TABLE 82-6 GENETIC APPROACHES FOR IDENTIFYING DISEASE GENES

Method	Indications and Advantages	Limitations
Linkage Studies		
Classical linkage analysis (parametric methods)	Analysis of monogenic traits	Difficult to collect large informative pedigrees
	Suitable for genome scan	Difficult to obtain sufficient statistical power for complex traits
	Control population not required	
	Useful for multifactorial disorders in isolated populations	
Allele-sharing methods (nonparametric methods)	Suitable for identification of susceptibility genes in polygenic and multifactorial disorders	Difficult to collect sufficient number of subjects
Affected sib and relative pair analyses	Suitable for genome scan	Difficult to obtain sufficient statistical power for complex traits
Sib pair analysis	Control population not required if allele frequencies are known	Reduced power compared to classical linkage, but not sensitive to specification of genetic mode
	Statistical power can be increased by including parents and relatives	
Association Studies		
Case-control studies	Suitable for identification of susceptibility genes in polygenic and multifactorial disorders	Requires large sample size and matched control population
Linkage disequilibrium	Suitable for testing specific allelic variants of known candidate loci	False-positive results in the absence of suitable control population
Transmission disequilibrium test (TDT)	Facilitated by HapMap data, making GWAS more feasible	Candidate gene approach does not permit detection of novel genes and pathways
Whole-genome association studies	Does not necessarily need relatives	Susceptibility genes can vary among different populations

Abbreviation: GWAS, genome-wide association study.

then assess whether certain marker alleles cosegregate with the disease. Markers that are closest to the disease gene are less likely to undergo recombination events and therefore receive a higher linkage score. Linkage is expressed as a lod (logarithm of odds) score—the ratio of the probability that the disease and marker loci are linked rather than unlinked. Lod scores of +3 (1000:1) are generally accepted as supporting linkage, whereas a score of −2 is consistent with the absence of linkage.

ALLELIC ASSOCIATION, LINKAGE DISEQUILIBRIUM, AND HAPLOTYPES *Allelic association* refers to a situation in which the frequency of an allele is significantly increased or decreased in individuals affected by a particular disease in comparison to controls. Linkage and association differ in several aspects. Genetic linkage is demonstrable in families or sibships. Association studies, on the other hand, compare a population of affected individuals with a control population. Association studies can be performed as case-control studies that include unrelated affected individuals and matched controls or as family-based studies that compare the frequencies of alleles transmitted or not transmitted to affected children.

Allelic association studies are particularly useful for identifying susceptibility genes in complex diseases. When alleles at two loci occur more frequently *in combination* than would be predicted (based on known allele frequencies and recombination fractions), they are said to be in *linkage disequilibrium*. Evidence for linkage disequilibrium can be helpful in mapping disease genes because it suggests that the two loci are tightly linked.

Detecting the genetic factors contributing to the pathogenesis of common complex disorders remains a great challenge. In many instances, these are low-penetrance alleles (e.g., variations that individually have a subtle effect on disease development, and they can only be identified by unbiased GWAS) (Catalog of Published Genome-Wide Association Studies; Table 82-1) **(Fig. 82-14)**. Most variants occur in noncoding or regulatory sequences but do not alter protein structure. The analysis of complex disorders is further complicated by ethnic differences in disease prevalence, differences in allele frequencies in known susceptibility genes among different populations, locus and allelic heterogeneity, gene-gene and gene-environment interactions, and the possibility of phenocopies. The data generated by the HapMap Project are greatly facilitating GWAS for the characterization of complex disorders. Adjacent SNPs are inherited together as blocks, and these blocks can be identified by genotyping selected marker SNPs, so-called *Tag SNPs*, thereby reducing cost and workload (Fig. 82-4). The availability of this information permits the characterization of a limited number of SNPs to identify the set of haplotypes present in an individual (e.g., in cases and controls). This, in turn, permits performing GWAS by searching for associations of certain haplotypes with a disease phenotype of interest, an essential step for unraveling the genetic factors contributing to complex disorders.

POPULATION GENETICS In population genetics, the focus changes from alterations in an individual's genome to the distribution pattern of different genotypes in the population. In a case where there are only two alleles, A and a, the frequency of the genotypes will be $p^2 + 2pq + q^2 = 1$, with p^2 corresponding to the frequency of AA, $2pq$ to the frequency of Aa, and q^2 to aa. When the frequency of an allele is known, the frequency of the genotype can be calculated. Alternatively, one can determine an allele frequency if the genotype frequency has been determined.

Allele frequencies vary among ethnic groups and geographic regions. For example, heterozygous mutations in the *CFTR* gene are relatively common in populations of European origin but are rare in the African population. Allele frequencies may vary because certain allelic variants confer a selective advantage. For example, heterozygotes for the sickle cell mutation, which is particularly common in West Africa, are more resistant to malarial infection because the erythrocytes of heterozygotes provide a less favorable environment for *Plasmodium* parasites. Although homozygosity for the sickle cell mutation is associated with severe anemia and sickle crises **(Chap. 127)**, heterozygotes have a higher probability of survival because of the reduced morbidity and mortality from malaria; this phenomenon has led to an increased frequency of the mutant allele. Recessive conditions are more prevalent in geographically isolated populations because of the more restricted gene pool.

APPROACH TO THE PATIENT: Inherited Disorders

For the practicing clinician, the family history remains an essential step in recognizing the possibility of a hereditary predisposition to disease. When taking the history, it is useful to draw a detailed