

## ● REVIEW

# Transcriptional dysregulation in neurodegenerative diseases: who tipped the balance of *Yin Yang 1* in the brain?

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## Abstract

*Yin Yang 1* (YY1) is a multi-functional transcription factor that regulates gene expression in a range of cell types, including neurons. It controls neuronal differentiation, as well as neuronal specification and migration during the development of the mammalian nervous system. Besides, YY1 also mediates the transcription of genes that are required for neuronal survival. An impairment of the transcriptional function of YY1 causes neuronal death. This review summarizes recent research findings that unveil the dysfunction of YY1 in multiple neurodegenerative disorders. The expression of disease proteins perturbs the function of YY1 via distinct molecular mechanisms, including recruitment to protein aggregates, protein degradation and aberrant nuclear/cytoplasmic shuttling. Understanding the pathogenic roles of YY1 will further broaden our knowledge of the disease mechanisms in distinct neurodegenerative disorders.

**Key Words:** Alzheimer's disease; amyotrophic lateral sclerosis; neurodegeneration; protein aggregates recruitment; protein degradation; subcellular localization; transcriptional regulation; *Yin Yang 1*

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## Historical Perspective of *Yin Yang 1* and Its Normal Function in the Nervous System

*Yin Yang 1* (YY1) was first identified in 1991 as a multi-functional transcription factor (Shi et al., 1991). The name YY1 is adopted from Chinese, and alludes to its dual transcriptional activities in both repressing ('*Yin*') and activating ('*Yang*') gene expression (Shi et al., 1991). The genes whose expression is modulated by YY1 have widespread implications for diverse signalling pathways, leading to the involvement of YY1 in multiple cellular processes including cell differentiation, proliferation and apoptosis. The YY1 protein is ubiquitous, exerting its transcriptional activity in a range of cell types, including neurons. It is now known that YY1 supports the normal development of the mammalian nervous system by controlling the expression of two categories of developmental genes, one of which encodes transcription factors involved in brain tissue patterning, and the other encoding proteins that regulate neuronal cell specification and migration (He and Casaccia-Bonnel, 2008). When YY1 is genetically ablated, mutant embryos display severe developmental retardation, including growth and neurulation defects (Morgan et al., 2004). Furthermore, Knauss et al. (2018) demonstrated that YY1 binds to the promoter region of a pluripotency gene, sex determining region Y-box 2, to repress its transcription in mouse cerebellar cortical neural progenitor cells. Sex determining region Y-box 2 promotes the proliferation of cerebellar cortical neural progenitor cells, and its expression is

downregulated when neural progenitor cells differentiate into neurons. The YY1-mediated inhibition of sex determining region Y-box 2 results in the suppression of neural progenitor cells proliferation, while accelerating neuronal differentiation. This finding therefore suggests a role of YY1 in governing neuronal differentiation in the developing cerebellum (Knauss et al., 2018). In addition to regulating neuronal development and differentiation, YY1 also controls neuronal viability. This review highlights recent advances in studying YY1 function in neuronal survival, and demonstrates several mechanisms that lead to neuronal death due to the dysfunction of the YY1 protein. The background information in this review was collected and discussed based on a Pubmed literature search of articles published from October 1991 to September 2018.

## *Yin Yang 1* Maintains Neuronal Survival

Several lines of evidence have demonstrated a correlation between YY1 and neuronal survival. In a recent study, Chen et al. (2018) reported that YY1 functions as a transcription repressor in regulating the expression of a pro-apoptotic gene, *Fuz*. When YY1 was overexpressed, *Fuz* promoter was hypermethylated, and *Fuz* expression was downregulated. Conversely, when YY1 expression was diminished, *Fuz* promoter was hypomethylated and *Fuz* transcription was induced. *Fuz* is a major player in planar cell polarity signalling, a pathway that directs the polarised cell migration along the tissue plane. Dominant mutations in the *Fuz* gene

have been uncovered in patients with neural tube defects, and a functional study revealed that *Fuz* mutants impair the directional cell movement and cell fusion, leading to the perturbation of neural tube closure (Seo et al., 2011). This finding highlights an important developmental role of *Fuz* in the human nervous system. Interestingly, Chen et al. (2018) found that when *Fuz* expression exceeded 2.5 times the normal level, an upregulation of neuronal apoptosis was observed, indicating a novel pro-apoptotic function of *Fuz*. The authors further demonstrated a Dishevelled-Ras-related C3 botulinum toxin substrate 1-mitogen-activated protein kinase-caspase signalling cascade that was exploited by *Fuz* to trigger neuronal apoptosis (Chen et al., 2018). In normal neurons, YY1 was found to associate with *Fuz* promoter to ensure sufficient DNA methylation, implying that the YY1-*Fuz* promoter interaction restricts the expression of *Fuz* to prevent the induction of neuronal apoptosis (Chen et al., 2018).

In addition to suppressing pro-apoptotic gene expression in normal neurons, YY1 also functions to promote pro-survival gene transcription. For example, YY1 was reported to bind directly to the promoter of glucose-6-phosphate dehydrogenase and stimulate its transcription. The induction of glucose-6-phosphate dehydrogenase expression subsequently leads to the activation of the pentose phosphate pathway in support of cell survival (Wu et al., 2018). It is noteworthy that in aged mice, upregulation of the brain glucose-6-phosphate dehydrogenase level alleviates neurodegeneration, suggesting a beneficial role of glucose-6-phosphate dehydrogenase in protecting against neuronal loss (Jeng et al., 2013). Taken together, YY1 maintains neuronal survival *via* inhibiting pro-apoptotic gene expression and simultaneously activating pro-survival genes (Chen et al., 2018; Wu et al., 2018). Any impairment of YY1's transcriptional function would result in an imbalance of pro-apoptotic and pro-survival gene expression, and compromise neuronal survival.

### **Yin Yang 1 Function Is Impaired *via* Distinct Mechanisms in Neurodegenerative Disease Models**

In 1997, Korhonen et al. (1997) first reported the impairment of functional YY1 in neuronal degeneration. The authors demonstrated that when cerebellar granule cells received excessive glutamate, a well-known excitotoxic agent that triggers neuronal death, a de-association of the YY1-DNA transcriptional complex was observed (Korhonen et al., 1997). This observation suggests a perturbation of functional YY1 during neurodegeneration. Because YY1 governs the expression of pro-apoptotic and pro-survival genes, it is possible to hypothesise that treatment with excitotoxic agents perturbs YY1's transcriptional function, which in turn causes an imbalance of cell apoptotic and survival events, leading to the stimulation of neuronal apoptosis and contributing to neurodegeneration.

However, the ultimate cause of the deterioration of YY1 transcriptional activity in neurodegeneration, especially in neurodegenerative diseases, remains elusive. We highlight some recent research findings that unveil the impairment of YY1 *via* distinct mechanisms in multiple neurodegenerative

diseases (Chen et al., 2018; Yin et al., 2018). More importantly, such impairment causes YY1-mediated gene dysregulation, which contributes to various pathologies.

### **The recruitment of Yin Yang 1 to protein aggregates**

Polyglutamine (polyQ) diseases comprise a group of neurodegenerative disorders, including Huntington's disease and several types of spinocerebellar ataxia such as spinocerebellar ataxia type 3 (SCA3). These diseases are caused by the expansion of glutamine-coding CAG trinucleotide repeats within the open reading frames of the disease genes (Lieberman et al., 2018). The formation of insoluble protein aggregates is one of the pathogenic features of polyQ diseases. Several essential cellular components, such as transcription factors, molecular chaperones and proteasomal subunits, are sequestered to polyQ protein aggregates, causing biological dysfunctions including transcriptional dysregulation, protein misfolding and perturbation of the ubiquitin proteasome system. These dysfunctions trigger the downstream cell death pathways, leading to neuronal deterioration, which contributes to the neurodegeneration in polyQ diseases (Lieberman et al., 2018).

In a recent study, Chen et al. (2018) described a novel pathogenic pathway that illustrates the relationship between polyQ protein aggregates and apoptosis induction in SCA3. This pathway involves two important partners, the transcriptional regulator YY1 and the planar cell polarity gene *Fuz*. The authors further showed that the level of soluble YY1 was downregulated due to the recruitment of YY1 protein to expanded SCA3-polyQ protein aggregates. Such recruitment depressed YY1 function, leading to *Fuz* promoter DNA hypomethylation followed by *Fuz* induction. The accumulation of *Fuz* protein consequently caused neuronal apoptosis in SCA3 disease models (Chen et al., 2018).

Similar to polyQ diseases, disease protein aggregates are observed in other neurological disorders as well. In Alzheimer's disease, the formation of protein aggregates is caused by the expression of toxic A $\beta_{1-42}$  peptide (Davis et al., 2018). *Fuz* induction has also been detected in A $\beta_{1-42}$  neurons. The authors further demonstrated that this upregulation also resulted from the decreased DNA methylation level of *Fuz* promoter accompanied by the recruitment of YY1 protein to A $\beta_{1-42}$  aggregates (Chen et al., 2018). These findings thus suggest a pathogenic mechanism that involves the recruitment of YY1 to disease protein aggregates, leading to the transcriptional dysregulation of a pro-apoptotic gene, *Fuz*, which in turn triggers apoptosis in polyQ disease and Alzheimer's disease models.

### **Proteolytic cleavage of Yin Yang 1 protein**

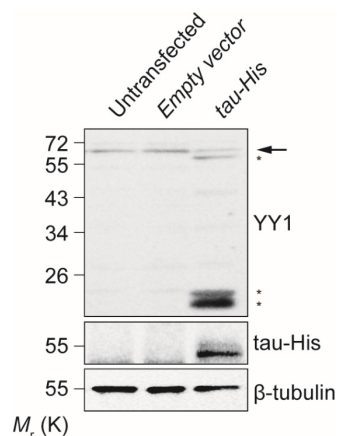
Krippner-Heidenreich et al. (2005) identified two caspase-recognised cleavage sites within the full-length YY1 protein sequence. They further provided experimental evidence that when caspases were activated, full-length YY1 was cleaved into shorter fragments, leading to the degradation of YY1 protein (Krippner-Heidenreich et al., 2005). The cleaved YY1 fragments retain the DNA-binding activity but lose the ability to regulate gene transcription, therefore behaving as a dominant negative product in occupying YY1-binding sites, in turn preventing the interaction between full-length YY1

and DNA sequences (Krippner-Heidenreich et al., 2005).

Apart from in the SCA3 and A $\beta_{1-42}$  neuronal models, *Fuz* upregulation has further been detected in tau-expressing neurons (Chen et al., 2018). Tau protein likewise aggregates when expressed in neurons. The formation of these pathological protein aggregates compromises the neuronal functions, causing a class of neurodegenerative disorders named tauopathy (Davis et al., 2018). Interestingly, YY1 was not recruited to tau protein aggregates, suggesting that an alternative mechanism may contribute to tau-mediated *Fuz* induction (Chen et al., 2018). The authors were then inspired to examine whether the YY1 protein level was attenuated in tau-expressing cells. Interestingly, as demonstrated by immunoblotting results, YY1 protein was found to undergo protein degradation, resulting in an accumulation of truncated YY1 fragments accompanied by a reduction of the full-length functional YY1 level (Figure 1). Based on this observation, we hypothesise that both the reduction of full-length YY1 and accumulation of truncated fragments contribute to the impairment of YY1's normal function, causing *Fuz* upregulation in tau-expressing neurons. More importantly, YY1 protein degradation was detected in the brains of Alzheimer's disease patients (Aubry et al., 2015), further suggesting a clinical implication of YY1 degradation in neurodegenerative disorders.

### Subcellular localisation of Yin Yang 1 protein

YY1 protein localises predominantly in the cell nucleus, which coincides with the fact that nuclear YY1 functions as a transcription factor to mediate gene transcription. In astrocytes derived from a SOD1<sup>G93A</sup> amyotrophic lateral sclerosis mouse model, an aberrant nuclear/cytoplasmic ratio of YY1 protein was reported. YY1 protein was found to be further enriched in the cell nuclei of diseased astrocytes (Yin et al., 2018). The accumulation of nuclear YY1 in turn caused



**Figure 1** Overexpression of tau promotes Yin Yang 1 (YY1) protein degradation.

Human embryonic kidney 293 cells were transfected with a *tau*-overexpressing DNA construct (Chen et al., 2018). The *pcDNA3.1(+)* DNA construct was used as an empty vector control. The expression of YY1, tau-His and  $\beta$ -tubulin proteins was determined using anti-YY1 antibody (1:1000, ab109237, Abcam, Cambridge, MA, USA), anti-His antibody (1:1000, 27-4710-01, Sigma-Aldrich, St. Louis, MO, USA) and anti- $\beta$ -tubulin antibody (1:2000, ab6046, Abcam), respectively. In tau-overexpressing cells, full-length YY1 protein (arrow) was found to undergo protein degradation, resulting in the accumulation of truncated YY1 protein fragments (asterisks). Beta-tubulin was used as a loading control. Experiments were independently repeated three times. Only one representative blot is shown.

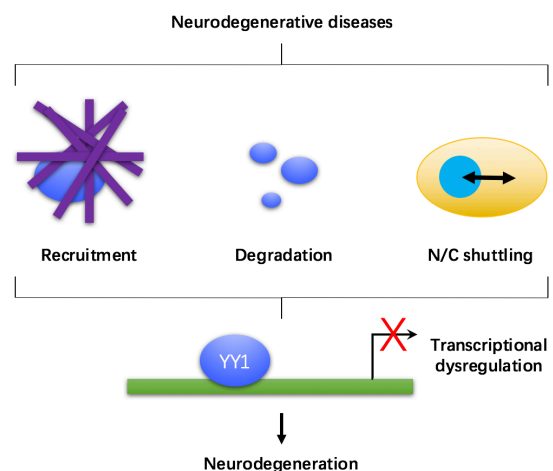
downregulation of excitatory amino acid transporter-2, whose gene product is responsible for re-translocating glutamate into neurons to eliminate excessive extracellular glutamate. The impairment of excitatory amino acid transporter-2 expression was accompanied by impaired glutamate clearance ability, and accumulation of toxic glutamate further caused neuronal cell death in SOD1<sup>G93A</sup> astrocytes (Yin et al., 2018). In addition to protein-aggregate recruitment and degradation, another contributor to YY1 dysfunction in neurodegenerative disease is aberrant nuclear/cytoplasmic shuttling.

### Concluding Remarks and Future Perspectives

Taken together, in multiple neurodegenerative disorders, the mutant disease proteins perturb the function of YY1 via distinct mechanisms, including recruitment to protein aggregates, promotion of protein degradation and alteration of nuclear/cytoplasmic distribution (Figure 2). The dysfunction of YY1 in turn causes the transcriptional dysregulation of downstream target genes (Figure 2). A future objective in YY1 research would be to uncover other potential mechanisms that lead to YY1 dysfunction in neurodegenerative diseases, such as aberrant post-translational modifications (He and Casaccia-Bonnel, 2008).

The central role of YY1 in governing diverse downstream genes/pathways highlights this protein as an essential therapeutic target in neurodegenerative disorders. In SCA3, when the functional level of YY1 is restored, *Fuz* upregulation is diminished, accompanied by the relief of neuronal apoptosis (Chen et al., 2018). Therefore, identification of potential activators of YY1, or the delivery of ectopic YY1, will help replenish YY1's transcriptional function and correct the dysregulation of downstream genes/pathways. The restoration of the gene transcription network will thus provide therapeutic benefits against the neuronal toxicity of neurodegenerative disorders.

Other than neurons, the function of YY1 is also impaired in glial cells of neurodegenerative diseases. In astrocytes



**Figure 2** Summarised diagram illustrating Yin Yang 1 (YY1) dysfunction and transcriptional dysregulation in neurodegenerative diseases.

In multiple neurodegenerative diseases, the function of YY1 is perturbed via distinct mechanisms, including recruitment to protein aggregates, protein degradation and aberrant nuclear/cytoplasmic (N/C) shuttling. These impairments hinder the transcriptional activity of YY1, leading to gene transcriptional dysregulation, which contributes to the disease pathologies.



derived from SOD1<sup>G93A</sup> mouse brain, aberrant nuclear/cytoplasmic distribution of YY1 causes dysregulation of excitatory amino acid transporter-2, which in turn leads to the accumulation of glutamate that hinders neuronal viability (Yin et al., 2018). Furthermore, YY1 controls expression of excitatory amino acid transporter-1 (*EAAT1*), another astrocytic glutamate transporter gene (Karki et al., 2015). The dysregulation of *EAAT1* is reported in multiple neurological disorders, including Alzheimer's disease and prion diseases (Scott et al., 2002; Chretien et al., 2004). Therefore, it would be interesting to examine whether the dysfunction of YY1 leads to *EAAT1* dysregulation, and contributes to disease pathologies.

Intriguingly, in addition to astrocytes, YY1 also modulates gene transcription in other types of glial cells, such as oligodendrocytes (He et al., 2007) and microglia (Zhang et al., 2018). Moreover, oligodendrocytes and microglia have been implicated in neurodegenerative disease pathogenesis (Nasrabady et al., 2018; Spiller et al., 2018). Another interesting perspective would be to investigate whether YY1's function is dysregulated in disease oligodendrocytes and microglia, and how such dysregulation contributes to the disease pathologies. Unravelling these novel mechanisms will broaden our knowledge of YY1's pathogenic role in various neurodegenerative diseases.

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