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The Role and Relationship of Different Bacteria in Alzheimer's Disease: Effects; Pathogenesis; Complication

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ABSTRACT

Background: The Alzheimer's association restated the necessity of the brain gut axis within the context of studying the disease. With its broad-spectrum impact cutting across mnemonics, degeneration of cortex, and neurology, Alzheimer's disease is known as a neurodegenerative disease. Rising guidance implicate AD as a progressive disease of the Gut microbe dysbiosis with the gut ecosystem destruction resulting in the cascade of neuroinconsistency, accumulation of amyloid- β ,



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compromise of blood brain barrier, and the impairment. Metabolic aberration along with the inflammation caused by microbes such as *Chlamydia pneumoniae*, *Helicobacter pylori* and *Porphyromonas gingivalis* have advanced the degeneration of the Alzhemers patient. The cyclic attack set forth by the bacterials in the brain together with the systemic cytokine secretion creates an inflammation and neurodegeneration enhancing loop which cannot be broken. Such potential microb target therapies which aim not on the total elimination of the disease but on its on-going replacement are being later on presented within this review alongside with detailed explanation of the above mechanism.

Conclusion: Alzheimer's disease relates to gut-brain axis; gut issues can cause inflammation and cognitive problems. Certain bacteria may worsen AD. Microbiome therapies could help; future research should target key microbial strains and conduct clinical trials for treatments.

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Introduction

Alzheimer's disease (AD) is a progressive neurodegenerative disorder characterized by the early extracellular deposition of diffuse and neuritic plaques (composed of amyloid- β peptides) followed by the intracellular formation of neurofibrillary tangles (formed by hyperphosphorylated tau protein) in the brain (1). While these aggregates represent the main pathological hallmarks of AD, the disease involves various other pathophysiological changes and processes, such as neuroinflammation, synaptic dysfunction, and metabolic dysregulation. Despite tremendous research efforts to understand the pathogenesis of the disease, the cause-and-effect relationships of the complex biological processes involved in AD are not fully understood. The lack of clarity poses significant challenges for developing effective treatments, highlighting the need for a comprehensive and multidimensional approach to tackle the disease (2).

AD is an age-associated neurodegenerative disorder characterized by loss of cognitive

function. The cognitive functions include behavioral changes, reduced mental capacity to learn, and memory deficit leading to dementia. AD is caused by the accumulation of beta-amyloid (A β) fibrils, oligomers, and neurofibrillary tangles (NFTs) in the hippocampus, cerebral cortex, and other areas of the brain (3).

Probiotics are living microorganisms that promote health benefits when consumed in adequate quantity. They regulate the level of pH in the body, help preserve the integrity of the intestinal lining, act as antibiotics, and enhance the brain-derived neurotrophic factor (3). These neurotrophic factors are made up of a type of protein in the brain that facilitates the survival and differentiation of neurons. Hence, it plays a crucial role in neurological development. Learning disabilities and memory impairments are some of the common issues that tend to arise if these factors are missing from the brain (4).

The effects of probiotics on the central nervous system (CNS) are achieved by alteration of gut microbiota, by increasing the diversity of the good bacterial composition, thereby boosting CNS

functions. Apart from brain neurotrophic factor, probiotics tend to provide good prognosis in curing memory deficits and psychiatric disorders by directly modifying brain biochemical components such as serotonin, γ -aminobutyric acid (GABA) and dopamine (5).

General discussions about the relationship between the gut microbiota and AD have already been reviewed in our previous review article. In this narrative review, we will briefly summarize and update the recent progress in the field and discuss emerging questions from the new observations that need further elucidation. Finally, we will discuss possibilities for disease modification by leveraging the capabilities of the gut microbiota. The presence of lipopolysaccharide (LPS) by gram-negative bacteria and the increased buildup of amyloids in the human gut are critical in the etiopathogenesis of neurological disorders characterized by amyloidogenic features (6, 7).

Alzheimer's disease

AD presents with diverse symptoms and progression patterns. Early stages often include amnesic mild cognitive impairment (MCI), strongly linked to underlying AD pathology, which significantly raises the risk of progressing to dementia. Biomarkers such as amyloid PET, CSF (cerebrospinal fluid) analysis, and neuroimaging help predict progression risks. Early signs of AD, often appearing years before diagnosis, include mood changes, anxiety, apathy, and sleep disturbances. In later stages, symptoms like impaired judgment, confusion, aggression, and neuropsychiatric issues emerge. Recognizing these signs early and conducting appropriate evaluations are essential for effective management (8).

AD is strongly linked to aging, with about 90% of cases occurring in individuals aged 65 and older. Its prevalence doubles every five years, highlighting a time-dependent, exponential increase. This association suggests that as people age, they face a significantly higher risk of developing AD, alongside other neurodegenerative

diseases like Parkinson's. Theories of aging provide a framework to understand how biological changes with age increase susceptibility to such conditions. These findings emphasize the broader vulnerability of the elderly to age-related diseases, even if not all individuals manifest them. The rising prevalence of AD and other dementias in aging populations calls for intensified research and healthcare strategies to address these challenges. Understanding the mechanisms of aging and their relationship with neurodegeneration is critical for developing preventative and therapeutic interventions to improve the health and quality of life of older adults (9).

AD is the most prevalent form of dementia, characterized as a progressively worsening neurodegenerative disorder. It is marked by the presence of neurotic plaques and neurofibrillary tangles caused by the accumulation of A β in brain regions most affected by the disease, including the medial temporal lobe and neocortical structures (10).

Two distinct neuropathological changes are associated with AD progression and symptomatology. The first category, termed positive lesions, arises from the accumulation of pathological structures such as neurofibrillary tangles, amyloid plaques, dystrophic neurites, neuropil threads, and other deposits found in the brains of individuals with AD. The second category, negative lesions, is characterized by significant brain atrophy resulting from the loss of neurons, neuropil, and synapses. Additional contributors to neurodegeneration include neuroinflammation, oxidative stress, and damage to cholinergic neurons (11).

AD is recognized as a multifactorial disease linked to various risk factors, including advancing age, genetic predisposition, head trauma, vascular conditions, infections, and environmental exposures (e.g., heavy metals and trace metals). Despite extensive research, the primary cause of the pathological changes in AD—such as A β accumulation, neurofibrillary tangles, and synaptic loss—remains unclear. While several hypotheses have been proposed, two are considered

predominant: one attributes the disease to impairments in cholinergic function as a key risk factor, while the other suggests that disruptions in amyloid-protein production and processing act as the primary triggers. However, no universally accepted theory currently explains the pathogenesis of Alzheimer's disease (11).

Related and effective bacteria in Alzheimer's disease

AD, which affects approximately 50,000,000 people worldwide, is the most frequent cause of dementia, constituting a real global health problem (12). The disease is characterized by the progressive deposition of A β plaques and tangles of hyperphosphorylated tau neurofibrils, leading to neuroinflammation and progressive cognitive decline (13). Synaptic dysfunction and neuronal death are at least in part due to the excessive or non-resolving activation of the immune response and any infections or traumatic events affecting the brain (traumatic brain injury) can interfere with central immune homeostasis and accelerate the progression of the disease (14). Although several hypotheses have been formulated about the causes of AD pathogenesis and progression, both the onset and the evolution of the disease remain not entirely clear. Therefore, although different therapeutic options have been proposed, many have failed in clinical trials and have not been found to produce significant benefits (15-17). It is widely thought that an early diagnosis could be essential to act at the earliest disease stages, but effective and reproducible biomarkers are still far from clinical application (18, 19).

AD is a deadly neurodegenerative illness that mostly impacts the elderly and is a major health concern for the geriatric population worldwide. AD prevalence increases substantially with age, reaching 50% in 85-year-olds (12). AD is expected to become significantly more common in the geriatric population as the median life expectancy grows. The worldwide incidence of dementia is about 24 million, and it is estimated to surge fourfold by the year 2050 (13). As such, there is a

need for modern treatment options given the probable risk factors for AD and treatments that can delay AD onset and occurrence (14). About 5000 species of gut microorganisms, notably Firmicutes, Bacteroidetes, Actinobacteria, and Proteobacteria, have been reported in the human intestinal lumen. These microbes play crucial roles in gut digestion and absorption functions (15). Among these microorganisms, in particular, *Chlamydia pneumoniae* and *Spirochetes* have multiple research findings pointing to their significance in the pathogenesis of AD (16).

According to the AD pathogen hypothesis, pathogens operate as triggers, in conjunction with genetic variables, in starting the accumulation and/or processing of A β , hyperphosphorylated tau proteins, and inflammation in the brains of AD patients (17). HSV1 and other pathogens, such as *C. pneumoniae* and *Spirochetes*, are commonly found in the brains of AD patients, as these may evade the host immune response and infect the brain (18, 19). In vitro and animal studies have demonstrated that pathogens facilitate amyloid plaque formation and increased levels of hyperphosphorylated tau (20, 21). Such pathogens induce a glial inflammatory response, damaging and killing neurons directly and indirectly (22). In the brains of AD patients, there are major inflammatory cascades (23, 24), and these pathways combine to cause further neurodegeneration and disease progression. Neurodegenerative illnesses occur and progress due to genetic and lifestyle factors and are significantly influenced by gene-environment interactions (25). The human gut is a reservoir of several bacterial species, and the human body is home to a variety of microorganisms, including bacteria, viruses, archaea, and microeukaryotes (26, 27).

Interestingly, patients with neurological, autoimmune, metabolic, and cancer illnesses have distinct gut microbiota compared with healthy individuals. The enteric nervous system (ENS) and central nervous system (CNS) communicate bidirectionally through the gut-brain axis (27, 28).

Role and relationship of different bacteria in Alzheimer's Disease

Alzheimer's Disease and Bacterial Infection

Bacteria, particularly *Porphyromonas gingivalis* (*P. gingivalis*), which is known for causing gum disease, have been proposed as possible contributors to Alzheimer's disease. Research indicates that infection with *P. gingivalis* in mice leads to higher levels of A β in peripheral macrophages, and this bacterium has also been detected in postmortem brain tissues of AD patients (29). Research suggests that individuals with AD have approximately seven times more oral bacteria in their brains compared to those who are cognitively healthy. Despite this, there is still ongoing debate regarding whether these microbes simply invade the brain or establish an ecosystem, as the concept of microbes existing within the brain remains controversial (30).

The influence of *P. gingivalis* on AD is thought to involve the production of toxic enzymes called gingipains, which have been found to correlate with tau pathology in AD patients (31). Furthermore, inhibiting gingipains has demonstrated neuroprotective effects in mice infected with *P. gingivalis* by reducing A β levels and markers of neuroinflammation. However, clinical trials of a drug targeting *P. gingivalis* did not yield significant benefits and were stopped due to concerns about liver toxicity (32).

Other bacterial species are also considered potential contributors to AD. For instance, the DNA of *Chlamydia pneumoniae*, a common respiratory bacterium in the elderly, has been discovered in the brain tissue of 80% of AD patients (33). Recent studies in mice have demonstrated that *Chlamydia pneumoniae* can infect the central nervous system, potentially traveling along the olfactory and trigeminal nerves (34).

In addition, *Borrelia burgdorferi*, the bacterium that causes Lyme disease, has been proposed as a contributor to the development of AD. This bacterium has been found in association with

plaques in AD patients, and studies have shown that its infection of mammalian cells in vitro results in elevated levels of beta-amyloid (A β) and phosphorylated tau (35).

Fusobacterium nucleatum, a prevalent bacterium associated with periodontitis, has been linked to AD. Importantly, this causal relationship is supported by evidence demonstrating worsened cognitive symptoms, increased A β accumulation, and tau phosphorylation in 5XFAD mice that were topically infected with *F. nucleatum* to induce periodontitis (36).

Gut Microbiota

Recent research indicates that gastrointestinal bacteria could influence the development of AD (37). The gut microbiome is mainly composed of various bacterial species, including *Lactobacillus*, *Bifidobacteria*, *Verrucomicrobia*, *Spirochetes*, *Proteobacteria*, *Fusobacteria*, *Firmicutes*, and *Cyanobacteria*. Evidence suggests that bacterial infections may initiate pathological processes linked to AD (38).

Bacteria such as *Helicobacter pylori*, *Borrelia burgdorferi*, *Chlamydia pneumoniae*, *Escherichia coli* (*E. coli*), *Shigella*, *E. rectale*, and *Bacteroides fragilis* have been linked to AD (39). These bacterial species can work together to heighten the infection burden in AD patients. One way these bacteria may cause pathological changes is through the release of neurotoxic substances (40).

Lactobacillus and actinobacteria can convert glutamate into gamma-aminobutyric acid (GABA) in the central nervous system. Elevated GABA levels in the gut can lead to higher GABA levels in the central nervous system, which might cause memory issues, depression, and problems with synapse formation (41).

Gut bacteria release inflammatory agents, beta-amyloid protein, and neurotoxic substances that disrupt the immune system. These bacteria produce endotoxins called lipopolysaccharides (LPS), found in the outer membrane of Gram-negative bacteria, which are common in the gut and other parts of the body. An imbalance in gut

microbiota is linked to diseases like AD. This imbalance weakens gut barrier function and increases intestinal permeability. When the gut barrier is compromised, microbial metabolites can enter the bloodstream. If the blood-brain barrier (BBB) is also compromised, proinflammatory cytokines can reach the central nervous system, causing neuroinflammation by activating microglia and astrocytes (40).

Role of Gut Microbiota in Alzheimer's Disease (AD) Pathogenesis

Studies have shown that the gut microbiome plays a role in the development of AD in both animals and humans. Research has found connections between specific microbial organisms and CSF biomarkers related to AD. For example, lower levels of biomarkers such as the A β 42/A β 40

and Bacteroidetes, have been observed in AD patients and animal models. Clinical studies have shown that individuals with amyloidosis have distinct gut microbiota compositions compared to those without the condition. Additionally, higher levels of proinflammatory cytokines such as IL-6, CXCL2, NLRP3, and IL1 β have been found in amyloid-positive patients (42).

Role of gram-negative bacteria in Alzheimer's Disease (AD) Pathogenesis

Gram-negative bacteria release outer membrane vesicles (OMVs) during both planktonic growth and in surface-attached biofilm communities. These small, spherical vesicles detach from the outer cell membrane and contain LPS, peptidoglycan (PG), proteins, DNA, RNA, and various virulence factors like enzymes and toxins

Table 1. Role of gram-negative bacteria in Alzheimer's Disease (AD) Pathogenesis.

Bacteria	Effects on Alzheimer's Disease (AD)	Mechanism	References
<i>Porphyromonas gingivalis</i>	- Increased A β levels - Neuroinflammation	Production of toxic gingipains correlated with tau pathology	(1)
<i>Chlamydia pneumoniae</i>	- Cognitive decline - Infection of central nervous system	- Invasion through olfactory and trigeminal nerves	(2)
<i>Borrelia burgdorferi</i>	- Elevated A β and phosphorylated tau levels	- Association with amyloid plaques	(3)
<i>Fusobacterium nucleatum</i>	- Increased A β accumulation - Worsened cognitive symptoms	- Induction of periodontitis	(4)
<i>Gut Microbiota</i>	- Memory issues - Depression - Disruption of immune system	- Production of inflammatory agents, beta-amyloid protein, and neurotoxic substances	(5-7)
<i>Helicobacter pylori</i>	- Increased intestinal permeability - Neuroinflammation	- Production of endotoxins (LPS)	(8)
<i>Escherichia coli</i>	- Increased proinflammatory cytokines	- Production of LPS	(9)
<i>Bacteroides fragilis</i>	- Disruption of blood-brain barrier (BBB)	- Release of microbial metabolites	(10)

ratio and phosphorylated tau (p-tau) are linked to Clostridiaceae and Erysipelotrichaceae, whereas higher levels of these biomarkers are associated with *Blautia* and *Bacteroides* species (42).

Changes in gut microbiota at the phylum level, including variations in Firmicutes, Proteobacteria,

(43, 44). OMVs are nanosized and carry higher concentrations of toxins and virulence factors compared to their parent bacteria (45). During infection, these vesicles deliver pathogenic factors to host cells and can bypass direct cell-to-cell contact (46). As a result, OMVs enable bacteria-

host communication and can trigger disease processes even in the absence of live bacteria. Recent studies have associated OMVs with a variety of inflammatory diseases, including chronic inflammatory conditions, autoimmune disorders, and inflammation-related tumors. OMVs have been thoroughly studied for their roles in diseases such as periodontal disease, gastrointestinal inflammation (including inflammatory bowel disease), pulmonary inflammation, sepsis, and inflammation-related tumors. For instance, *F. nucleatum* OMVs increase osteoclast numbers and inflammatory cytokine production in gingival connective tissues, exacerbating periodontitis symptoms (47).

Helicobacter pylori (*H. pylori*) OMVs, containing virulence factors, are rapidly internalized by gastric epithelial cells, contributing to mucin barrier destruction and bacterial colonization in gastric diseases (43). OMVs from *P. gingivalis* significantly disrupt tight junction proteins in lung epithelial cells, causing cytotoxic effects and pulmonary inflammation (48, 49). *E. coli* OMVs increase the expression of IL-6, P-selectin, and intercellular adhesion molecules while significantly decreasing thrombomodulin, triggering the coagulation cascade. Additionally, small RNA23392 (sRNA-23392) packed in *P. gingivalis* OMVs promotes the migration and invasion of oral squamous cell carcinoma cells by targeting desmocollin-2 (50).

Conclusion

Alzheimer's disease (AD) pathogenesis is strongly associated with the gut-brain axis, and gut microbiome dysbiosis is causative of neuroinflammation and cognitive impairment. The literature indicates that integrity compromise of this axis in association with inflammation, endothelial dysfunction, and amyloid β deposition propels neurodegeneration (51, 52). Certain bacterial infections, such as *Chlamydia pneumoniae*, *Helicobacter pylori*, and *Porphyromonas gingivalis*, have been seen to be involved in the aggravation of AD through

chronically promoting inflammation and sustaining neuroinflammatory reactions (53). This indicates the involvement of microbial imbalance in AD development and onset. Precision microbiome therapies, such as probiotics, prebiotics, and antimicrobials, are promising in the restoration of microbial balance, the alleviation of inflammation, and the maintenance of cognitive health (54, 55). But there would need to be accurate application of antimicrobials to prevent disturbance of gut homeostasis that has an effect on disease outcome. The key focus for future studies would be to determine the most significant microbial strains, their metabolites, and their involvement in AD pathology. Clinical trials of microbiome-guided treatments will be vital in taking lab-based findings to clinic-based treatments. Because the gut-brain interaction is so pivotal in AD, microbiome-targeted strategies offer an intriguing avenue for the creation of new therapies.

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