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# Role of Genetic Factors in the Cause of Alzheimer's Disease: Literature Review

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**Annotation:** Alzheimer's disease (AD) is a chronic, progressive neurological disorder that primarily affects older adults, accounts for 1 to 5% of all cases, and is the leading cause of death worldwide, with a dominant familial or autosomal presentation. It accounts for 1 to 5% of all cases and is the leading cause of death worldwide. This review discusses the current understanding of the relationship between genetically related and environmental influences closely associated with the development of neurodegeneration, as well as the pathophysiology of AD, which is the pathological accumulation of multifactorial etiology, significantly contributing to the development of genetic and non-genetic factors. The alteration of pathologic amyloid-beta (Aβ) plaques and neurofibrillary tangles leads to extensive neuronal damage, greatly compromising daily functioning and quality of life, which causes dementia in older persons. It has complex symptoms and influences the development of both affective factors. Genetic factors account for approximately 60-80% of AD risk, with specific genes such

as apolipoprotein E (APOE), amyloid precursor protein (APP), presenilin 1 (PSEN1), and presenilin 2 (PSEN2) being crucial in both early- and late-onset forms of the disease. Early biomarkers are necessary to advance diagnostic methods and identify effective therapeutic targets for AD.

**Keywords:** epigenetic, genetic, dementia, GWAS, neuropathology.

## INTRODUCTION

Alzheimer's disease (AD) is a neurological disease that causes considerable brain cell death, resulting in loss of memory, cognitive decline, and dementia. Hyperphosphorylated tau protein is present in neurons, and extracellular plaques are composed of accumulated β-amyloid (*Aβ*). Neurofibrillary tangles (NFTs) are the pathological etiology of AD, present in tissue that has progressively fewer nerve cells and connections due to a shrinking of the total brain size. It affects an estimated fifty million people worldwide, with 60–80% of dementia diagnostic cases rising life expectancy rates, and it is expected to affect 139 million people globally by 2050, with major socioeconomic and healthcare system impacts (Nwadiugwu *et al*., 2023). Alois Alzheimer, a German physician, characterized AD as a complicated neurological disorder with progressive and long-term characteristics. The primary cause of AD is a reduction in acetylcholine levels in the brain, which is common in Alzheimer's patients, as well as nerve degeneration, particularly of cholinergic nerves (Kabra and Ramteke, 2021; Arjmand *et al*., 2024). Multifactorial, advanced, and irretrievable neurological brain disease (NBD), specifically the most frequent dementia and pathogenic AD, with neuroinflammation and vascular alterations, begins many years before any symptoms appear (Wang *et al*., 2025). Alzheimer's disease is a progressive neurological ailment that usually affects older persons. It is marked by persistent memory loss, cognitive impairment, and deficiencies in areas such as language and executive function, which eventually lead to a deterioration in personal autonomy. The illness is characterized by an excessive buildup of proteins in the brain, amyloid-β (*Aβ*) plaques and tangle formation damage and putting to death neurons, first affecting memory centers and later causing widespread brain atrophy (Chen *et al*., 2023). Neuropathological examination for clinical symptoms of AD reveals significant overlap with multiple other NBDs and provides a clear diagnosis of AD after brain autopsy (Alzheimer's Disease International, 2019). Care for AD and AD-related dementias (ADRD) comes at a crippling cost; it was estimated in 2024, in the United States (US), to be about $360 million, and globally, costs in 2019 were over USD 1313.4 billion (Gaugler *et al*., 2022). The result of AD and its various forms of dementia, conditions, and their complications account for 15% of the most common causes of death each year. It is a worrying statistic suggesting that approximately 1.1 million females die each year (Li *et al*., 2022; Andrade *et al*., 2023).

The cognitive manifestations of AD primarily arise from two neuropathological processes: the accumulation of extracellular *Aβ* plaques and aggregation of intracellular hyperphosphorylated tau into neurofibrillary tangles (NFTs) (Hardy & Selkoe, 2002; Bloom, 2014). In addition to advanced age, several factors, including lifestyle, family history, and genetic polymorphisms, contribute to AD pathogenesis (Scheltens *et al*., 2021). Alzheimer's disease accounts for as high as 82% of cases of heritability estimates (Gatz *et al*., 2006). Sporadic Alzheimer's disease (SAD) accounts for approximately 95% of cases after the age of 65, in contrast to early-ons*et al*zheimer's disease (EOAD) and represents about 10% of all cases of manifests before age 65 that associated with a

strong hereditary component, approaching 100% in some instances (World Health Organization [WHO], 2022; Van der Flier & Scheltens, 2005). Clinically and pathologically, EOAD and late-onset alzheimer's disease (LOAD) are largely indistinguishable, with both familial and sporadic forms reported (Honig *et al*., 2018; Masurkar *et al*., 2024). Among EOAD patients, 35–60% report a positive family history of dementia, with 10–15% linked to autosomal dominant inheritance across at least three generations (Honig *et al*., 2018). Pathogenic variants in the *APP*, *PSEN1*, and *PSEN2* genes have been identified as causal mutations in EOAD families, all of which encode critical proteins in the *Aβ* production pathway (Bird, 2008; De Strooper & Karran, 2016). Furthermore, the presence of the *APOE* ε4 allele, in either heterozygous or homozygous form, significantly increases familial risk in EOAD patients (López-Cerdán *et al*., 2024).

The amyloid-β hypothesis, which has been explored in AD research for more than 25 years, proposes that the accumulation of *Aβ* plaques in the brain serves as a primary pathogenic trigger. This hypothesis is supported by the identification of disease-causing defect mutations in three major AD-related genes: *APP*, *PSEN1*, and *PSEN2*, as well as evidence that *Aβ* aggregation induces localized oxidative stress within membrane microdomains (Alzheimer's Association, 2023). According to this framework, *Aβ* deposition initiates a cascade of pathological processes, including tau hyperphosphorylation and tangle formation, neuroinflammation, and synaptic dysfunction. However, the presence of *Aβ* plaques in cognitively normal older adults, as well as the absence of detectable *Aβ* in certain patients with clinically confirmed AD, has generated significant controversy. Cases of suspected non-*Aβ* AD, characterized by the presence of *Aβ* biomarkers in cerebrospinal fluid or the absence of *Aβ* deposition on positron emission tomography (PET) imaging, provide evidence that alternative pathological mechanisms may contribute to AD independently of the *Aβ* cascade (Serrano-Pozo *et al*., 2019). Moreover, mutations in non-*Aβ* pathways have been linked to only 5-10% of early-onset AD (EOAD) cases, suggesting that multiple mechanisms beyond *Aβ* pathology are involved in disease onset and progression (Andrade *et al*., 2023; Nicolas *et al*., 2024).

The early-onset AD appears to be determined by genetic factors; 95% of all cases may result from a combination of risk and environmental influences (Bourquard *et al*., 2023). *FAD* and *LOAD* are the two main types of AD. The genetic mutations in the *FAD*, *APP*, *PSEN1*, *PSEN2*, and *LOAD* genes have different effects. The *FAD* gene mutations are relatively rare and typically occur before the age of 65, while mutations in the *PSEN2* gene are an even rarer cause of AD. The *APP* gene was an abnormal *Aβ* protein that causes Alzheimer's pathology. Concordance studies between parents and offspring, as well as between siblings, revealed an offspring concordance of less than 10% and a sibling concordance of 21.6% (Hoogmartens *et al*., 2021). Alzheimer's disease is caused exclusively by fully penetrant autosomal dominant alleles; the concordance rate between parent and offspring is approximately 50%, indicating that other genes, pathways, and inheritance patterns are involved. Although at least one disease-modifying therapy is currently accessible, treatments that break or reverse the disease remain elusive (Budd *et al*., 2022; Van der *et al*., 2023). This review aims to investigate the genetic and clinical factors that may impact AD development and be used for gene therapy strategies based on various genetic profiles.

## Factors Affecting Alzheimer's Disease

### 1. Demographic and Physiological Factors

Alzheimer's disease was developed and increased by several demographic and physiological factors, suggesting the risk of it, including advanced age, sex, race, and lifestyle activities such as diet, smoking, and alcohol consumption. Age remains the strongest predictor of AD, with prevalence estimated at 5–10% among individuals aged 60–69 years, rising to more than 25% in those over 70 years in developed countries. There were an estimated 200,000 cases before the age of 65, about 3.7% of all dementia diagnoses in the United States, approximately 5.4 million (Gustavsson *et al*., 2023). Among patients diagnosed after age 65, about 11% have AD, with prevalence markedly increasing with advancing age: 32% of cases occur in individuals older than

85, and 81% of those aged 75 years and above (Gustavsson *et al*., 2023). These findings underscore the steep age-related progression of AD, with incidence rates peaking in the mid-ninth decade of life (Nwadiugwu *et al*., 2023).

Sex variations affect various aspects of AD, especially in females, 32% of sex-related differences in all AD patients, with evident patterns of disease appearance and the rates of cognitive decline and brain atrophy, including brain aging, metabolic dysfunction, and gene expression (Shokouhi *et al*., 2020). The involvement of the sex factor role and relationship with sex hormones was a vital variable in disease heterogeneity. The development targeted therapeutic interventions, as fluctuations in ovarian sex hormones, particularly estrogens, were linked to mitochondrial dysfunction in AD and may be a potential therapeutic target through estrogen receptors, which play a role in glucose metabolism during perimenopause and may provide insights into sex-specific AD pathophysiology (Mishra *et al*., 2025). The female sex factor is a risk factor and accounts for all diagnosed cases of AD, especially in individuals aged 60-70% in the eighth or ninth decade. The accumulation of β-amyloid plaques is quantitatively higher in females, who exhibit a higher percentage of tau protein accumulation, a pathological trait of AD progression, than males.

The origin of ethnocracies is also recorded as a significant risk factor for AD, ranging from 3.5% to 14.4% of total dementia cases based on racial and ethnic backgrounds in the US, and rates are influenced by factors such as race, age, comorbidities, and related diseases (Scheltens *et al*., 2021). In addition, nutritional deficiencies, particularly of folates and vitamins B12, B1, and B3, have a complex role in the evolution of AD disease. A combination of oxidative stress with malnutrition and homocysteine-related vitamins can synergistically increase a patient's risk of developing AD (Mertaş & Boşgelmez, 2025); refer to Figure 1.

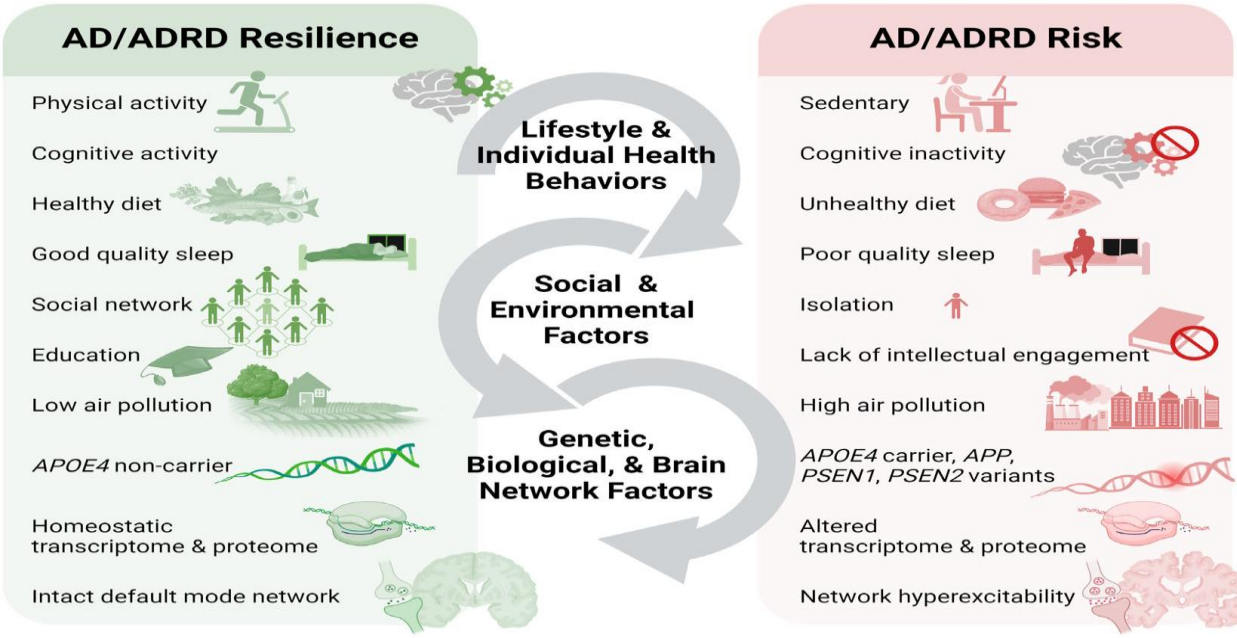


**Figure 1:** Alzheimer's disease factors and dementias [Color figure can be viewed at www.annalsofneurology.org].

Other lifestyle factors that influence cholinergic deficiencies in the brain include reduced nicotinic acetylcholine receptors. Smoking, on the other hand, causes an increase in nicotinic receptor expression and improves cholinergic metabolic function. In addition to genetic predispositions, the presence of epigenetic factors; the effect of environmental conditions such as harmful substances like aluminum, solvents, pesticides, heavy metals, organic solvents, and organophosphorus pesticides; and the effect of the release of nicotine, increases in nicotinic receptors, and high emission of oxidative stress and free radicals to alter inflammatory immunological responses, phagocyte activation, and increases in oxidative and degenerative effects (Safiri *et al*., 2024).

Heavy metals such as aluminium, mercury, zinc, copper, cadmium, magnesium, and manganese hurt the central nervous system (CNS), leading to neurodegeneration. Additionally, the combination of these metals might disrupt cellular homeostasis and initiate an amyloidogenic cascade with fluctuations (Twarowski & Herbet, 2023). These factors may be a reduction in intraneuronal connections and a limited cognitive reserve, which are critical in mitigating the onset and progression of neurodegenerative diseases (Fu and Nancy, 2023; Saragea, 2024).

## 2. Alzheimer's Disease Comorbidities

Obesity, diabetes mellitus type 2, dyslipidemia, hypercholesterolemia, hypertension, and a history of traumatic brain injury were considerably more prevalent comorbidities related to Alzheimer's disease. Obesity is correlated directly with body mass index (BMI) and increases the risk of neurodegenerative processes; it is also a modifiable risk factor for AD, associated with higher rates of neuronal apoptosis and necrosis within the CNS.

The metabolic alterations caused by weight increase and decreased neuroplasticity (Gęborys *et al*., 2025). Variations in glycemic levels and insulin, an essential neuromodulator, significantly influence the relationship between AD and type 2 diabetes mellitus. Diabetics may develop extracellular neurotic plaques and intracellular neurofibrillary tangles due to the cell-surface receptor for advanced glycation end products (RAGE) interacting with *Aβ* peptides. Furthermore, excess adipocytes can exacerbate this process by producing pro-inflammatory cytokines and adipokines, rendering the likelihood of AD development in diabetic individuals twice that of non-diabetics. Insulin resistance, hyperinsulinemia, and hyperglycemia, along with leptin, adiponectin, and interleukin-6 (IL-6). Tumor necrosis factor-alpha (TNF-α) has been shown to potentiate the formation of *Aβ* plaques, particularly in patients with type 2 diabetes who are homozygous or heterozygous for the ε4 risk allele. High insulin levels may impair *Aβ* peptide clearance by competing with insulin-degrading enzymes (IDE), thereby contributing to the onset of Alzheimer's disease (Scheltens *et al*., 2021).

Genetic variants were associated with strong, rare mutations that clarify pathogenic pathways, therapeutic risk, and resilience in the development of AD/ADRD. A family history of FOAD and LOAD is associated with an increased risk of AD heritability, with EOAD being 90-100% heritable and LOAD being 60-80% heritable, as well as connections with specific genetic variations in some cases of inheritance (Hussain *et al*., 2023). Traumatic brain injuries (craniocerebral trauma) disrupt the blood–brain barrier, exposing normal brain antigens and depleting plasma proteins, which in turn alter immune responses. As part of the acute phase reaction to neuronal damage, trauma increases the expression of the *APP* gene. Infections such as meningitis, encephalitis, tuberculosis, neuroborreliosis, parasitosis, and meningoencephalitis are usually considered exclusion criteria when differentiating AD. However, recent studies suggest a link between herpes simplex virus (HSV) and AD. Antibodies against viral antigens can accumulate in the cerebrospinal fluid (CSF). Abnormal tau protein aggregates and infectious agents such as HSV or slow viruses may contribute to the onset of AD. In response to infection, the immune system activates reactive astrocytes and pericytes, which stimulate amyloid deposition. Interestingly, this process may temporarily improve cognitive function and senile plaque formation (Gao *et al*., 2022).

Environmental factors play a crucial role in the etiology of AD, inducing both early and late stages of disease progression. Interactions between environmental exposures and genetic predispositions can accelerate disease onset, with estimates suggesting that such factors contribute to 20–40% of heritable risk in late-LOAD, where overall heritability ranges from 60% to 80% (Burrai *et al*., 2022). A variety of non-genetic environmental exposures have been implicated in the development of dementia and AD pathology, including occupational contact with aluminum, pesticides, and organic solvents; chronic alcoholism and nicotine dependence; toxic exposures such as chronic intoxication or carbon monoxide poisoning; heavy metal accumulation; infectious agents; and comorbid medical conditions (Burrai *et al*., 2022).

On a neuropathological level, environmental risk factors may contribute to the formation of neurofibrillary tangles, metabolic dysfunctions, and alterations in apolipoprotein E4 expression. They also disrupt neurotransmitter systems, particularly noradrenaline, dopamine, and serotonin, as well as impair mitochondrial function, which is central to oxidative phosphorylation and cellular energy metabolism (Galluzzi *et al*., 2022). Such mitochondrial dysfunction and neurotransmitter imbalance exacerbate neurodegenerative processes characteristic of AD. Collectively, these findings highlight the substantial impact of environmental risk factors on AD pathophysiology (Masurkar *et al*., 2024). Figure 2 provides a schematic overview of genes implicated in the neuropathological mechanisms underlying AD.

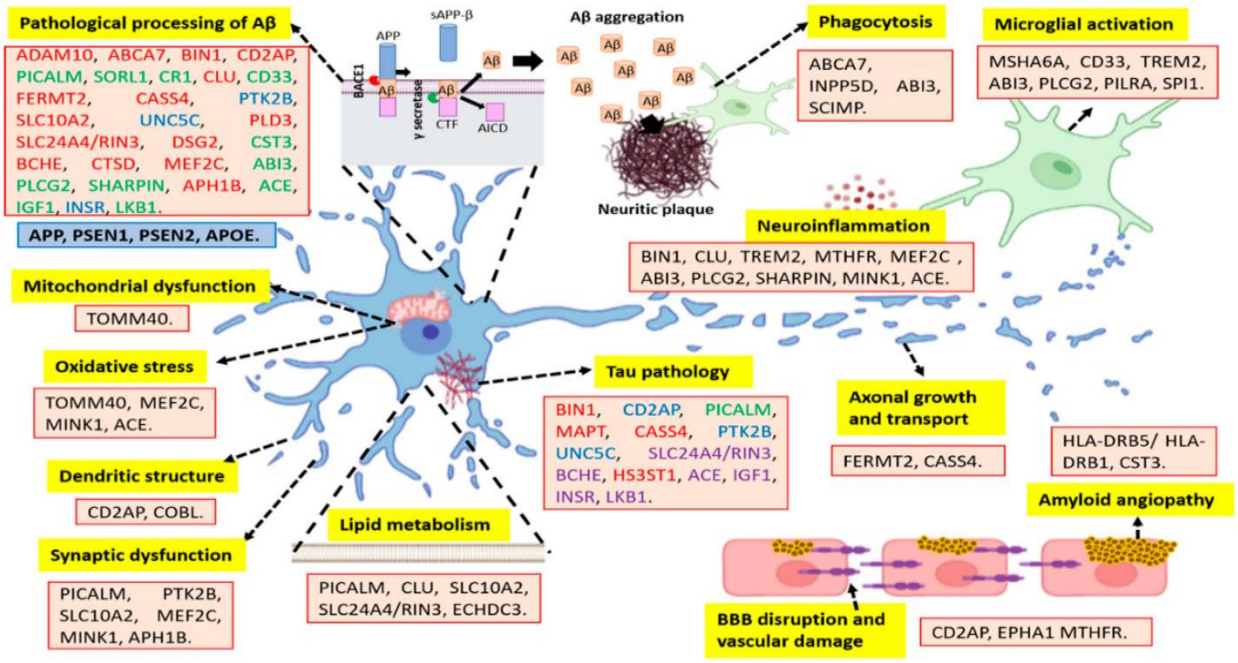


**Figure 2**: Schematic diagram of neuropathological mechanisms and gene associations with AD. This figure was created with biorender.com (Andrade *et al*., 2023).

## 3. Genetic and Epigenetic Risk Factors

Alzheimer's disease is characterized by a multifaceted and extensive etiology influenced by both genetic and epigenetic modifications. Environmental factors, including epigenetic alterations of genetic material such as DNA methylation and histone modification, play a crucial role in AD development. Early-onset AD is linked to mutations in *APP*, *PSEN1*, and *PSEN2*, accounting for 1-5% of cases, and the various polymorphisms in genes like CYP46, BACE1, and UBQLN1 have been associated with AD development (Saragea, 2024). The modification of post-transcription of non-coding RNA and protein-coding RNA is associated with gene expression and RNA sequencing in both non-coding and genes altered in AD risk (Wainberg *et al*., 2023). Brain tissue has identified altered transcripts associated with RNA-seq differentially vulnerable brain regions by tau pathology, including the less vulnerable occipital cortex and the more vulnerable precuneus (Guennewig *et al*., 2021; Holstege *et al*., 2022).

Genetic mutations on chromosomes 1, 14, 19, and 21 are important, with many cases resulting in an autosomal-dominant inheritance pattern and associated with monogenic transmission. Traumatic brain injuries, cerebrovascular amyloidosis, and vascular diseases are also recognized as contributing factors in mixed dementia cases. Genetic analysis techniques are essential for understanding biological mechanisms, identifying risk factors, and potential therapeutic targets associated with AD. The relationship between genetic risk and SAD is complex, as variants do not directly cause the condition, and personal risk perception may be subject to misinterpretation. Genetic risk factors, such as those identified through GWAS, APOE, APP, PSEN-1, and PSEN-2 genes, play a critical role in genetic counselling and testing for inherited neurodegenerative

diseases and dementia (Ranson *et al*., 2021). Genetic studies demonstrated the role in AD pathogenesis.

The initial group of early-onset genes, APP, PSEN1, and PSEN2, are genetically associated with the disease. The APP is responsible for producing the APP, which is an integral membrane protein. This protein is commonly found in various tissues, especially in synapses, and is located on chromosome 21. Missense mutations occur at a frequency at least four times more than APP genomic duplications and develop symptoms between 45 and 60 years in AD patients (Rolf *et al*., 2021). Amyloid precursor protein, an essential membrane protein, is being dissociated into *Aβ* peptides. Neurons, endothelial cells, and platelets produce the three primary splice variants of the APP gene: APP695, APP751, and APP770. Analysis of EOAD: 10% of all AD patients (Öztan and İşsever, 2023).

The apolipoprotein E (APOE) gene is a main genetic risk factor for late-onset AD (LOAD) and significantly increases amyloid plaque accumulation in the brains of AD patients. The APOE is a lipoprotein that facilitates the repair and remodeling of the cell membrane, and variants with amino acids at positions 112 and 158 produce 3 main alleles (Martens *et al*., 2022; Brase *et al*., 2023). The APOE protein plays a significant role in metabolism by breaking down *Aβ* and preventing plaque formation. The APOE protein in humans has three different amino acid substitutions that influence the risk of carriers developing the disease status. The APOE is a polymorphic amino-acid glycoprotein with a molecular mass of 34,200 Da, and it is essential for the body's processing of cholesterol transport and triglyceride lipid metabolism through the bloodstream, instructs the formation of apolipoprotein E, and forms lipoproteins. The APOE1 gene has three alleles, including APOE2, APOE3, and APOE4, present at one gene locus in humans, such as ε2, ε3, and ε4, whose relative frequencies in the world population were approximately 7%, 78%, and 14%, respectively, and the major genetic risk factor for both late-onset and SAD (Chen *et al*., 2022).

According to Öztan and Halim (2023), the APOE e2 allele can delay the onset of AD and minimize neuropathological changes associated with aging. The ε2 allele may offer protective effects and provide instructions for producing a protein called APOE (Kamboh, 2022; Saragea, 2024). The apolipoprotein E e4 allele (APOE e4) represents the predominant genetic risk factor for AD, with GWAS accounting for approximately 23.52% of all AD inheritance, compared to less than 1% contributed by the majority of other genetic risk mechanisms related to APOE e4 and increased risk of developing AD due to *Aβ* aggregation. It is associated with lipid metabolism, temporal lobe atrophy, and altered cerebral blood flow (CBF). The gene polymorphism of the APOE-ϵ4 allele is a risk factor for sporadic AD (SAD) and is characterized by a twelvefold increase in the general population with the common genotype (homozygous). It shows symptoms of AD well before the age of 65 and is affected by the number of alleles present (Bennett *et al*., 2025). The presence of one APOE ϵ4 allele increases the chance of developing AD threefold compared with the ϵ3/ϵ3 individuals' genotype (Van der Ende *et al*., 2023). The PSEN2 gene is located on chromosome 1 and consists of twelve exons grouped into ten translated exons that encode a peptide having 448 amino acids. A mutation related to PSEN2 increases the ratio between two types of *Aβ* proteins, specifically *Aβ*42 and *Aβ*40 (Oikawa and Walter, 2019; Bennett *et al*., 2025).

Transcriptomics for both RNA non-coding and RNA protein-coding have associations with AD risk. MicroRNAs (miRNAs), noncoding RNAs that regulate and modulate gene expression, are implicated in AD risk and include miR-129-5p, miR-132-5p, and miR-138-5p, with target genes that include functions involved in synaptic transmission (GABRB1), immune response (HCFC2), and AD-associated methylation (SLC16A3). In addition, miRNA expression can be modified by methylation, and miRNAs are differentially methylated in the temporal cortex of AD patients (Cochran *et al*., 2023). Long non-coding RNA (lncRNA) can modify gene expression and inflammation in AD to influence both proinflammatory and anti-inflammatory gene expression in brain tissue and blood samples (Nikolac *et al*., 2021; Dey *et al*., 2024).

Proteomics analyses have identified some protein changes associated with AD risk, including genetic risk contributions, environmental factors, correlations to pathology severity, and vulnerable brain regions (Askenazi *et al*., 2023). Protein changes in brain tissue from APOE ε4 AD patients are associated with the matrisome, which consists of the extracellular matrix. Proteins that interact with hyperphosphorylated tau in AD brain tissue are associated with RNA processing in APOE ε3 patients and with the synaptic compartment and cellular transport in APOE ε4 patients (Thierry *et al*., 2024). In ADAD patients, protein changes in CSF paralleled those in SAD. Genetic regulation by protein quantitative trait loci analyses that included APOE, CD33, and GRN in AD, as well as MMP10 in preclinical AD (Wainberg *et al*., 2023).

## DISCUSSIONS

This literature review of AD as a neurodegenerative syndrome is defined by amyloid β and tau pathology that cause dementia. Genetic, lifestyle, and environmental factors all contribute to determining AD risk and susceptibility, according to Karachanak *et al*. (2023). It indicates that controlling these factors could delay up to 40% of cases. It suggests that addressing these issues could delay up to 40% of instances. Although the disease has permanent characteristics, and failure occurs at variable rates, current research suggests that around one-third of dementia cases may be preventable or delayed in onset. This can be accomplished by identifying and managing modifiable risk factors, monitoring the oncogene population, comparing with genetic and non-genetic factors, and preventing neurodegeneration (Mazzarino *et al*., 2024). The documentation of specific genes related to AD has improved prospects of developing effective pharmacological treatments of the disease due to advances in genetic technology that facilitate understanding of the function of genes and integration of chronic diseases with complex pathogenesis, such as AD, through genetic testing and gene-targeted therapies in the future. As genetic research continues to evolve, it emphasises the importance of multi-omics approaches, incorporating genomic, transcriptomic, and proteomic data, to provide a comprehensive understanding of AD (Colijn & Ismail, 2024). The integration of genetic risk estimates to increase the evidence base and facilitate the development of more inclusive clinical studies and research communities. a) Genetic counseling is an essential element of AD management. B) Personalized medicine involves customizing treatment based on an individual's unique genetic AD profile; however, genetic testing for AD susceptibility is not currently recommended in clinical settings. Focus on personalized risk reduction is under development. Genomic biomarkers, which include genetic variants, can be used to diagnose or predict the risk of AD. C) Genetic epistasis refers to the interplay of many genetic variants that contribute to AD risk (Kamaljeet and Lovekesh, 2024). Biomarker analysis allows for earlier detection and intervention. The National Institute on aging and AD's Disease Association are working with modified diagnostic criteria to include biomarker data analysis, which will improve early diagnosis and allow for earlier detection and intervention using breakthrough neuroimaging techniques (MRI, PET).

## CONCLUSIONS

Alzheimer's disease is an advanced and irreversible neurological disease that is becoming more prevalent as the population ages and modifiable pathogenic risk factors increase. The accumulation of *Aβ* plaques and tau protein tangles can affect brain transmission and homeostasis. Research understanding the formative causes of AD, as well as the development of new therapeutics, is critical to improving patient outcomes. The interaction of genetic and environmental factors contributes to the risk of AD. Advanced genetic research techniques, such as GWAS and next-generation sequencing (NGS), are vital for determining the genetic foundations of the disease. Recent advances in multi-omics approaches, combined with datasets derived from both human AD samples and animal models, provide a valuable framework for investigating sex-specific molecular mechanisms and pathway alterations (meta-analyses of gene expression profiles in human AD patients have highlighted distinct patterns that may inform targeted therapeutic strategies). The current care of AD primarily relies on pharmacological approaches that provide symptomatic relief but fail to alter the underlying disease trajectory.

Novel therapeutic avenues under investigation include amyloid-β and tau-directed therapies, gene-based therapies, and immunotherapies. Given the complex and multifaceted nature of AD, a comprehensive approach that integrates clinical, genetic, and environmental determinants is vital to evolving treatment strategies and improving quality of life for both patients and caregivers.

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