

Genetics & Anxiety

The genetic epidemiology of anxiety disorders has focused mostly on specific disorders such as obsessive-compulsive disorder (OCD) and panic disorder. Family, twin and segregation studies strongly suggest a genetic influence in these disorders, however, due to phenotypic and genetic heterogeneity specific genetic loci and genes have not been yet discovered. Linkage studies have renewed interest as they may provide clues to ‘private mutations’ that are family-specific which can be pursued with next-generation sequencing technologies (rare variant approach). Other methods include using chromosomal aberrations to localize putative loci and genes as well as exploration of disease-gene association with candidate genes which are attractive from a biological perspective. Recent genome-wide studies (GWAS) are used to detect genetic variants of modest effect but which are common in the population (common variant approach). Endophenotypes which may point to genetic candidate loci or variants can also be used to pursue genetic association to disease, by identifying a trait in unaffected relatives that is linked to disease. Epigenetic, alternative splicing, copy number repeat and micro-RNA mechanisms plausibly influence behavioral traits, but research in these areas is only emerging.