

Online encyclopedias and field synopses of genetic association studies in Alzheimer's and Parkinson's disease

Bertram, L.*

Head, Neuropsychiatric Genetics Group, Dept. of Vertebrate Genomics, Max-Planck Institute for Molecular Genetics, Berlin, Germany

Alzheimer's disease (AD) and Parkinson's disease (PD) are genetically complex and heterogeneous disorders. To date, a small number of genes have been pinpointed for both diseases causing predominantly early-onset forms with Mendelian inheritance. The majority of AD and PD cases, however, show no obvious familial aggregation and are likely governed by a variety of genetic and non-genetic factors that define an individual's risk. In the past decades, more than 2,000 papers have been published across both disorders claiming or refuting genetic association between hundreds of putative AD/PD genes and disease risk or other phenotypic variables. Similar to the situation in other genetically complex diseases, this wealth of information is becoming increasingly difficult to follow, evaluate, and most importantly to interpret. To alleviate this situation, we have recently created two online databases that serve as unbiased, continuously updated and publicly available encyclopedias of all AD or PD genetic association studies ("AlzGene": www.alzgene.org, and "PDGene": www.pdgene.org), including genome-wide association studies (GWAS). Data for both databases is collected following systematic searches of the scientific literature. For each eligible study, essential characteristics are summarized online, including study design, sample size and ethnicity of the investigated populations, as well as gene-specific results and genotyping details (e.g. genotype and allele frequencies). For all polymorphisms with genotype data available in at least four independent case-control samples, we routinely calculate meta-analyses based on allelic crude odds ratios from each study. All data and results, including those of over 400 up-to-date meta-analyses, can be retrieved online at the respective websites. In addition to separately highlighting loci containing at least one nominally significant polymorphism by meta-analysis ("Top Results"), there is extensive cross-linking to overlapping entries across both databases. At the symposium, I will discuss the most compelling results from each database, with a particular focus on loci showing significant associations across both disorders. In addition, I will outline the difficulties and pitfalls encountered when attempting to systematically curate and synthesize data from thousands of individual publications.