Intervention of next-generation sequencing in diagnosis of Alzheimer's disease: challenges and future prospects

Abstract

Clinical diagnosis of several neurodegenerative disorders based on clinical phenotype is challenging due to its heterogeneous nature and overlapping disease manifestations. Therefore, the identification of underlying genetic mechanisms is of paramount importance for better diagnosis and therapeutic regimens. With the emergence of next-generation sequencing, it becomes easier to identify all gene variants in the genome simultaneously, with a system-wide and unbiased approach. Presently various bioinformatics databases are maintained on discovered gene variants and phenotypic indications are available online. Since individuals are unique in their genome, evaluation based on their genetic makeup helps evolve the diagnosis, counselling, and treatment process at the personal level. This article aims to briefly summarize the utilization of next-generation sequencing in deciphering the genetic causes of Alzheimer's disease and address the limitations of whole genome and exome sequencing.

Keywords: Alzheimer Disease; Exome Sequencing; High-Throughput Nucleotide Sequencing; Neurodegenerative Diseases; Whole Genome Sequencing.

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