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Review

Genomic profile of Parkinson's disease in Asians

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ABSTRACT

Parkinson's Disease (PD) has witnessed an alarming rise in prevalence, highlighting the suboptimal nature of early diagnostic and therapeutic strategies. To address this issue, genetic testing has emerged as a potential avenue. In this comprehensive review, we have meticulously summarized the variants associated with PD in Asian populations. Our review reveals that these variants exert their influence on diverse biological pathways, encompassing the autophagy-lysosome pathway, cholesterol metabolism, circadian rhythm regulation, immune system response, and synaptic function. Conventionally, PD has been linked to other diseases; however, our findings shed light on a shared genetic susceptibility among these conditions, implying an underlying pathophysiological mechanism that unifies them. Moreover, it is noteworthy that these PD-associated variants can significantly impact drug responses during therapeutic interventions. This review not only provides a consolidated overview of the genetic variants associated with PD in Asian populations but also contributes novel insights into the intricate relationships between PD and other diseases by elucidating shared genetic components. These findings underscore the importance of personalized approaches in diagnosing and treating PD based on individual genetic profiles to optimize patient outcomes.

1. Introduction

In recent years, Asian countries, particularly Korea, have observed a concerning increase in the prevalence of Parkinson's disease (PD) among individuals under the age of 50. As per data from 2010, the incidence rate for this age group was recorded as 1.2 cases per 100,000 individuals. By 2015, this rate had risen to 1.7 cases per 100,000 individuals [1]. The increasing frequency and widespread occurrence of PD highlight a pressing demand for the development of biomarkers that can be utilized in both prevention and therapy.

PD has been associated with various conditions such as hypertension or hypotension, type-2 diabetes (T2DM), constipation, depression, epilepsy and hearing loss [2]. This suggests a shared pathophysiology between PD and other diseases; however current research has yet to fully explore these connections.

Pharmacogenetics has received increasing attention in recent years due to its potential in personalizing medical treatments. Genetic variants can influence an individual's response to drugs by either enhancing or diminishing their effects [3]. Therefore, detecting these variants through genome wide association study (GWAS) and other approach is valuable for both prevention and treatment as it can predict future risk of Parkinson's disease and related disease while also informing more effective therapeutic strategies.

In recent literature, comprehensive analyses have been conducted on the molecular genetics of PD, yet there remains a gap in the focus on Asian populations [4]. This review aims to bridge this gap by providing a detailed examination of genetic variations associated with PD within Asian demographics. The significance of ethnic-specific genetic variants is well-documented, as evidenced by the differing risk and protective profiles observed between Asian and Caucasian populations in stroke review [5]. Our review extends beyond a mere cataloging of these variations; it delves into exploring potential interconnections between these genetic factors and other disorders, reflecting on the shared pathophysiological underpinnings that PD may have with various diseases. A critical aspect of our study is the investigation into the influence of PD-specific genetic variants on pharmacological outcomes. This area, particularly in relation to the Asian population, has not been extensively explored in existing scientific discourse and represents a frontier for potential breakthroughs in personalized medicine for PD.

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