UNEQUAL CROSSING-OVER Normally, DNA recombination in germ cells occurs with remarkable fidelity to maintain the precise junction sites for the exchanged DNA sequences (Fig. 82-6). However, mispairing of homologous sequences leads to unequal crossover, with gene duplication on one of the chromosomes and gene deletion on the other chromosome. A significant fraction of growth hormone (*GH*) gene deletions, for example, involve unequal crossing-over (Chap. 402). The *GH* gene is a member of a large gene cluster that includes a GH variant gene as well as several structurally related chorionic somatomammotropin genes and pseudogenes (highly homologous but functionally inactive relatives of a normal gene). Because such gene clusters contain multiple homologous DNA sequences arranged in tandem, they are particularly prone to undergo recombination and, consequently, gene duplication or deletion. On the other hand, duplication of the *PMP22* gene because of unequal crossing-over results in increased gene dosage and type IA Charcot-Marie-Tooth disease. Unequal crossing-over resulting in deletion of *PMP22* causes a distinct neuropathy called *hereditary liability to pressure palsy* (Chap. 459).

Glucocorticoid-remediable aldosteronism (GRA) is caused by a gene fusion or rearrangement involving the genes that encode aldosterone synthase (*CYP11B2*) and steroid 11β-hydroxylase (*CYP11B1*), normally arranged in tandem on chromosome 8q. These two genes are 95% identical, predisposing to gene duplication and deletion by unequal crossing-over. The rearranged gene product contains the regulatory regions of 11β-hydroxylase fused to the coding sequence of aldosterone synthetase. Consequently, the latter enzyme is expressed in the adrenocorticotropic hormone (ACTH)–dependent zona fasciculata of the adrenal gland, resulting in overproduction of mineralocorticoids and hypertension (Chap. 406).

Gene conversion refers to a nonreciprocal exchange of homologous genetic information. It has been used to explain how an internal portion of a gene is replaced by a homologous segment copied from another allele or locus; these genetic alterations may range from a few nucleotides to a few thousand nucleotides. As a result of gene conversion, it is possible for short DNA segments of two chromosomes to be identical, even though these sequences are distinct in the parents. A practical consequence of this phenomenon is that nucleotide substitutions can occur during gene conversion between related genes, often altering the function of the gene. In disease states, gene conversion often involves intergenic exchange of DNA between a gene and a related pseudogene. For example, the 21-hydroxylase gene (*CYP21A2*) is adjacent to a nonfunctional pseudogene (*CYP21A1P*). Many of the nucleotide substitutions that are found in the *CYP21A2* gene in patients with congenital adrenal hyperplasia correspond to sequences that are present in the *CYP21A1P* pseudogene, suggesting gene conversion as one cause of mutagenesis. In addition, mitotic gene conversion has been suggested as a mechanism to explain revertant mosaicism in which an inherited mutation is "corrected" in certain cells. For example, patients with autosomal recessive generalized atrophic benign epidermolysis bullosa have acquired reverse mutations in one of the two mutated *COL17A1* alleles, leading to clinically unaffected patches of skin.

INSERTIONS AND DELETIONS Although many instances of insertions and deletions occur as a consequence of unequal crossing-over, there is also evidence for internal duplication, inversion, or deletion of DNA sequences. The fact that certain deletions or insertions appear to occur repeatedly as independent events indicates that specific regions within the DNA sequence predispose to these errors. For example, certain regions of the *DMD* gene, which encodes dystrophin, appear to be hot spots for deletions and result in muscular dystrophy (Chap. 462e). Some regions within the human genome are rearrangement hot spots and lead to CNVs.

ERRORS IN DNA REPAIR Because mutations caused by defects in DNA repair accumulate as somatic cells divide, these types of mutations are particularly important in the context of neoplastic disorders (Chap. 102e). Several genetic disorders involving DNA repair enzymes underscore their importance. Patients with xeroderma pigmentosum have defects in DNA damage recognition or in the nucleotide excision and repair pathway (Chap. 105). Exposed skin is dry and pigmented and is extraordinarily sensitive to the mutagenic effects of ultraviolet irradiation. More than 10 different genes have been shown to cause the different forms of xeroderma pigmentosum. This finding is consistent with the earlier classification of this disease into different complementation groups in which normal function is rescued by the fusion of cells derived from two different forms of xeroderma pigmentosum.

Ataxia telangiectasia causes large telangiectatic lesions of the face, cerebellar ataxia, immunologic defects, and hypersensitivity to ionizing radiation (Chap. 450). The discovery of the ataxia telangiectasia mutated (*ATM*) gene reveals that it is homologous to genes involved in DNA repair and control of cell cycle checkpoints. Mutations in the *ATM* gene give rise to defects in meiosis as well as increasing susceptibility to damage from ionizing radiation. Fanconi's anemia is also associated with an increased risk of multiple acquired genetic abnormalities. It is characterized by diverse congenital anomalies and a strong predisposition to develop aplastic anemia and acute myelogenous leukemia (Chap. 132). Cells from these patients are susceptible to chromosomal breaks caused by a defect in genetic recombination. At least 13 different complementation groups have been identified, and the loci and genes associated with Fanconi's anemia have been cloned. HNPCC (Lynch's syndrome) is characterized by autosomal dominant transmission of colon cancer, young age (<50 years) of presentation, predisposition to lesions in the proximal large bowel, and associated malignancies such as uterine cancer and ovarian cancer. HNPCC is predominantly caused by mutations in one of several different mismatch repair (MMR) genes including MutS homologue 2 (*MSH2*), MutL homologue 1 and 6 (*MLH1, MLH6*), *MSH6*, *PMS1*, and *PMS2* (Chap. 110). These proteins are involved in the detection of nucleotide mismatches and in the recognition of slipped-strand trinucleotide repeats. Germline mutations in these genes lead to microsatellite instability and a high mutation rate in colon cancer. Genetic screening tests for this disorder are now being used for families considered to be at risk (Chap. 84). Recognition of HNPCC allows early screening with colonoscopy and the implementation of prevention strategies using nonsteroidal anti-inflammatory drugs.

UNSTABLE DNA SEQUENCES *Trinucleotide repeats* may be unstable and expand beyond a critical number. Mechanistically, the expansion is thought to be caused by unequal recombination and slipped mispairing. A premutation represents a small increase in trinucleotide copy number. In subsequent generations, the expanded repeat may increase further in length and result in an increasingly severe phenotype, a process called *dynamic mutation* (see below for discussion of anticipation). Trinucleotide expansion was first recognized as a cause of the fragile X syndrome, one of the most common causes of intellectual disability. Other disorders arising from a similar mechanism include Huntington's disease (Chap. 448), X-linked spinobulbar muscular atrophy (Chap. 452), and myotonic dystrophy (Chap. 462e). Malignant cells are also characterized by genetic instability, indicating a breakdown in mechanisms that regulate DNA repair and the cell cycle.

Functional Consequences of Mutations Functionally, mutations can be broadly classified as gain-of-function and loss-of-function mutations. Gain-of-function mutations are typically dominant (e.g., they result in phenotypic alterations when a single allele is affected). Inactivating mutations are usually recessive, and an affected individual is homozygous or compound heterozygous (e.g., carrying two different mutant alleles of the same gene) for the disease-causing mutations. Alternatively, mutation in a single allele can result in *haploinsufficiency*, a situation in which one normal allele is not sufficient to maintain a normal phenotype. Haploinsufficiency is a commonly observed mechanism in diseases associated with mutations in transcription factors (Table 82-2). Remarkably, the clinical features among patients with an identical mutation in a transcription factor often vary significantly. One mechanism underlying this variability consists in the influence of modifying genes. Haploinsufficiency can also affect the expression of rate-limiting enzymes. For example, haploinsufficiency in enzymes involved in heme synthesis can cause porphyrias (Chap. 430).