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# Systematic Review Article

# Physiological Roles of Hippo Signaling Pathway and Autophagy in Dementia











# Abstract

Background: Dementia is a neurocognitive disorder associated with the aging brain and mainly affects the hippocampus and cerebral cortex. The Hippo signaling pathway and autophagy proteins have been found to be perturbed in the brain affected by dementia processes.

Objective: This systematic review aims to elaborate on the involvement of the Hippo signaling pathway and autophagy in modulating the progression and severity of dementia in aging.

Methods: Searches were conducted on MEDLINE, Google Scholar, Scopus, and Web of Science databases.

Results: The Hippo signaling pathway is dependent upon the transcriptional co-activator YAP/TAZ, which forms complexes with TEAD in the nucleus in order to maintain cell homeostasis. When the expression YAP/TAZ is reduced, transcriptional repression-induced atypical cell death, ballooning cell death, and necrosis will consequently occur in the neurons. Moreover, the autophagic proteins, such as LC3, ATG proteins, and Beclin, are reduced, resulting in the disruption of autophagosome formation and accumulation and the spread of misfolded proteins in the brain suffering from dementia.

Conclusion: The impairment of the Hippo signaling pathway and autophagy in the dementia process in aging should be considered since it might predict the severity, treatment, and prevention of dementia.

Keywords: Aging, autophagy, brain, dementia, Hippo signaling pathway, neurodegeneration.



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# Physiological Roles of Hippo Signaling Pathway and Autophagy in Dementia

Andreas Christoper<sup>1</sup>, Herry Herman<sup>2</sup>, Rizky Abdulah<sup>3</sup>, Felix Zulhendri<sup>4,5,6</sup>, Ardo Sanjaya<sup>7,8</sup> and Ronny Lesmana<sup>9,10,11,\*</sup>

<sup>1</sup>Basic Biomedical Sciences Master Program, PMDSU Program Batch VI, Faculty of Medicine, Universitas Padjadjaran, Bandung, Indoran, Bandung, Indonesia; <sup>2</sup>Department of Orthopaedics, Faculty of Medicine, Universitas Padjadjaran, Bandung, Indonesia; <sup>3</sup>Department of Pharmacology and Clinical Pharmacy, Faculty of Pharmacy, Universitas Padjadjaran, Bandung, Indonesia; <sup>4</sup>Kebun Efi, Kabanjahe 22171, North Sumatera, Indonesia <sup>5</sup>Center of Excellence in Higher Education for Pharmaceutical Care Innovation, Universitas Padjadjaran, Bandung, Indonesia; <sup>6</sup>Division of Physiology, Department of Biomedical Sciences, Faculty of Medicine, Universitas Padjadjaran, Bandung, Indonesia; <sup>7</sup>Department of Anatomy, Faculty of Medicine, Maranatha Christian University, Bandung, Indonesia; <sup>8</sup>Postgraduate Program of Biomedical Science, PMDSU Program Batch V, Faculty of Medicine, Universitas Padjadjaran, Bandung, Indonesia; <sup>9</sup>Department of Biomedical Sciences, Physiology Division, Faculty of Medicine, Universitas Padjadjaran, Bandung, Indonesia; <sup>10</sup>Division of Biological Activity, Central Laboratory, Universitas Padjadjaran, Bandung, Indonesia; <sup>11</sup>Center of Excellence in Higher Education for Pharmaceutical Care Innovation, Universitas Padjadjaran, Bandung, Indonesia

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Received: June 07, 2022 Revised: November 25, 2022 Accepted: November 29, 2022

ARTICLE HISTORY

DOI: 10.2174/1874609816666230206144212 **Results:** The Hippo signaling pathway is dependent upon the transcriptional co-activator YAP/TAZ, which forms complexes with TEAD in the nucleus in order to maintain cell homeostasis. When the expression YAP/TAZ is reduced, transcriptional repression-induced atypical cell death, ballooning cell death, and necrosis will consequently occur in the neurons. Moreover, the autophagic proteins, such as *LC3*, *ATG* proteins, and *Beclin*, are reduced, resulting in the disruption of autophagosome formation and accumulation and the spread of misfolded proteins in the brain suffering from dementia.

*Conclusion*: The impairment of the Hippo signaling pathway and autophagy in the dementia process in aging should be considered since it might predict the severity, treatment, and prevention of dementia.

PROSPERO registration number CRD42022337445.

Keywords: Aging, autophagy, brain, dementia, Hippo signaling pathway, neurodegeneration.

# **1. INTRODUCTION**

Dementia is a term that refers to a group of neurocognitive disorders marked by gradual memory impairment and cognitive and motor deterioration. It is mainly a form of neurodegeneration that typically occurs during and is associated with aging [1, 2]. However, the dementia process is not the norm and does not occur in all aging processes. The loss of executive and memory function and attention, the reduction of grey and white matter volume, and other alterations of activity level in the brain occur in normal aging, but more gradually [3]. The progression of dementia accelerates in some populations with various risk factors, such as cardio-

<sup>\*</sup>Address correspondence to this author at the Department of Biomedical Science, Faculty of Medicine, Universitas Padjadjaran, Jl. Raya Bandung Sumedang KM 21, Jatinangor 45363, West Java, Indonesia; Tel: +6287736671707, E-mail: ronny@unpad.ac.id

vascular diseases. According to the CDC, African Americans and Hispanics have the highest prevalence of dementia among other races or ethnic groups. Alarmingly, the future generations of these groups are predicted to have a threefold increase in risks of dementia in their old age [4].

Moreover, the dementia progression in aging is accelerated in certain diseases, such as Alzheimer's disease, vascular dementia, or Lewy body disease. These diseases affect parts of the brain, albeit manifested in different types and levels of protein changes and gene expression belonging to similar pathways [5, 6]. Consequently, the hippocampus and cerebral cortex, the crucial structures in learning and memory functions, are damaged morphologically and functionally in dementia [2, 7].

The alteration and inactivation of the Hippo signaling pathway in the hippocampus and cerebral cortex have been causally linked to dementia-causing diseases. The reduction of Hippo signaling effectors proteins in the hippocampus and cerebral cortex is associated with the progression and severity of dementia [8, 9]. The Hippo signaling pathway modulates cell growth and death. It has been identified in Drosophila melanogaster and mammals [10]. Yes-Association Protein (YAP) and the transcriptional co-activator with PDZ-binding motif (TAZ) are essential components of the Hippo pathway. In Drosophila, YAP/TAZ or Yorkie binds to the TEA domain family member 1 (TEAD) transcription factor to regulate cell survival and death. Increased TEAD activity mediated by YAP is linked to cell proliferation and differentiation. An increase in p73 activity and a decrease in TEAD activity, on the other hand, promoted apoptosis and necrosis [10, 11].

The modulation of the Hippo pathway by amyloid precursor protein (APP) and amyloid  $\beta$  peptides has been studied. In agreement with the study by Tanaka *et al.*, intracellular amyloid  $\beta$  (A $\beta$ ) accumulation removes YAP from the nucleus in Alzheimer's disease. Reduced levels of nuclear YAP due to activation of the Hippo pathway in cortical neurons stimulate Hippo pathway-dependent necrosis and accumulation of the inflammatory cytokines [9, 11-13]. Therefore, the Hippo signaling pathway appears to be induced by A $\beta$  accumulation in the hippocampus, which promotes neuronal cell death and triggers neurodegeneration [14].

Proteins, such as amyloid  $\beta$  peptides and tau, accumulate in the brain and cause the simultaneous occurrence of microglia activation and neuronal damage. The activation of microglia is initiated by the senescence-associated secretory cytokines and chemokines, such as IFN $\gamma$ , IL-6, and IL-8, produced by astrocytes that undergo senescence [15, 16]. A $\beta$ accumulation has also been associated with the occurrence of fewer neurons and more microglia [14, 17]. In the hippocampus, the accumulation of A $\beta$  can cause aberrant mitochondrial dynamics and biogenesis defects [18].

According to the research conducted by Chen *et al.* and Manczak *et al.*, autophagy and mitophagy also play a significant role in the progression of dementia. The expression of the autophagy-associated genes, such as *ATG5*, *Beclin1*, and *LC3*, and mitophagy genes *BNIP3L*, *PINK1*, and *BCL2*, increases in the early onset of Alzheimer's disease but decreases in the late onset of disease. The dysregulation of autophagy genes will reduce misfolded protein degradation and consequently promote the accumulation of those proteins, thus increasing the severity of neurodegeneration and dementia [17-19].

The Hippo signaling pathway proteins, YAP/TAZ, play a role in regulating the autophagic flux by controlling the autophagosome and autolysosome. In addition, the autophagic flux maintains the homeostasis of cell proliferation and death by keeping YAP/TAZ at a constant level to prevent them from overpromoting nuclear cell growth [20]. When the Hippo signaling pathway is activated by external stimuli and the co-activator protein YAP/TAZ expression is reduced, the dysregulation of the formation and maturation of intracellular autophagosome and autolysosome occurs. This dysregulation will result in the failure of 'recycling' misfolded or damaged proteins and organelles, and consequently, untimely cell death occurs [11, 14]. To our knowledge, there is no systematic review exploring the relationship between the Hippo signaling pathway and autophagy in neurodegeneration and neuronal death in terms of the progression of dementia. Thus, the present review attempted to discuss the involvement of the Hippo signaling pathway and autophagy in modulating the progression and severity of dementia in aging.

#### 2. MATERIALS AND METHODS

The systematic review was conducted by searching the MEDLINE database, Scopus, Google Scholar, and Web of Science in August 2021. The guiding question was as follows: Are the Hippo pathway and autophagy involved in the process of dementia, and what are the roles of the Hippo pathway and autophagy in the progression of dementia? The search strategy is shown in Supplementary Table S1. The search was limited to papers published between 2011 and 2021. We included articles, not limited to in vitro studies, animal models, and clinical trials, that describe the outcome of any process of dementia concerning the Hippo pathway and autophagy and any condition influencing the Hippo pathway and autophagy in dementia. This study's exclusion criteria were review articles as they might impart biases and studies that do not explicitly illustrate the role of the Hippo pathway and autophagy in relation to dementia and aging.

The titles and abstracts of the papers that fulfilled the eligibility criteria were evaluated independently by two investigators. If feasible, the full text of the publications was retrieved. Only English-language publications were included. Any disagreements regarding the eligibility of a particular article were resolved through discussion with a third investigator. The papers were then exported to Mendeley. The data were collected from the article, such as methodology, the outcome of the study, and references. The collected data were then tabulated in Microsoft Excel.

#### **3. RESULTS AND DISCUSSION**

#### 3.1. Characteristics of the Included Studies

A total of 425 scientific articles were retrieved from MEDLINE, Scopus, Google Scholar, and Web of Science (Fig. 1). The articles were first screened through the titles and abstracts, resulting in sixty articles. Further screening of the full texts was carried out, and nineteen articles were excluded because they did not explore the relationship between



Fig. (1). The screening process of the included studies. Forty-one research articles from 425 articles were included in the systematic review. The screening process was adopted by Page *et al.* [21].



Fig. (2). The characteristics of the study. (A) The majority of the studies in the review were animal studies, followed by mixed studies, *in vitro* experiments, and microarray studies; (B) The majority of the experimental animals involved in the studies in the review were mammals (transgenic mice) and insects (*Drosophila melanogaster*). (A higher resolution / colour version of this figure is available in the electronic copy of the article).

the Hippo pathway or autophagy and dementia. As a result, forty-one articles were included in the present systematic review. A summary of the included studies and their findings are shown in Supplementary Table **S2**.

A total of 24 animal studies (59%) were included in this review, followed by 9 (22%) mixed studies (*in vitro* and *in vivo* animal studies), 7 (17%) *in vitro* studies, and 1 (2%) microarray study (Fig. 2). From the animal and mixed studies, 27 (77%) studies conducted the research using mammals, and 5 (23%) studies using insects.

## 3.2. Dementia and Hippo Signaling Pathway

The Hippo signaling pathway, often called Salvador/Warts/Hippo (SWH) pathway, was first discovered in *Drosophila melanogaster* and, subsequently, in mammals. The Hippo signaling pathway is a serine/threonine kinase signaling cascade, with the involvement of prostate-derived sterile 20-like kinases/TAO kinases (PSK/TAOK), mammalian Ste20-like kinases 1/2 (MST1/2), large tumor suppressor 1/2 (LATS1/2), and transcriptional co-activator yes association protein (YAP) and its paralog TAZ, as well as TEA domain-containing sequence-specific (TEAD) transcription factors. PSK/TAOK phosphorylates and activates MST1/2 when the Hippo pathway is active, and MST1/2 activation phosphorylates SAV1 and MOB1A/B, consequently promoting the phosphorylation of LTS1/2 (Fig. **3**). The YAP/TAZ transcriptional co-activator is inactivated when LATS1/2 is phosphorylated and activated. When the Hippo pathway is not active, the active proteins of YAP and TAZ bind directly to the nucleus and interact with TEAD, activating several genes involved in cell growth and organ size control [10, 22].

Cell death can occur when the Hippo signaling system is disrupted. The accumulation of  $A\beta$  peptide, the product of amyloid precursor protein miscleavage, in the hippocampus



**Fig. (3).** Hippo signaling pathway. When the Hippo signaling pathway is inactive (left-hand side), PSK/TAOK protein kinases do not activate MST1/2 protein kinases. Therefore, YAP and TAZ can interact with TEAD and bind directly to the nucleus to activate several genes that regulate organ size and cell proliferation. However, when the Hippo signaling pathway is active (right-hand side), external stimuli activate PSK/TAOK protein kinases, and then the kinases phosphorylate and activate MST1/2. The activation of MST1/2, in turn, phosphorylates LATS1/2 and inactivates YAP/TAZ. The inactive form of YAP/TAZ cannot bind to TEAD in the nucleus, causing the sequestration of the YAP/TAZ with 14-3-3 protein or the degradation of YAP/TAZ protein in the cytoplasm. (*A higher resolution / colour version of this figure is available in the electronic copy of the article*).

and cerebral cortex, as well as the downregulation and activation of the Hippo signaling pathway, are linked to dementia, specifically in Alzheimer's disease [23]. YAP deficiency enhances transcriptional repression-induced atypical cell death (TRIAD), ballooning cell death (BCD), and necrosis in Alzheimer's disease and Huntington's disease, resulting in TEAD suppression [14, 24, 25]. Intracellular Aβ also subsequently activates the Hippo signaling pathway, which in turn induces the JNK signaling pathway, which initiates neuroinflammation and neuronal cell necrosis [11, 12, 14]. YAP expression is found to be down-regulated in a Hippo pathway-dependent manner in the hippocampus astrocytes of aged mice and mice models of Alzheimer's disease. Consequently, at least in the in vitro and in vivo models, the signaling cascade appears to promote astrocyte senescence [13]. In addition, the core component MST1 appears to provoke neuronal apoptosis via regulator Bcl-2. Moreover, the increased level of MST1 activates Bax and inhibits the Bcl-2 expression in cells, thus promoting mitochondrial dysfunction [26]. Furthermore, PSK/TAOK, an upstream regulator of the Hippo pathway, is also involved in the pathogenesis of Alzheimer's disease-related dementia. In cell cultures, tau phosphorylation had been shown to be modulated by the activation of PSK1 and PSK2 in the cortex and the hippocampus. Other kinases stimulated by PSKs, such as JNK, p38, and MARK, have also been found to aggravate tau phosphorylation, and consequently promote neurodegeneration [27].

In neurodegenerative diseases, the overexpression of YAP and the inactivation of the Hippo pathway are beneficial in ameliorating neurodegeneration and suppressing the progression of the illness. In the research conducted by Dubey *et al.*, the neurodegeneration of eye disks mediated by

mutant huntingtin (Htt) was overcome by Yorkie, the effector protein YAP in Drosophila melanogaster [23]. Moreover, the activation of the Hippo pathway and the phosphorylation of MST1/2 and LATS 1/2 can phosphorylate and inactivate YAP by sequestration or degradation in the cytoplasm. The inactivation of the Hippo pathway results in the unphosphorylated YAP, essential for cell longevity as YAP can bind with nuclear TEAD to express the protein. The unphosphorylated YAP helps the cortical neurons from degeneration and cell death, as reported in the study by Mao et al.. In the report, YAP/YAPdeltaC and the transcription of YAP and TEAD1 prevented neuronal death by suppressing BCD and TRIAD in primary cortical neurons affected by Htt proteins [25]. Thus, the expression and nuclear transcription of YAP and TEAD are essential in neuronal health and survival from neurodegeneration.

#### 3.3. Dementia and Autophagy

Autophagy is a cellular mechanism in which damaged cell structures are degraded and recycled from the cytoplasm through the lysosomes [28]. There are several forms of autophagy, each with its purposes and processes. Macroautophagy, often generalized as autophagy, is the non-selective process of degrading damaged cell organelles with autophagosome involvement. It starts when *ULK1/2* induces and nucleates the phagophore. Subsequently, the elongation of the phagophore is induced and transformed into an autophagosome (Fig. 4). The autophagosome would then fuse with the damaged structure or the targeted cargo. The process is regulated by *ATG12-ATG5-ATG16L1*, *ATG9*, *LC3-II*, and *Class III PtdIns3K*. The autophagosome subsequently combines with lysosomes to generate autolysosomes, which degrade the structure/cargo, after which the resulting broken-



**Fig. (4).** The typical pathway of autophagy and mitophagy. (1) The process of autophagy is initiated by ULK1/2 protein kinase complex activated by AMPK; (2) The phagophore is induced and nucleated by ULK1/2 and regulated by ATG9, ATG12-ATG5-ATG16L1, LC3-II, and Class III PtdIns3K; (3) The elongation of phagophore to the targeted cargo appears after the nucleation of phagophore and later develops into autophagosome; (4) The autophagosome fuses with the damaged structure or the targeted cargo; (5) The autophagosome then merges with the lysosome to form autolysosomes; (6) The formed autolysosome degrades the cargo. The proteins are subsequently transferred back to the cytoplasm. In mitophagy, the dysfunctional or damaged mitochondria on the outer membrane of PINK1 attach to PARK2 to stimulate the elongation of phagophore and mitophagy. (*A higher resolution / colour version of this figure is available in the electronic copy of the article*).

down components are transferred back to the cytoplasm *via* the lysosomal permeases [29, 30].

Microautophagy is a selective degradation process using small parts of the cytoplasm without autophagosome involvement. The cytoplasmic material reaches the lysosome by a lysosomal membrane invagination [31]. A microautophagy process has been known to include the delivery of cytosolic proteins directly into the vesicle of late endosome multivesicular bodies [32].

The other type of autophagy, called chaperone-mediated autophagy, involves the KFERQ motifs in transferring cytosolic proteins into the lysosomal membrane. In this process, KFERQ motifs are linked to the HSPA8/HSC70 and other co-chaperones, which are then delivered to lysosomes *via* the LAMP2A substrate receptor and degraded in the lysosomal lumen [30].

Another type of autophagy is called mitophagy. Mitophagy focuses on mitochondrial breakdown involving BNIP3L/NIX, *PINK1*, and *PARK2* proteins. BCL2 Interacting Protein 3 Like (BNIP3L/NIX) is an autophagy-selective protein found on the mitochondria's outer membrane, which is required for mitochondrial elimination [33, 34]. PTENinduced putative kinase-1, often known as *PINK1*, is a serine/threonine-protein kinase that sticks to the depolarized mitochondria. *PARK2*, also known as Parkin, is an E3ubiquitin-protein ligase that binds to *PINK1* and ubiquitinates the mitochondrial outer membrane protein, which subsequently interacts with *LC3* with the assistance of SQSTM1 to initiate the process of mitophagy [35]. Both the BNIP3L-mediated mitophagy and *PINK1-PARK2*-mediated mitophagy have been shown to be critical in cell maturation and the removal of aged or defective mitochondria to support cellular functions. In the maturation of red blood cells, BNIP3L is the mitochondrial outer membrane protein that binds to the microtubule-associated protein 1A/1B-light chain 3 (*LC3*) and gamma-aminobutyric acid receptor-associated protein (GABARAP) on the phagophore to allow the recognition and the subsequent degradation of mitochondria. The removal of damaged mitochondria is assumed to be aided by *PINK1* and *PARK2*. The outer membrane kinase *PINK1* connects to the cytosolic E3 ubiquitin ligase *PARK2* in defective mitochondria, leading to the ubiquitination of *PARK2* mitochondrial proteins and mitophagy [30].

The autophagy processes to clear misfolded or damaged proteins are needed in a healthy human brain to preserve brain functions. Defective autophagy processes have been linked to the pathophysiology of dementia (Fig. 5). In Alzheimer's disease and other forms of dementia, circulating levels of autophagic markers, including *ATG5*, *ATG7*, *Beclin*, *LC3*, and *NRBF2*, are significantly reduced. The deficiency of these markers leads to the gradual deterioration of brain neurons, which manifests in physiological and behavioral impairments [19, 36-39].

Autophagy has been demonstrated to be inhibited by the aggregation of amyloid precursor protein (APP), A $\beta$  peptide, and tau protein, particularly in the hippocampal neurons [40–43]. When autophagic markers are reduced or depleted, the autophagosome formation is disrupted and consequently



Fig. (5). The autophagy impairment in dementia. In defective autophagy, activated mTOR inhibits the *ULK1/2* protein kinase complex, resulting in the disturbance in the formation of the phagophore. Other autophagic proteins, such as *ATG5*, *ATG7*, *Beclin*, and *LC3*, are depleted in dementia, which results in decreased autophagosome synthesis or accumulation of autophagosomes, decreased autophagy dysfunction, and reduction of protein degradation. Neurodegeneration and the build-up of damaged proteins can result from the autophagy dysfunction. (*A higher resolution / colour version of this figure is available in the electronic copy of the article*).

exacerbates the aggregation and spread of A $\beta$  and tau proteins in the brain [37, 44, 45]. Interestingly, in studies conducted by Yu *et al.* (2011), Chen *et al.* (2015), Ma *et al.* (2017), and Villamil Ortiz *et al.* (2021), autophagy was shown to be boosted in the early stages of Alzheimer's disease but deteriorated as the disease progressed [2, 17, 46, 47].

Furthermore, Joshi *et al.* (2015) found that in the late stage of Alzheimer's disease, p62 and pAkt/mTOR kinase activity were enhanced in transgenic mice models, but Bcl-2 levels were considerably lowered. Since the inactivation of Akt/mTOR promotes autophagy, it implies that p62 and mTOR activities inhibit autophagy in dementia [48].

Mitophagy also decreases in dementia and aging. The progression of Alzheimer's disease is exacerbated by, among other factors, the accumulation of defective and dysfunctional mitochondria [49]. The simultaneous rise in *PINK1* levels and reduction in *PARK2* levels are some of the consequences of severe mitochondrial breakdown. In addition, APP and Tau suppress the action of the mitochondrial-targeting *PINK1/PARK2* complex, resulting in the failure of mitophagy [50, 51]. The mitophagy impairment appears to be related to the early tau accumulation in the brain [52].

Vascular and Lewy body dementia have different pathophysiology compared to Alzheimer's disease with regards to autophagy regulation. The activation of autophagy-mediated chronic cerebral hypoperfusion exacerbates the degree of dementia in vascular dementia patients. Therefore, in vascular dementia patients, cognitive and motor function decline can be alleviated by inhibiting autophagy [53-55]. There is an ongoing debate about whether autophagy activation or inhibition by synuclein expression causes Lewy body dementia development and severity [56-58].

## 3.4. Dementia and Aging

The brain functions deteriorate progressively with age, which manifests in cognitive and motor decline. The hallmarks of aging found in brain tissues include DNA oxidative damage and repair defect, epigenetic alterations, telomeric attrition, loss of proteostasis, mitochondrial dysfunction, neuronal senescence, stem cells exhaustion, altered cellular network, and inflammation (Fig. 6) [59, 60].

The types of neuronal DNA damage in an aging brain are DNA single-strand breaks, double-strand breaks, abasic sites, bulky adducts, base mismatches, insertions, and deletions [60]. Increased Reactive Oxygen Species (ROS) generation and DNA repair failure can be regarded as both a cause and/or a consequence of oxidative-stress-related DNA damage by endogenous ROS. More importantly, the DNA double-strand breaks caused by oxidative stress have been shown to be the most destructive type of DNA damage [61]. This particular damage has been found to be the etiology of dementia and linked to methionine-35, an amino acid responsible for the production of amyloid  $\beta$  and the subsequent plaque formation in Alzheimer's disease [61, 62].

The DNA repair systems, such as homologous combinational repair, non-homologous end-joining repair, and base excess repair (BER), are reduced in dementia, resulting in a decreased ability of cells to remove DNA lesions [61, 63]. BER enzymes, such as APE1 and OGG1, are increased in normal brain tissues but reduced in the frontal cortex of brain tissues suffering from Alzheimer's disease [64].

The poly (ADP-ribose) polymerase-1 (PARP-1) is an essential enzyme in maintaining memory and synaptic plasticity in the brain. The reduction of this enzyme activity and expression has been observed in the hippocampus and the



**Fig. (6).** The hallmarks of brain aging include DNA oxidative damage and repair defect, epigenetic alterations, telomeric attrition, loss of proteostasis, mitochondrial dysfunction, neuronal senescence, stem cells exhaustion, altered cellular network, nutrient sensing problem, and inflammation [59, 60]. (*A higher resolution / colour version of this figure is available in the electronic copy of the article*).

cerebral cortex of dementia patients, displaying DNA damage, cellular senescence, and inflammation [65, 66].

Some of the hallmarks of aging, such as epigenetic alterations, telomeric attrition, and the loss of proteostasis, have been linked to dementia progression. Memory, learning, and behavior deficits in dementia are strongly associated with epigenetic alterations, such as DNA methylation and histone acetylation. Bradley-Whitman et al. (2013) and Coppieters et al. (2014) found active DNA methylation of 5methylcytosine and 5-hydroxymethylcytosine in aging brain tissues, implicating epigenetic changes in the early progression and clinical features of dementia [67, 68]. Furthermore, histone H3 Ser57 and Thr58 dephosphorylation and histone H4K16ac deacetylation have been shown to be associated with dementia neuropathology and progression. The dephosphorylation and deacetylation cause a reduction in neuronal gene transcription by stabilizing the nucleosomes and condensing the chromatin [69, 70].

The severity of dementia-related neurodegenerative disorders, such as vascular dementia, Lewy body dementia, and Alzheimer's disease, has also been associated with telomeric attrition or shortening. Accelerated telomere shortening has been associated with the increased formation of ROS, cellular oxidative damage, and inflammation in patients with high-risk dementia [71-73]. Meanwhile, the loss of proteostasis has been found in the hippocampal neurons of brains in aging mice. Proteostasis failure results in the accumulation of poly-ubiquitin and amyloid, exacerbating cellular senescence and autophagic activity impairment [74-76]. The configuration of mitochondria in the dendrites and axons of neurons is designed to produce ATP for neurotransmission, preservation, and cellular recovery. The proliferation and differentiation of mitochondria in the form of mitochondrial biogenesis are modulated by mitophagy. Mitophagy is crucial in maintaining cell functions and homeostasis to prevent the accumulation of dysfunctional mitochondria [77]. The analyses of mitochondria from brain tissues of patients with cognitive decline demonstrate abnormal fission and morphology, reduced mitochondrial function, diminished mitochondrial membrane potential, and mitophagy dysfunction, which results in the disturbance of ATP production as well as oxidative stress [78-81].

In addition, the amyloid  $\beta$  peptides and tau-containing neurofibrillary tangles have been found to promote cellular senescence, aging, and neurodegeneration. The A $\beta_{42}$  peptides increase intracellular ROS by activating FPR2 in the brain and the downstream ROS-p38 MAPK signaling pathway, inhibiting neurogenesis and triggering astrocyte senescence *in vitro*. These processes upregulate the expression of inflammatory cytokines, such as IL-6, RANTES, IL-8, and ICAM-1. The secretion of IL-6 is promoted by the activation of p38MAPK. IL-6 is considered the central chronic inflammation mediator in aging and dementia. Moreover, the insoluble tau is considered to be causative factor for the senescence of neurons and astrocytes, marked by the elevated levels of p16<sup>INK4a</sup>, the astrocyte marker GFAP, and senescenceassociated secretory phenotype [15, 82-84].

Lifestyle changes, such as the control of calorie intake and physical activities, are associated with nutrient-sensing gene expression during aging. Caloric restriction is neuroprotective by reducing the levels of amyloid  $\beta$  and the activation of microglia [85, 86]. Insulin, insulin-like growth factor 1 (IGF-1), mammalian target of rapamycin (mTOR), AMPactivated protein kinase (AMPK), and sirtuins are some of the significant nutrient-sensing pathways and molecules involved in aging. Central insulin resistance, marked by the increased level of IRS-1 pSer<sup>616</sup> and decreased level of IGF-1, is found in dementia patients and is related to worsening cognitive function [87, 88]. mTOR and AMPK have been found to be involved in dementia pathophysiology. The studies by Caccamo et al. (2013) and Zimmerman et al. (2013) reveal that the elevation of mTOR and reduction of AMPK activity levels are both associated with learning and memory deficits in dementia [89, 90]. On the other hand, the neuroprotective sirtuins (SIRT1) usually decrease during aging and are significantly reduced in dementia [91].

Furthermore, there is evidence that aging causes alteration in autophagy function and the Hippo pathway. Nutrient sensing and epigenetic alterations are some of the hallmarks of aging, which can affect autophagic flux [92, 93]. As mentioned, mTOR, AMPK, and SIRT1 levels have been associated with aging. SIRT1 can activate AMPK via deacetylation of LKB1 kinase, in which the activation of AMPK can phosphorylate forkhead transcription factors (FoxO) proteins. SIRT-1 can also deacetylate FoxO1 and FoxO3 to elevate levels of autophagy-related proteins, such as *BNIP3*, *ULK1/2*, ATG5, ATG7, ATG8, and LC3.

Additionally, AMPK can regulate the ULK/mTOR pathway to control autophagy by inhibiting the expression of mTOR and enhancing the expression of the ULK complex. The increased mTOR and reduced AMPK and SIRT1 levels in aging may be related to the altered autophagy function [93, 94]. On the other hand, the nuclear protein YAP/TAZ in the Hippo signaling pathway deteriorates in aging, although the biochemical and molecular mechanisms are not yet precise. The decreased level of YAP can activate p53/p21 expression and lysosomal activity to develop cellular senescence and senescence-associated secretory phenotypes [95]. In neurodegenerative diseases, such as Alzheimer's disease, astrocyte senescence in the hippocampus can occur by YAP deficiency or the suppression of YAP activity due to the activation of the Hippo pathway [13].

In this context, the pathophysiology of the progression of dementia has been linked to physiological changes in aging. The hallmarks of aging will affect several pathways that promote cellular senescence. We propose that the elucidation of the complex relationships between the Hippo signaling pathway and autophagy in dementia is one of the key factors to a better understanding of the progression of dementia in aging.

#### 3.5. Dementia, Hippo Signaling Pathway, and Autophagy

The interaction of the Hippo signaling pathway and autophagy plays an essential role in neurodegeneration. The role of Hippo signaling is to maintain organ and cell homeostasis. Hippo signaling co-activator YAP/TAZ controls autophagy by promoting the formation of autophagosomes and autolysosomes and the degradation of the autophagosome. The knockdown of YAP/TAZ is shown to cause the disturbance of the autophagic flux, with the accumulation of *LC3-II* in the cells and downregulation of Armus, a RAB7-GAP, which assists the autophagosome-lysosome fusion [96]. YAP/TAZ is also found to interact with the F-actin cytoskeleton and myosin-II complex in regulating the autophagy proteins *ATG16L1* and *ATG9*, signaling the formation of autophagosomes. YAP/TAZ collaborates with autophagy to preserve homeostasis in cells by clearing unused or damaging substances [97]. The other components of the Hippo signaling pathway, STK4/MST1 and STK3/MST2, have been considered important in controlling autophagy. The MST1/2 plays a role in phosphorylating *LC3* Thr50 to induce autophagosome and autolysosome formation and increase autophagic flux [98].

It is still unclear whether the activation or the inhibition of autophagy by Hippo pathway inactivation is beneficial for maintaining cell survival or harmful (inducing cell death). The declining level of MST1 can significantly promote autophagic flux. Western blot analysis of motor neuron samples from the MST1<sup>-/-</sup> group in the spinal cord experiment revealed an increase in LC3-II expression and a reduction in p62 expression, demonstrating autophagy to be triggered in response to spinal cord injury [99]. Another study showed that when titanium implants containing spherical silica nanoparticles were placed, the level of YAP rose, and mesenchymal stem cells underwent osteogenic differentiation after autophagy activation, as evidenced by an increase in LC3-II following the suppression of Akt/mTOR signaling [100]. Conversely, YAP expression suppresses autophagy to accelerate tumor progression in cancer cells. In the study by Jin et al. (2021) on colorectal cancer cells, YAP interacted with TEAD in the nucleus of SW620 cells to generate and bind to the target gene Bcl-2. YAP/Bcl-2 expression inhibited autophagy, which was shown by the decrease in LC3-II level in the western blot analysis. Further, the SW620 cell growth was also found to be enhanced as a result [101]. Another study claimed that the downregulation of LATS, an upstream kinase in the Hippo pathway, led to a 2-fold increase in YAP expression. YAP could assist the proliferation of lung cancer cells in lung adenocarcinoma by stimulating Akt/mTOR signaling pathway to inhibit autophagy [102]. Numerous research studies have focused on the relationship between the Hippo pathway and autophagy in several human body systems and cancer cells. Still, relatively few researchers have addressed these topics in the neurological system.

Hypothetically, when the Hippo signaling pathway is activated in the neurons of the brain suffering from neurodegenerative diseases, it causes YAP reduction in the nucleus. Degradation of YAP occurs when it enters the cytoplasm. The reduction of YAP then lowers the autophagic flux, causing the cell's inability to mark misfolded and damaged protein to be degraded in autophagy, leading to protein accumulation and aggregation in neurons (Fig. 7). The accumulation and aggregation of proteins directly induce BCD and TRIAD to initiate the necrosis and apoptosis of neurons [11, 25]. The accumulation of misfolded proteins in neurons can activate Hippo signaling and the JNK signaling pathways. The interaction between the activated Hippo signaling and JNK signaling pathways indirectly induces neurodegeneration through the promotion of apoptotic neuronal death [14, 103].



**Fig. (7).** The YAP/TAZ knockdown affects autophagy, causing neuron necrosis and apoptosis. A reduction in the autophagy protein and activation of the Hippo signaling pathway can inhibit the development of autophagosomes and autolysosomes in the neuron, leading to the sequestration of YAP/TAZ and 14-3-3 protein as well as the downregulation of Armus synthesis from the nucleus. These are two ways in which the inactivated version of YAP/TAZ can change the autophagy flux. Due to the buildup of misfolded protein brought on by the disruption of the autophagic flux, BCD and TRIAD-induced neuron necrosis and apoptosis can subsequently develop. (*A higher resolution / colour version of this figure is available in the electronic copy of the article*).

#### CONCLUSION

This review provides information on the roles of the Hippo signaling pathway and autophagy in the development of dementia in aging. The Hippo signaling pathway and autophagy alterations play a major role in the progression of dementia as demonstrated in animal, *in vitro*, *in vivo*, and microarray studies. The Hippo signaling pathway is dependent on the transcriptional co-activator YAP/TAZ, which connects with TEAD in the nucleus to maintain cell homeostasis. When YAP/TAZ is reduced, TRIAD, BCD, and necrosis will occur in the neurons. Moreover, the autophagic proteins, such as *LC3*, *ATG* proteins, and *Beclin*, are reduced in dementia, resulting in the disruption of autophagosome formation and accumulation and spread of misfolded proteins in the brain.

Although the relationship between the Hippo signaling pathway and autophagy in dementia is not clear, it has been shown that when Hippo signaling co-activator YAP/TAZ is reduced in neurons, the autophagic flux is decreased, causing misfolded proteins to accumulate in the brain leading to neurodegeneration. Further research should be carried out to determine the specific relationships between the Hippo signaling pathway and autophagy in dementia, as they are clearly essential in the progression of dementia.

The studies that describe the contribution of the Hippo signaling pathway and autophagy to dementia in aging are limited. To date, there is no available article on the relationship between the Hippo signaling pathway and autophagy in dementia involved in aging. Although articles that discuss the relationship between the Hippo signaling pathway and autophagy are available, no specific theory or evidence has been found to describe this relationship in the aging brain. From the results, we found that the disturbance of the Hippo signaling pathway and autophagy could affect the progression of dementia. We believe this systematic review can pave the way for new research on the relationship between Hippo signaling pathway and autophagy in the brain, especially with respect to dementia in aging. By understanding these relationships, new treatment and/or prevention strategies could be developed by targeting the Hippo pathway and autophagy in aging-related dementia.

# LIST OF ABBREVIATIONS

- YAP = Yes-Association Protein
- TAZ = Transcriptional Co-activator with PDZ-Binding Motif
- APP = Amyloid Precursor Protein

$$A\beta = Amyloid \beta$$

- TRIAD = Transcriptional Repression-Induced Atypical Cell Death
- BCD = Ballooning Cell Death

# **CONSENT FOR PUBLICATION**

Not applicable.

## **STANDARDS OF REPORTING**

PRISMA guidelines and methodology were followed.

# FUNDING

This project was supported by World Class Researcher Grant 2021 with Grant No. WCR/2022 from the Kementerian Pendidikan, Kebudayaan, Riset, dan Teknologi Republik Indonesia to RL.

# **CONFLICT OF INTEREST**

The authors declare no conflict of interest, financial or otherwise

## **ACKNOWLEDGEMENTS**

The authors thank Hanna Goenawan, MD., Ph.D. (Faculty of Medicine, Universitas Padjadjaran) for critical discussion during manuscript preparation.

# SUPPLEMENTARY MATERIAL

Supplementary material is available on the publisher's website along with the published article.

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