

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 is challenging. 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 466-1](#)) ([Fig. 466-16](#)). 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. Catalogues of human variation and genotype data (HapMap, International Genome Sample Resource) have greatly facilitated 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. 466-4](#)). 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