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Review Article

Metabolic Risk Factors of Sporadic Alzheimer's Disease: Implications in the Pathology, Pathogenesis and Treatment

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ABSTRACT: Alzheimer's disease (AD), the major cause of dementia among the elderly world-wide, manifests in familial and sporadic forms, and the latter variety accounts for the majority of the patients affected by this disease. The etiopathogenesis of sporadic AD is complex and uncertain. The autopsy studies of AD brain have provided limited understanding of the antemortem pathogenesis of the disease. Experimental AD research with transgenic animal or various cell based models has so far failed to explain the complex and varied spectrum of AD dementia. The review, therefore, emphasizes the importance of AD related risk factors, especially those with metabolic implications, identified from various epidemiological studies, in providing clues to the pathogenesis of this complex disorder. Several metabolic risk factors of AD like hypercholesterolemia, hyperhomocysteinemia and type 2 diabetes have been studied extensively both in epidemiology and experimental research, while much less is known about the role of adipokines, pro-inflammatory cytokines and vitamin D in this context. Moreover, the results from many of these studies have shown a degree of variability which has hindered our understanding of the role of AD related risk factors in the disease progression. The review also encompasses the recent recommendations regarding clinical and neuropathological diagnosis of AD and brings out the inherent uncertainty and ambiguity in this area which may have a distinct impact on the outcome of various population-based studies on AD-related risk factors.

Key words: Metabolic, risk factors, sporadic, Alzheimer's disease, pathogenesis, treatment

With the general increase in the life span of the population across the globe, Alzheimer's disease (AD), a progressive neurodegenerative disorder presenting with insidious loss of memory and cognition, is fast becoming a major disease burden and socio-economic challenge for many countries. AD is the commonest form of dementia above the age of 65 years, and the estimated prevalence of this disease was 24 million in the world in 2011 which would be doubled by the year 2030 [1, 2]. The majority (more than 95 %) of the AD dementia cases belong to sporadic variety of the disease which is a multi-factorial disorder in which both genetic predisposition and environmental factors contribute to the genesis of the disease [1, 2, 3]. In contrast, the familial form of the disease (less than 5% of AD population) arises from the mutations of any of the three genes e.g. amyloid precursor protein (*APP*), presenilin 1 (*PS 1*) and presenilin 2 (*PS 2*) and usually appears in somewhat younger age-group than the sporadic form and follows a more aggressive downhill course [2, 3,4]. The clinical features and post-mortem neuropathological hallmarks of both forms of AD are nearly identical, and thus it has been tacitly assumed that ante-mortem pathogenesis is the same in either form of the disease. The neuropathological lesions of AD are characterized by abnormal accumulation of amyloid beta protein (AB) derived from APP and a microtubule associated protein tau [5]. The experimental research in AD for exploring disease pathogenesis has been dominated by the attempts for identification of various consequences abnormal neurotoxic of protein accumulation on one hand, and on the other by an extensive use of transgenic AD models harboring single or multiple mutant gene(s) of human familial AD [5, 6, 7, 8]. However, this approach so far has neither explained the complexity and heterogeneity of sporadic human AD, nor produced any reasonably efficacious drug for this condition. It is now increasingly understood that in sporadic AD multiple risk factors from gene- environment interactions working in the backdrop of the aging brain activate and reinforce the disease pathogenesis [1, 2, 8]. The molecular nature of gene-environment interaction or its temporal relationship with the pathogenesis of sporadic AD is largely unknown. However, one interesting theory, the Latent Early-life Associated Regulation (LEARn) model, has envisaged that exposure to environmental risk factors (e.g. heavy metal exposure, nutritional deficiency etc.) in early developmental life brings about epigenetic modifications of AD related genes (e.g. Amyloid Precursor Protein or APP gene) that remain latent for many years till a second 'hit' (e.g. aging associated elevated pro-inflammatory cytokines, unhealthy mid-life diet etc.) results in sustained alterations in the expressions of these early-affected genes manifesting the full-blown disease [9, 10]. The epigenetic modifications of AD related genes affected by the early life exposure to environmental risk factors may include DNA methylation or oxidation or chromatin re-organization [9, 10]. The novel and attractive LEARn model which advocates the role of environmental risk factors and traces the origin of AD to early developmental stage, however, needs further support from experimental and epidemiological studies. On the other hand, many AD researchers tend to suggest that the environmental risk factors operate during the preclinical phase of the disease decades before the appearance of clinical dementia. In either way, there is overwhelming support for environmental or extra-genetic risk factors as inducers of AD pathogenesis. These environmental or extra-genetic risk factors are varied in nature and origin, but for the sake of the present review we may club a few of them as metabolic risk factors and attempt to understand their biological implications in the context of disease pathogenesis and therapeutic strategies (Fig.1). The growing literature of metabolic risk factors of sporadic Alzheimer's disease (AD) extending from epidemiology to molecular pathogenesis and therapeutic management, however, is replete with controversies and contradictions. Nevertheless, this is an active area of research and one that holds enormous promise in the future development of treatment strategies to combat AD primarily because much of the data are obtained directly from clinical cases. Secondly, the identification of clear metabolic risk factors for AD will give us an opportunity to halt the progress of AD by dietary manipulation or lifestyle management. The idea of blocking or halting AD pathogenesis by dietary manipulations (e.g. supplementation with folate and vitamin B12) or life-style changes during the early developmental phase or latent phase of the disease has also been espoused by those proposing the LEARn model of sporadic AD [10, 11]. This review will try to present an overview of AD bringing out the dilemmas and uncertainties of clinical diagnosis, neuropathology and molecular pathogenesis before providing an account of predisposing metabolic risk factors of this disease.

Alzheimer's disease: clinical diagnosis, pathology and molecular pathogenesis.

Clinical Diagnosis

The clinical diagnosis of AD requires thorough history and neuropsychological evaluation following the criteria NINCDS/ADRDA (Neurological set bv and Communicative Disorders and Stroke and Alzheimer's Disease and Related Disorders Association) in 1984, which are comparable to those used by other expert bodies e.g. DSM IV (Diagnostic and Statistical Manual of Mental Disorders) [12]. Fundamentally, an insidious onset of progressive dementia with impairment of multiple cognitive domains documented by Mini Mental State Examination or Blessed Dementia Scoring or similar tests usually after 65 years of age is considered as diagnostic of probable AD in the absence of any other dementia producing systemic illness or neurological disease [12, 13]. Various mood or behavioral alterations like depression, agitation, apathy, social withdrawal, insomnia, delusion, emotional or physical outburst are also typical characteristics of AD [12, 13]. The diagnosis can be supported by MRI (magnetic resonance imaging) evidence of diffuse atrophy involving hippocampus and neocortex of the brain. However, the clinical diagnosis is often confused with other forms of dementia like Lewy body dementia, HIV dementia, Huntington's disease, frontotemporal dementia, dementia due to Parkinson's disease and hydrocephalus, Cruetzfeldt-Jacob disease and other conditions [12, 14]. Vascular dementia poses a special problem because of overlapping clinical features and etiopathogenesis [15, 16]. Thus, in a significant number of cases of clinically diagnosed probable AD, the final autopsy report does not confirm the presence of AD pathology. Over the last two decades, the understanding of the pathogenesis of AD and other types of dementias at the cellular and molecular level has enormously increased, and coupled with this the PET imaging methods of reduced glucose uptake or increased amyloid beta deposition in AD brain and the identifications of CSF biomarkers of this disease condition have been developed. This has necessitated some modifications of the original diagnostic criteria and introduction of new terminologies and classifications, which could help in identifying the AD patients with greater degrees of certainty. Thus, as recommended by National Institute of Aging -Alzheimer's Association (NIA - AA) workgroups, AD is a continuum of disease process which includes preclinical AD, mild cognitive impairment (MCI) and AD dementia [17, 18, 19]. AD dementia patients would be further categorized as 'probable AD' and 'possible AD (i.e. AD dementia with an atypical course or with another co-morbidity such as cerebro-vascular disease, Lewy

body dementia or any other disease affecting cognition)' on the basis of history and neuropsychological examination, while the diagnosis of 'probable AD' or 'possible AD' with AD pathophysiologic process will require CSF biomarker examination (AB42, total tau or phosphorylated tau) or PET evidence of decreased ¹⁸F-2 deoxyglucose uptake or increased accumulation of amyloid beta peptide in brain [19]. The present recommendations have emphasized that ' probable AD' or ' possible AD' diagnosis is sufficient in clinical settings, while for research purposes a more definitive diagnosis of 'probable' or 'possible' AD with AD pathophysiologic process is necessary [19]. Similarly, pre-clinical AD is to be used only for research purposes e.g. for selection of cohorts for longitudinal clinical studies [17]. The inherent uncertainty and ambiguity of AD diagnosis as outlined here is to be kept in mind in the context of our current discussion on AD and its multiple risk factors, since the former can confound the results of epidemiological studies significantly.

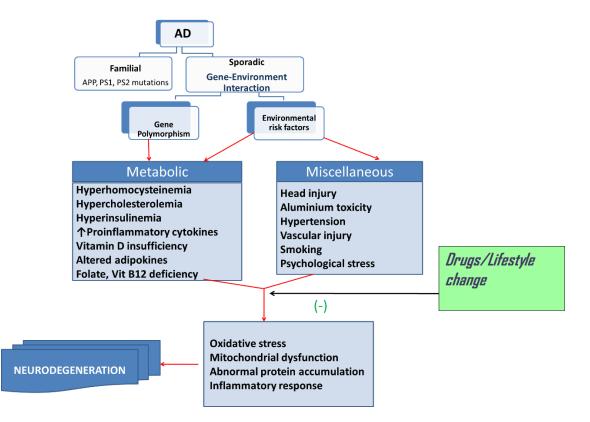


Figure 1. Risk factors of Alzheimer's disease. Gene -environment interactions may be the underlying mechanism of sporadic AD. Environmental risk factors include those present in external environment or extra-genetic internal milieu of the body. The risk factors may affect the functions of AD-related genes or their regulatory regions by methylation, oxidation or other mechanisms. Gene polymorphisms, on the other hand, may aggravate the effects of the risk factors on AD pathogenesis. Drugs, diet and life-style may prevent the interaction of risk factors with AD pathogenic mechanisms.

Neuropathology of AD

The histopathology of AD brain has two hallmarks of extracellular amyloid or senile plaques and neurofibrillary tangles in neuronal perikarya [20, 21, 22]. The amyloid plaques appear in several varieties e.g. neuritic plaques, diffuse amyloid plaques, amyloid lakes, cotton-wool plaques etc. [20]. The neuritic plaques are composed of a core deposit of amyloid beta peptide (predominantly A β 42 and A β 40, but also several other amyloid peptides of different chain lengths) in different degrees of oligomerization state surrounded by dystrophic neurites [20, 22]. The neurofibrillary tangles, on the other hand, are composed of paired helical filaments of hyperphosphorylated tau proteins detected bv histochemical stains or immuno-histochemistry [20, 22]. The distributions of these typical AD lesions are approximately in the same regions and involve enterorhinal cortex, hippocampus, amygdala and different areas of neocortex [20, 21, 22]. There are other accompaying features of AD pathology like neuronal loss, degeneration of synapses, dendrites and axons, gliosis, white matter rarefaction, ganulovacuolar degeneration and cerebral amyloid angiopathy [20, 22]. Further, apart from amyloid beta peptides or abnormal tau protein, several other proteins also accumulate in various degrees in AD brain like α- synuclein, TDP-43 (TAR DNA binding protein), actin giving rise to various forms of inclusion bodies like Lewy bodies, Hirano bodies etc. [20, 22]. Since the post-mortem confirmation of AD diagnosis rests on autopsy findings, attempts have been made over the years for systematic and well standardized criteria, qualitative and quantitative, for identifying the neuropathology of AD brain [23, 24, 25]. The NIA-REGAN (National Institute of Aging / Regan Institute of the Alzheimer Association) criteria set in 1997 have been revised recently by NIA - AA workgroups and provided guidelines for autopsy reporting of AD neuropathology irrespective of clinical presentations of the subjects [20, 25]. The present recommendations have outlined the ABC scoring for describing AD neuropathology: A for amyloid deposit, B for Braak staging of neurofibrillary tangles and C for neuritic plaques as per CERAD (Consortium to Establish a Registry for Alzheimer's Disease) criteria. By this ABC scoring, AD neuropathlogy can be graded as 'No', 'Low', 'Intermediate' and 'High', and further NIA -AA suggestions include pathological description of all comorbidities e.g. vascular brain injury, hippocampal sclerosis etc. [20, 22].

Clinical AD vs. AD Neuropathology: Ambiguity and Controversy

It is to be emphasized that the impairment of cognitive domains on which the clinical diagnosis of AD is based is in most cases but not always correlate well with the extent of post-mortem AD neuropathology [26, 27]. In some cases significant AD neuropathology has been observed after autopsy in aged individuals who were non-demented before death which has been explained by the assumption that neuropathology of AD predates the clinical cognitive deficits by many years [17, 20]. In other cases cognitive decline is much higher in comparison to existing AD neuropathology, which implies that other co-morbidities like vascular brain injury or Lewy body disease etc. may have contributed to the dementia in such instances [20, 26]. Alternatively, such discrepancies may mean different degrees of 'brain reserve' or 'cognitive reserve' among the affected individuals [17]. Moreover, this discrepancy between the extent of neuropathology and clinical severity of the disease in many cases may also mean that AD pathology which causes dementia and cognitive impairment is not driven solely by the toxic effects of amyloid plaques or neurofibrillary tangles, but other cellular and molecular damage mechanisms such as oxidative damage or mitochondrial dysfunction or other metabolic alterations may be playing more crucial roles in the genesis of this disease [5, 20]. It remains uncertain at this moment whether histopathologic diagnosis of AD should take in to account the features of molecular damage e.g. accumulation of oxidative damage markers, structural and functional alterations in mitochondria, presence of proinflammatory markers etc. in post-mortem AD brain to obtain a better correlation of neuropathology and cognitive decline. The incongruity between neuropathology and clinical severity of AD may also explain, at least partially, the discrepancy often observed between epidemiological studies and autopsy findings with regard to the association of a particular risk factor with AD.

Pathogenesis of Alzheimer's Disease

The central mechanisms in the pathogenesis of AD have generally revolved round two themes clearly linked to two hallmark lesions found in brain after autopsy in this disease condition. The first and foremost is the abnormal accumulation of oligomeric A β 42 or related peptides and their multiple toxic effects on neurons and glia leading to oxidative damage, mitochondrial dysfunction, calcium dysregulation, inflammation and ER stress, which together may set in programmed death of neurons [5, 28]. This is the so called 'Amyloid Cascade Hypothesis'. The formation of amyloid beta peptide (predominantly A β 42) from APP through sequential actions of β and γ secretases in the amyloidogenic pathway, the intracellular trafficking of APP-AB from endoplasmic reticulum through protein secretory pathway to plasma membrane and outside, the degradation of A β 42 by neprilysin, insulin degrading enzyme (IDE), endothelin converting enzyme, plasmin etc. and the clearance of $A\beta 42$ from the brain have been the subject of several excellent reviews in the context of AD pathogenesis [28, 29, 30]. It is conceivable that the increased accumulation of amyloid beta peptides in sporadic AD results from increased expression of APP gene and / or increased processing of the APP gene product in the amyloidogenic pathway by means of β and γ secretases and / or decreased catabolism and clearance of the peptides from the brain. In case of familial AD, the mutations in APP, PS1 or PS2 gene may lead to similar effects with accumulation of amyloid beta peptides in the brain, and the 'Amyloid Cascade Hypothesis' as the pathogenic mechanism of AD has gained huge support from identification of these familial AD mutation [29, 31]. The other suggested mechanism in AD pathogenesis emphasizes the neuronal and synaptic dysfunctions caused by the abnormal accumulation of phosphorylated tau protein (tauopathy) [32, 33]. Tau protein acts as a substrate for phosphorylation at multiple sites by several different kinases e.g.GSK-3β, Cdk5, PKA, MARK etc. in vitro, but it is not clear which of these kinases are responsible for in vivo phosphorylation of tau in physiological or pathological conditions [33]. Under normal physiological conditions the reversible and transient phosphorylation of tau is involved in many neuronal functions such as axonal transport and neurite outgrowth, but pathological hyperphosphorylation of tau leads to oligomerization and fibrillization and decreased binding to microtubules [32, 33]. Despite a plethora of evidence from animal models (transgenic and chemical induced), cell based models and post-mortem brain of AD subjects supporting the 'Amyloid Cascade Hypothesis' or 'tauopathy', it is not fundamentally clear how these alterations of abnormal protein accumulation and aggregation are triggered in the aging brain especially in the case of sporadic AD. The LEARn model mentioned earlier posits that environmental risk factor like heavy metal exposure or nutritional deficiency can bring about epigenetic modifications in the regulatory regions of APP or β -secretase gene to cause increased production of amyloid beta peptide [9, 10]. In general, it may be surmised that the risk factors tend to affect the expression, processing and trafficking of APP and amyloid beta peptide or change the phosphorylation state of tau proteins through multiple kinases and phosphatases. Furthermore, extensive post-mortem evidence of accumulation of oxidative damage markers of phospholipids (malondialdehyde, 4-hydroxynonenal (4-HNE). F₂ isoprostane etc.), protein (protein carbonyls, HNE-protein adducts) and nucleic acids in AD brain is available [34, 35, 36]. Likewise evidence of mitochondrial dysfunction and intramitochondrial accumulation of amyloid beta peptide in AD brain has been clearly documented in postmortem AD brain [37, 38]. The inflammatory response by activated microglia and also astrocytes leading to production of cytokines, chemokines and reactive oxygen species (ROS) with associated neuronal damage is another important feature of AD pathogenesis [39, 40]. A growing body of recent evidence has indicated the activation of several types of inflammosomes in microglia, and also possibly in neurons, that drives the inflammatory response and neurodegeneration in AD brain [41, 42]. It is a moot point whether all these alterations are simply the secondary consequences of abnormal accumulation of amyloid beta peptide or hyperphosphorylated tau in AD brain or they represent independent damage mechanisms working in concert in the backdrop of an aged brain to bring about neurodegeneration as well as characteristic AD proteinopathy.

Metabolic and Endocrine Components in AD pathogenesis:

One of the earliest manifestations of AD is the decreased cerebral utilization of glucose as evidenced by PET imaging of ¹⁸F -2 deoxyglucose uptake in the AD brain, and the phenomenon is progressive with the disease and well correlated with the degree of cognitive decline in AD brain [43, 44]. The multiple reasons for cerebral glucose hypometabolism in AD, its relationship with oxidative stress and the use of alternative substrates under such condition have been well reviewed [43, 44]. The metabolic implications of AD pathogenesis in the context of brain insulin deficiency and insulin resistance have been extensively discussed in several recent publications [45, 46]. Although multiple causes have been attributed to altered food intake and loss of body weight in AD, the fact also implies a role of hormones like insulin and adipokines in its pathogenesis [48, 49, 50]. The mitochondrial dysfunction and inhibition of key metabolic enzymes involved in energy production like the glycolytic enzymes as also pyruvate dehydrogenase, α -ketoglutarate dehydrogenase, cytochrome oxidase are established features of AD pathology indicating general metabolic perturbation in brain in this condition [50, 51]. The transcriptome data from neurodegenerative and neurological diseases incorporated in brain-specific metabolic network models have indicated alterations in several key metabolites and pathways in AD brain that are related to energy, lipid and ROS metabolism [52]. The role of glucose and lactate metabolism in AD brain has been recently analyzed from the proposed alternative view of brain metabolism based on astrocyte-neuron-lactateshuttle [53]. Metabolic syndrome, a condition characterized by multiple biochemical and physiological alterations like hyperglycemia, dyslipidemia, hypertension, obesity etc., has been linked with the genesis of sporadic AD [54]. Thus, there is substantial evidence supporting a strong metabolic component in AD pathogenesis which calls for a systematic discussion of metabolic risk factors of sporadic AD.

Metabolic Risk Factors of AD: Present Status

Although in the context of the present discussion, we are primarily concerned with the metabolic risk factors of sporadic AD, it is to be understood that gene polymorphisms associated with sporadic AD may modulate the role of these risk factors in multiple ways in the disease pathogenesis. The polymorphism of *APOE is* considered as a definite risk factor for AD with $\varepsilon 4$ allele (*APOE4*) showing strong association with the disease, but the estimated risk attributable to *APOE4* varies in different populations depending on the frequency of this allele in a particular population [55]. The protein coded is apolipoprotein E which is involved in by APOE cholesterol transport in the periphery as well as cholesterol trafficking within the brain, and APOE genotype and serum total cholesterol interaction has been suggested in AD progression [56]. Recent large genomewide association studies have identified several other genetic susceptibility loci for AD which include CR 1, SORL 1, PICALM, CLU etc. [57]. Apart from the gene polymorphisms, population based long-term prospective as well as cross-sectional retrospective studies have identified many risk factors of sporadic AD, and some of hypercholesterolemia, type 2 diabetes, these like hyperhomocysteinemia, elevated circulating proinflammatory cytokines, vitamin D deficiency and altered blood levels of adipokines have obvious metabolic connotation. The possible links of these metabolic risk factors with disease pathogenesis are presented in Fig.2.

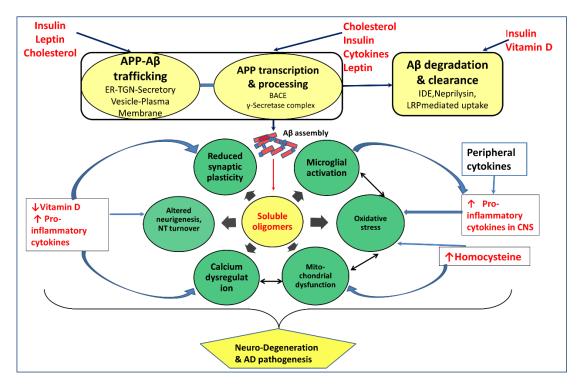


Figure 1. Metabolic risk factors and molecular pathogenesis of AD. AD pathogenesis is represented by interacting damage pathways spearheaded by soluble oligomers of amyloid beta peptide. Altered levels of metabolic risk factors e.g. hormones, vitamins, cytokines, metabolites etc. can affect APP expression and processing or intracellular trafficking, catabolism and clearance of amyloid beta peptide or induce oxidative stress or inflammatory response through interactions at multiple sites leading to neurodegeneration and characteristic proteinopathy of AD. ER-TGN, Endoplasmic reticulum trans- golgi network; BACE, Beta-site APP cleaving enzyme; IDE, Insulin degrading enzyme; LRP, Low density lipoprotein receptor related protein; NT, Neurotransmitter.

Hypercholesterolemia:

Large-scale population-based prospective studies have indicated that mid-life hypercholesterolemia is an independent risk factor for AD even when corrected for age and other confounding factors [58, 59]. Several other studies have prospective also reported that hypercholestolemia is a risk factor for AD even after adjustment of APOE4 attributed risk [60]. One population based study of African Americans has shown that higher serum cholesterol is associated with increased risk of AD in APOE4 negative subjects, but not in those carrying at least one ɛ4 allele [61]. Many case - control studies have confirmed that mild hypercholesterolemia also accompanies late-onset AD [49, 62, 63]. However, a 32year long follow-up study of 1462 women has failed to find an association of mid-life hypercholesterolemia with increasing risk of AD, and even some studies have indicated that a high blood cholesterol especially in latelife is actually protective against AD [64, 65, 66]. The statin group of cholesterol lowering agents has been shown to produce beneficial effects in AD subjects in some studies [67]. A recent careful analysis of existing literature has shown that the association of hypercholesterolemia with AD is quite compelling, but the beneficial effect of statin therapy is not firmly established [68, 69].

In experimental cell based research, cholesterol distribution within membrane is seen to have effects on APP metabolism, trafficking of APP, activities of β , γ and α secretases and A β synthesis [70, 71]. In transgenic AD mice promotes high cholesterol diet brain amyloidogenesis [72]. The human brain contains a high amount of cholesterol, mostly in the unesterified form, in two pools of which the major one is in myelin and the minor pool in the plasma membranes of glia and neurons [73, 74]. Since very little cholesterol is transported from the plasma via lipoproteins through the blood-brain barrier, the brain cholesterol is maintained by in situ synthesis and recycling with a small amount moving out from the CSF to the plasma [73, 74]. The recycling and trafficking of cholesterol in the brain requires apoE, lowdensity lipoprotein receptor related protein (LRP) and VLDL receptor, and the details of this complex pathway have been worked out [71, 75]. In the cell membrane cholesterol is associated with special lipid microdomains known as lipid rafts, and because amyloidogenic processing of APP and oligomerization of AB peptide take place within lipid rafts, cholesterol could modulate the latter phenomena [75]. What is not clearly understandable is how hypercholesterolemia can be an important risk factor for AD when circulating cholesterol containing lipoproteins do not gain entry in to brain in significant amount. However, high serum total cholesterol is an important vascular risk factor and vascular brain injury mav confound epidemiological data linking hypercholesterolemia and AD. Alternatively, vascular brain injury and hypoperfusion of brain can initiate and promote brain amyloid pathology as has been suggested earlier [16]. APOE polymorphism is considered as a strong risk factor for sporadic AD in subjects carrying E4 allele, and it has been shown in experiments with cultured neurons that apoE4 isoform is less efficient compared to apoE2 or apoE3 in carrying out efflux of cholesterol from the neurons [76]. The latter effect may promote neuronal production of amyloid β peptide. The cholesterol/ ApoE isoform interaction in the progression of AD pathogenesis has also been observed in population based study [77]. Another interesting connection with cholesterol and AD is through the oxidation product of cholesterol, 24hydroxyhydroxy cholesterol, which is formed exclusively in the brain [73, 78, 79]. This oxysterol can pass through the blood brain barrier and constitutes an efflux pathway of cholesterol from the brain, and thus the plasma level of 24-hydroxycholesterol is an indicator of brain cholesterol turnover [73, 79]. In AD, the plasma level of 24 hydroxycholesterol is increased presumably as a result of neuronal death and membrane cholesterol turnover [78, 79].

Type 2 Diabetes:

A population based cohort study has estimated the Relative Risk (RR) of 2.27 for men and 1.37 for women relating AD with type 2 diabetes [80]. Large- scale population based prospective studies have shown that type 2 diabetes increases the risk of late-onset AD, and different studies have calculated the RR varying from 1.44 to 1.9 [81, 82, 83, 84]. Another population based follow up study showed that hyperinsulinemia or type 2 diabetes increases the risk of of AD with a hazard ratio of 2.2 [85]. A mean follow-up study of 5.5 years for a population of 1138 persons has shown that diabetes is a strong risk factor for AD (hazard ratio 2.4) and the risk is further augmented when other risk factors like hypertension, heart disease and smoking are simultaneously present [86]. Several meta-analysis studies from published literature have estimated an aggregated relative risk of approximately 1.5 linking type 2 diabetes with AD, and the relative risk increases considerably by the presence of hypertension, smoking and APOE4 positivity [87, 88, 89, 90]. A population based cross-sectional study has also shown the significant association of hyperglycemia and hyperinsulinemia with AD independent of APOE4 status [91]. However, many epidemiological studies have linked type 2 diabetes more with vascular dementia than AD, and cognitive decline as a consequence of type 2 diabetes per

se is also well documented [92, 93, 94]. On the other there is a clear discrepancy hand between epidemiological results and neuropathological autopsy findings in linking AD with type 2 diabetes. Neuropathological autopsy studies do not support that type 2 diabetes predisposes to development of AD pathology in the brain of aged persons when compared to Several epidemiological age-matched controls [95]. studies also have examined a proportion of their study cohorts at autopsy for neuropathological changes typical of AD and concluded that type 2 diabetes does not promote AD pathology in the brain and instead vascular pathologies in brain are more commonly associated with type 2 diabetes [89, 96].

While the controversy is persisting between epidemiological findings and neuropathological observations in relating type 2 with AD, in experimental AD research insulin and insulin resistance have been linked to AD pathogenesis in multiple ways. In the brain insulin and IGF signaling regulates a broad range of functions such as glucose and energy metabolism, growth, differentiation, migration, survival and plasticity of neurons [97, 98]. In particular in the context of amyloid beta metabolism, insulin stimulates APP-AB trafficking from trans-golgi network to plasma membrane and the extra-cellular release of A β , and insulin resistance in mice induced by high fat diet causes increased activities of β and γ secretases with accumulation of amyloid beta peptide [45, 99, 100]. Likewise in db/db mice brain or in insulin resistant cultured cells of neural origin, an accumulation of autophagosomes and amyloid beta peptide has been noticed [100]. In addition, insulin competes with AB for degradation by IDE (insulindegrading enzyme) and thus may promote $A\beta$ accumulation in the brain in hyperinsulinemic condition, although the evidence suggests that the peripheral hyperinsulinemia of type 2 diabetes actually causes a decreased entry of insulin into brain [101]. The role of insulin in tau phosphorylation has also been explored in different experimental models, and it is suggested that insulin resistance through impaired PI3/Akt signaling may lead to activation of GSK-3ß and increased phosphorylation of tau [101, 102].

It has been envisaged that Alzheimer's disease may be a type of 'brain diabetes' or 'type 3 diabetes' resulting from both insulin deficiency and insulin resistance in the brain [46, 84, 101]. This is supported by a body of evidence such as the decreased level of insulin, insulin mRNA and insulin receptor protein in brain, de-sensitization of insulin receptor and decreased levels and impaired functioning of downstream components of insulin signaling pathway in AD brain [46, 103, 104, 105, 106, 107]. Although the reasons for brain insulin deficiency or resistance in AD are not clear, it is worthwhile to state in this context that AB oligomers which accumulate in AD brain as a primary pathologic process can bind to brain insulin receptors and induce the re-distribution of the receptors from the membrane to the cytosol leading to impaired insulin signaling [98]. Likewise, AB oligomers can abnormally activate TNF- α /JNK pathway causing phosphorylation of serine residues of IRS-1 and blocking insulin signaling downstream [98]. Whatever may be the mechanism, insulin deficiency and resistance of 'type 3' diabetes can directly contribute to the genesis of AD pathology in the brain as a primary process by enhancing Aß accumulation and tau phosphorylation. In conformity with this idea of brain insulin deficiency and resistance in intracerebro-ventricular administration AD. of streptozotocin in mice causes AD like neuropathology and cognitive deficits [46, 108]. However, this proposition of AD per se as a case of 'brain diabetes', though attractive, needs further scrutiny, and rather it may be more logical to think that insulin deficiency and resistance is conferred on AD brain secondarily by coexisting peripheral insulin resistance diseases like type 2 diabetes. In turn, the brain insulin resistance aggravates the AD pathologic process presumably by altering APP expression, processing, trafficking and degradation and / or phosphorylation of tau or by causing metabolic perturbations, oxidative stress and mitochondrial dysfunctions through inter-dependent pathways. The possibility that co-existing type 2 diabetes accelerates AD pathogenesis is not only supported by epidemiological evidence, but also by studies in transgenic Tg2576 AD mice in which dietary high fat induced insulin resistance promotes $A\beta$ peptide generation and amyloid plaque formation in the brain [109]. Another recent study has shown that cross-mating of ob/ob or NSY diabetic mice models with APP transgenic mice results in double transgenic animals in which both AD and type 2 diabetes pathologies are aggravated [110]. Although acute infusion of insulin in peripheral circulation tends to raise CSF insulin, in type 2 diabetes, chronic hyperglycemia and hyperinsulinemia lead to decreased entry of insulin in to brain resulting in lower CSF and brain insulin levels and a state of brain insulin deficiency [101, 111, 112]. Thus both insulin deficiency and insulin resistance would be present in AD brain as a result of co-existing type 2 diabetes. However, the molecular defect that generates insulin resistance in type 2 diabetes is neither precisely known, nor it is known whether the mechanism of insulin resistance is the same for all tissues like skeletal muscles. adipose tissue or liver. Thus, it will be an interesting area of exploration to elucidate the mechanism of brain insulin resistance in type 2 diabetes and its consequence on the co-existing AD pathology. A corollary of this complex interaction of type 2 diabetes and AD is the possibility of a beneficial effect of insulin or insulin-sensitizers in blocking the genesis and progression of sporadic AD, but the results are still not unequivocal in this respect [103, 113, 114].

Hyperhomocysteinemia

Hyperhomocysteinemia has been well recognized as a cardiovascular risk factor from epidemiological and experimental studies [115]. The causes of hyperhomocysteinemia in general population are multiple and include both genetic and non-genetic mechanisms. The mutations of genes coding for major enzymes involved homocysteine remethylation in or transulfuration pathways e.g. cystathionine β synthase, synthase, methylene tetrahydrofolate methionine reductase etc. can lead to hyperhomocysteinemia [116]. The deficiency of vitamin cofactors of homocysteine metabolism like vitamin B12, folate and pyridoxine may also be responsible for hyperhomocysteinemia in general population [116].

Many case-control as well as prospective studies have associated high plasma homocysteine with AD which has been well reviewed in a recent publication [117]. Several large -scale long follow-up studies have demonstrated an increased risk of AD with high plasma total homocysteine after adjustment of other variables [118, 119]. In the Framingham Offspring Study, 2096 participants have been examined seven times for multiple parameters for 30 years followed by a battery of neuropsychological tests, and an inverse association of plasma total homocysteine with multiple cognitive domains has been noted in subjects above 60 years or above [120]. A recent meta-analysis of eight cohort studies has also confirmed the association of hyperhomocysteinemia with increased risk of AD with an odds ratio of 1.35 for every 5 µmol/L increase in plasma homocysteine [121]. Many epidemiological studies have simultaneously measured plasma total homocysteine, folate, vitamin B12, vitamin B6 in cohorts in relation to AD risk and established that hyperhomocysteinemia is associated with deficiency of these vitamins [118, 122, 123, 124, 125]. There has been a general optimism that corrections of hyperhomocysteinemia by supplementation with folate, vitaminB12 and vitamin B6 would be beneficial in preventing or halting AD progression [126]. However, several interventional epidemiological studies have shown that while hyperhomocysteinemia can be reversed by supplementation with vitamin B12, folate, pyridoxine etc., the dementia is not improved [127, 128]. Since homocysteine is a known vascular risk factor, it is likely that hyperhomocysteinemia probably contributes to vascular component of AD pathology. Several casecontrol studies have shown that the degree of hyperhomocysteinemia is more in typical vascular

dementia than in AD [129, 130]. Nevertheless, many experimental studies have shown that homocysteine in higher than physiological concentrations can induce a wide range of neurotoxic effects involving oxidative stress, excitotoxicity, mitochondrial dysfunction, DNA damage and apoptosis implying that hyperhomocysteinemia may directly contribute to AD neurodegeneration [117, 131, 132, 133].

Adipokines

The fact that AD is accompanied by significant metabolic changes in the brain and altered food intake and body weight, some significant studies, epidemiological and experimental, have been made on the role of adipokines like leptin and adiponectin in AD. Adiponectin regulates glucose, lipid and energy metabolism and insulin sensitivity in many tissues through AdipoR1 and AdipoR2 receptors using complex signaling mechanisms involving AMPK, p3-MAPK, PPAR-α and NF-kβ [134, 135, 136]. The role of adiponectin in regulating brain metabolism and function is less established, but the globular, trimeric and hexameric forms of the hormone are believed to cross the blood-brain barrier and act on receptors present in different brain areas [137]. Under physiological conditions, adiponectin may be responsible for regulation of energy metabolism of the brain and control of food intake [137]. The other important adipokine, leptin, acts through Ob-Rb (the long form of the receptor) utilizing an array of downstream signaling mechanisms e.g. Jak-Stat, Erk, PI3K/Akt and AMPK [138, 139] Leptin is known to affect satiety, food intake and body weight through its action in hypothalamus, but the hormone has more diverse neurotrophic and neuroprotective actions in the brain and also affects hippocampal neurigenesis and long-term potentiation [138, 139, 140]. Several case-control and large population based prospective studies have shown an inverse association of circulating leptin levels with AD or general cognitive decline [141, 142, 143]. In case of adiponectin the epidemiological link with AD risk is less clear. Some case-control and large follow-up studies have shown an association of higher circulating level of adiponectin with increased risk of AD, but others have not replicated these findings [144, 145, 146]. A recent case-control study has measured the serum levels of adiponectin and leptin in the same cohorts of AD and confirmed a raised level of adiponectin and a lower leptin level in serum of AD subjects which are in good correlation with the severity of the disease as measured by MMSE scores [49]. Extensive experimental studies in cell lines and AD transgenic mice have indicated that leptin can affect APP-AB trafficking, A β accumulation and clearance, β secretase expression as also phosphorylation of tau protein [139, 140, 147].

Adiponectin on the other hand may have a proinflammatory role in AD brain [137].

Proinflammatory cytokines

The AD brain elicits a strong inflammatory response primarily by activated microglia and to a lesser extent by astrocytes. The microglia during inflammatory response show typical morphological changes with expression of specific surface markers and release of proinflammatory interleukins, interferons, chemokines and reactive oxygen species [39, 40, 148, 149]. On the other hand, as part of this inflammatory response, an alternative activation of microglia and acquired deactivation take place which helps in repair, resolution and neuroprotection [149]. In AD brain the activation of the microglia is triggered by oligomeric amyloid beta peptide and amyloid fibrils and the resulting pro- inflammatory response mediated by IL-1, IL-6 and TNF- α , complement system, chemokines etc. plays an important role in neurodegeneration of AD, while anti-inflammatory cytokines IL-4, IL-10 and TGF-B also liberated from the microglia may assist in neuroprotection [40, 148, 150, 151, 152]. The role of pro-inflammatory cytokines in AD pathogenesis has recently gained some intense attention because of the evidence suggesting the activation of the inflammosome, NLRP3, in the brain of transgenic AD mice and patients of mild cognitive impairment and AD dementia [153, 154]. The inflammosomes. intracellular the multi-protein complexes consisting of nucleotide binding oligomerization domain (NOD)- like receptor proteins adaptor proteins and downstream effector (NLRP), proteins, become activated by a wide array of pathogen and danger related molecular patterns through NLRP [42, 154]. There are several types of inflammosomes, but the microglial NLRP3 which is coupled to ASC (apoptosis associated spec-like protein containing caspase recruitment domain) and caspase 1 probably plays a key role in AD pathogenesis [42, 154]. The phagocytosed fibrillar amyloid beta peptide within microglia activates NLRP3 through lysosomal degradation leading to activation of caspase 1 that induces maturation and secretion of pro-inflammatory cytokines IL-1ß and IL-18 [41, 154]. However, independent of the brain immune response, raised levels of circulating proinflammatory cytokines have been generally reported in AD subjects in both longitudinal as well as case-control studies, though significant variability has also been noted [155, 156, 157, 158]. A systematic meta-analysis of published reports has clearly shown that raised serum levels of IL-6, TNF- α and IL-1 are associated with increased risk of AD [159]. Some studies have measured serum and CSF levels of cytokines simultaneously in AD subjects, but generally serum level is not reflective of that of CSF [159]. A recent casecontrol study of a relatively small sample size has suggested that raised levels of proinflammatory cytokines like IL-6, IL-1 β and TNF- α are present only in AD patients with associated depression [160]. The communication pathways between the peripheral immune system and the CNS have been identified in details which include both humoral and neural mechanisms, and through the raised levels of peripheral this proinflammatory cytokines can increase the CNS production of cytokines which have varied actions in CNS through widely distributed receptors [161, 162]. The cytokines have neuromodulatory and neurotrophic actions and can also affect neurigenesis, synaptic plasticity, synaptic scaling, neurotrasmitter turnover and the activity of hypothalamus-pituitary axis [162, 163]. Thus, the activation of peripheral immune system during systemic infection after systemic injection or of lipopolysaccharides or endotoxins or interleukins can cause behavioral and cognitive alterations in animals and human beings [164, 165, 166]. Additionally, this mechanism may be causal to many psychiatric and neurological diseases [148, 167, 168]. In the context of AD pathogenesis, the central pro-inflammatory cytokines have been shown to enhance the phosphorylation of tau or production of amyloid beta peptide and potentiate the neurodegeneration process [148, 169, 170].

Vitamin D

Vitamin D₃ synthesized from 7-dehydrocholesterol in the epidermis by photochemical reaction is sequentially hydroxylated in liver and kidney by cytochrome P450 dependent enzymes to produce 1,25 dihydroxy vitamin D_3 , the active form of vitamin D_3 , which acts as a hormone producing diverse effects in tissues apart from its classical role in Ca^{2+} and phosphate metabolism [171]. The serum level of vitamin D₃ is typically monitored by measuring 25-hydroxy vitamin D₃. Vitamin D has both genomic and non-genomic actions mediated by nuclear and membrane receptors respectively, and the receptor VDR is identical in both the locations [171, 172]. The nuclear VDR heterodimerizes with retinoid X receptor and in concert with several coactivators regulates the transcription of a wide variety of genes in different tissues [171, 172]. In CNS development, vitamin D helps in neuronal differentiation and axonal growth, and in the adult brain it regulates the synthesis of neurotrophic factors and neurotransmitters and also exhibits neuroprotective and antioxidative functions [173, 174, 175].

The association of VDR polymorphism with increased risk of AD has been shown in several studies. The polymorphism in intron 8 recognized by ApaI, but not one recognized by TaqI in exon 9, is associated with increased risk of AD [176]. Another promoter SNP

(single-nucleotide polymorphism) corresponding to the transcription factor Cdx-2 binding region of VDR gene has also been linked to increased risk of AD [177]. Haplotype analysis of 5 polymorphic sites has shown that the frequency of TaubF haplotype (alleles of TaqI, ApaI, Tru9I, BsmI, FokI) is significantly higher in AD patients [178]. Several observational case-control studies have indicated that the deficiency of plasma 25-hydroxy vitamin D₃ is associated with cognitive decline in elderly or with AD [179, 180]. A large population based prospective studies of Danish subjects over a follow up period of 30 years has concluded that 25-hydroxy vitamin D3 deficiency increases the risk of AD [181]. Other studies have shown that plasma vitamin D is an important determinant of cognitive status, CSF Aβ42 level and brain volume in patients of AD, MCI and subjective cognitive impairment [182].

In cell based experiments, vitamin D has been shown to inhibit A β induced cytotoxicity and apoptosis in cultured cortical neurons [183]. In post-mortem AD brain, a decreased level of VDR mRNA has been reported in hippocampal region [184]. 1, 25 dihydroxy vitamin D has been shown to increase the clearance of A β peptide from mouse brain [185]. In neuroblastoma cells, VDR overexpression or vitamin D treatment increases APP transcription [177]. The macrophages from AD subjects show decreased phagocytosis of soluble A β , and thus delay the clearance of amyloid beta load of the brain [186]. 1, 25, dihydroxy vitamin D₃ alone or in combination with curcuminoids can strongly activate the macrophages from AD subjects to remove $A\beta$ by phagocytosis [186]. A vitamin D3-enriched diet has been shown to decrease the amyloid plaque load and inflammatory reaction and increase NGF production in the brain of AD transgenic mice [187]. It appears plausible that vitamin D, because of its diverse genomic and non-genomic effects in CNS, will impact amyloid pathogenesis at multiple levels.

Metabolic Risk Factors of AD: Future Possibilities

Epidemiological studies as mentioned here have identified several important metabolic risk factors having moderate to strong association with AD, but these reports also exhibit extreme variability in many cases. Moreover, neuropathological autopsy studies in large cohorts have often not supported the epidemiological data. The experimental studies have also not convincingly elucidated the pathways that could link these risk factors to the disease pathogenesis. Much of this confusion has arisen from the inherent uncertainty of AD diagnosis, absence of simple and specific biomarkers for disease identification, ambiguity in neuropathology, incomplete understanding of pathogenesis and frequent absence of correlation between clinical severity and the extent of neuropathology. Thus, the effectiveness of risk factor modification by drugs (e.g. statins, B vitamins, vitamin D, insulin or other anti-diabetic agents and anti-depressants) or life-style management to halt the progression of AD has not been firmly established. However, this is a possibility with significant optimism because of the scarcity of effective drugs for the treatment of AD, the recent major failure of anti-amyloid therapeutics in clinical trials and uncertain effectiveness of potential disease-modifying agents [188, 189]. Another important issue should also be addressed at this point with regard to experimental models used for AD research. There is no proper animal model for sporadic AD, but an overwhelming emphasis has been given on transgenic AD models to understand the disease pathogenesis. It is intuitively illogical to assume that the pathogenesis of sporadic AD which occurs without any definite mutation would be explained by a transgenic model harboring single or multiple mutations. The clear identification of metabolic risk factors may help us to develop a disease model that would truly simulate sporadic AD pathogenesis.

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Conflicts of Interest:

The authors declare no conflict of interest.

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