(e.g., multiple endocrine neoplasia [MEN]), the severity of the disorder (e.g., cystic fibrosis), or the age of disease onset (e.g., Alzheimer's dementia). MEN 1 illustrates several of these features. In this autosomal dominant tumor syndrome, affected individuals carry an inactivating germline mutation that is inherited in an autosomal dominant fashion. After somatic inactivation of the alternate allele, they can develop tumors of the parathyroid gland, endocrine pancreas, and the pituitary gland (Chap. 408). However, the pattern of tumors in the different glands, the age at which tumors develop, and the types of hormones produced vary among affected individuals, even within a given family. In this example, the phenotypic variability arises, in part, because of the requirement for a second somatic mutation in the normal copy of the *MEN1* gene, as well as the large array of different cell types that are susceptible to the effects of *MEN1* gene mutations. In part, variable expression reflects the influence of modifier genes, or genetic background, on the effects of a particular mutation. Even in identical twins, in whom the genetic constitution is essentially the same, one can occasionally see variable expression of a genetic disease.

Interactions with the environment can also influence the course of a disease. For example, the manifestations and severity of hemochromatosis can be influenced by iron intake (Chap. 428), and the course of phenylketonuria is affected by exposure to phenylalanine in the diet (Chap. 434e). Other metabolic disorders, such as hyperlipidemias and porphyria, also fall into this category. Many mechanisms, including genetic effects and environmental influences, can therefore lead to variable expressivity. In genetic counseling, it is particularly important to recognize this variability, because one cannot always predict the course of disease, even when the mutation is known.

*Penetrance* refers to the proportion of individuals with a mutant genotype that express the phenotype. If all carriers of a mutant express the phenotype, penetrance is complete, whereas it is said to be *incomplete* or *reduced* if some individuals do not exhibit features of the phenotype. Dominant conditions with incomplete penetrance are characterized by skipping of generations with unaffected carriers transmitting the mutant gene. For example, hypertrophic obstructive cardiomyopathy (HCM) caused by mutations in the *myosin-binding protein C* gene is a dominant disorder with clinical features in only a subset of patients who carry the mutation (Chap. 283). Patients who have the mutation but no evidence of the disease can still transmit the disorder to subsequent generations. In many conditions with postnatal onset, the proportion of gene carriers who are affected varies with age. Thus, when describing penetrance, one has to specify age. For example, for disorders such as Huntington's disease or familial amyotrophic lateral sclerosis, which present later in life, the rate of penetrance is influenced by the age at which the clinical assessment is performed. *Imprinting* can also modify the penetrance of a disease. For example, in patients with Albright's hereditary osteodystrophy, mutations in the Gsα subunit (*GNAS1* gene) are expressed clinically only in individuals who inherit the mutation from their mother (Chap. 424).

***SEX-INFLUENCED PHENOTYPES*** Certain mutations affect males and females quite differently. In some instances, this is because the gene resides on the X or Y sex chromosomes (X-linked disorders and Y-linked disorders). As a result, the phenotype of mutated X-linked genes will be expressed fully in males but variably in heterozygous females, depending on the degree of X-inactivation and the function of the gene. For example, most heterozygous female carriers of factor VIII deficiency (hemophilia A) are asymptomatic because sufficient factor VIII is produced to prevent a defect in coagulation (Chap. 141). On the other hand, some females heterozygous for the X-linked lipid storage defect caused by α-galactosidase A deficiency (Fabry's disease) experience mild manifestations of painful neuropathy, as well as other features of the disease (Chap. 432e). Because only males have a Y chromosome, mutations in genes such as *SRY*, which causes male-to-female sex reversal, or *DAZ* (deleted in azoospermia), which causes abnormalities of spermatogenesis, are unique to males (Chap. 410).

Other diseases are expressed in a sex-limited manner because of the differential function of the gene product in males and females. Activating mutations in the luteinizing hormone receptor cause dominant male-limited precocious puberty in boys (Chap. 411). The phenotype is unique to males because activation of the receptor induces testosterone production in the testis, whereas it is functionally silent in the immature ovary. Biallelic inactivating mutations of the follicle-stimulating hormone (FSH) receptor cause primary ovarian failure in females because the follicles do not develop in the absence of FSH action. In contrast, affected males have a more subtle phenotype, because testosterone production is preserved (allowing sexual maturation) and spermatogenesis is only partially impaired (Chap. 411). In congenital adrenal hyperplasia, most commonly caused by 21-hydroxylase deficiency, cortisol production is impaired and ACTH stimulation of the adrenal gland leads to increased production of androgenic precursors (Chap. 406). In females, the increased androgen level causes ambiguous genitalia, which can be recognized at the time of birth. In males, the diagnosis may be made on the basis of adrenal insufficiency at birth, because the increased adrenal androgen level does not alter sexual differentiation, or later in childhood, because of the development of precocious puberty. Hemochromatosis is more common in males than in females, presumably because of differences in dietary iron intake and losses associated with menstruation and pregnancy in females (Chap. 428).

**Chromosomal Disorders** Chromosomal or cytogenetic disorders are caused by numerical or structural aberrations in chromosomes. For a detailed discussion of disorders of chromosome number and structure, see Chap. 83e. Deviations in chromosome number are common causes of abortions, developmental disorders, and malformations. *Contiguous gene syndromes* (e.g., large deletions affecting several genes) have been useful for identifying the location of new disease-causing genes. Because of the variable size of gene deletions in different patients, a systematic comparison of phenotypes and locations of deletion breakpoints allows positions of particular genes to be mapped within the critical genomic region.

**Monogenic Mendelian Disorders** Monogenic human diseases are frequently referred to as *Mendelian disorders* because they obey the principles of genetic transmission originally set forth in Gregor Mendel's classic work. The continuously updated OMIM catalogue lists several thousand of these disorders and provides information about the clinical phenotype, molecular basis, allelic variants, and pertinent animal models (Table 82-1). The mode of inheritance for a given phenotypic trait or disease is determined by pedigree analysis. All affected and unaffected individuals in the family are recorded in a pedigree using standard symbols (Fig. 82-11). The principles of allelic segregation, and the transmission of alleles from parents to children, are illustrated in Fig. 82-12. One dominant (A) allele and one recessive (a) allele can display three Mendelian modes of inheritance: autosomal dominant, autosomal recessive, and X-linked. About 65% of human monogenic disorders are autosomal dominant, 25% are autosomal recessive, and 5% are X-linked. Genetic testing is now available for many of these disorders and plays an increasingly important role in clinical medicine (Chap. 84).

***AUTOSOMAL DOMINANT DISORDERS*** These disorders assume particular relevance because mutations in a single allele are sufficient to cause the disease. In contrast to recessive disorders, in which disease pathogenesis is relatively straightforward because there is loss of gene function, dominant disorders can be caused by various disease mechanisms, many of which are unique to the function of the genetic pathway involved.

In autosomal dominant disorders, individuals are affected in successive generations; the disease does not occur in the offspring of unaffected individuals. Males and females are affected with equal frequency because the defective gene resides on one of the 22 autosomes (Fig. 82-13A). Autosomal dominant mutations alter one of the two alleles at a given locus. Because the alleles segregate randomly at meiosis, the probability that an offspring will be affected is 50%. Unless there is a new germline mutation, an affected individual has an affected parent. Children with a normal genotype do not transmit the disorder. Due to differences in penetrance or expressivity (see above), the