Three decades of genetic research in Alzheimer's disease (AD) have substantially broadened our understanding of the pathogenetic mechanisms leading to neurodegeneration and dementia. Positional cloning led to the identification of rare, disease-causing mutations in APP, PSEN1, and PSEN2 causing early-onset familial AD, followed by the discovery of APOE as the single most important risk factor for late-onset AD. Recent genome-wide association approaches have delivered several additional AD susceptibility loci (e.g. BIN1, CD33, CLU, CR1, PICALM) that are common in the general population, but exert only very small risk effects. As a result, a large proportion of the heritability of AD continues to remain unexplained by the currently known disease genes. It seems likely that much of this "missing heritability" may be accounted for by rare sequence variants, which owing to recent advances in high-throughput sequencing technologies can now be assessed in unprecedented detail. In this lecture, I will present a comprehensive overview of the current status of genetics research in AD, and will provide an outlook into what comes next in the field.