA closely positioned along a chromosome to segregate together at meiosis and therefore be inherited together
Marker:	An identifiable segment of DNA (e.g., microsatellite) with enough variation among individuals that its inheritance and co-inheritance with alleles of a given gene can be traced; used in linkage analysis
Microsatellite (synonyms: satellite DNA, short tandem repeats):	Repetitive segments of DNA two to five nucleotides in length (dinucleotide/trinucleotide/tetranucleotide/pentanucleotide repeats), scattered throughout the genome in noncoding regions between genes or within genes (introns), often used as markers for linkage analysis because of the naturally occurring high variability in repeat number between individuals. These regions are inherently unstable and susceptible to mutations
Monozygotic twins:	Referred to as identical twins. Occurs when a single egg is fertilized to form one zygote, but the zygote then divides into two separate embryos. The two embryos develop into fetuses sharing the same womb
Mutation:	Any alteration in a gene from its natural state; may be disease causing or a benign, normal variant
Phenotype:	The observable physical and/or biochemical characteristics of the expression of a gene. Also, the clinical presentation of an individual with a particular genotype.
Polymorphism:	Natural variations in a gene, DNA sequence, protein, or chromosome that have no adverse effect on the individual and occur with fairly high frequency in the general population
SNP (single nucleotide polymorphism):	A DNA sequence variation occurring when a single nucleotide—A, T, C, or G—in the genome (or other shared sequence) differs between members of a species (or between paired chromosomes in an individual)
Trait:	A distinct variant of a phenotypic character of an organism that may be inherited, environmentally determined or somewhere in between

Sources: Gene reviews: Full glossary. Retrieved from <http://www.genetests.org/servlet/access?qry=ALLTERMS&db=genestar&fcn=term>rreport2=true&id=8888891&key=cmFOvYe0NXOBb>. Genomicseducation.ca. Retrieved from <http://www.genomicseducation.ca/glossary/t.asp>.

Lawrence, E. (2005). *Henderson's dictionary of biology*. Pearson: Prentice Hall. Allele: A genetics definition. Retrieved from About.com at biology.about.com/od/geneticsglossary/g/alleles.htm.

Table 2**Online Resources for Genetic Information**

Family Medical History
American Medical Association, Genetics and Molecular Medicine
www.ama-assn.org/ama/pub/category/2380.html
Tools for gathering family history
GeneTests
National Center for Biotechnology Information
www.genetests.org/
Information for health professionals about hundreds of genetic tests
Genetics Education Program for Nurses
Cincinnati Children's Hospital Medical Center
www.gpnf.org
Links to genetics resources of particular interest to nurses.
Genetics Home Reference
U.S. National Library of Medicine
http://ghr.nlm.nih.gov
Provides consumer information about genetic conditions and the genes or chromosomes responsible for those conditions
Genomics and Health
Centers for Disease Control and Prevention
http://www.cdc.gov/genomics/public/index.htm
Resources on genetics, health, and diseases, etc.
Human Genome Resources
National Center for Biotechnology Information (NCBI), National Library of Medicine (NLM)
www.ncbi.nlm.nih.gov/genome/guide/human/
Comprehensive one-stop genomic information center
International Society of Nurses in Genetics (ISONG)
http://www.isong.org/
Website of the global nursing specialty organization dedicated to fostering the scientific and professional growth of nurses in human genetics and genomics worldwide.
Learn.Genetics—Genetic Science Learning Center
Eccles Institute of Human Genetics, University of Utah
http://learn.genetics.utah.edu/
Website created to help people understand how genetics affects their lives and society.
National Coalition for Health Professional Education in Genetics
www.nchpeg.org/
Core competencies in genetics and reviews of education programs.
National Newborn Screening and Genetics Resource Center
http://genes-r-us.uthscsa.edu/
Genetic information and resources for newborn screening
Online Mendelian Inheritance in Man (OMIM)
National Center for Biotechnology Information and Johns Hopkins University
http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=OMIM
Search engine for human genes and links to human genomes resources
Understanding Cancer Series: Gene Testing
National Cancer Institute
http://www.cancer.gov/cancertopics/understandingcancer/genetesting
An informative, illustrated tutorial on genes and genetic testing

Note. Adapted from the National Human Genome Research Institute's Online Genetics Education Resources at <http://www.genome.gov/10000464>.