Genetic contributions to stroke range from classic Mendelian (a single gene leads to disease) to complex (multiple genes contribute to risk for disease in combination with other genetic and/or environmental factors). In addition to traditional candidate gene and linkage approaches to defining the genetic causes of stroke, technological advances in genotyping and the development of bioinformatics solutions for managing large-scale genetic and phenotypic datasets have made it feasible to perform genomewide association studies. Genomewide association studies are discovery-based and make no a priori assumptions about mechanism. Genomewide association studies permit detection of genetic variants that only modestly contribute to disease susceptibility. Clearly defined phenotypic criteria, standardized data collection, and rigorous data management are essential to gene discovery in stroke. Large sample size requirements will require collaborative research. It is hoped that in the future, identification of genetic factors will allow development of tools for the early detection and treatment of stroke.

KEY WORD: genetics

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