PKR, the double stranded RNA-dependent protein kinase as a critical target in Alzheimer’s disease

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Abstract

Amyloid β-peptide (Aβ) deposits and neurofibrillary tangles are key hallmarks in Alzheimer’s disease (AD). Aβ stimulates many signal transducers involved in the neuronal death. However, many mechanisms remain to be elucidated because no definitive therapy of AD exists. Some studies have focused on the control of translation which involves eIF2 and eIF4E, main eukaryotic factors of initiation. The availability of these factors depends on the activation of the double-stranded RNA-dependent protein kinase (PKR) and the mammalian target of rapamycin (mTOR), respectively. mTOR positively regulates the translation while PKR results in a protein synthesis shutdown. Many studies demonstrated that the PKR signalling pathway is up-regulated in cellular and animal models of AD and in the brain of AD patients. Interestingly, our results showed that phosphorylated PKR and eIF2α levels were significantly increased in lymphocytes of AD patients. These modifications were significantly correlated with cognitive and memory test scores performed in AD patients. On the contrary, the mTOR signalling pathway is down-regulated in cellular and animal models of AD. Recently, we showed that p53, regulated protein in development and DNA damage response 1 and tuberous sclerosis complex 2 could represent molecular links between PKR and mTOR signalling pathways. PKR could be an early biomarker of the neuronal death and a critical target for a therapeutic programme in AD.

Keywords: Alzheimer’s disease • control of translation • PKR • mTOR • apoptosis

Introduction

Alzheimer’s disease (AD) is a neurodegenerative disease and the most common form of dementia which causes serious impairments of cognitive functions. The majority of AD cases in people over the age of 65 are of the sporadic (or ‘late onset’) form, suggesting that the disease has no family link. However, about 2–5% per cent of the Alzheimer population have ‘familial’ (FAD) or ‘early onset’ AD via autosomal dominant inheritance. FAD is identical to the sporadic form but it occurs because of the inheritance of certain genes which at some point in the family’s history ‘mutated’ from having normal to abnormal characteristics. Most cases of FAD result from mutations in one of the three following genes: the amyloid precursor protein (APP), the presenilin 1 and 2 (PS1, PS2). All mutations result in elevated levels of amyloid-β (Aβ) peptide [1]. The most important genetic risk factor for both familial and sporadic forms of AD is the apoE4 gene [2, 3]. ApoE4 enhances the rate of amyloid fibril formation, interacts with the microtubule-associated proteins (MAPs) [4, 5] and directly affects cholinergic activity in the brains of AD patients [6]. Two studies
also confirm the association between genetic variants in sortilin-related receptor (SORL1) and AD [7, 8]. SORL1 binds APP and acts as a sorting receptor for APP. Absence of SORL1 switches APP away from the recycling endosomes pathway and instead leads APP to the β- and γ-secretase cleavage pathways to generate Aβ [7]. However, it is unclear whether these changes are causal or simply reactive to AD.

AD is characterized by three major pathologic hallmarks: extracellular plaques of the 39–43 amino acid Aβ aggregated, intracellular neurofibrillary tangles (NFTs) composed of hyperphosphorylated τ-protein and neuronal death. Aβ is derived by proteolytic cleavage of APP. The action of β-secretase liberates a C-terminal fragment, which is subsequently processed by γ-secretase to release Aβ. Cleavage by γ-secretase releases a number of Aβ species, which vary in length. Presenilin proteins are an integral part of γ-secretase complex involved in the processing of APP. The major form of Aβ contains 40 amino-acid residues (Aβ 40), although minor C-terminally extended forms (Aβ42 and Aβ43) are also produced. Aβ42 has a higher propensity to aggregate than Aβ40 and evidence from several studies indicates that increased production of Aβ42 is closely associated with the development of AD [9–11]. Besides amyloid plaques, NFTs are composed of arrays of paired helical filaments as described for the first time by Kidd [12]. NFTs are mainly localized in the hippocampus, entorhinal cortex and amygdala. Paired helical filaments are structures generated by self-aggregation of hyperphosphorylated τ-proteins making a compact filamentous network [13].

Furthermore, increasing evidence suggests that inflammation significantly contributes to the pathogenesis of AD. Research performed in the last 20 years supports the hypothesis of Fisher [14]. Senile plaques might be the result of an inflammation mediated regenerative response of surrounding nerve fibres against extracellular deposits of a foreign substance. In the following years, it was shown that the ‘foreign’ substance, now identified as Aβ fibrils, could indeed induce a local inflammatory response [15, 16]. However, the chronic inflammatory response in AD brains is described in the plaques containing fibrillar Aβ deposits but not in the diffuse plaque with the non-congophilic low-fibrillar Aβ depo-
sitions [17, 18]. A spectrum of inflammatory mediators up-regulated in AD has been demonstrated [16, 19–22] and indicates that such inflammation is an important part of pathology and suggests many routes for future therapeutic intervention.

Yet, it is clear that a variety of cellular mechanisms can lead to this neurodegenerative disorder. Elucidation of the factors that trig-
er the sequence changes in the normal neuronal machinery leading to neurodegeneration and the mechanisms underlying signal trans-
ductions that determine neuronal death in AD brains is of utmost importance because no definitive therapy exists for resolution.

Some works reported the mitotic hypothesis in which vulnerable neurons in the AD brain do not only show activation of cell cycle components, but at least in some cases, show evidence of DNA replication (S-phase) prior to neuronal death [23]. Studies of the lysosomal system in AD identified a robust mobilization of this system and its impairment in neurons, which may actively promote disease pathogenesis not only by accelerating amyloidogen-

**Control of translation**

In eukaryotes, protein translation includes four consecutive phases: initiation, elongation, termination and ribosome recycling. The initiation phase corresponds to the connection between mRNA and ribosomes. The elongation phase includes the links between amino acids at the ribosomal level, and is followed by the termination phase at the level of stop codon and then by the dissociation of ribosomal subunits. All phases are regulated by proteins called translation factors, which can interact directly with mRNAs but most regulation is exerted at initiation where the start codon is identified and decoded by the methionyl tRNA specialized for initiation (Met-tRNAi). The process of initiation can be divided into three stages: (1) association of Met-tRNAi and several initiation factors with the 40S ribosomal subunit to form the 43S pre-initiation complex (PIC); (2) the binding of this complex to mRNA, followed by its migration to the correct start codon and (3) the addition of the 60S ribosomal subunit to assemble an 80S ribosome at the initiation codon, ready for elongation [31, 32]. In the first stage, the binary eukaryotic initiation factor (eIF)2-GDP complex requires eIF2B, a guanine nucleotide exchange factor to catalyze the regeneration of the eIF2-GTP complex for recruitment of the initiator tRNA and conduct it as a eIF2-GTP-Met-tRNAi ternary complex (TC), [33, 34]. Then, the TC is associated to eIF1, eIF1A, eIF3 and eIF5 to form the PIC. eIF1 collaborates with eIF1A to promote scanning from the 5′ end in order to select the start codon [35, 36]. The multi-subunit factor eIF3 plays a role in the PIC assembly and in the recruitment of PIC to the mRNA [37]. The 43S PIC binds near the cap with the eIF4F complex (eIF4E, eIF4G and eIF4A) which covers the 5′ terminal methyl-GTP cap of the mRNA. In mammals, eIF3 forms a protein bridge to the mRNA by interacting with eIF4G [36]. The poly(A) binding protein interacts with eIF4G and mediates circularization of the mRNA by linking the cap to the poly(A) tail in a ‘closed loop’. The mRNA is activated and the 48S assembly can start the scanning of the start codon in

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an ATP-dependent reaction and partial hydrolysis of eIF2-bound GTP in the TC to eIF2-GDP-Pi [31]. When start codon is recognized, eIF1 is dissociated from the 40S, allowing the release of Pi and eIF2-GDP. Then, eIF5B-GTP catalyses the joining of the 60S subunit and then this second GTP hydrolysis triggers release of eIF5B-GDP and eIF1A to yield the final 80S initiation complex [36].

Translation of mRNAs into proteins is recognized as an important site of regulation of gene expression, with the initiation stage as the most commonly observed target for physiological control. Two particular steps of the initiation pathway appear to be hot spots for physiological regulation, the binding of Met-tRNAi to the 40S ribosomal subunit, mediated by eIF2, and the initial binding of the 43S PIC to the 5'-end of mRNA, mediated by eIF4E and associated factors (Fig. 1). In addition, various cis-regulatory elements located in the 5'- and 3' UTRs (untranslated regions) control the synthesis of protein by employing one of the many mechanisms such as alterations in the stability of the mRNA, its accessibility to the ribosomes, its circularization and interaction with the translation machinery [38]. In the 5' UTR of an mRNA, multiple upstream open reading frames (uORFs) influence translation rate and the impairment of these elements result in several human diseases, for example hereditary thrombocytopenia by efficient expression of thrombopoietin [39], AD by enhancing B-site APP-cleaving enzyme 1 (BACE1) expression [40], bipolar affective disorder by mutation in the uORFs of 5-hydroxytryptamine receptor 3 [41]. The exact process by which these inhibitory uORFs are bypassed is currently unknown. The microRNAs (miRNAs) are cis-regulatory elements in the 3' UTR and also regulate the translation by controlling the localization and stability of the mRNA. Mutations affecting the termination codon, polyadenylation signal and secondary structure of 3' UTR of mRNA can cause diseases but this association needs to be confirmed [42, 43].

The control of eIF2 is linked to the state of phosphorylation at serine 51 site on the α-subunit. When phosphorylated, eIF2α becomes a competitive inhibitor of the 5-subunit guanine nucleotide exchange factor, eIF2B, and decreasing TC assembly [44, 45] (Fig. 1). There are four different eIF2α kinases in mammals activated by different stress, PKR (double-stranded (ds) RNA-dependent protein kinase), PKR-like endoplasmic reticulum kinase, heme regulated kinase and amino-acid regulated kinase, which phosphorylate the same residue in eIF2α, resulting in down-regulation of general translation [46]. However, in mammalian cells there is a reinitiation mechanism as in the yeast which overcomes the inhibitory effects of uORFs and allows the transcriptional activation of stress response genes including the regulatory subunit of an eIF2(αP) phosphatase (GADD34) to provide a negative feedback [46].

Several studies revealed an increased PKR expression with ageing [47] or in neurodegenerative diseases such as AD, Parkinson's disease, Huntington's disease [48–50] or the phosphorylation of eIF2α in cerebral ischemia-reperfusion, hypoxia or zinc toxicity [51–53]. It is demonstrated that these kinases play an important role in the process of cellular apoptosis by interacting with protein synthesis and apoptotic factors. Besides, the β-isoform of the glycogen synthase kinase-3 (GSK3β) can phosphorylate the ε subunit of eIF2B blocking the GDP/GTP exchange eIF2 and
induce memory deficits in vivo and may be involved in neuronal defence systems [55].

PKR is an interferon (IFN) inducible eIF2α kinase that binds to dsRNA and then undergoes homodimer formation and autophosphorylation at several sites, resulting in its activation [56]. Considerable evidence confirmed that PKR, an ubiquitous protein, plays an important role in host defence against virus infection. However, in response to stress signals, an additional dsRNA-independent mechanism of activation of this enzyme is mediated by the human protein PACT (PKR-associated activator) or murine RAX (PKR activator X) in vitro and in vivo [57, 58]. Important roles in the regulation of protein synthesis and the control of cell growth and survival were demonstrated for PKR [44, 59, 60]. Several studies established that activation of PKR can either induce apoptotic cell death or at least enhance this process when apoptosis is initiated by other agents [61, 62]. Conversely, in cells deficient for the kinase or containing a dominant-negative form, there is substantial resistance to apoptosis [30, 61, 63]. It is not clear whether the phosphorylation of eIF2α is sufficient to mediate the pro-apoptotic effects of PKR. The cell expression of an inhibitor of eIF2α phosphorylation or the non-phosphorylatable eIF2α mutant does partially protect cells from apoptosis [63]. Many studies performed in virus-infected cells reported that PKR regulates also different signal transducers, in particular, p53 [64], NF-κB (nuclear factor-κB) [65], mitogen-activated protein kinases (MAPK) [66], FADD (Fas-associated protein with a death domain)/caspase-8 [65, 67], signal transducers and activators of transcription (STAT) [68] and activating transcription factor 3 (ATF-3) [69].

The availability of the eIF4E factor is linked to the binding of specific proteins called 4E-BPs. When these proteins are non-phosphorylated, they have a great affinity for eIF4E, which is unable to bind the eIF4F complex, leading to the inhibition of the recognition of the mRNA 5’ cap structure [70], (Fig. 1). These proteins are mainly phosphorylated by a kinase called mTOR (mammalian target of rapamycin) or FRAP (FKBP12-rapamycin complex-associated protein) [71, 72] (Fig. 1). mTOR, is an essential serine/threonine protein kinase that functions in two distinct multiprotein complexes, mTOR complex 1 and 2 [73, 74]. mTOR complex 1 is inhibited by rapamycin and is thought to couple growth cues to cellular metabolism; mTOR complex 2 is not inhibited by rapamycin and appears to regulate spatial aspects of growth such as cell polarity. mTOR can also phosphorylate eIF4G, the ribosomal S6 kinases (RSK) such as p70S6K which phosphorylate eIF4B, enhancing its interaction with eIF3 and stimulate protein synthesis [75–77] (Fig. 1). The regulation of mTOR activity is important for the availability of eIF4E. mTOR is activated by the phosphoinositide 3-kinase (PI3K) and protein kinase B (Akt/PKB) pathway [70], (Fig. 1). The mTOR signalling is physiologically active and allows protein and ribosome synthesis. Many studies have shown that cellular stress can increase the binding of 4E-BPs to the eIF4E factor and can reduce protein translation [59]. Recently, it has been demonstrated that two tumour suppressor genes, the tuberous sclerosis complex (TSC) gene TSC1 (or Hamartin) and TSC2 (or Tuberin) were negative regulators of mTOR phosphorylation [78] by blocking the small GTPase Rheb activity, which is a positive regulator of mTOR [79, 80].

In addition, the reduction of eIF4E level is not enough to induce cellular apoptosis [81] and PKR can induce dephosphorylation of the proteins 4E-BPs by increasing the activity of the phosphatase 2A after its interaction with the regulatory subunit B56α, leading to cell apoptosis [82–84]. Electrophysiological results have also demonstrated that mTOR could play a role in neuronal plasticity and in the process of learning and memory. In brain slices treated with the mTOR inhibitor rapamycin, the authors have observed a decrease of the late phase of LTP induced by synaptic stimulation or brain-derived neurotrophic factor (BDNF) exposure [85, 86]. Another signalling pathway is the Ras-MAPK pathway, which is responsible for the phosphorylation of eIF4E and eIF4B and strongly impacts translation [76] (Fig. 1).

According to these results, it appears interesting to study these two pathways: PKR (pro-apoptotic) and mTOR (anti-apoptotic), involved in the control of initiation, in different models of neurodegenerative disorders and in AD patients. Both these molecular signalling pathways were largely described in AD. Studies have also reported that brain tissues from patients with Parkinson’s and Huntington’s diseases displayed strong induction of phosphorylated PKR in hippocampal neurons compared with age-matched disease controls [49].

Dysfunctions of protein synthesis mediated by PKR- and mTOR-dependent signalling pathways

It has been recognized for several years that the mRNA translation was disturbed in the brains of AD patients [87]. The inhibition of the ribosomal translation could be responsible for the modifications of gene expression detected in affected brain regions. An increased phosphorylation of the elongation factor 2 was also noted in the AD brains [88].

For the last 8 years, studies have focused on the control of translation, in particular the control of initiation. Aβ exposure induces a sustained reduction of mTOR/p70S6K signalling in neuroblastoma cell cultures marked by a progressive decrease of phosphorylated mTOR and phosphorylated p70S6K [27, 89]. In addition, the mTOR signalling is reduced in the cortex but not in the cerebellum of APPSL/PS1 mutant transgenic mice. We also studied the control of translation in the newly engineered APPSL/PS1 knock in transgenic mice (APPSL/PS1 KI) which display, in addition to extracellular Aβ deposits, more than 50% CA1 neuron loss at 10 months of age, starting approximately at 6 months combined with intraneuronal Aβ accumulations [90]. In the brains of APPSL/PS1 KI mice at 3 and 6 months of age, we also analysed upstream and downstream factors of mTOR. Although...
mTOR levels were not modified, we found a great activation of Akt with a robust accumulation of PT389-Akt in non-apoptotic neurons at 6 months of age. By contrast, a significant decrease of the p70S6K phosphorylation was observed in brains of PS1 KI and APPSL/PS1 KI mice with a very weak or no nucleocytoplasmic PT389-p70/85S6K staining in apoptotic neurons of APPSL/PS1 KI mice. These findings demonstrate a clear dissociation between Akt and ribosomal S6K signalling markers in these mice which could be involved in the AD pathological process [91]. Furthermore, in the lymphocytes of AD patients the PT389-p70S6K/total p70S6K ratio was reduced in AD patients (n = 26) compared to control individuals (n = 28) and levels were positively correlated with Mini Mental Status Examination (MMSE) scores [27]. However, in a larger cohort, our recent results showed no significant difference between AD and control groups for the levels of PT1462-TSC2 (control: 2.39 ± 0.59 [n = 36]; AD: 2.48 ± 0.51 [n = 50]), PS2448-mTOR (control: 0.9 ± 0.1 [n = 38]; AD: 1.34 ± 0.2 [n = 49]) and PT389-p70S6K (Control: 4.83 ± 1.01 [n = 32]; AD: 3.87 ± 0.53 [n = 50]). Other studies showed significant increases of P-p70S6K (T389 and T421/S424), P-mTOR (S2481), P-4E-BP1 (T70 and S65) in homogenates of the medial temporal cortex in AD patients as compared to control brains [92, 93]. The levels of the mTOR signalling markers were significantly and positively correlated with total tau and P-tau [92, 93]. Taken together, one may propose that there are two different neuronal responses: some neurons are characterized by a highly reactive Akt/mTOR/RS6K signalling pathway in adult brains of AD patients compared to control brains [92, 93].

Crosslink between the up-regulation of PKR/eIF2α and the down-regulation of mTOR/RS6K in AD

Besides the eIF2α factor, PKR can phosphorylate other targets, which could explain the role of PKR in the control of translation. It is known that PKR is physically associated with p53 and phosphorylated it in mouse embryo fibroblasts cells treated with IFN [64]. Furthermore, reports showed that p53 activation is able to inhibit the activity of mTOR through a pathway involving the subsequent activation of TSC gene products TSC1 and TSC2, which are tumour suppressors and negative regulators of mTOR [78, 103–105]. In addition, authors have discovered a new transcriptional target of p53, Redd1 (regulated protein in development and DNA damage response) named also DDIT4/RTP 801/dig 2 [106, 107]. Redd1 is a new stress-induced protein and is known as a negative regulator of mTOR through TSC1/TSC2 complex [106–115]. Redd1 appears to function in the regulation of cellular ROS, a pathway linked to both stress responses and modulation of growth factor signalling [110]. Data demonstrated that endogenous Redd1 is induced following energy stress and inhibition of endogenous Redd1 increases cell size in a rapamycin-sensitive manner [111]. The interaction between these factors and PKR was mainly described in IFN-treated or virus-infected models and in hypoxia-induced models. However, the possible link between these two signalling pathways through p53, Redd1 and TSC2 remains yet unknown in AD.

A clinical study was conducted in lymphocytes of AD patients isolated from whole blood. The results showed that the expression of p53 and Redd1 genes, the activation of p53 and the levels of Redd1 protein were significantly higher in lymphocytes of AD patients compared to age-matched controls. Furthermore, statistical correlations between proteins and genes suggest that active PKR could phosphorylate p53, which could induce the transcription of Redd1 gene. However, p53 and Redd1 at transcriptional and translational levels were not correlated with the MMSE scores.
the cells from A
releases TSC2 which is dephosphorylated to inhibit the mTOR to hypoxia [127]. In fact, Redd1 can bind 14–3-3 proteins and so nous TSC2/14–3-3 proteins and inhibition of mTOR in response endogenous Redd1 is required for both dissociation of endoge- nously regulates TSC2 [125, 126]. A recent study showed that interaction is dependent of the TSC2 phosphorylation and nega- tively regulates TSC2 [125, 126]. A recent study showed that endogenous Redd1 is required for both dissociation of endoge- nous TSC2/14–3-3 proteins and inhibition of mTOR in response to hypoxia [127]. In fact, Redd1 can bind 14–3-3 proteins and so releases TSC2 which is dephosphorylated to inhibit the mTOR activity. Authors showed that the antisense Redd1 gene protected the cells from A9 neurotoxicity [128]. Recently, we showed that the transfection of PKR siRNA to A942 peptide induced the expres- sion of a repertoire of proteins in neurons involved in the control of cell cycle until the phase G2 with the expression of the cyclin B1 for the maturation promoting factor in order to re-enter the cell cycle [133–137]. However, little is known about the possible causes of the neuronal cell cycle re-entry and its subsequent regu- latory failure. In neurons that express high levels of Bax (apop- totic mRNA transcriptionally activated by p53), the G2 arrest will lead to apoptosis and in neuronal populations that are not-apop- tosism competent, a prolonged G2 arrest could lead to the develop- ment of AD-type pathology with hyperphosphorylation of TSC2 negative regulation of CDK2 and positive CDKI. Interestingly, some CDK trigger phosphorylation of TSC2 levels, leading to its proteasomal degradation [125]. In our recent work, the PKR gene silencing induced an increase in the levels of PT146-TSC2 protein in A942-exposed SH-SY5Y cells. Thus, PKR also controls this state of phosphorylation of TSC2 perhaps through the activation of the proteasomal degradation of cyclin D1 involved in the increased phosphorylation of TSC2 when it is associated to CDK4/6 [139]. Then, TSC2 in PKR gene-silencing conditions can be blocked by sequestration with 14–3–3 proteins to prevent the inhibitory effect of TSC2 in the apoptosis dependent of PT146-TSC2 protein in A942-exposed SH-SY5Y cells. Thus, PKR: a potential biomarker of AD diagnosis

At present, AD cannot be diagnosed until dementia appears and the specificity in the discrimination of AD and other dementia with cerebrospinal fluid biomarkers (total-β, phospho-β and Aβ 1–42) is not absolute. Thus, the identification of early disease-related tar- gets is crucial to improve diagnostic accuracy and/or to facilitate the development of new drug therapies. Candidate biomarkers should be molecules representing the altered cerebral molecular and cellular processes observed in AD. Furthermore, these bio- markers should be easily accessible. In this regard, many reports underline the great importance of the peripheral cells such as fibroblasts, platelets and mononuclear cells [101, 118, 124, 140–144]. Ray et al. [145] have found 18 signalling proteins in blood plasma that can be used to classify blinded samples from Alzheimer’s and control patients with close to 90% accuracy and to identify patients with mild cognitive impairment that progressed to AD 2–6 years later. Biological analysis of the 18 proteins points to systemic deregulation of haematopoiesis, immune responses, apoptosis and neuronal support in pre-symptomatic AD [145]. Thus, peripheral cell’s biomarkers, easily accessible, could facilitate an early diagnosis or help following the severity of disease. The control of translation through PKR/eIF2α signalling pathway is altered in AD lymphocytes as it was observed in brains of AD patients [50, 95]. In addition, we reported that PKR represents an initiator of deregulated translation via two consecutive targets p53 and Redd1 in AD lymphocytes [102]. However, our data showed that the number of mononuclear cells was significantly higher...
that such pro-inflammatory cytokines enter the CNS and activate microglia and astrocytes, or peripheral activated T cells promote activation of myeloid cells such as monocytes, macrophages and dendritic cells that secrete pro-inflammatory cytokines such as tumour necrosis factor (TNF-α), interleukin (IL)-1β and IL-6. In fact, there is some evidence of elevated IL-6 levels in monocytes derived from AD patients [154–156]. Recently, it was demonstrated that a blockade of TNF-α production at the periphery prevented histological lesions induced by IL-1β in CNS [157].

Furthermore, activated T cells also exist as infiltrates in the brains of AD patients [158–160]. In vitro data showed a ‘cross-talking’ between microglia and T cells, microglia can serve as antigen-presenting cells for Aβ-reactive T cells and, in turn, T cells themselves can influence microglial differentiation [161–163]. Different types of T cells would be expected to have different effects on microglial cell activation and therefore on amyloid clearance. T-helper 1 cells can promote microglial cell activation through the secretion of IFN-γ, which also up-regulates the expression major histocompatibility complex class II molecules by microglial cells, thereby enhancing the interaction between T cells and microglial cells [164, 165]. A study has shown that the interaction of CD40 (expressed on the surface of microglia) and CD40L (T-cell receptor) promotes pro-inflammatory microglial cell activation in
response to Aβ [166]. Furthermore, recent evidence revealed that peripheral T cells of AD patients overexpressed CXCR2 (XC chemokine receptor 2), which is intracerebral microglial TNF-α-dependent and is associated with T-cell adhesion on brain endothelia and transendothelial migration [167]. It is also known that glial cells can mediate the permeability of blood brain barrier to recruit specialized immune cells from the periphery such as T cells [164]. Besides these roles of peripheral immune cells in AD brains, further studies would be investigated to understand the deep interactions between glia and peripheral immune cells. These researches may reveal new targets modulating brain inflammation and help in developing novel immunotherapeutic approaches to AD.

Nevertheless, despite these several defence mechanisms, authors showed a cell cycle regulatory failure in lymphocytes as it was observed in neurons [130–132, 168, 169].

PKR is not specific to AD because it is also known to be active in other neurodegenerative diseases like Parkinson’s disease [49, 170]. Huntington’s disease [48] and amyotrophic lateral sclerosis [96]. PKR is not specific to neurodegenerative disease because it is also implied in infectious [61, 171], inflammatory [172, 173] and ischemic [171] pathology without cognitive decline. So, PKR may not be a biomarker of cognitive decline but rather an early biomarker of cell death. Indeed, many studies revealed the role of PKR in apoptosis induction. We can remember that the levels of phosphorylated PKR were significantly increased in brains of APP/PS1 KI mice as early as 3 months of age associated with intraneuronal amyloid peptide before the massive neuronal death observed at 6 months [97]. At present, there are five major effectors, eIF2α, FADD, p53, NF-κB and ATF-3 implicated in mediatingPKR-induced apoptosis [171]. In AD, eIF2α and p53 are targets of PKR [28, 30, 97, 102, 129]. NF-κB and ATF-3 activation by PKR is also involved in apoptosis induction as shown in virus-infected cells [69, 174–176]. However, NF-κB could be under the control of PKR in AD because this factor is activated in AD [177, 178]. In addition, FADD and the subsequent caspase-8 are responsible for PKR-induced apoptosis in virus-infected cells [179] and an overexpression of a dominant-negative FADD construct rescued SH-SYSY cells from either TNF-related apoptosis-inducing ligand or Aβ-induced neurotoxicity [180]. Recently, we demonstrated the physical and functional interactions between PKR and FADD in Aβ neurotoxicity (data submitted). Taken together, PKR could be a critical target in AD because of its early activation and its apoptotic effectors shared with Aβ.

Conclusion and perspectives

In conclusion, data revealed that PKR can represent an initiator of the dysfunction of the control of translation described in AD. In the brain, this disturbance is associated with the neuronal death while in peripheral mononuclear cells of AD patients, PKR can control the cell cycle and the inflammatory reaction. In brains of APP/PS1 KI mice, PKR was early up-regulated before the massive neuronal loss [97]. In patients, the PKR levels were correlated to the severity of the disease [101]. Thus, it is now interesting to develop molecules able to cross the blood brain barrier in order to target this early active kinase for the treatment of the disease which represents a great problem of public Health. However, PKR is a constitutive protein and all its physiological roles are yet unknown. Besides its role in the antiviral defence mechanism of the host, PKR controls the cell cycle, the proliferation and differentiation of cells. Thus, further studies will be needed to determine the best concentration of specific inhibitors only inhibiting the excessive active form of PKR or will have to use a therapeutic strategy specifically directed to neurons to prevent the activation of PKR involving in their apoptosis.

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