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Review

Neurogenomics of Alzheimer's disease (AD): An Asian population review

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ABSTRACT

Alzheimer's disease (AD) is on the rise worldwide. Generally, AD is considered neurodegenerative when the production and clearance of amyloid-β (Aβ) are imbalanced. Recent research on genome-wide association studies (GWAS) has been explosive; GWAS indicates a relationship between single nucleotide polymorphism (SNP) and AD. GWAS also reveals ethnic differences between Caucasians and Asians. This indicates that pathogenesis between ethnic groups is distinct. According to current scientific knowledge, AD is a disease with a complex pathogenesis that includes impaired neuronal cholesterol regulation, immunity regulation, neurotransmitters regulation, Aβ clearance, Aβ production, and vascular regulation. Here, we demonstrate the pathogenesis of AD in an Asian population and the SNP risk of AD for future AD screening before onset. According to our knowledge, this is the first review of Alzheimer's disease to demonstrate the pathogenesis of AD based on SNP in an Asian population.

Introduction

Alzheimer's disease (AD) are neurodegenerative disease with complex pathologies. AD and other dementias increased by 147.95% worldwide between 1990 and 2019 [1]. Neurodegenerative diseases have extremely complex etiologies, and considered genetic susceptibility makes individuals susceptible to these diseases [2]. Although genetics play a significant role, lifestyle modifications can prevent neurodegenerative disorders [3]. The increasing prevalence of AD necessitates an early examination, as it is closely linked to genetics, to prevent this neurodegenerative disease.

The genome is the repository of information for an organism, containing millions or billions of information, whereas genetics is a component of DNA or DNA segments from the genome [4]. A genome-wide association study GWAS was conducted to determine the relationship between genetics and phenotype. This method typically analyses SNP and tests on hundreds of thousands of genetic variants across many genomes to identify statistically specific associations between a trait or disease [5].

The explosive study of GWAS recently has made a new theory in the pathogenesis of AD. GWAS on Caucasians and Asians produces different results. For example, the SNP BIN1 rs7561528 allele Aβ is protective against AD in Asians but not in Caucasians [6]. Another example is SNP rs689021 of SORL1 allele A, which has a protective function in Caucasians but not Asians [7]. This observation suggests variations in pathogenesis between individuals of Caucasian and Asian descent. Our aim is to perform a thorough analysis of GWAS in order to investigate the potential risk of developing AD in the Asian population, as well as to explore the comprehensive pathogenesis of this condition. The genetic SNP associated with Alzheimer's Disease was derived from clinical research on individuals of Asian descent. Nonetheless, the underlying mechanism of this SNP is based on pre-clinical trials, as outlined in this review.

1. Search strategy and selection criteria

The sources cited in this review were obtained through comprehensive searches of various academic databases, including PubMed, Google Scholar, and Semantic Scholar, and by examining the reference lists of pertinent articles. Temporal constraints do not limit the search strategy employed. The study employed specific search terms, including "Alzheimer," "single nucleotide polymorphism," "SNP," "Asian,", "Caucasian," [gene of interest] such as "BIN1," and [mechanism of interest] such as "immunity." Limitations were imposed on the use of the English language. The final compilation of references was produced based on their pertinence to the subjects discussed in this credible review.

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