

UNIVERSIDADE DE LISBOA
FACULDADE DE MEDICINA DE LISBOA



**AMYLOID β PEPTIDE AND p63:
TWO PRIME TRIGGERS OF NEURAL APOPTOSIS
AND DIFFERENTIATION**

Maria Benedita Pereira de Vasconcelos Fonseca

**Doutoramento em Ciências Biomédicas (Neurociências), apresentada à
Universidade de Lisboa através da Faculdade de Medicina**

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Supervisor: Cecília M. P. Rodrigues, Ph.D.

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Resumo

A doença de Alzheimer (AD) é uma doença neurodegenerativa caracterizada pela ocorrência de perturbações na função sináptica e perda massiva de neurónios nas regiões cerebrais relacionadas com as funções cognitivas, como o hipocampo e o córtex cerebral. A deposição do péptido β amilóide ($A\beta$) na AD foi desde cedo reportada como sendo um aspeto crucial nos fenómenos patológicos da doença, nomeadamente na formação de placas senis. Vários estudos mostram que o stress oxidativo, a inflamação, a perturbação dos fluxos de cálcio e a morte celular programada estão envolvidos na toxicidade induzida pelo $A\beta$. Contudo, os mecanismos pelos quais o péptido $A\beta$ desencadeia a morte neuronal não são, ainda, completamente conhecidos. Um melhor conhecimento desses mecanismos básicos, desencadeados pelo péptido $A\beta$, poderá constituir um importante contributo para retardar, ou até prevenir, a neurodegenerescência associada à AD. Por outro lado, alguns dos fatores associados ao processo apoptótico podem também modular a proliferação e a diferenciação. Os mecanismos regulatórios desta tomada de decisão, quanto ao destino das células, dependem do balanço e da conjugação de sinais de sobrevivência e de morte celular. De facto, o nosso grupo demonstrou já que caspases, calpaínas, p53 e microRNAs associados à apoptose aceleram o processo de diferenciação neural. Além disso, foi recentemente sugerido que o péptido $A\beta$ pode também regular a proliferação e diferenciação de células estaminais neurais (NSCs). Estas células são capazes de originar os principais tipos de células neurais, incluindo neurónios e células da glia, como os astrócitos e os oligodendrócitos. Em cada divisão celular, as NSCs podem seguir destinos celulares diferentes, nomeadamente continuar o processo proliferativo, ou iniciar a diferenciação. Assim, propusémo-nos identificar e caracterizar novos fatores e vias moleculares envolvidas na regulação da apoptose e da diferenciação neural, que sejam relevantes no contexto da AD.

Explorámos, inicialmente, mecanismos moleculares subjacentes à apoptose induzida pelo $A\beta$ em células neuronais PC12 e em neurónios corticais de cultura primária. A incubação com o péptido $A\beta$ resultou na estabilização da isoforma pro-apoptótica da proteína p63, pertencente à família p53, TAp63, bem como na degradação da isoforma anti-apoptótica, $\Delta Np63$, através de um mecanismo dependente do proteossoma e de cinases de proteínas ativadas pelo mitogénio. Este efeito encontrou-se associado a um aumento dos níveis proteicos de c-Jun, um fator de transcrição envolvido na regulação do destino das células, já anteriormente reportado como sendo modulador da abundância de TAp63. Curiosamente, a pré-incubação das

células com um agente anti-apoptótico, o ácido tauro-ursodesoxicólico (TUDCA), reverteu o efeito do A β nas proteínas TAp63 e c-Jun. De igual forma, em células tratadas com compostos genotóxicos, como a cisplatina e a doxorrubina, verificámos um aumento da expressão de c-Jun, associado a uma redução dos níveis proteicos da isoforma Δ Np63. A expressão endógena e ectópica de Δ Np63 foi também dramaticamente reduzida aquando da sobreexpressão de c-Jun. Recorrendo à tecnologia de silenciamento com siRNAs, silenciámos c-Jun em células tratadas com A β , o que preveniu a degradação da isoforma Δ Np63. Por outro lado, a sobreexpressão de c-Jun originou a redução dos níveis de Δ Np63. Por fim, verificámos que o tempo de semi-vida de Δ Np63 foi significativamente reduzido na presença de c-Jun, confirmando assim o papel de c-Jun na regulação da estabilidade de Δ Np63. Estes resultados indicaram que a abundância de Δ Np63, em resposta à morte apoptótica induzida pelo A β , é regulada por um mecanismo dependente de c-Jun.

De seguida, investigámos o envolvimento da proteína p63 na regulação do potencial de proliferação e diferenciação de NSCs. De facto, a proteína p53, homóloga de p63, foi recentemente descrita como fator limitante do potencial proliferativo das células estaminais, desempenhando mesmo um papel crucial durante a neurogénese. Por outro lado, foi também demonstrado que os efeitos pró-neurogénicos da proteína p53 resultam da sua interação com reguladores importantes da diferenciação neural, como a desmetilase JMJD3, específica para o resíduo de lisina-27 da histona 3. Considerando as semelhanças funcionais e estruturais entre as proteínas p53 e p63, investigámos uma possível interação molecular entre a desmetilase JMJD3 e a proteína p63 durante o processo de neurogénese. A proteína p63 já foi descrita como estando envolvida na diferenciação da epiderme e de outros tecidos epiteliais. Contudo, o seu envolvimento durante a diferenciação neural não foi inteiramente esclarecido. Os resultados obtidos demonstraram que a isoforma TAp63 γ interage diretamente com a desmetilase JMJD3 e que esta regula os níveis de p63, estabelecendo-se um programa de expressão de marcadores neurais. De facto, a sobreexpressão de JMJD3 promoveu um aumento dos níveis de TAp63 γ , de forma dependente da sua atividade de desmetilase. A sobreexpressão de TAp63 γ aumentou os níveis do marcador de neurónios β -III tubulina, enquanto que o silenciamento de TAp63 γ resultou em efeitos significativamente diferentes. Ensaio de imunoprecipitação permitiram-nos confirmar a interação direta entre TAp63 γ e JMJD3, durante a diferenciação de NSCs, assim como a modulação dos níveis de metilação de TAp63 γ pela JMJD3. Curiosamente, a JMJD3

regulou também a estabilidade e a distribuição celular da isoforma TAp63 γ , bem como o processo de neurogênese regulado pela TAp63 γ . Estes resultados clarificam o papel da proteína p63 na diferenciação das células precursoras neurais e demonstram que a isoforma TAp63 γ é um alvo direto da JMJD3, sendo esta interação importante para a neurogênese.

Por fim, avaliámos a capacidade de diferentes péptidos A β modularem os processos de proliferação e diferenciação de NSCs, clarificando o papel da autofagia nos efeitos mediados pelos péptidos A β . De facto, embora considerados neurotóxicos, os péptidos A β estão também envolvidos em diversos eventos celulares não patogénicos. Por outro lado, a autofagia tem sido implicada na sobrevivência celular em resposta à toxicidade do A β , mas também em processos de diferenciação. Contudo, o seu papel concreto na diferenciação neural continua por esclarecer. Os resultados obtidos demonstraram que os péptidos A β_{1-40} e A β_{1-42} promovem preferencialmente a neurogênese e a gliogênese, respetivamente, enquanto que o péptido A β_{25-35} não parece ter qualquer efeito nestes processos. Verificámos também que o papel do A β_{1-40} na neurogênese é parcialmente dependente da sua função na proliferação de NSCs. Tal foi comprovado pelo aumento da fase S do ciclo celular e pelo aumento da marcação com bromodeoxiuridina em células expostas a A β_{1-40} . Além disso, o péptido A β_{1-40} aumentou a atividade do promotor de Tuj1, validando assim os resultados anteriores que mostram o papel importante do péptido A β_{1-40} na diferenciação neuronal. Observámos também que o processo autofágico parece estar envolvido nos efeitos mediados pelos diferentes péptidos A β nas NSCs, independentemente da produção de espécies reativas de oxigénio e da ocorrência de fenómenos apoptóticos. Inibindo a autofagia, através da adição do inibidor autofágico 3-metiladenina, verificou-se que os níveis proteicos de marcadores neuronais e gliais não aumentaram, mesmo na presença dos diferentes péptidos A β . Assim, estes resultados suportam e clarificam o papel de diferentes péptidos A β na regulação do destino celular das NSCs e sublinham a importância da autofagia no controlo deste processo.

Em conclusão, estes estudos contribuem com dados novos relativamente ao papel do péptido A β e da proteína p63 no controlo da decisão entre diferenciação e morte celular, os quais se poderão revelar úteis na modulação do destino celular na AD.

Palavras-chave: Ácido tauro-ursodesoxicólico; Apoptose; Autofagia; Células estaminais neurais; c-Jun; Neurogênese; p63; Péptido β amilóide

Abstract

Amyloid β ($A\beta$) peptide accumulation and apoptosis play an important role in the pathogenesis of Alzheimer's disease. However, the mechanisms by which $A\beta$ mediates neuronal apoptosis are not completely elucidated. Mounting evidence also supports the involvement of specific apoptosis factors in neural stem cell (NSC) differentiation. Therefore, we set to identify and characterize new molecular pathways involved in $A\beta$ -induced regulation of neural apoptosis and differentiation.

First, we further explored the molecular mechanisms of $A\beta$ -induced neuronal death. We found that $A\beta$ elicited stabilization of the pro-apoptotic isoform of p63, TAp63, which in turn was partially inhibited by tauroursodeoxycholic acid. In addition, in response to $A\beta$ -induced apoptosis, the abundance of the anti-apoptotic isoform of p63, $\Delta Np63$, was clearly reduced and tightly regulated in a c-Jun-dependent mechanism.

Next, we investigated whether apoptosis-associated molecule p63, member of the p53 family, might also be involved in differentiation of NSCs. We showed that TAp63 γ interacted with the histone H3 lysine 27-specific demethylase JMJD3, a key regulator of neurogenesis, to redirect NSCs to differentiation, as an alternative to cell death. In addition, both TAp63 γ and JMJD3 were coordinately regulated to establish a neural-specific gene expression pattern during NSC differentiation. We also found that JMJD3-demethylase activity was crucial in regulating TAp63 γ half-life and nuclear accumulation.

Finally, we evaluated the ability of $A\beta$ peptides to modulate NSC proliferation and differentiation, and investigated whether autophagy was involved in $A\beta$ -induced alterations of NSC fate. We showed that $A\beta_{1-40}$ and $A\beta_{1-42}$ strongly enhanced neurogenesis and gliogenesis, respectively, while $A\beta_{25-35}$ did not influence NSC fate. Notably, autophagy was implicated in $A\beta$ -mediated effects in NSCs, independently of reactive oxygen species production and apoptosis induction.

In conclusion, the work presented here provides additional insights into the molecular mechanisms implicated in $A\beta$ - and p63-induced cell death signaling pathways, and extends our knowledge in considering these prime triggers of apoptosis as integral components of neural proliferation and differentiation.

Keywords: Amyloid β peptide; Apoptosis; Autophagy; c-Jun; Neural stem cells; Neurogenesis; p63; Tauroursodeoxycholic acid

Abbreviations

3-MA	3-methyladenine
AD	Alzheimer's disease
Aβ	amyloid β
AIF	apoptosis-inducing factor
AP	autophagosome
AP-1	activator protein-1
Apaf-1	apoptosis protease-activating factor 1
APP	amyloid precursor protein
ATG	autophagy-related
Bcl-2	B-cell lymphoma-2
Bcl-x_L	B-cell leukemia/lymphoma extra long
BH	Bcl-2 homology
BrdU	bromodeoxyuridine
C99	99-residue membrane-bound fragment
CHX	cycloheximide
CNS	central nervous system
Cyt <i>c</i>	cytochrome <i>c</i>
DG	dentate gyrus
EGF	epidermal growth factor
ESC	embryonic stem cells
FBS	fetal bovine serum
FGF	fibroblast growth factor
KO	knockout
NGF	nerve growth factor
GFAP	glial fibrillary acidic protein
GFP	green fluorescent protein
IAP	inhibitor of apoptosis protein
Id1	inhibitor of differentiation 1
JMJD3	histone H3 lysine 27-specific demethylase

JNK	c-Jun N-terminal kinase
LC3	microtubule-associated protein light chain 3
LDH	lactate dehydrogenase
MAP2	microtubule-associated protein 2
MAPK	mitogen-activated protein kinase
MeK	methylated lysine
miRNAs	microRNAs
MOMP	mitochondrial outer membrane permeabilisation
NeuN	neuronal nuclei
NG2	neuronal/glial 2
NPCs	Neuronal precursor cells
NSCs	neural stem cells
NTR	neurotrophin receptor
PBS	phosphate buffer saline
PC12	rat pheochromocytoma
PI3K	phosphatidylinositide 3 kinase
PS1	presenilin-1
PS2	presenilin-2
PTM	post-translational modifications
RG	radial glia
ROS	reactive oxygen species
SGZ	subgranular zone
siRNA	short-interference RNA
SVZ	subventricular zone
TNF	tumor necrosis factor
TrkA	tyrosine kinase receptor type 1
TUDCA	tauroursodeoxycholic acid
UDCA	ursodeoxycholic acid

Publications

The present thesis was mostly based on work that has been published in international peer-reviewed journals:

Fonseca MB, Nunes AF, Rodrigues CMP. c-Jun regulates the stability of anti-apoptotic $\Delta Np63$ in amyloid β -induced apoptosis. *Journal of Alzheimer's Disease* 2012; 28 (3): 685-94.

Fonseca MB, Nunes AF, Solá S, Rodrigues CMP. p63 demethylation by JMJD3 modulates p63 stability and cellular distribution during neural stem cell differentiation. *Plos One* 2012; 7 (12): e52417.

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1. General Introduction

1.1 Neural Apoptosis

The term apoptosis was first introduced in 1972 by Kerr *et al.* to describe the morphological processes leading to controlled cellular destruction (Kerr et al., 1972). The apoptosis term has a Greek origin, meaning "falling off" or "dropping off", in analogy to leaves falling off trees or petals dropping off flowers. This analogy emphasizes that the death of living matter is a necessary part of the life cycle of organisms, being apoptosis an extremely coordinated and highly efficient form of cell death that plays a considerable role during physiological conditions, including development, differentiation, proliferation and function of the immune system; and in the removal of harmful cells.

During development of the central (CNS) and peripheral nervous systems, naturally occurring neuronal death is required during a specific time window to ensure the establishment of a correct match between the neuronal numbers and the size of the target tissue and for morphogenetic processes, such as neural tube closure (Oppenheim, 1991). The ultimate survival of any given neuron is determined by its capacity to sequester sufficient amounts of target-derived trophic factors, such as the nerve growth factor (NGF) (Kaplan and Miller, 2000). NGF binds to the neurotrophic tyrosine kinase receptor type 1 (TrkA) on the terminal axonal arbor and mediates cellular survival signaling. A second neurotrophin receptor (NTR), the p75^{NTR}, plays an antagonistic role in this system, promoting the elimination of the neurons that do not compete for target-derived NGF. The initial overproduction of neurons, followed by death of some, represents an adaptive process that provides enough neurons to form nerve cell circuits that are precisely matched to their functional specifications. Neuronal loss subsequent to this development window is still physiologically appropriate but may also contribute to neurological deficits. Notably, the cell death machinery has vital components of the maintenance and differentiation programs of adult stem cells (Aranha et al., 2009; Solá et al., 2012), which must be restrictively activated to assure differentiation efficiency, and carefully regulated to avoid cell loss. Therefore, it is not surprising that during differentiation, specific cellular changes occur in a similar manner to those observed during apoptosis (Chasis and Schrier, 1989). In addition, Biebl *et al.* (Biebl et al., 2000) have also reported that apoptosis may have an important regulatory function by eliminating

supernumerous cells from neurogenic regions, and may thus contribute to a self-renewal mechanism in the adult mammalian brain. Furthermore, several studies have demonstrated that neuronal apoptosis also occurs as a pathological event following excitotoxic, ischemic or traumatic nervous system injury. Finally, there is increasing evidence that apoptotic cell death is one of the mechanisms leading to neuronal loss in neurodegenerative diseases (Yuan and Yankner, 2000), including Huntington's disease, Parkinson's disease, and Alzheimer's disease (AD) (Lassmann et al., 1995; Ohyagi et al., 2005; Smale et al., 1995; Tang et al., 2005; Yao and Wood, 2009).

Deposition of amyloid β (A β) peptide in AD was earlier thought to initiate the pathological cascade of this disease, including the formation of senile plaques and neurofibrillary tangles (NFTs), neuronal loss, and dementia. Previous studies have demonstrated that A β causes neurotoxicity and neuronal cell apoptosis *in vivo* and *in vitro* (Alvarez et al., 2004; Cancino et al., 2008; Laurén et al., 2009). However, the mechanisms of A β -induced apoptosis remain to be clarified.

1.1.1 Apoptosis signaling pathways

Classic apoptosis consists in at least two phases, initiation and execution, which in turn results in the activation of cysteine-dependent aspartate directed proteases, termed caspases. Most morphological changes of apoptotic cells are caused by caspases, in a sequence of biochemical events. The death receptor (extrinsic) and mitochondrial (intrinsic) apoptosis pathways represent the canonical routes of caspase activation during the initiation phase (Kroemer et al., 2007).

1.1.1.1. Extrinsic pathway

Death receptors belong to the tumor necrosis factor (TNF) superfamily of cell surface receptors, and contain a cytoplasmic protein motif termed death domain that enables receptors to engage the cell apoptotic machinery. Caspase activation by the death receptor involves the binding of extracellular death ligands, such as Fas ligand (FasL) or TNF α to transmembrane death receptors, causing the recruitment and oligomerization of the adapter molecule Fas-associating death domain-containing protein (FADD) within the death-inducing signaling complex. Oligomerized FADD, in turn, binds the procaspase-8 and -10, causing their dimerization and activation

(Debatin and Krammer, 2004). Cytosolic and active caspase-8 and -10 then mediate the activation of the effector caspases-3, -6 and -7, causing further caspase activation events, and finally substrate proteolysis and cell death (Debatin and Krammer, 2004; Mattson, 2006).

1.1.1.2. Intrinsic pathway

Mitochondria play a key role in the regulation of apoptosis, collecting and integrating both pro- and anti-apoptotic signals, such as pro- and anti-apoptotic B-cell lymphoma-2 (Bcl-2) family proteins, p53, kinases, phosphatases, reactive oxygen species (ROS), calcium overload, viral proteins or toxins. Unlike in extrinsic apoptosis, caspase activation is not always a requirement for mitochondrial-induced apoptosis, although caspases accelerate the process. The mitochondrial pathway of apoptosis begins with mitochondrial outer membrane permeabilization (MOMP), and subsequent release of apoptotic factors from the mitochondria, including cytochrome *c* (cyt *c*), second mitochondria-derived activator of caspase/direct inhibitor of apoptosis protein (IAP) binding protein with a low pI (Smac/DIABLO) and Omi stress-regulated endoprotease/high temperature requirement protein A2 (Omi/HtrA2), which act through caspase activation; and the caspase independent apoptosis-inducing factor (AIF) and endonuclease G (EndoG) (reviewed in (Kroemer et al., 2007)).

This process is strongly regulated by Bcl-2 family proteins. The anti-apoptotic members of this family have four Bcl-2 homology (Oda et al.) regions that mediate protein-protein interactions (Youle and Strasser, 2008) and contain transmembrane domains that mediate their insertion into the outer membranes of mitochondria as well as into the endoplasmic reticulum (Kelly and Strasser, 2011). This group includes Bcl-2, Bcl-w, Mcl-1, A1, BOO/DIVA, NR-13 and Bcl-x_L, which are responsible for inhibition of both MOMP and release of apoptotic factors from the mitochondria. The pro-apoptotic Bcl-2 proteins Bax, Bak, Bok, Bcl-x_S, Bcl-g_L and Bfk are multi-domain proteins with up to four BH domains, while Bid, Bad, Bik, Hrk, Puma, Noxa, Bmf and Bim have only the BH3 domain, hence called BH3-only proteins. The pro-apoptotic Bcl-2 family members reside in the cytosol but following death signaling, they are translocated to mitochondria to promote MOMP. Bad translocates to mitochondria and forms a pro-apoptotic complex with Bcl-x_L. This translocation may also be inhibited by

survival factors that induce the phosphorylation of Bad, leading to its cytosolic sequestration (Pradelli et al., 2010). Bax and Bim, in turn, translocate to mitochondria in response to death stimuli or survival factor withdrawal.

Upon release from mitochondria, cyt *c*, together with dATP and the apoptotic protease-activating factor-1 (Apaf-1), form an activation complex with caspase-9, the apoptosome. Another level of regulation is provided by the IAP family members that promote survival signaling pathways and interfere with the activation of caspases (Fulda and Vucic, 2012). Smac/DIABLO and Omi/HtrA2, in turn, can sequester and/or degrade IAPs, thereby facilitating caspase activation. AIF and EndoG do not interact with caspases and instead translocate to the nucleus to promote DNA fragmentation and chromatin condensation.

Although apparently independent, in some instances, extrinsic death signals can crosstalk with the intrinsic pathway through caspase-8-mediated proteolysis of the BH3-only protein Bid. Truncated Bid (tBid) can promote mitochondrial cyt *c* release and assembly of the apoptosome, comprising ATP, seven molecules of Apaf-1 and the same number of caspase-9 homodimers (reviewed in (Kroemer et al., 2007)).

1.1.2. p53 family of proteins

The p53 family includes the products encoded by the *p53* gene and its homologues, *p63* and *p73*. The three members of the family share a high level of similarity, which allows p63 and p73 to transactivate p53-responsive genes causing cell cycle arrest and apoptosis (Dötsch et al., 2010; Murray-Zmijewski et al., 2006). The complexity of the family has been enriched by the use of alternative promoters, splicing and translational sites (Moll and Slade, 2004; Murray-Zmijewski et al., 2006). Consequently, several protein isoforms with distinct N- and C- termini are encoded. Transcribing from P1 promoter principally gives rise to full-length isoforms with the transactivation domain (TAD), including p53, TAp63 and TAp73, whereas using the alternative P2 promoter produces N-terminal truncated isoforms without TAD, such as Δ Np53, Δ Np63 and Δ Np73 (Bourdon, 2007) (Fig. 1.1).

Combining the alternative splicing with different promoter usage, additional protein isoforms of p53, p63 and p73 arise. The p73 gene expresses at least 7 alternatively spliced C-terminal isoforms (α , β , γ , δ , ϵ , ζ , η) and at least 4

alternatively spliced N-terminal isoforms, which contain different parts of the transactivation domain.

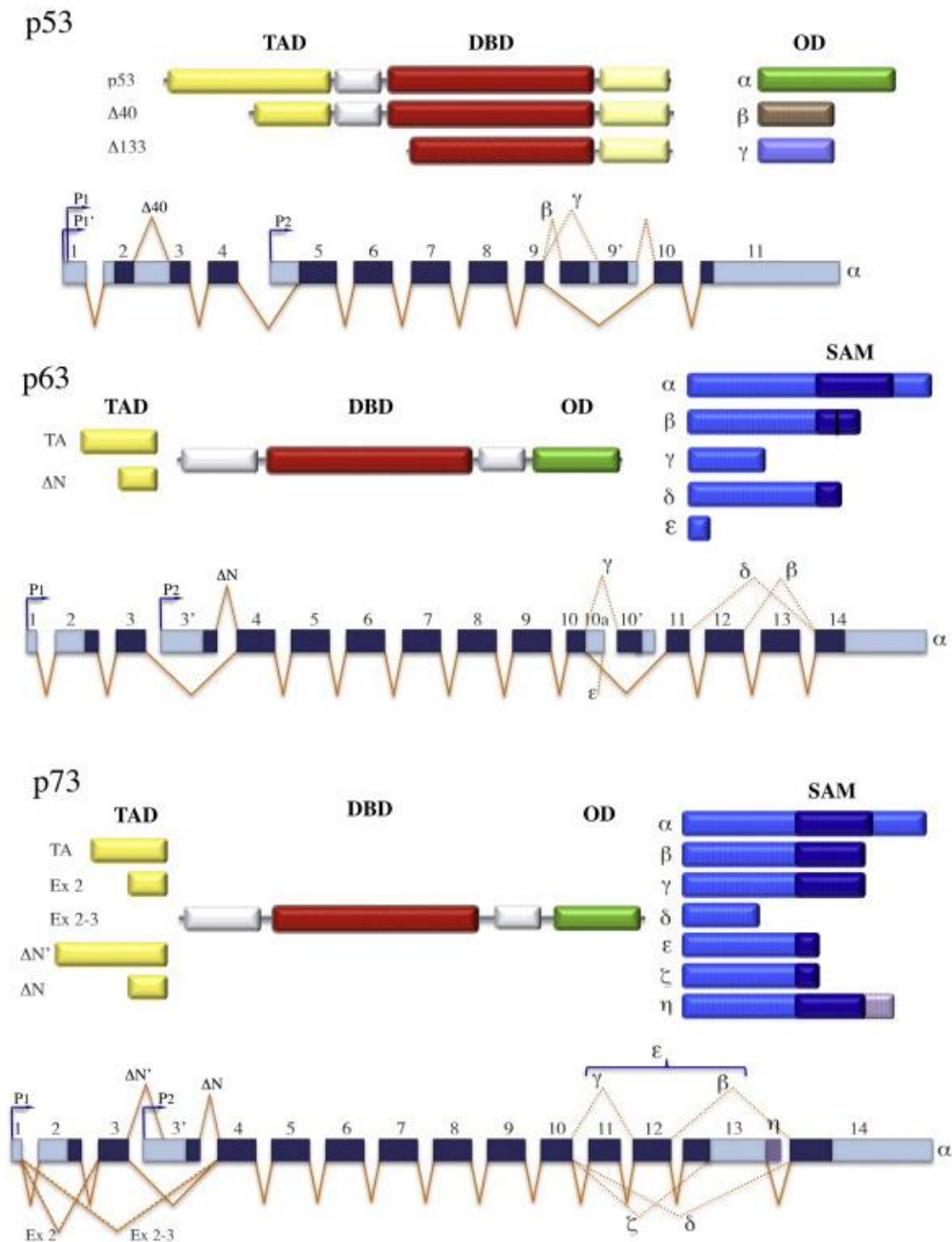


Figure 1.1. p53 family gene and protein structure. The main p53 family protein domains include the transactivation domain (TAD), DNA binding domain (DBD), oligomerization domain (OD), and sterile alpha motif (SAM). All p53 family proteins produce two groups of mRNAs controlled by different promoters. The isoforms generated may or may not contain the transactivation domain, depending on whether they are generated by the activity of the promoter P1 (TA forms) or from the promoter P2 (ΔN forms). Adapted from Allocati et al., 2012.

Similarly to p73, the human and mouse p63 gives rise to three different splice variants that differ in their C-termini: a full-length α form; a β form that is truncated after exon 12; and a γ form that lacks exons 12-14 and uses an additional exon 15. Each of these isoforms may or may not contain the TAD, depending on whether they are generated by the activity of the promoter upstream of exon 1 (P1) (TA forms) or from the alternative promoter in intron 3 (Δ N forms). Although Δ N isoforms of p63 do not activate transcription, they can act dominant negatively and inhibit transactivation by TAp63, TAp73 and p53 proteins, through a different transactivation domain present in their distinct N-terminal end (Helton et al., 2006).

1.1.2.1. p53

p53 functions mainly as a DNA-binding, sequence-specific transcription factor, which has well-established roles in promoting neuronal cell death during development (Tedeschi and Di Giovanni, 2009), and in adult individuals after exposure to stress and/or DNA damage. Indeed, the p53 protein is a downstream target of the DNA damage signaling network that is expressed at low levels under physiological conditions and whose activity is promoted by a wide range of stress signals; once activated, and depending on cell type and cell environment, p53 stimulates the expression of multiple pro-apoptotic genes involved in either reversible cell cycle arrest or apoptosis, including p21, GADD45, Bax, and many other, as well as targets of p63 and p73 (Irwin and Kaelin, 2001; Melino et al., 2002; Mills, 2006; Vousden and Lu, 2002).

The pro-apoptotic activity of p53 is often evident after irreversible damage in circumstances of exposure to genotoxic stress, oxidative stress or NGF withdrawal in developing or mature cortical and sympathetic neurons (Aloyz et al., 1998; Anderson and Tolkovsky, 1999; Bonaguidi et al., 2011; Cregan et al., 2004; Song and Xu, 2007). In addition, p53 regulates the expression of proteins that modulate its own activation and stability, such as the E3 ligase Mdm-2, forming multiple positive and negative feedback loops (Harris and Levine, 2005). In fact, in response to DNA damage, the p53 protein accumulates upon a number of post-translational modifications (Sims and Reinberg), which reduce its affinity for Mdm-2 and hence favor its stabilization (Kruse and Gu, 2009). Alternatively, Mdm-2-repressing mechanisms such as those mediated by the onco-suppressor

protein ADP ribosylation factor (ARF), which acts by sequestering Mdm-2 and preventing the Mdm-2-p53 interaction in response to oncogenic stress, can stabilize p53 (Iwakuma and Lozano, 2003).

Lethal proteins whose promoter contains a functional p53 responsive element of the activator type include pro-apoptotic members of the Bcl-2 protein family such as Bad, Bak, Bax, Bid, Bok, Noxa, and PUMA, as well as other components of the mitochondrial apoptotic pathway like the cytosolic adaptor Apaf-1, AIF, AIF-homologous mitochondria-associated inducer of death, p53-regulated apoptosis-inducing protein 1, oxidative stress-induced growth inhibitor 1, which has recently been discovered to contribute to p53-dependent MOMP in response to DNA damage, and caspase-6 (Galluzzi et al., 2011). Moreover, a number of genes are transcriptionally repressed by p53. These genes code for negative regulators of MOMP, such as Bcl-2, Bcl-x_L, and Mcl-1, as well as for anti-apoptotic proteins that operate downstream of mitochondria (Galluzzi et al., 2011).

Curiously, until recently, p53 was believed to promote MOMP only by transactivating pro-apoptotic genes and/or by repressing genes that exert anti-apoptotic effects. Recently, it has become clear that the cytoplasmic pool of p53 mediates a direct apoptogenic effect at mitochondria by physically interacting and inhibiting anti-apoptotic Bcl-2 family members (Chipuk et al., 2005; Chipuk et al., 2004; Moll et al., 2005; Morselli et al., 2008; Vaseva et al., 2009), and directly stimulating pro-apoptotic proteins, including mitochondria Bak (Pietsch et al., 2008), cytosolic Bax (Chipuk et al., 2004), Bad (Jiang et al., 2006), and Bid (Song et al., 2009). Finally, caspase-dependent proteolysis of p53 may also generate fragments that translocate to mitochondria and induce MOMP, thereby activating a feedforward loop for the amplification of the apoptotic signal (Robles et al., 2001).

1.1.2.2. p63 and p73

Much like p53, both p63 and p73 are clearly implicated in apoptosis regulation (Rocco and Ellisen, 2006). The TAp63 isoforms are pro-apoptotic, while the Δ Np63 isoforms are anti-apoptotic, similarly to the TA and Δ N isoforms of p73 (Flores et al., 2002; Wu et al., 2003).

Several studies have highlighted an essential role of endogenous TAp73 in regulating apoptosis in response to DNA damage (Jost et al., 1997; Lin et al., 2004). Upon this stress, not only $\Delta Np73$ but also $\Delta Np63\alpha$ (Chatterjee et al., 2008; Müller et al., 2006; Westfall et al., 2005) are rapidly degraded. Thus, they do not exert their dominant negative effect on p53, TAp63 and TAp73, allowing cell cycle arrest and apoptosis to proceed. Moreover, previous studies have already shown that treatment of cells with various DNA-damaging agents resulted in increased expression of TAp63 and TAp73 isoforms (Hershkovitz Rokah et al., 2010; Sayan et al., 2007b; Yao et al., 2010c).

p73 is a target of the tyrosine kinase c-Abl in response to DNA damage induced by cisplatin or ionizing radiation, thereby resulting in apoptosis (Agami and Bernards, 2000; Gong et al., 1999; Yuan et al., 1999). In turn, the role of p63 in apoptosis pathways is still under debated. Gressner *et al.* (Gressner et al., 2005) described the role of TAp63 α in activating apoptosis through death receptor signaling and mitochondria by activating transcription of p53 targets (Testoni et al., 2006). In fact, it was shown that TAp63 can induce the expression of death receptors including Fas, TNF-R, and TRAIL-R, as well as pro-apoptotic Bcl-2 family members, such as Bax (Gressner et al., 2005). Furthermore, inhibition of TAp63 function results in chemoresistance. Sayan *et al.* (Sayan et al., 2007b) have also demonstrated that after induction of apoptosis, the transactivation-inhibitory domain of the $\Delta Np63\alpha$ isoforms is cleaved by activated caspases. Cleavage of $\Delta Np63\alpha$ relieves its inhibitory effect on transcriptionally active p63 proteins, and the cleavage of TAp63 α results in production of a TAp63 protein with enhanced transcriptional activity, promoting apoptosis.

Nevertheless, the involvement of p63 and p73 in neural p53-mediated apoptosis is still controversial (Benchimol, 2004). In fact, there is intense debate on whether and how p63 and p73 interact with p53 in apoptosis context. During development, the p53 family has been considered pivotal in determining the life *versus* death of developing peripheral sympathetic neurons (Jacobs et al., 2005; Pozniak et al., 2000; Walsh et al., 2004). p53 has a partial but essential role for efficient neuronal apoptosis *in vivo* (Aloyz et al., 1998; Jacobs et al., 2005; Slack et al., 1996). TAp63 can induce neuronal apoptosis on its own, but p53 requires TAp63, indicating that p63 is dominant to p53 during developmental sympathetic neuronal death (Jacobs et al., 2006). In addition, analysis of the embryonic

superior cervical ganglion shows that TAp63 is also essential for naturally occurring sympathetic neuronal death *in vivo*. Sympathetic neuron survival is largely regulated by pro-apoptotic signals deriving from p75^{NTR} and pro-survival signals deriving from the NGF/TrkA receptor (Kaplan and Miller, 2000). In addition, NGF withdrawal and p75^{NTR} activation converge on TAp63 and p53, which then activate Bax gene and protein expression to induce mitochondrial apoptosis (Jacobs et al., 2005). Interestingly, Dugani *et al.* (Dugani et al., 2009) have also demonstrated that the Δ Np63 isoform is crucial for the survival of neural precursors, namely embryonic cortical precursors, and newly born neurons, antagonizing the pro-apoptotic actions of p53. NGF induced anti-apoptotic Δ Np73 protein functions, at least in part, by antagonizing the pro-apoptotic actions of p53 (Pozniak et al., 2000), and potentially TAp63. Thus, p73 acts as an essential pro-survival protein (Lee et al., 2004; Pozniak et al., 2000). Thus, coordinated regulation of the abundance of p53 family proteins appears to be critical in influencing the outcome of neural apoptosis.

1.1.3. JNK/c-Jun signaling pathway

Several stimuli including growth factors, proinflammatory cytokines, neurotransmitters, cell-matrix interactions, physical and chemical stresses activate MAPK signaling pathways (Chang and Karin, 2001; Ip and Davis, 1998; Karin et al., 1997; Whitmarsh and Davis, 1996). In mammalian cells, the MAPK family is comprised of 3 groups: c-Jun N-terminal kinase (JNK), extracellular signal-regulated kinase, and p38. The JNK pathway is a central stress signaling pathway implicated in neuronal plasticity, regeneration and death (Herdegen et al., 1997). Signaling cascades activate the activator protein-1 (AP-1) through the phosphorylation of distinct substrates. AP-1 is linked to various cellular responses, including proliferation, differentiation, oncogenic transformation and apoptosis (Angel and Karin, 1991; Shaulian and Karin, 2002). The AP-1 capacity to control several biological processes is primarily due to its structural and regulatory complexity. In fact, AP-1 is a collective term referring to dimeric basic/leucine zipper transcription factors that belong to several subfamilies, including the Jun (Estus et al., 1997) subfamily. These DNA binding proteins may form homodimers or heterodimers with each other (Chinenov and Kerppola, 2001). c-Jun is an essential regulator of both cell survival and death, with its levels being increased upon exposure to a variety of stress

signals and chemotherapeutic agents as well as growth factors (Eferl and Wagner, 2003). Its activity is regulated by phosphorylation at serines 63 and/or 73 through JNKs (Dérijard et al., 1994; Ham et al., 1995; Kyriakis et al., 1994).

The detailed mechanisms by which c-Jun regulates apoptosis is not fully understood. The role of c-jun in apoptosis may be stimulus- and cell type-specific. JNK increases the ability of c-Jun to activate the transcription of target genes (Estus et al., 1994; Ham et al., 1995) that are more proximal to promote caspase activation and neuron apoptosis (Edwards and Tolkovsky, 1994; Putcha et al., 2000). Indeed, induction of pro-apoptotic Bcl-2 family members Bim (Whitfield et al., 2001) and death protein 5/harakiri were shown to be JNK/c-Jun-dependent in neurons (Harris and Johnson, 2001). In addition, some studies have reported that after NGF withdrawal in sympathetic neurons, c-Jun protein levels increased and the N-terminal c-Jun transcriptional activation domain became more phosphorylated (Eilers et al., 1998; Eilers et al., 2001), in correlation with an increase in JNK activity (Bruckner et al., 2001; Eilers et al., 1998). Moreover, microinjection of an expression vector for a c-Jun dominant negative mutant, which inhibited AP-1 activity, resulted in protection of neurons against NGF withdrawal-induced death, whereas overexpression of wild-type c-Jun was sufficient to induce apoptosis in the presence of NGF (Estus et al., 1994; Ham et al., 1995). The role for c-Jun in CNS neurons has also been reported, namely in cerebellar granule neurons (Watson et al., 1998). In addition, the c-Jun pathway has also been implicated in the induction of apoptosis in differentiated PC12 cells deprived of NGF (Xia et al., 1995), in striatal neurons treated with neurotoxic concentrations of dopamine (Luo et al., 1998), or in a hippocampal neuron cell line transfected with an expression vector for polyglutamine-expanded Huntingtin (Liu, 1998).

Curiously, JNK may also phosphorylate p53 (Fuchs et al., 1998), and subsequently up-regulate Bax (Miyashita and Reed, 1995). However, the interplay between p53 and c-Jun in regulating neuronal survival and death genes remains to be determined. Regarding p73, it was already demonstrated that JNK and c-Jun is required for the stabilization of TAp73 (Jones et al., 2007; Toh et al., 2004) and degradation of Δ Np73 under stress stimulation (Dulloo et al., 2010). Importantly, c-Jun has also been shown to regulate the abundance of p63. Yao *et al.* (Yao et al., 2010b) showed that the transcriptional activity of the TAp63 promoter and TAp63

protein levels were both up-regulated by an increased c-Jun activity in the Hep3B human hepatocellular carcinoma cell line.

However, since c-Jun null mice die during embryonic development at embryonic day 12.5 (E12.5) due to hepatic failure (Hilberg et al., 1993), *in vivo* studies focused on the role of c-Jun in the nervous system were only possible due to knockout (KO) mice models for the three mammalian JNK genes, *Jnk1*, *Jnk2*, and *Jnk3*. JNK3 is mainly expressed in the CNS (Junyent et al., 2011), whereas JNK1 and JNK2 are expressed in many other tissues (Ip and Davis, 1998). In fact, c-Jun phosphorylation and neuronal cell death was inhibited in neurons from JNK3 null mice (Bruckner et al., 2001). Finally, JNK1/JNK2 double KO mice, but not single, showed that both JNKs are required for developmental cell death in the neural tube, whereas in the developing cortex they promote neuronal survival (Kuan et al., 1999; Sabapathy et al., 1999). Thus, although JNKs and c-Jun may be pro-apoptotic in many neuronal cell types, they can have other cellular roles.

1.1.4. Role of apoptosis in Alzheimer's disease

AD is the most common human age-related, sporadic neurodegenerative disorder, characterized by a global, progressive and irreversible cognitive decline that is strongly correlated with synaptic dysfunction and death of neurons from hippocampus and associated regions of the cerebral cortex. The affected brain shows extracellular deposits of A β peptides, known as amyloid or senile plaques (Mattson, 2004), and intracellular accumulation of paired helical filaments that form NFTs (McKee et al., 1990), consisting of polymerized hyperphosphorylated tau protein (Spillantini and Goedert, 1998). Although activation of apoptotic signaling has been reported in AD brains (Raynaud and Marcilhac, 2006), the precise intracellular signaling pathways by which A β peptides trigger cell death are not fully understood.

The study of apoptosis in neurodegenerative diseases has become a challenging task and a controversial area of research, especially because synaptic loss and electrophysiological abnormalities typically precede cell loss. In addition, given the slow progression of most neurodegenerative diseases, in contrast with the rapid progression of a cell through apoptosis, the detection of representative apoptotic neurons in AD patients could be difficult. Further, apoptotic processes may be terminated or not yet initiated by the time of tissue examination. In fact, the collected

tissue is usually representative of the end-stage disease, being removed much later than it would be ideal to treat patients and prevent neuronal cell death. Finally, the criteria used to classify the type of cell death as apoptosis has often been based on morphological assessment and biochemical assays, which may also account for other forms of programmed cell death.

Although many AD mouse models have been reported, there is no single model that exactly mimics human AD (Elder et al., 2010). Thus, it is important to keep in mind the limitations when research data generated from using these AD animal models are interpreted.

Knowledge of the production and degradation pathways acting on the toxic proteins that cause AD, and various other proteinopathies, could help in the design and improvement of therapeutic strategies. Specifically, the reduction of A β load has given many insights into drug development strategies for potential therapies in AD aimed at preventing A β formation or accelerating its degradation. β - and γ -secretases have been considered as possible drug targets. Targeting secretases may, however, have unforeseen effects because a physiological role for A β has also been proposed (Atwood et al., 2003; Chen and Dong, 2009; Pearson and Peers, 2006).

1.1.4.1. A β production and accumulation

The amyloid precursor protein (APP) in mammals belongs to a family of conserved type I membrane proteins that include APP, APP-like protein 1 (Aydin et al.) and 2 (APLP2) (Aydin et al., 2012). Although the APP family is abundantly expressed in the brain and APLP1 expression is restricted to neurons (Lorent et al., 1995), APP and APLP2 can also be found in the majority of other tissues. The human *APP* gene encodes a single transmembrane polypeptide, whose primary structure contains a signal peptide for secretion, a large extracellular N-terminal domain, a transmembrane domain, and a cytoplasmic C-terminal tail.

During normal development, APP can undergo amyloidogenic or non-amyloidogenic processing via cleavage by three different secretases, α -, β -, and γ -secretases (Ling et al., 2003). In the non-amyloidogenic pathway, cleavage of APP occurs via presenilin-containing α -secretase complex, which cleaves within A β sequence and consequently abrogates A β formation, leading to the release of a large soluble extracellular fragment (Mattson), which can be neuroprotective, and retention of an 83-residue membrane-bound fragment (C83). Alternatively, APP can be

cleaved by β -secretase, which cuts at the N-terminus of $A\beta$, generating a smaller extracellular fragment (Mattson) and a 99-residue membrane-bound fragment (C99). Peptide fragments C83 and C99 may then undergo conformational alterations and become targets for the presenilin (PS1/PS2)-dependent γ -secretase, which cleaves within the plasma membrane domain. C99 proteolysis generates $A\beta_{1-40}$ and $A\beta_{1-42}$ (Selkoe and Wolfe, 2007). The cleavage of either C83 or C99 by γ -secretase may also generate an amyloid intracellular domain (AICD), which moves to the nucleus where it may modulate transcription of target genes.

$A\beta$ is produced as a monomer, but readily aggregates to form multimeric complexes. Therefore, the term “soluble $A\beta$ ” is generally applied either to newly generated, cell-secreted $A\beta$ or to that fraction of tissue or synthetic $A\beta$ that is taken into the aqueous phase of a non-detergent containing extraction buffer. In contrast, “misfolded” and “aggregated” $A\beta$ are terms used to describe very early, nonspecific changes in $A\beta$ folding states or solubility states, respectively. In addition, “oligomeric” $A\beta$ refers to peptide assemblies with limited stoichiometry, such as dimers and trimers, while protofibrils are structures of intermediate order between aggregates and fibrils (Gandy, 2005).

$A\beta$ peptide is detected in human cerebrospinal fluid (CSF) as a range of isoforms between 38 and 43 amino acids in length. The predominant isoforms secreted are $A\beta_{1-40}$ (90%) whereas $A\beta_{1-42}$ isoform represents less than 10% (Thinakaran and Koo, 2008). In patients with AD, the relative proportions of $A\beta_{1-40}$ and $A\beta_{1-42}$ change to approximately 50% each (Mehta et al., 2001). The accumulation of $A\beta$ is progressive and strongly accepted as an important contributor to the neuronal dysfunction and loss (Hardy and Selkoe, 2002). The pattern and distribution of the different $A\beta$ species varies among the different topographical lesions.

1.1.4.2. Cytotoxicity of $A\beta$

Several studies suggest that $A\beta$ -induced oxidative stress leads to apoptotic neuronal cell death that can be inhibited by antioxidants (Behl et al., 1994; Mattson and Goodman, 1995; Pillot et al., 1999). In fact, many lines of evidence suggest that mitochondria dysfunction and oxidative damage have a central role in aging-related neurodegenerative diseases, being key regulators of cell survival and death (Danial and Korsmeyer, 2004).

The involvement of apoptosis in AD has been corroborated by studies showing that A β alters the expression of the Bcl-2 family of apoptosis-related genes (Yao et al., 2005) and that survival pathways play a pivotal role in preventing A β -mediated apoptosis (Watson and Fan, 2005). On the other hand, studies in an anti-NGF transgenic mouse model and PC12 cells suggest that discontinued or limited NGF supply induces an overproduction of A β peptides, triggering downstream apoptotic cell death (Capsoni et al., 2000; Matrone et al., 2008). Furthermore, p75^{NTR} has been consistently linked to changes occurring in AD (Schliebs, 2005; Sothibundhu et al., 2009), including cell death of basal forebrain cholinergic neurons, where this receptor is highly expressed (Dechant and Barde, 2002). Both *in vitro* and *in vivo* evidence suggests that the JNK/c-Jun cascade is a critical event during neuronal death in AD (Anderson et al., 1994; Kihiko et al., 1999; Viana et al., 2010), where JNK mediates the activation of several molecules, including caspase-2 (Viana et al., 2010), p53 (She et al., 2002), and Bcl-2 family members (Sorenson, 2004) and potentiate inflammatory responses via AP-1 activation (Manning and Davis, 2003). Viana *et al.* (Viana et al., 2010) showed that A β exposure in PC12 cells resulted in activation and nuclear translocation of JNK, and caspase-2 activation. Caspase-2 triggers apoptosis through activation of the mitochondrial apoptosis pathway. The induction of c-Jun was shown to occur *in vitro* after A β treatment (Estus et al., 1997; Iwasaki et al., 1996; Kihiko et al., 1999) and in AD brains (Anderson et al., 1994; Anderson et al., 1996), suggesting a possible requirement for this transcription factor in A β toxicity.

Curiously, p53 family members have also been associated with A β -induced neuronal apoptosis. The first indication that the p53 family may play a role in AD came in 1996 with the demonstration that intracellular A β up-regulates p53 in the brains of transgenic mice overexpressing the A β fragment of APP (LaFerla et al., 1996). The use of pifithrin- α , an inhibitor of p53-dependent gene transcription, was shown to protect neurons against A β -induced apoptosis (Culmsee et al., 2001; Hooper et al., 2007). p53 was also found to be up-regulated in the brain of AD patients [43, 44]. In 2004, Caricasole *et al.* (Caricasole et al., 2004) showed that A β activates the expression of the soluble Wnt antagonist Dickkopf-1 (Caricasole et al.), a p53 target gene. Knockdown of Dkk1 in primary neurons, in turn, almost completely blocked A β -induced tau phosphorylation, implicating the p53 family in the “amyloid cascade” pathway.

More recently, it has been demonstrated that p53 participates in A β -induced apoptosis of PC12 neuronal cells through modulation of Bax expression (Ramalho et al., 2004). Furthermore, A β -induced apoptosis in rat primary cortical neurons was associated with translocation of Bax to the mitochondria, followed by cyt *c* release, caspase activation, and DNA and nuclear fragmentation (Solá et al., 2003). Interestingly, a novel biological function of intracellular A β ₁₋₄₂ has been suggested, where it acts as a transcription factor for the p53 promoter, enhancing p53-dependent neuronal apoptosis in AD (Ohyagi et al., 2005).

Several reports have also demonstrated p73 involvement in apoptosis triggered by A β ₂₅₋₃₅, being probably vital for mediating the process of AD (Zhang et al., 2011). It has been shown that in primary cortical neurons generated from p73 KO mice, the activity of JNK increased, while JNK inhibition decreased tau phosphorylation in these neurons (Wetzel et al., 2008). Since Δ Np73, and not TAp73, can bind and inhibit JNK, the loss of Δ Np73 forms may result in tau phosphorylation and neurodegeneration. As mentioned before, A β peptide activates c-Abl and increases p73 levels (Alvarez et al., 2004; Vázquez et al., 2009), while the Swedish mutant form of APP increases expression from both the TA and Δ N promoters of the p73 gene, only inducing an overall increase in the TA forms (Vázquez et al., 2009). Surprisingly, the mechanisms regulating p63 levels under A β -mediated apoptosis have yet to be elucidated.

A β peptides accumulate within mitochondria, strongly affecting their function and morphology, particularly in the synaptic compartment (Baliatti et al., 2012). Increasing evidence indicates that the mitochondrial dysfunction is an important early factor in the development of AD-like pathology (Blass and Gibson, 2006; Yao et al., 2009). Accumulation of A β in mitochondria appears to be also associated with diminished enzymatic activity of respiratory chain complexes III and IV, and reduction of oxygen consumption (Caspersen et al., 2005).

Finally, several studies have demonstrated that A β triggers the formation of tau pathology. Inflammatory processes are strongly correlated with AD onset and progression in humans, and could have a pivotal role in disease etiology (Kitazawa et al., 2005; Krstic and Knuesel, 2013). Interestingly, it has been suggested that different forms of A β may be responsible for inducing tau hyperphosphorylation in different settings (Blurton-Jones and LaFerla, 2006; LaFerla, 2010).

1.1.5. Regulation of apoptosis by autophagy

Autophagy is a cellular process in which isolated membrane sequesters part of the cytoplasm to form a double-membrane vesicle, called autophagosome (AP) that fuses with lysosomes for the degradation of its contents, long-lived cytoplasmic proteins or damaged organelles, by acidic lysosomal hydrolases, maintaining normal cell homeostasis (Nixon and Yang, 2011). There are at least three types of autophagy; macroautophagy (delivery of cytosolic contents to the lysosome by autophagosomes), microautophagy (inward invagination of the lysosomal membrane) and chaperone-mediated autophagy (direct translocation across the lysosomal membrane). Among these, macroautophagy referred to as autophagy has been the most studied. Autophagy-related (Atg) proteins are a set of evolutionarily conserved gene products, originally identified in yeast and followed by the identification of homologs in higher eukaryotes (Huang and Klionsky, 2002), which are required for autophagy.

Among Atg proteins, one subset is essential for AP formation, and is referred to as the “core” molecular machinery (Xie and Klionsky, 2007). In mammalian cells, most of the Atg proteins are observed in isolated membranes but not in complete APs (Longatti and Tooze, 2009; Tooze and Razi, 2009). Only microtubule-associated protein light chain 3 (LC3), a mammalian homolog of yeast Atg8, is known to exist in APs, and therefore, this protein serves as marker for APs and is widely used to monitor autophagy (Kabeya et al., 2000).

Since autophagy can block apoptosis, one might expect that their regulation would be tightly coordinated. Curiously, the same proteins can regulate both processes. Some molecular connections occur upstream of the autophagic and apoptotic machinery itself, where signaling pathways regulate both processes (Thorburn, 2008). p53, which is a potent inducer of apoptosis, can also induce autophagy through increased expression of a direct p53 target gene called DRAM (Crighton et al., 2006). Similarly, activation of the phosphatidylinositide 3 kinase (PI3K)/Akt pathway, which is well-known to inhibit apoptosis, also inhibits autophagy (Arico et al., 2001). Thus, important signaling pathways simultaneously increase or decrease both autophagy and apoptosis. In addition, proteins that are themselves central components of the apoptosis machinery, including Bcl-2 family proteins and FADD regulate both processes directly. In addition, in normal cytoprotective autophagy, activation of JNK can up-regulate Beclin-1 (Li et al.,

2009), a marker for autophagy activation that was originally identified as an interaction partner of the anti-apoptotic protein Bcl-2 (Kang et al., 2011). When Bcl-2 and Bcl-x_L proteins form Beclin-1-Bcl-2/Bcl-x_L complexes, the pro-autophagic function of Beclin-1 is inhibited (Maiuri et al., 2007).

Although autophagy is crucial in survival and suppression of apoptosis, it can also lead to cell death (Lum et al., 2005; Mizushima, 2005; Yu et al., 2004b), either in collaboration with apoptosis or as a backup mechanism when apoptotic machinery is disabled (Eisenberg-Lerner et al., 2009; Shimizu et al., 2004; Yu et al., 2004a). One example of autophagic cell death is caused by increased ROS resulting from autophagic degradation of catalase (Yu et al., 2006). Interestingly, neurons presenting accumulation of autophagic vacuoles (AVs) seem to have dysfunction of this degradation pathway (Nixon et al., 2005; Yu et al., 2005; Yu et al., 2004c). Autophagy is normally efficient in the brain as reflected by the low number of AVs at any given moment (Boland et al., 2008). Interestingly, it has been reported an elevated number of AVs in brains of AD patients and in transgenic mouse models, associated with dystrophic neuritis and deformed synaptic membranes (Nixon et al., 2005; Yu et al., 2005). This suggests impairment of clearance mechanisms, thus indicating that autophagy is involved in AD pathogenesis. In addition, Lipinski *et al.* (Lipinski et al., 2010) has shown that ROS play an essential role in mediating autophagy upstream of PI3K in brains of AD patients. This pathway is critical for the initiation of autophagy by A β . Zheng *et al.* (Zheng et al., 2006b) have also demonstrated that ROS induce intralysosomal A β accumulation in cultured differentiated neuroblastoma cells through the activation of autophagy. However, it remains to be elucidated whether intralysosomal A β corresponds to autophagocytosed cytoplasmic A β , or a derivative of autophagocytosed APP, or both.

Interestingly, autophagy has also been reported as a mechanism of neuronal protection from A β -induced cytotoxicity (Cheung et al., 2011; Hung et al., 2009; Wang et al., 2010), and serves as a mechanism that mediates clearance of ubiquitinated A β to eliminate molecular debris and restore neurotransmitter balance (Khandelwal et al., 2011) (Fig. 1.2). In fact, Hung *et al.* (Hung et al., 2009) have demonstrated in SH-SY5Y/pEGFP-LC3 cells that A β treatment activates autophagy, and inhibition of this process increases neuronal death, indicating that the clearance of A β plays a neuroprotective role. Furthermore, the decreased activity of the proteasomal system and consequent accumulation of A β induced autophagy (Iwata et

al., 2005; Khandelwal et al., 2011), concurrent with ubiquitination (Nedelsky et al., 2008; Ravikumar and Rubinsztein, 2004; Wong and Cuervo, 2010). When proteins are aggregate-prone and poor proteasome substrates, autophagy becomes a major clearance route by default.

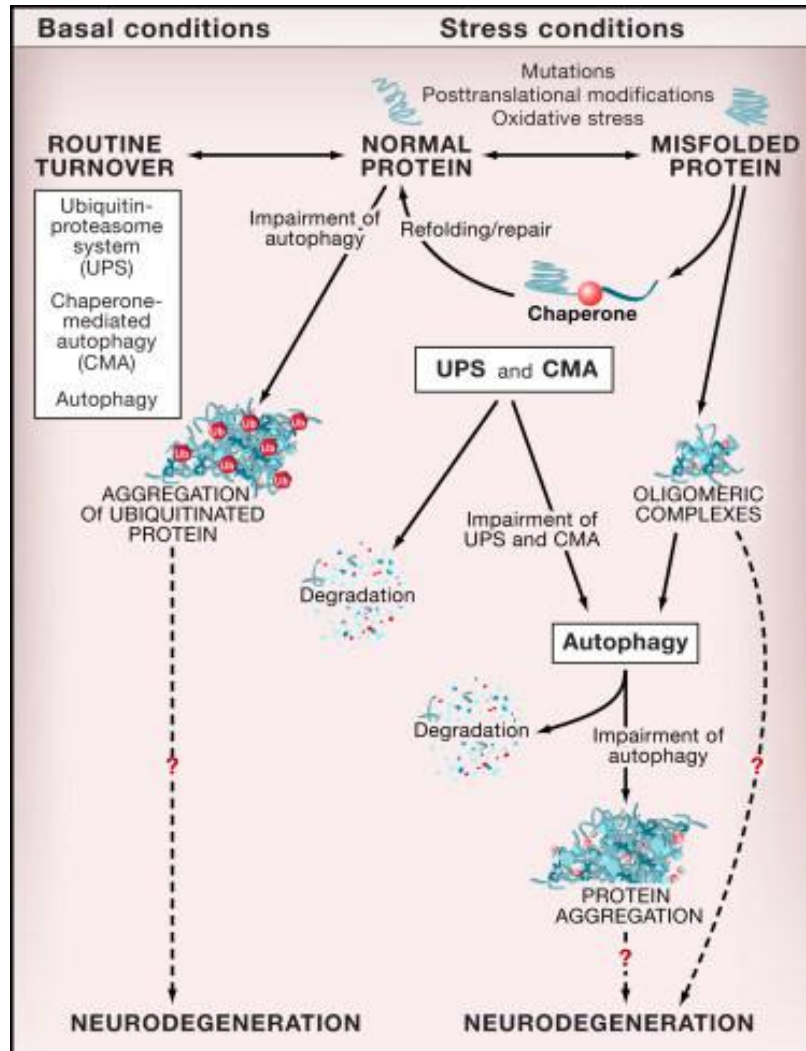


Figure 1.2. Autophagy is crucial for intracellular clearance of neurons. Normal proteins are routinely turned over by different protein degradation systems, including the ubiquitin-proteasome system (UPS), chaperone-mediated autophagy (CMA), and autophagy. In autophagy-deficient neurons, there is an accumulation of ubiquitinated protein aggregates that is associated with neurodegeneration. Proteins altered by mutations, posttranslational modifications, or stress undergo a conformational change, are recognized by molecular chaperones, and are either refolded and repaired or delivered to protein degradation systems, usually UPS or CMA. If these protein degradation systems are impaired or if the altered proteins form oligomeric complexes that cannot be recognized by the UPS or CMA, autophagy may be the primary route for the removal of these abnormal and potentially toxic proteins. Impaired autophagy is associated with the formation of protein aggregates and increased neurodegeneration. Adapted from Levine and Kroemer, 2008.

In 3xTg-AD mice, the E3-ubiquitin ligase parkin clears vesicle-containing defective mitochondria, suggesting that the clearance of intraneural A β reduces oxidative stress (Geisler et al., 2010; Khandelwal et al., 2011), and may modulate autophagy. These issues deserve further investigation since autophagy might be one of the key checkpoints responsible for neural differentiation, as an alternative to cell death.

1.1.6. Modulation of neural apoptosis by bile acids

Bile acids are the major component of bile, produced in the liver and secreted via the bile ducts and gallbladder into the intestine (Setchell et al., 1992), where they act as detergents being crucial in the solubilization of lipids in the human intestinal lumen. Ursodeoxycholic acid (UDCA) is an endogenous bile acid used during the past several decades for the treatment of certain liver diseases (Lazaridis et al., 2001; Paumgartner and Beuers, 2002). It is normally present in human bile in low concentrations. The anti-apoptotic effects of UDCA have been demonstrated both *in vivo* and *in vitro* in the rat liver [48, 68], and in human hepatocytes [69]. Furthermore, it has been shown that both UDCA and its taurine conjugated form, tauroursodeoxycholic acid (TUDCA), play a unique role in modulating cell death in response to a variety of agents, by interrupting classic pathways of apoptosis in both hepatic and non-hepatic cells, including neurons (Rodrigues et al., 1998; Rodrigues et al., 2002a; Rodrigues et al., 2000b; Solá et al., 2003) (Fig. 1.3). A possible explanation for this ubiquitous anti-apoptotic effect appears to involve the mitochondrial membrane stabilization (Rodrigues et al., 2003b). Indeed, both UDCA and TUDCA are antioxidant molecules (Oveson et al., 2011; Phillips et al., 2008), modulating mitochondrial apoptosis in a number of animal models (Rodrigues et al., 1998; Rodrigues et al., 2002a; Rodrigues et al., 2000b). In fact, UDCA and, more efficiently, TUDCA inhibited bilirubin- and A β -induced MOMP and consequent cyt *c* release in isolated mitochondria of neural and glial cells (Rodrigues et al., 2000a). Moreover, using electron paramagnetic resonance spectroscopy analysis, it has been demonstrated that TUDCA prevents A β -driven modifications in mitochondrial membrane redox status, lipid polarity and protein order (Rodrigues et al., 2001). The effects of TUDCA on the A β -affected mitochondria were further confirmed by the

observation of decreased Bax translocation in the presence of this bile acid (Solá et al., 2003).

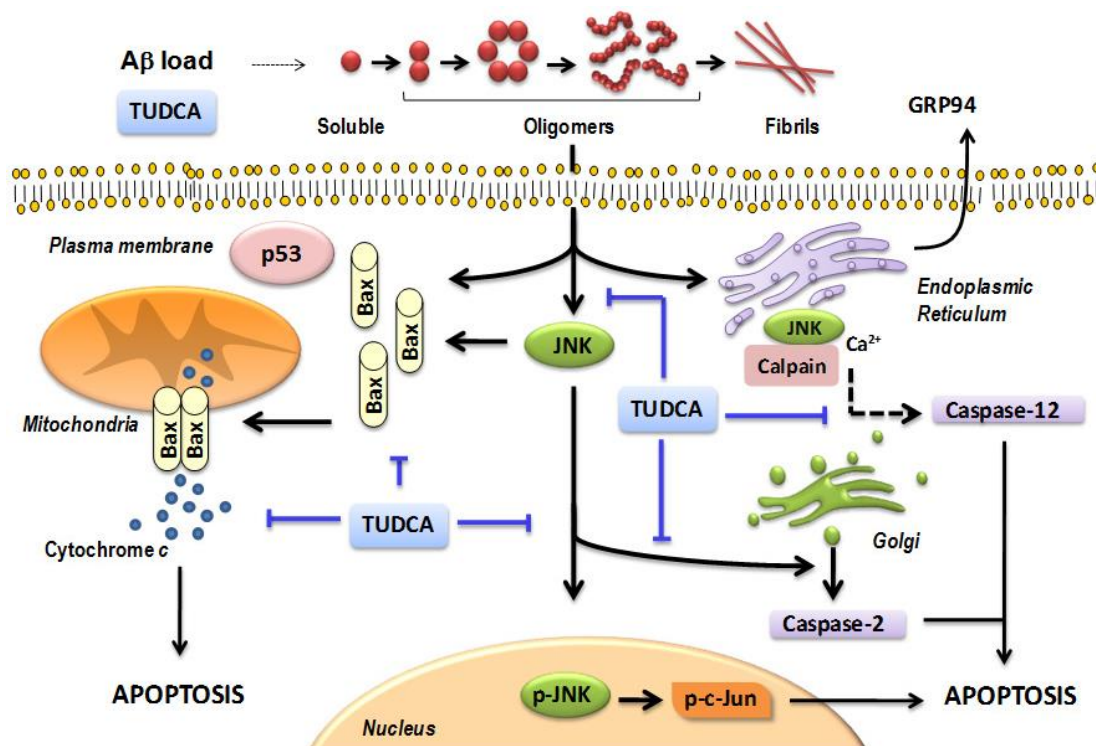


Figure 1.3. Tauroursodeoxycholic acid modulates amyloid β -induced toxicity by inhibiting organelle-driven apoptosis. Soluble $A\beta$ is a hydrophobic peptide that is prone to aggregation. Equilibrium is produced between several extracellular and intracellular $A\beta$ species, including monomeric, oligomeric, and fibrillar forms. Cell death by toxic $A\beta$ appears to involve a complex signaling network of inter-organellar cross-talk that involves mitochondria, ER, Golgi and nucleus. TUDCA effectively abrogates this signaling network. Intracellular calcium (Ca^{2+}) free levels are tightly regulated by the ER to avoid cell death induced by Ca^{2+} deregulation. Inside the ER, Ca^{2+} is maintained elevated by Ca^{2+} -binding buffering proteins, such as GRP94, promoting cellular Ca^{2+} homeostasis. Caspase-12 can be activated via Ca^{2+} -activated protease calpain during ER stress-induced apoptosis. $A\beta$ -induced cell death requires the activation of caspase-2, which is localized at the Golgi complex and has been described as a target of the JNK pathway that triggers apoptosis through activation of the mitochondrial pathway. In fact, $A\beta$, p53 and activated JNK trigger Bax translocation to the mitochondria, formation of pore complex, cytochrome c release, and subsequent mitochondrial apoptosis. In addition, JNK activates the pro-apoptotic transcription factor c-Jun, enhancing the expression of apoptosis proteins. Adapted from Viana et al., 2012.

In addition, UDCA and TUDCA interfere with upstream targets of mitochondria, in a caspase-independent manner (Solá et al., 2003b). The anti-apoptotic effects of these bile acids appear to be dependent on other molecular

targets upstream of the E2F-1/p53 apoptotic pathway (Solá et al., 2003b), namely the nuclear steroid receptors. In fact, as cholesterol-derived molecules, UDCA and TUDCA interact with specific regions of glucocorticoid (GR) and the mineralocorticoid (MR) receptors (Solá et al., 2006; Solá et al., 2005; Solá et al., 2004). A β incubation reduces MR nuclear translocation while increasing nuclear GR levels. Notably, pretreatment with TUDCA markedly altered A β -induced changes in nuclear steroid receptors.

The protective role of TUDCA has been extended to several mouse models of neurological disorders, including Huntington's disease (Keene et al., 2002), Parkinson's disease (Duan et al., 2002), and acute ischemic (Rodrigues et al., 2002b) and hemorrhagic stroke (Rodrigues et al., 2003a). Notably, in an *in vitro* AD pathologic model, TUDCA prevented the reduction of dendritic spine number and the decrease in the frequency of spontaneous excitatory synaptic activity (Ramalho et al., 2013; Shankar et al., 2007), supporting the idea that the protective role of this bile acid goes beyond its capacity to modulate neuronal death.

It is becoming increasingly evident that activation of survival pathways may also represent an important additional mechanism by which TUDCA inhibits apoptosis. In primary rat hepatocytes, TUDCA was shown to protect mitochondria-controlled apoptosis by activating the PI3K and the MAPK survival pathways (Bradham et al., 1998; Schoemaker et al., 2004). PI3K signaling is also activated by TUDCA in A β -induced neuronal apoptosis (Solá et al., 2003). In fact, incubation with wortmannin, an inhibitor of the PI3K pathway, significantly reduced the ability of TUDCA to modulate p53-induced apoptosis (Ramalho et al., 2006). Moreover, by interfering with apoptotic pathways, TUDCA not only increases the survival of neurons but also prevents downstream abnormal conformations of tau (Ramalho et al., 2008). Finally, TUDCA was shown to abrogate A β -induced apoptosis of neuronal PC12 cells by inhibiting the E2F-1/p53 apoptotic pathway, hence modulating the expression of Bcl-2 family members (Ramalho et al., 2004). Similar results were seen *in vitro* models of familial AD that consist of mouse neuroblastoma cells expressing APP with the Swedish mutation or double-mutated human APP and PS1 (Ramalho et al., 2006), as well as in primary rat neurons incubated with A β (Solá et al., 2003). A recent study in primary rat cortical and hippocampal cultures exposed to A β , and brain tissue of APP/PS1

transgenic mice also showed that TUDCA suppresses A β -induced decrease of the neuronal marker postsynaptic density-95 protein (PSD-95). Of note, TUDCA was capable of reducing A β deposits, glial activation (Itagaki et al., 1989) and neuronal integrity loss in the APP/PS1 double transgenic mouse model of AD, rescuing memory and learning deficits (Nunes et al., 2012). This effect may be partially explained by the effect of TUDCA in regulating lipid-metabolism mediators that influence A β production and intracellular accumulation (Nunes et al., 2012).

1.2. Neural Differentiation

The defining hallmark of metazoan multicell life forms is cell specialization and adaptation that results from the process commonly referred to as differentiation. In fact, during differentiation, stem cells give rise to committed and specialized cells. Stem cells are unspecialized precursor cells, capable of generating identical progeny (self-renewal), thereby sustaining a stem cell pool, with the ability to develop into other cell types (differentiation) carrying out particular tissue functions. *In vivo*, stem cells are thought to reside in specific cellular niches that constitute privileged sites for support of self-renewal (Doetsch, 2003; Spradling et al., 2001; Watt and Hogan, 2000). They can be found both in the embryo and adult organisms, and may also differ in their differentiation potential. Stem cells can be somatic (fetal or adult) or embryonic. Embryonic stem cells (ECs) have attracted a lot of attention because of their origin and plasticity, being currently used to create transgenic animals, and proposed for use in a wide variety of commercial and clinical applications (Gage, 2000; Thomson et al., 1998). These cells are derived from the inner mass cell of developing blastocysts (Evans and Kaufman, 1981; Martin, 1981) and are considered pluripotent, capable of transforming into cells from all three somatic germ layers as well into germ cells. In contrast, adult stem cells are considered multipotent because they only originate different cell types of a particular lineage.

Neural stem cells (NSC) are defined as clonogenic cells, having some capacity of self-renewal, and also as multipotent cells, being able to differentiate into neuronal and glial precursor cells (Brüstle et al., 1997) (Fig. 1.4). Neuronal precursor cells (NPCs) can further generate motor, sensory, or dopaminergic

neurons, while glial precursor cells generate astrocytes or oligodendrocytes (Reynolds and Weiss, 1996).

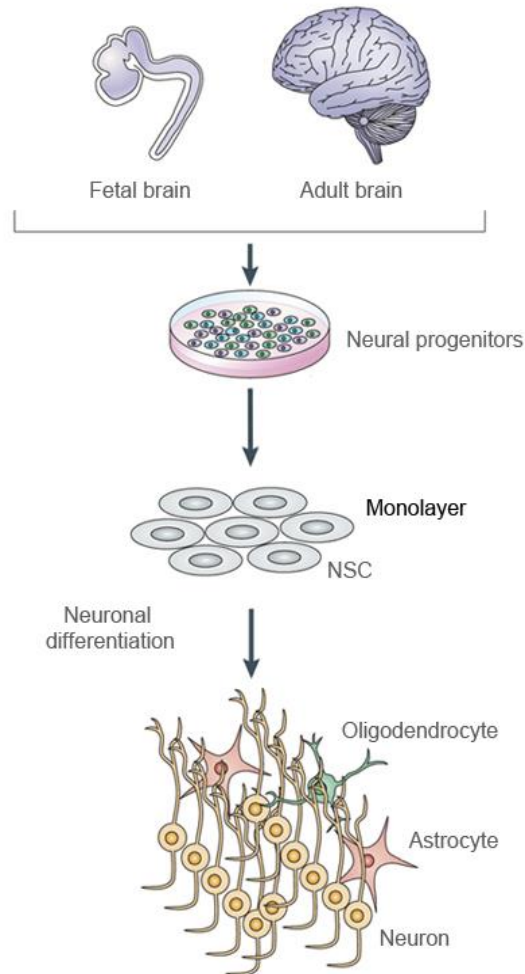


Figure 1.4. Monolayer culture system of neural stem cells. Monolayer NSC lines can be derived from fetal and adult brains and display multipotency, generating neurons, astrocytes and oligodendrocytes under appropriate culturing conditions. The cellular composition of the monolayer NSC culture system is highly homogeneous. This property of monolayer NSC lines results in higher reproducibility of differentiation protocols and higher neurogenic potential. Adapted from Conti and Cattaneo, 2010.

Neurogenesis, the process of generating integrated neurons from progenitor cells, was traditionally believed to occur only during embryonic stages in the mammalian CNS. Only recently neurogenesis was shown to also occur in the adult mammalian brain (Alvarez-Buylla and Garcia-Verdugo, 2002; Christie and Cameron, 2006; Gage, 2000; Pignatelli et al., 2009).

Neurogenesis in mammals begins with thickening of the ectoderm, leading to the induction of neuroectoderm, which forms the neural plate, at E7.5 in mice, and

then folds to give rise to the neural tube. These structures are made up by a layer of neuroepithelial cells (Götz and Huttner, 2005), which contact both apical (ventricular) and basal (pial) surfaces. Initially, neuroepithelial cells divide symmetrically at the ventricular surface to increase the pool of stem cells. However, at a certain point, they start dividing asymmetrically, generating stem cells that remain in the ventricular zone, and other cells that migrate radially outward (Haubensak et al., 2004). These cells are responsible for the first wave of neurogenesis in the neural tube, after which they give rise to radial glia (RG) (Conti and Cattaneo, 2010).

The name of RG was attributed due to several characteristics shared with astrocytes, including the presence of glycogen granules and the expression of glial fibrillary acidic protein (GFAP) (Choi and Lapham, 1978; Levitt and Rakic, 1980), astrocyte-specific glutamate transporter (Shibata et al., 1997) and brain lipid binding protein (Feng et al., 1994). RG cells act as guide wires for the migration of neurons (Malatesta et al., 2008). It is now clear that in many regions of the CNS, RG also represents the main population of neural progenitors and that their progeny includes neurons, astrocytes, oligodendrocytes, ependymocytes and adult NSCs (Conti and Cattaneo, 2010; Malatesta et al., 2003; Merkle et al., 2004; Spassky et al., 2005). While in many species RG persists into adulthood, in the mammalian brain RG disappears soon after birth, giving rise to the adult astrocyte-like NSCs (Merkle and Alvarez-Buylla, 2006).

1.2.1. Adult NSCs

The existence of adult NSCs, capable of self-renewing and generating both neuronal and glial derivatives has been an area of great controversy. Adult NSCs were first isolated from the adult CNS of rodents (Reynolds and Weiss, 1992), and later from humans (Kukekov et al., 1999). Full acceptance of postembryonic mammalian neurogenesis was not immediate until Luskins *et al.* (Luskin, 1993) described neurogenesis in the anterior portion of the subventricular zone (SVZ) in postnatal mice, Lois and Alvarez-Buylla (Lois and Alvarez-Buylla, 1993) demonstrated neurogenesis in the adult mouse SVZ, and several groups showed neurogenesis in the subgranular layer of the hippocampus (Altman and Das, 1965; Cameron et al., 1993; Kaplan and Bell, 1984; Kuhn et al., 1996). The discovery of the “no new neuron” dogma suggested that ongoing adult neurogenesis might be supported by a population of multipotent NSCs. This idea was based on the

following observations: (1) primary precursors within CNS germinal zones continue to produce neurons and glia throughout an organism life; and (2) cells from the adult brain with properties of NSCs can be grown *in vitro* with growth factors.

Along the lateral walls of the lateral ventricles lies the largest germinal zone of the adult mammalian brain, the SVZ. NSCs in the SVZ give rise predominantly to committed progenitor cells that migrate inferiorly into the olfactory bulb (OB) via the rostral migratory stream (Kornack and Rakic), where they differentiate into two kinds of local olfactory interneurons, granule and periglomerular cells (Altman, 1969; Kornack and Rakic, 2001; Luskin, 1993). SVZ NSCs can be dissociated and grown in culture as free-floating spheres, or neurospheres, in the presence of epidermal growth factor (EGF), fibroblast growth factor (FGF), or combination of both growth factors (Gage, 2000; Temple and Alvarez-Buylla, 1999; Weiss et al., 1996). Some of these primary spheres are capable of generating other spheres upon dissociation and can be renewed through many passages.

The hippocampus is other major site of neurogenesis in adult mammals. Granule neurons in the dentate gyrus (DG) are born locally in the subgranular zone (SGZ). The progenitors in the SGZ migrate into the granular cell layer (Kuhn et al.) and also differentiate into neurons (Eriksson et al., 1998).

In the SVZ, the NSC pool is larger than in the SGZ (Yao et al., 2012), and three types of progenitors can be found, defined by their morphology, ultrastructure, and molecular markers: SVZ neuroblasts (type A cells) migrate in homotypic chains (Lois et al., 1996) into to OB through the RMS, where they differentiate into several types of neurons, depending on their place of origin within the SVZ (Lois and Alvarez-Buylla, 1994; Merkle et al., 2007). These chains are unsheathed by slowly proliferative type B cells (Lois et al., 1996). B cells have properties of astrocytes, including light cytoplasm, thick bundles of GFAP-positive intermediate filaments, gap junctions, glycogen granules, and dense bodies (Doetsch et al., 1999), which have been hypothesized to represent the primary neuronal precursors *in vivo* (Mu et al., 2010). Scattered along the chains of type A cells are clusters of spherical and rapidly dividing C cells. The SVZ is largely separated from the ventricle cavity by a layer of ependymal cells. In contrast to the SVZ, the subgranular layer is deep within the brain at the interface of the GCL of the DG and the hilus of the hippocampus and, opposite

to the extensive tangential migration undertaken by OB neurons, hippocampal granule neurons move only a short distance into the GCL (Seri et al., 2001). The NSCs from this region are radial astrocytes, also known as RG-like cells or type 1 progenitors. Although expressing the astrocyte marker GFAP, these cells are morphologically and functionally different from mature astrocytes.

Recently, type 1 cells were also shown to be indeed multipotent NSCs, as they are capable of undergoing self-renewing symmetric and asymmetric divisions and can differentiate into both neurons and astrocytes (Bonaguidi et al., 2011). Radial astrocytes have long radial processes that penetrate the GCL. Dividing radial astrocytes generate immature, non-radial intermediate progenitors termed type 2 or type D cells. These D cells can differentiate into neuroblasts, which migrate into the nearby granule layer and differentiate into glutamatergic neurons (Kuhn et al., 1996). D cells developed a branched apical process that becomes the dendrites of the new granule neuron, and later an axon that projects to area CA3 (Stanfield and Trice, 1988). Approximately half of these cells survive and integrate the pre-existing neuronal circuits (Toni et al., 2007; van Praag et al., 2002). The demonstration of neurogenesis in adult human brains not only proves the unforeseen regenerative capacity of CNS, but also gives hope for strategies to repair damaged adult CNS after injury of neurodegenerative diseases.

1.2.3. Apoptosis-associated factors in neural differentiation

The mechanisms controlling the neural differentiation process remain poorly understood, and many molecules and their specific functions are yet unknown. Emerging evidence suggests that apoptosis players and inducers may also control cell fate, without involving cell death *per se* (Fernando et al., 2002; Fernando and Megeney, 2007; Galluzzi et al., 2012). In fact, essential players of apoptotic executioner pathways cannot be totally blocked to assure differentiation efficiency but, at the same time, must be carefully regulated to avoid cell loss (Chasis and Schrier, 1989; Solá et al., 2012). Specifically, apoptosis-related microRNAs (miRNAs), such as miRNA-34a, -16 and let-7a, and proteins, including caspases, calpains, and Bcl-2 and p53 family members are involved in mouse NSC differentiation by mechanisms independent of cell death (Aranha et al., 2011; Aranha et al., 2010; Aranha et al., 2009; Solá et al., 2011a).

1.2.3.1. Proteases

Caspases are cysteinyl aspartate-specific proteases with a number of properties that make them highly effective as cellular remodeling enzymes. Although their critical function in apoptosis is firmly established, caspase activation is also essential for dynamic, non-apoptotic cell processes, such as innate immune response, neural regeneration, NSC fate determination, and neural activation. Indeed, caspases have recently been implicated in the differentiation process for a variety of model systems, including neural cells (Santos et al., 2012b; Schwerk and Schulze-Osthoff, 2003). It has been demonstrated that NSC differentiation depends on endogenous caspase-3 activity that may influence kinase activities associated with changes in phenotype (Fernando et al., 2005). In addition, caspases modulate FOXO3A/inhibitor of differentiation 1 (Id1) signaling during mouse NSC differentiation (Aranha et al., 2009). In fact, caspase inhibition and silencing of p53 synergistically delayed neural differentiation, with no evidence of apoptosis. Recently, the role of caspases in neural differentiation has been further elucidated and suggested to be required for neuronal growth cones (Campbell and Holt, 2003), learning and memory (Lu et al., 2002), axon routing, synaptic connections (Ohsawa et al., 2010), among others. Several mechanisms for regulating non-apoptotic caspase function in neural differentiation have been proposed, including transient caspase activation, local caspase activation and regulation of endogenous caspase inhibitors (Solá et al., 2012).

Although the available literature on calpain activity in NSCs is scarce, recent data has also elucidated the role of calpain 1 and 2 during NSC self-renewal and differentiation. Santos *et al.* (Santos et al., 2012b) showed that calpain 1 maintains stemness and represses neural differentiation, while calpain 2 acts as potential modulator of gliogenesis. These results underscored the distinct regulatory functions of calpain 1 and 2 in NSC fate decision.

1.2.3.2. Bcl-2 family

Bcl-2 family proteins suffer developmental regulation in the nervous system, being highly expressed in neuroepithelial cells of the SVZ, and in post-mitotic neurons before adulthood (Merry et al., 1994). Bcl-2 acquired immunoreactivity signal in the brain of squirrel monkeys, specifically in areas involved in neurogenesis and morphogenesis (Bernier and Parent, 1998). Therefore, it has been suggested that Bcl-2 might be important, but not crucial, during neuronal cell differentiation.

In vitro, Bcl-2 expression was associated with both neural differentiation of human neural-crest-derived tumor cell line, Paju (Zhang et al., 1996), and RA (Sarkar and Sharma)-mediated differentiation of CNS neurons (Wang et al., 2001). In PC12 cells, in turn, Bcl-2 was shown to trigger differentiation as a result of prevention of cell death induced by serum free medium (Sato et al., 1994). In addition, other studies indicate that Bcl-2 may act as an intercellular factor that controls neurite extension and axonal regeneration (Eom et al., 2004; Suzuki and Tsutomi, 1998). It was recently reported that Bcl-x_L and Bax play an instructive role in determining the fate of embryonic cortical precursor cells (Chang et al., 2007). Bcl-x_L and Bax appear to mediate neurogenesis and astrogliogenesis, respectively, independently from their roles in cell survival and apoptosis (Solá et al., 2012). These findings support the possibility that determination of neuronal versus astroglial lineages is actively regulated by balanced levels of anti- and pro-apoptotic Bcl-2 family proteins in NPCs (Chang et al., 2007). Finally, pro-apoptotic Bim was associated with the neurogenesis of adult-born NPCs (Bunk et al., 2010).

1.2.3.3. p53 family

p53 family members, p53, p63 and p73 play crucial roles as regulators of NSC proliferation and differentiation (Murray-Zmijewski et al., 2006).

p53

In the past several years, a specific novel function for p53 in neuronal biology has emerged. In fact, increased evidence points to a role for p53 in neural progenitor proliferation and differentiation, independent of its apoptotic role (Solá et al., 2013; Tedeschi and Di Giovanni, 2009). p53 was shown to be required to the differentiation of mouse embryonic stem cells (ESCs) by suppressing expression of Nanog, a transcription factor essential to the maintenance of pluripotency of ESCs (Chen et al., 2008; Mitsui et al., 2003) (Fig. 1.5). In addition, it was also reported that in neurons from a p53^{-/-} mouse, p53 plays an important role in neuronal differentiation (Ferreira and Kosik, 1996). Curiously, high levels of p53 mRNA have also been detected in the developing brain in areas showing little or no apoptosis. Some p53-null embryos die during development, and a percentage of the surviving mice exhibit neuronal abnormalities, namely defects in neural tube closure (Armstrong et al., 1995), resulting in exencephaly

(Sah et al., 1995). Curiously, this exencephalic phenotype is identical to that observed in animals with mutations in other members of the intrinsic death pathway, including Apaf-1, caspase 3 (Kuida et al., 1996), and caspase 9 (Kuida et al., 1998). p53 was already shown to promote neurogenesis through downregulation of the Akt/p-FOXO3A/Id1 pathway (Aranha et al., 2009) (Fig. 1.5). Furthermore, the role of p53 during mouse NSC differentiation has been further dissected by other studies (Solá et al., 2012).

p53 might also play a key role in neural differentiation as a limiting factor of stem cell proliferative competence (Armesilla-Diaz et al., 2009; Krizhanovsky and Lowe, 2009). Recent experiments of NSCs extracted from the OB of wild-type and p53-null mouse embryos showed that p53 controls proliferation, chromosomal stability, and differentiation pattern of mouse OB stem cells (Armesilla-Diaz et al., 2009). In fact, p53-null NSCs have increased proliferation with tendency to a neuronal phenotype, with concomitant reduction of astrocytes. This effect had been previously reported in SVZ-derived stem cells from adult mice (Gil-Perotin et al., 2006). Studies in neuronal-like PC12 and neuroblastoma cells have also suggested that p53 plays a role in cell survival following NGF administration (Hughes et al., 2000; Zhang et al., 2006a), and that the interaction of p53 with neuronal-specific transcription factors, such as Brn-3a, may determine a shift from cell death to neuronal survival (Hudson et al., 2005; Hudson et al., 2004). In fact, when forming a complex with Brn-3a, p53 cannot activate pro-apoptotic genes, such as Bax and Noxa, but rather shows increased affinity for the pro-differentiation gene p21. p53 was also reported to bind to the NGF receptor TrkA, which is required for PC12 neuronal differentiation (Browes et al., 2001), and to activate TrkA expression and consequent MAPK pathways (Zhang et al., 2006a) (Fig. 1.5). Also in PC12 cells, p53 regulates the expression of both actin-binding protein Coronin 1b and the GTPase Rab13, which are needed for correct neurite outgrowth and maturation of cortical neurons *in vitro* (Di Giovanni et al., 2006; Tedeschi and Di Giovanni, 2009) (Fig. 1.5). Integrated transcriptomic profiling, *in silico* promoter analysis, and functional studies of murine NSCs established that inactivation of both p53 and phosphatase and tensin homolog (PTEN) promotes an undifferentiated state, with high self-renewal potential, and increased Myc protein levels (Zheng et al., 2008). In agreement, increased Myc activity was validated as a potent contributor to impaired

differentiation and enhanced self-renewal of NSCs in murine double-null mice for p53 and PTEN. Thus, due its dual actions on cell cycle and cell death, p53 plays a versatile role in the regulation of cellular growth and differentiation, being considered a gatekeeper of self-renewal in NSCs that may function either as a pro-apoptotic or differentiation factor in neural precursors.

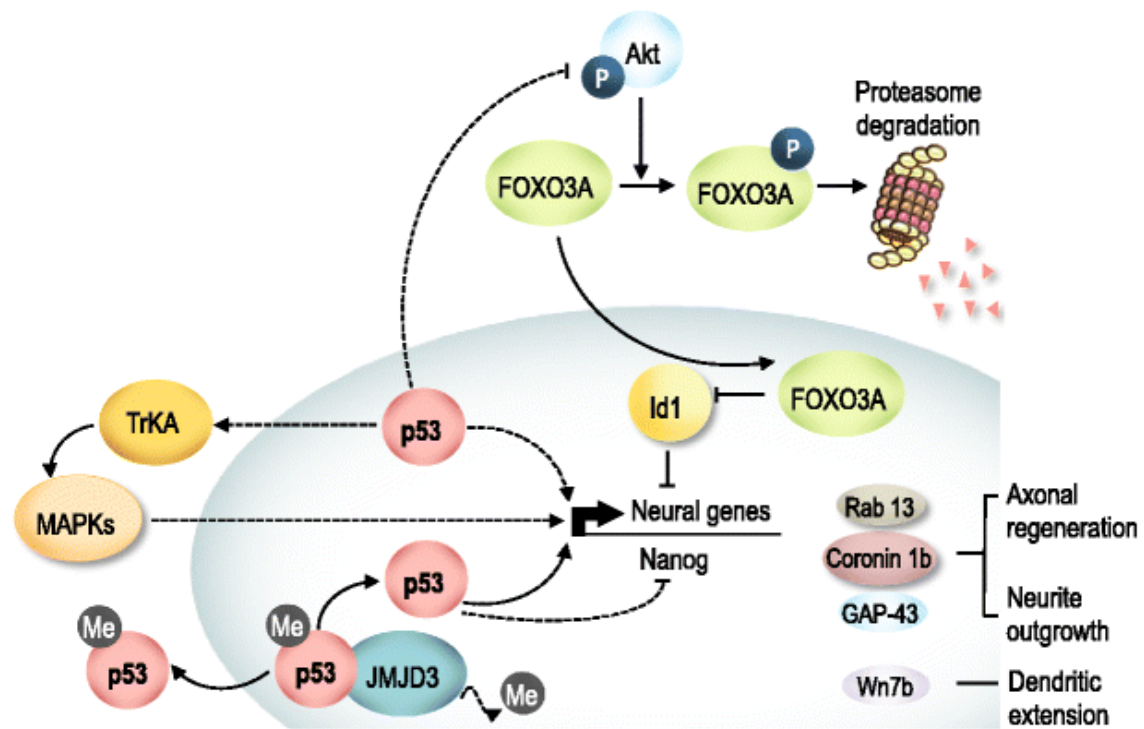


Figure 1.5. p53 in neurogenesis. p53 is involved in non-apoptotic processes such as cell-fate determination and actin-cytoskeleton reorganization. p53 plays a critical role in neuronal differentiation, in part via regulation of TrkA and MAPK pathways in PC12 cells. Moreover, Wnt7b is a new putative p53 target during NGF-mediated PC12 neuronal differentiation, involved in dendritic extension. p53 also regulates the expression of actin-binding protein Coronin 1b and the GTPase Rab13 in primary cultured neurons, both of which associate with the cytoskeleton and regulate neurite outgrowth, as well as the expression of the axonal growth-associated protein GAP-43, which is involved in pro-axon outgrowth and regeneration protein. In mouse NSC, p53 promotes neurogenesis by downregulating the Akt/p-FOXO3A/Id1 proliferation pathway. Interestingly, p53 and the demethylase JMJD3, a key regulator of neurogenesis, are coordinately regulated during adult neural differentiation. JMJD3 directly interacts with p53 to induce demethylation of p53 and subsequent p53 nuclear accumulation during specific stages of neural differentiation. Adapted from Solá et al. 2012.

Epigenetic mechanisms have an important role in control maintenance of stem cell state and in the differentiation process (Li and Zhao, 2008; Wu and Sun, 2006). In this regard, during the past decades, covalent modifications have been

discovered to play fundamental roles in either homeostatic maintenance or stress-induced activation of p53.

Specific targets and cofactors of p53 during neuronal differentiation may be unique and different from those regulated in genotoxic stress and apoptosis. This is possible by the multiple PTMs that target p53 on its N- and C-termini, which are not limited to phosphorylation, but may also include acetylation, sumoylation, neddylation, ubiquitination, or methylation (Collavin et al., 2010; Lavin and Gueven, 2006; Solá et al., 2011). In fact, specific combination of PTMs differentially regulates the interaction of p53 with co-activators and co-repressors and produces distinct gene expression profiles, which may also dictate cell fate.

p53 PTMs directly affect the transcriptional activity of p53 and regulate its affinity to several cofactors, which in turn regulate the occupancy of p53 specific promoters (Sims and Reinberg, 2008). Phosphorylation at Ser 15, Ser 20, Ser 33, Ser 46 and Thr 18 promotes p53 stabilization by preventing either its nuclear export or its recruitment to specific promoters. Early in the differentiation of ESCs, phosphorylation of p53 at Ser 15, Ser 315 and Ser 392 is significantly increased, which is thought to activate p53 (Xu, 2003). p53 phosphorylation at Ser 315 was also shown to be important for p53-dependent suppression of Nanog during differentiation of ESCs (Lin et al., 2005). The acetylation of p53 in neurons is mediated by the activity of at least these two histone acetyltransferases, CREB-binding protein (CBP)/p300 and p300/CBP-associated protein (P/CAF). CBP/p300 acetylates Lys370, Lys372, Lys373 and Lys382, and P/CAF acetylates only Lys320 (Brooks and Gu, 2003). These kinase and acetyltransferase pathways are activated downstream from NGF and BDNF signaling during neuronal differentiation and axon outgrowth. Interestingly, the acetylation of p53 at Lys 320 leads to increased transcriptional activation of the p21 promoter, which triggers G1/S arrest and promotes neuronal differentiation in PC12 cells (Wong et al., 2004). Interestingly, p53 acetylation in the same residue was reported to be involved in promotion of neurite outgrowth (Di Giovanni et al., 2006). Additionally, acetylated p53 at Lys372, Lys373 and Lys382 was shown to drive axon outgrowth and GAP43 expression, and to bind to specific elements on the neuronal GAP43 promoter (Tedeschi and Di Giovanni, 2009) (Fig. 1.5).

p53-induced control of cell fate may also be associated with p53 subcellular distribution. In fact, it has been reported that p53 translocates to the nucleus

following induction of differentiation (Brynczka and Merrick, 2007; Solá et al., 2011). SIRT1, a p53 deacetylase, inhibits p53 nuclear translocation in mouse ESCs and inhibits p53-mediated suppression of Nanog expression (Han et al., 2008). Moreover, p53 demethylation appears to be also essential in p53 nuclear distribution in mouse NSC differentiation, associated with an increase in neuronal markers (Solá et al., 2011b). In fact, recent studies have already established protein methylation as a novel mechanism of p53 regulation (Scoumanne and Chen, 2008). Recently, it has been shown that this proapoptotic protein cross-talks with key regulators of neurogenesis, such as the histone H3 lysine 27-specific demethylase JMJD3. In fact, Solá *et al.* have demonstrated that JMJD3 increases total levels of p53 by a mechanism dependent, at least in part, of ARF, a mechanism that is not associated with cell death. Importantly, they have also shown that JMJD3 directly interacts with p53 to modulate p53 methylation levels and regulate p53 cellular distribution during mouse neural differentiation (Solá et al., 2011) (Fig. 1.5). The molecular crosstalk between the transcription factor p53 and the histone lysine specific demethylase 1 has been previously demonstrated by Huang *et al.* (Huang et al., 2007).

While p53 is ubiquitously expressed, p63 exhibits a tissue-specific distribution that it is most detectable in embryonic ectoderm and in basal regenerative layers of stratified epithelial tissues in the adult (Yang et al., 1998). However, both TA and Δ Np63, as well as TA and Δ Np73 proteins are also expressed in the cortex of embryonic, postnatal, and adult brains (Jacobs et al., 2005).

p73

p73 is known to play an important role in controlling neuronal development, being an essential regulator of NSC maintenance and differentiation in both embryonic and adult neurogenesis (Fujitani et al., 2010; Talos et al., 2010). The first evidence for the role of *p73* in neural differentiation of a normal mammalian cell came from studies showing that both p53 and *p73*, but not p63, are involved in thyroid hormone-induced oligodendrocyte precursor cells differentiation, and that *p73* also plays a crucial role in platelet-derived growth factor withdrawal-induced differentiation (Billon et al., 2004).

p73 developmental role is supported by the phenotype of total *p73* KO mice. Unlike p53 null mice, total *p73* KO mice do not develop tumors; however, they show developmental defects in the CNS with 100% penetrance (Yang et al., 2000),

including congenital hydrocephalus and hippocampal dysgenesis, with loss or truncation of the lower blade of the neurogenic DG (Talos et al., 2010), thinning of the SVZ in the forebrain and loss of the Cajal-Retzius neurons (Hernández-Acosta et al., 2011). The total p73 KO mice also have defects in both embryonic and adult neurogenesis, suggesting that p73 isoforms may be important factors for the maintenance of NSCs (Fujitani et al., 2010; Holembowski et al., 2011; Talos et al., 2010). p73^{-/-} mice also have a reduction in cortical thickness as a consequence of loss of mature cortical neurons (Pozniak et al., 2002). Curiously, ΔNp73 variants are the predominant expression product of the p73 gene in developing and adult tissues. ΔNp73 isoforms are expressed in postmitotic neurons and act as survival factors of differentiated mature postmitotic neurons in discrete regions of the brain (Tissir et al., 2009; Wilhelm et al., 2010). Their loss explains this neurological phenotype (Pozniak et al., 2000). In addition selective TAp73 null mice also show hippocampal dysgenesis with loss of the lower blade of the DG, a phenotype intermediate between the phenotypes of p73^{-/-} and p53^{-/-} mice (Tomasini et al., 2008), reflecting a reduction in neurogenesis in the SGZ of the DG, and suggesting that TAp73 may be required for NSC proliferation (Michalak et al., 2008). Therefore, these studies suggest a role for p73 in neurogenesis and a cooperation or redundancy between the isoforms during this process. p73 also maintains an adequate neurogenic pool by promoting self-renewal and proliferation and inhibiting premature senescence of NSC and early progenitor cells in both embryonic and adult neurogenesis (Talos et al., 2010). Curiously, TAp73 appears to act via the basic helix-loop-helix Hey2 to promote long-term maintenance of neural precursors (Fujitani et al., 2010). Further, p73 deficiency results in impaired self-renewal and premature neuronal differentiation of mouse NPCs independently of p53 [103].

Neuroblastoma cell differentiation *in vitro* requires activation of a molecular pathway by p73, which is not shared by p53. p73 protein increases in cells induced to differentiate by RA (De Laurenzi et al., 2000). Exogenously expressed p73, in turn, is sufficient to induce neurite outgrowth, expression of neurofilaments and neural adhesion molecule, (N-CAM), downregulation of N-Myc and upregulation of pRb, all markers of neural differentiation (De Laurenzi et al., 2000). An *in vitro* neurosphere assay from p73 KO mice and their wild-type counterparts, demonstrated that p73 KO results in decreased capacity to form neurospheres, and smaller neurosphere sizes with fewer cells per neurosphere, indicating an impairment in the proliferation of

progenitors (Talos et al., 2010). Together, these results indicate that p73-deficient NSCs are not only deficient in self-renewal but also in proliferation and generation of progeny. Finally, p73 drives the expression of miRNA-34a in mouse cortical neurons, which then modulates the expression of synaptic targets, including synaptotagmin-1 and syntaxin-1A (Agostini et al., 2011b). In fact, p73 was shown increased during postnatal development of the brain, when synaptogenesis occurs (Agostini et al., 2011a).

p63

The p63 protein, in turn, has been extensively described as a key regulator of development and maintenance of stratified epithelial tissues, having a tissue-specific distribution, mostly detectable in the basal layer of epithelia, including epidermis (Yang et al., 1998). In fact, the phenotype of *p63*-deficient mice presents several developmental defects, suggesting that the primary biological function of p63 proteins is to regulate development. However, brain malformations have not been reported in humans with p63 mutations. This phenotype contrasts with mice lacking p73 gene, which have immunological, neurological, and pheromone defects (Yang et al., 2000). This raises the question whether p63 has a similar important role in neural differentiation as p53 and p73. Thus far, it is not clear whether p63 contributes to brain development. Dugani *et al.* (Dugani et al., 2009) have reported that p63 is a crucial pro-survival regulator of NPCs. Jacobs *et al.* (Jacobs et al., 2005) have also investigated the role of p63 in developing sympathetic neurons of the autonomous nervous system, concluding that the TAp63 isoforms play pro-apoptotic functions in these neurons. Furthermore, during embryonic stages, p73 and p63 are co-expressed in Cajal Retzius cells derived from a marginal zone of developing cortex, the cortical hem, which is a putative signaling center and the main place for the generation of CR cells. However, in contrast with the previous studies, the analysis of *p63*^{-/-} and *p73*^{-/-} mice shows that only p73 is essential for brain development and CR cell formation (Tissir et al., 2009), indicating that p63 expression and signaling in the cortical hem seems to be an accessory feature of these cells, and not essential for brain development in general (Hernández-Acosta et al., 2011).

Despite these divergences, it has been reported that p63 expression during development of the CNS is scant. Indeed, TAp63 and ΔNp63 mRNA levels are very low in murine embryonic cortex (Holembowski et al.; Jacobs et al., 2005), which is in

contrast to the essential role of p73 in neurogenesis (Agostini et al., 2010; Fujitani et al., 2010; Holembowski et al., 2001; Talos et al., 2010). In the SVZ of the lateral ventricle of postnatal mice, the three members of the p53 family are detected and may influence cell fate in this region of the adult brain. However, in contrast to p73, the detection levels of p63 and p53 were weak. In fact, immunohistochemistry revealed co-expression of p73 and a marker of proliferating cells, the proliferating cell nuclear antigen (Uberti et al.) in the SVZ, where the same double staining was not possible with either p63 or p53 (Hernández-Acosta et al., 2011; Lois and Alvarez-Buylla, 1993). Nevertheless, in contrast to p63-restricted expression observed during brain development, high levels of p63 were visualized in adult human cerebral cortex and hippocampus (Hernández-Acosta et al., 2011), suggesting a role for p63 in the adult brain. Furthermore, in postnatal mice, p63 is expressed in neurogenic niches, such as the SVZ of the lateral ventricle (Hernández-Acosta et al., 2011). This suggests that p63 may have a role during adult neurogenesis that remains to be explored.

1.2.4. Role of A β peptides in neural differentiation

A β peptides are highly multifunctional identities, which may display significant non-pathological activities (Fig. 1.6). Indeed, proposed functions of A β peptides include trophic and neuronal survival, neural differentiation, control of synaptic activity and memory consolidation, cholesterol transport and antioxidant functions (Parihar and Brewer, 2010; Pearson and Peers, 2006; Plant et al., 2003). The A β cellular functions are evident only when the peptides are present at physiological concentrations, before they aggregate and form amyloid fibrils (Parihar and Brewer, 2010; Pearson and Peers, 2006; Plant et al., 2003; Ramsden et al., 2002). In fact, Plant *et al.* (Plant et al., 2003) showed that, in rodent and human neuronal cells, *in vitro* inhibition of γ - or β -secretase culminates with toxicity. Recovery of cell viability using physiologically concentrations of exogenous A β suggests that this peptide may have a role in the normal function of neuronal cells as suggested previously by Ramsden and co-workers (Ramsden et al., 2001). Recent studies indicate that A β plays an important role at the synapse as well as in synaptic structure and functional plasticity, critical to learning and memory (Parihar and Brewer, 2010). A necessary role of A β in synaptic plasticity and memory in normal brain is also supported by the observation that APP KO mice show impaired LTP and memory (Dawson et al., 1999). The impaired synaptic plasticity and memory found in beta-

site APP-cleaving enzyme 1 KO mice also suggest a crucial role of A β (Laird et al., 2005).

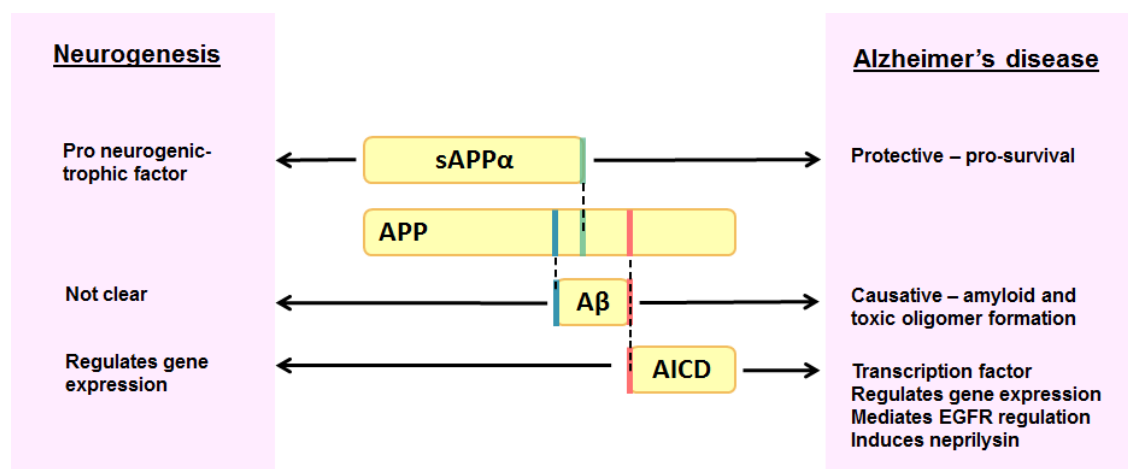


Figure 1.6. Pathological versus proneurogenic effects of amyloid β peptides. A summary of suggested function of β - and γ -secretases-generated APP fragments, including A β peptides, in AD neuropathology and in neurogenesis. sAPP α , soluble amyloid precursor protein α . Adapted from Lazarov and Marr, 2010.

The evidence that A β is present in the CSF of healthy individuals and in media from neuronal cell cultures (Blennow and Zetterberg, 2009; Tamaoka et al., 1997) indicates that A β may also play a role in the normal physiology of the CNS. Importantly, it was already reported that non-aggregated peptide at low doses exhibits neurotrophic effects including enhancement of neuronal survival and neurite-promoting effects (Luo et al., 1996; Pike et al., 1991; Whitson et al., 1990; Yankner et al., 1990). Indeed, A β_{1-42} monomers were shown to promote the survival of developing neurons under conditions of trophic deprivation, and protect mature neurons against excitotoxic death (Giuffrida et al., 2009). In addition, A β_{1-42} increased the number of newborn neurons in cultured NSCs (Chen and Dong, 2009; López-Toledano and Shelanski, 2004). Neurotrophic function of A β_{1-40} was obtained in a cell culture treated with picomolar and micromolar levels of A β_{1-40} (Chen and Dong, 2009; Plant et al., 2003; Yankner et al., 1990). These findings provide compelling evidence for a role for A β in neuronal survival.

Recently, *in vitro* and *in vivo* studies revealed that A β is also able to drive the differentiation of NPCs toward neurons (Calafiore et al., 2006; Chen and Dong, 2009; Heo et al., 2007; López-Toledano and Shelanski, 2004; Sothibundhu et al., 2009). However, the precise role of different forms of monomer, oligomer, and fibrillar A β

on the neurogenesis are still poorly understood. Indeed, there is a lot of variance in the literature regarding the experimental conditions used to address the neurogenic effects of A β . The experiments differ, not only in the form of A β used, but also in the type of NSC culture used, and in the concentrations of A β incubated (Calafiore et al., 2012; Haughey et al., 2002a; Haughey et al., 2002b; Heo et al., 2007; Kim et al., 2007; López-Toledano and Shelanski, 2004; Sotthibundhu et al., 2009). In cultures of NSCs derived from striatum and hippocampus it was demonstrated that A β has a role on the survival and neuronal differentiation (López-Toledano and Shelanski, 2004). The authors showed that this peptide increases the total number of neurons *in vitro* in a dose-dependent manner. In addition, they have shown that neurogenesis is induced by A β_{1-42} but not by A β_{1-40} or A β_{25-35} , and that the pro-neurogenic activity appears to be a property of A β oligomers and not fibrils. In concordance, other studies showed that low micromolar concentrations of oligomeric A β_{1-42} enhance neuronal differentiation of adult NSCs and their ability to migrate (Heo et al., 2007). An *in vivo* study also demonstrated that A β_{1-42} promotes amyloid deposition while A β_{1-40} inhibits it. Chen *et al.* (Chen and Dong, 2009) have reported notable neurogenic and survival effects of soluble A β_{1-40} in primary NPCs; A β_{1-42} treatment both *in vitro* and *in vivo*, as well as endogenous generation of A β in transgenic models of AD, stimulated neurogenesis of young adult SVZ precursors (Sotthibundhu et al., 2009). The neurogenic effect of A β_{1-42} was found to require expression of the p75^{NTR} by the precursor cells, and activation of p75^{NTR} by metalloprotease cleavage. In neurospheres incubated with oligomers of synthetic A β_{1-42} , the expression levels of DNA polymerase- β , an enzyme that represses proliferation and promotes differentiation, were rapidly increased (Calafiore et al., 2012).

On the other hand, studies using animal models of AD have proposed the opposite effect of A β peptides in neurogenesis (Haughey et al., 2002a; Haughey et al., 2002b). In fact, it has been reported that A β compromises the survival and differentiation processes (Haughey et al., 2002b; Mazur-Kolecka et al., 2006; Millet et al., 2005). However, these results appear to be correlated with the decreased levels of soluble A β peptide observed in AD. Consistent with this, others have demonstrated that higher levels of A β monomers, oligomers, and fibrils in the brain of individuals with amyloidosis- β induce oxidative stress and do not promote adult endogenous neurogenesis (Mazur-Kolecka et al., 2006). AD is a dynamic disease

process, and it is plausible that an increase in neuronal differentiation is followed by an overall decline as A β aggregates and loses its neurogenic functions.

1.2.5. Autophagy during neural differentiation

Autophagy acts as a quality control mechanism in differentiated cells by promoting basal turnover of long-lived proteins and organelles, and selectively degrading damaged cellular components (Wirawan et al., 2012). In addition, autophagy promotes morphological and structural remodeling (Singh et al., 2009). In fact, as a dynamic and highly inducible catabolic process, it can drive the rapid cellular changes necessary for proper differentiation and/or development.

In mammals, autophagy plays key roles in pre-implantation embryonic development (Levine and Ranganathan, 2010; Tsukamoto et al., 2008), survival during neonatal starvation (Aburto et al., 2012; Mizushima and Levine, 2010), cancer (Chen and Karantza, 2011; Edinger and Thompson, 2003), neuronal degeneration (Hara et al., 2006; Komatsu et al., 2006; Wong and Cuervo, 2010), and cell differentiation during erythropoiesis, lymphopoiesis, adipogenesis (Asanuma et al., 2003; Mizushima and Levine, 2010; Pua et al., 2007; Vessoni et al., 2012), and neurogenesis (Aburto et al., 2012; Zeng and Zhou, 2008; Zhao et al., 2010) (Fig. 1.7). Targeted mutagenesis of a few Atg genes in mice substantiated these hypotheses. Severe neural tube defects and embryonic lethality were associated with impaired autophagy in mice lacking the autophagy regulator Ambra1 (Cecconi et al., 2007; Fimia et al., 2007). In embryos homozygous for the gene-trapped (gt) allele Ambra1^{gt/gt}, it was observed reduced expression of neurogenic genes, accumulation of ubiquitinated proteins, unbalanced cell proliferation and excessive apoptotic cell death (Fimia et al., 2007). These interesting results suggest that autophagy may also be involved in the proliferative state or in the maintenance of pluripotency of NPCs. Activation of autophagy was also shown to be required for differentiation of glioma progenitor cells (Zhang et al., 2006b). It was shown that the autophagy inhibitors bafilomycin and 3-methyladenine could inhibit differentiation, while the autophagy activator and mTOR inhibitor, rapamycin, could promote it (Zhao et al., 2010). The basal low autophagic activity in glioma progenitor cells appears to be correlated with the inhibition of differentiation.

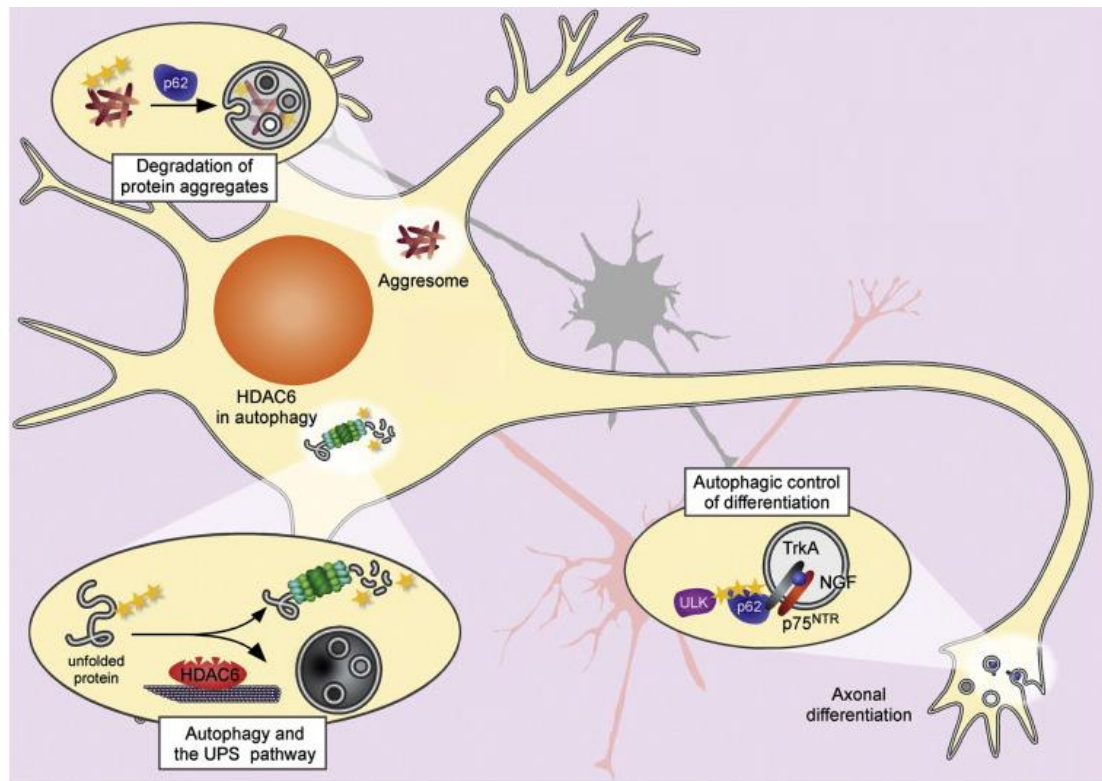


Figure 1.7. Autophagy is involved in neural differentiation. Autophagy is involved in multiple aspects of neuronal physiology, including axonal differentiation and maintenance, UPS-independent removal of unfolded cytosolic proteins and elimination of aggresomes. HDAC6, histone deacetylase 6. Adapted from Tooze and Schiavo 2008.

Zhuang *et al.* (Zhuang *et al.*, 2011) have also reported the relevance of autophagy in glioma-initiating cell differentiation and radiosensitization *in vitro* by rapamycin. The authors propose that autophagy deficiency in these cells contributes to the differentiation impairment and glioma radioresistance. NPCs from the mouse embryo olfactory bulb are also a well-characterized tool for the study of neuronal differentiation. Vazquez *et al.* (Vázquez *et al.*, 2012) have recently investigated whether basal autophagy occurs in these cells using this *in vivo* model during development. In fact, in wild-type mouse OB, they observed a progressive increase in the expression of the autophagy genes Atg7, Beclin1 (the orthologue of yeast Atg6), LC3 and Ambra1, during the differentiation of mitral neurons *in vivo*, associated with upregulation of Ngn1, NeuroD and β III-tubulin neurogenic markers. In addition, an increase of autophagic activity in NPCs from mouse embryo OB undergoing differentiation was also observed *in vitro* (Vázquez *et al.*, 2012).

The requirement of autophagy for neural differentiation was further confirmed in *Ambra1* haploinsufficient mice, where it was shown the generation of smaller neurospheres and fewer differentiated neurons (Vázquez et al., 2012). Importantly, these changes were reversed, to a large extent, by the metabolic substrate methylpyruvate, suggesting that in the context of neural differentiation, autophagy is crucial to energy supply, maintaining the ATP levels necessary for correct transition from proliferative precursor to postmitotic neuron. This hypothesis is indeed supported by previous studies in the developing retina, where autophagy was shown crucial for cell corpse clearance during naturally occurring cell death associated with neurogenesis (Mellén et al., 2008).

Objectives

The studies presented in this thesis were driven by the ambition to further understand the role of apoptosis in AD, and the function that AD-related apoptosis effectors may play in neural differentiation. Three main objectives were designed. First, our goal was to elucidate the precise role of p63 during A β -induced apoptosis and TUDCA protection. Second, we sought to investigate the potential involvement of p63 in regulating neural differentiation. Finally, we aimed to further explore the effect of soluble A β fragments in modulating neural proliferation and differentiation.

The specific questions addressed in this thesis are:

1. Does p63 play a role in A β -mediated cell death and/or TUDCA protection? Which molecular pathways does p63 modulate?
2. Does p63 modulate mouse NSC differentiation?
3. Can soluble A β peptides enhance neuronal-specific lineage of NSCs? How does A β regulate NSC fate determination?

The overarching goal of the research presented in this thesis is to increase our understanding on the pathogenic mechanisms of A β in AD as well as the role of apoptosis-regulatory players in NSC fate decision. The results may have broad implications in advancing our knowledge of neural degeneration and differentiation, and their interplay with the apoptosis machinery. Ultimately, our findings may prove useful in the comprehension of the key checkpoints responsible for neural degeneration *versus* differentiation, as an alternative to cell death, thus contributing to a better therapeutic management of apoptosis-associated AD and to a more efficient use of stem cells in neural-replacement therapy.

c-Jun Regulates the Stability of Anti-apoptotic Δ Np63 in Amyloid β -induced Apoptosis

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2.1. Abstract

p63, the structural and functional homologue of p53, is expressed either as a full-length isoform, containing a transactivation (TA) domain (TAp63), or as a truncated isoform, which lacks TA (Δ Np63). Amyloid β (A β) incubation of neuronal cells results in stress-induced cell death through poorly understood mechanisms. We investigated the role of p63 in A β -induced stress. Our results show that A β -induced apoptosis of rat PC12 neuronal-like cells and primary cortical neurons was associated with stabilization of pro-apoptotic TAp63 and, most importantly, degradation of anti-apoptotic Δ Np63 through a MAPK- and proteasome-dependent mechanism. This was associated with increased c-Jun, and partially modulated by tauroursodeoxycholic acid. As expected, classic genotoxic insults resulted in c-Jun upregulation and concomitant Δ Np63 reduction. Endogenous and ectopic Δ Np63 expression was also markedly reduced by c-Jun overexpression. Further, A β -mediated Δ Np63 degradation occurred in a c-Jun-dependent manner. Downregulation of c-Jun expression by specific c-Jun siRNA abrogated the reduction of Δ Np63 levels following A β insult, whereas overexpression of c-Jun led to its degradation. c-Jun significantly decreased Δ Np63 half-life. Together, these findings demonstrate that the abundance of anti-apoptotic Δ Np63 in response to A β -induced cell stress is regulated by a c-Jun-dependent mechanism, and highlight the importance of finding novel targets for potential therapeutic intervention.

Keywords: Amyloid β peptide; Apoptosis; c-Jun; Δ Np63; Tauroursodeoxycholic acid

2.2. Introduction

Alzheimer's disease (AD) is the most common human age-related, sporadic neurodegenerative disorder, and is characterized by a global cognitive decline. The major histopathological hallmarks of the disease are deposition of amyloid β ($A\beta$) peptide in neuritic plaques, formation of neurofibrillary tangles, and synaptic loss (Selkoe, 2001a). $A\beta$ has been shown to play a critical role in the pathogenesis of AD. Among its two predominant forms, $A\beta_{1-42}$ possesses stronger aggregation and deposition propensity than $A\beta_{1-40}$ (Selkoe, 2001a). Previous studies have shown that $A\beta$ -induced toxicity involves oxidative stress, inflammation, perturbation of calcium homeostasis, and most importantly apoptosis (Anderson et al., 1996; Estus et al., 1997; Loo et al., 1993; Selkoe, 2001a). In this respect, we have previously demonstrated that p53 participates in $A\beta$ -induced apoptosis of PC12 neuronal cells through modulation of Bax expression (Ramalho et al., 2004). Furthermore, $A\beta$ -induced apoptosis in rat primary cortical neurons was associated with translocation of pro-apoptotic Bax to the mitochondria, followed by cytochrome *c* (cyt *c*) release, caspase activation, and DNA and nuclear fragmentation (Solá et al., 2003a). Interestingly, a novel biological function of intracellular $A\beta_{1-42}$ has been suggested, where it acts as a transcription factor for the p53 promoter, enhancing p53-dependent neuronal apoptosis in AD (Ohyagi et al., 2005).

The role of apoptosis in $A\beta$ -induced toxicity suggests that its modulation may slow the neurodegenerative process. Ursodeoxycholic acid (UDCA) and its taurine conjugate, tauroursodeoxycholic acid (TUDCA) are well characterized endogenous potent inhibitors of apoptosis in different cell types and their effects have expanded to several experimental models of neurological disorders, including AD (Ramalho et al., 2008). Several lines of evidence suggest that TUDCA modulates $A\beta$ -induced neuronal death by inhibiting the mitochondrial machinery and enhancing survival signaling (Ramalho et al., 2006; Ramalho et al., 2004; Solá et al., 2006; Solá et al., 2003a). TUDCA is also a potent suppressor of $A\beta$ -induced changes of lipid/protein fluidity and oxidative status in mitochondrial membranes (Rodrigues et al., 2001). Finally, TUDCA prevents an endoplasmic-reticulum-specific apoptotic pathway involved in $A\beta$ neurotoxicity (Viana et al., 2011).

The p63 protein is a member of the p53 family that includes p53, p63 and p73. Alternative splicing and promoter usage results in multiple p63 isoforms with different biological activities. The p63 gene contains two promoters, leading to the

expression of two groups of proteins. Full-length proteins contain a transactivation (TA) domain (TAp63), whereas truncated proteins lack the TA domain (Δ Np63) (Yang et al., 1998). Additionally, both groups of proteins undergo carboxi-terminal alternative splicing giving rise to at least 6 different isoforms. TA isoforms act similarly to p53 and have the ability to transactivate p53 target genes and induce apoptosis. In contrast, Δ N isoforms have little transactivation activity and are thought to play a role in blocking transactivation of target genes of both p53 and TA isoforms (Yang et al., 2002). Therefore, Δ N isoforms function, at least in part, as naturally occurring dominant-inhibitory p53 family members. Both TA and Δ Np63 proteins are expressed in the cortex of embryonic, postnatal, and adult brains (Jacobs et al., 2005). Moreover, TAp63 has been shown to be required for growth factor-deprivation-mediated apoptosis of developing sympathetic neurons (Jacobs et al., 2005).

Given its key biological role, p63 is normally kept under tight regulatory control, mainly at the level of protein stability (Galli et al., 2010). Apoptotic doses of UV irradiation or genotoxic drugs promote phosphorylation-induced, proteasome-mediated degradation of the pro-survival isoform Δ Np63 α (Chatterjee et al., 2008; Lazzari et al., 2011; Liefer et al., 2000; Papoutsaki et al., 2005; Westfall et al., 2005). Surprisingly, the mechanisms regulating p63 levels under cellular insults such as A β -mediated apoptosis have yet to be elucidated.

The c-Jun transcription factor, a component of the AP-1 family, is a critical regulator of both cell survival and death that responds to genotoxic stress. Importantly, c-Jun induction has been shown to occur after A β treatment *in vitro* (Estus et al., 1997; Iwasaki et al., 1996; Viana et al., 2010) and in AD brains (Anderson et al., 1994; Anderson et al., 1996), suggesting a possible requirement of this transcription factor for A β toxicity. In this respect, it was also reported that sympathetic neurons from c-Jun-deficient mice were resistant to A β ₁₋₄₀ toxicity (Kihiko et al., 1999) and that extracellular application of aggregated A β induces neuronal apoptosis with c-Jun activation (Estus et al., 1997; Kihiko et al., 1999). Additionally, in AD patients, an increase in c-Jun immunoreactivity was reported in the brain (Anderson et al., 1996). These results suggest that c-Jun activation is a predominant feature of AD pathology and extracellular A β accumulation is a trigger of c-Jun activation. As c-Jun has been shown to regulate the abundance of TAp63

(Yao et al., 2010a), we hypothesized that c-Jun would have a key role in A β -mediated potential regulation of p63 stability.

The results presented here demonstrate that A β -induced apoptosis is associated with increased TAp63 and decreased Δ Np63 levels. Furthermore, our results strongly support the existence of a c-Jun-dependent mechanism regulating the abundance of anti-apoptotic Δ Np63 in the context of A β -induced stress. Importantly, TUDCA was efficient in partially modulating these effects.

2.3. Material and methods

2.3.1. Cell culture and treatments

Rat adrenal pheochromocytoma PC12 cells were grown in RPMI-1640 medium (Sigma-Aldrich, St. Louis, MO, USA) supplemented with 10% heat-inactivated horse serum (Sigma-Aldrich), 5% fetal bovine serum (Invitrogen Corp., Carlsband, CA, USA) and 1% penicillin/streptomycin (Invitrogen Corp.), and maintained at 37°C in a humidified atmosphere of 5% CO₂. Cells were plated and differentiated in the presence of nerve growth factor (Promega Corp., Madison, WI, USA) for 6 days, as previously described (Viana et al., 2010). Cell density was either 1×10^5 cells/cm² for morphological assessment of apoptosis, or 4×10^5 cells/cm² for protein extraction, and transfection assays. PC12 neuronal-like cells were then preincubated in medium supplemented with 100 μ M TUDCA (Sigma-Aldrich), or no addition (control), for 12 h, and then exposed to 25 μ M of peptide active fragment A β _{25–35} (Bachem AG, Bubendorf, Switzerland) for 2, 8, and 24 h. This was found to be the ideal concentration of soluble A β to achieve maximum cellular response with minimum exacerbated toxic effects in neuronal-like PC12 cells (Viana et al., 2010). In parallel experiments, cells were incubated with either 10 μ M soluble A β _{1–40} (Bachem AG), or 20 μ M fibrillar A β _{1–42} (Bachem AG) for 24 h (Viana et al., 2011). The predominant aggregates in these preparations are thought to be low N-oligomers, mainly monomeric to tetrameric, as fibrillogenesis usually requires longer incubation times and higher concentrations of the peptides [27]. Although high, the concentration of A β peptides used in this study are below the concentration of A β _{1–42} found in the cerebrospinal fluid of AD patients [28, 29]. For the experiments with the MAPK and proteasome inhibitors, cells were pretreated with the JNK inhibitor SP600125 (10 μ M), ERK inhibitor U0126 (50 μ M), p38 inhibitor SB202190 (50 μ M) (all from Sigma-Aldrich) or the proteasome inhibitor MG132 (5 μ M; Calbiochem,

San Diego California, USA) for 1 h, in the presence or absence of A β ₂₅₋₃₅ incubated for 24 h. Differentiated PC12 cells were also incubated for 6 h with genotoxic drugs doxorubicin (5 μ M; Sigma-Aldrich) and cisplatin (20 μ M; Sigma-Aldrich) as controls.

2.3.2. Primary culture of cortical neurons

Primary cultures of cortical neurons were prepared from embryonic (gestational day 18) CD1 mice and maintained in MEM Eagle's HBSS medium (Invitrogen). After dissociation with trypsin 0.25% (Invitrogen Corp.) and centrifugation, the cells were resuspended in Neurobasal medium (Invitrogen Corp.), supplemented with 2% B-27 (Invitrogen), 0.5 mM glutamine (Invitrogen Corp.), 25 μ M glutamic acid (Merck, Darmstadt, Germany), and 10 mg/mL gentamycin (Invitrogen Corp.). Neurons were plated onto 35 mm dishes coated with poly-D-lysine (0.05 mg/ml, Sigma-Aldrich) at a density of 1.0×10^6 cells/cm². The cultures were kept at 37°C in a humidified incubator with a 5% CO₂ atmosphere. The medium was replaced half on day 4 with Neurobasal medium without glutamic acid. TUDCA and A β ₂₅₋₃₅ treatment was performed as described before for PC12 cells, starting at day 4 in culture.

2.3.3. Measurement of cell death

Apoptotic nuclei were detected by Hoechst labeling after cell fixation with 4% formaldehyde in phosphate buffer saline (PBS), for 10 min at room temperature. Following incubation with Hoechst dye 33258 (Sigma-Aldrich) at 5 μ g/mL in PBS for 5 min, and PBS washes, slides were mounted with Fluoromount-G (Beckman Coulter, Inc, Fullerton, CA, USA) and fluorescence visualized with an Axioskop fluorescence microscope (Carl Zeiss GmbH, Hamburg, Germany). Fluorescent nuclei were scored and categorized according to the condensation and staining characteristics of chromatin. Normal nuclei showed non-condensed chromatin dispersed over the entire nucleus. Apoptotic nuclei were independently identified by condensed and fragmented chromatin contiguous to the nuclear membrane, as well as nuclear fragmentation and presence of apoptotic bodies. Three random microscopic fields per sample of ~250 nuclei were counted and mean values expressed as the percentage of apoptotic nuclei.

2.3.4. Plasmids, siRNAs and transfections

For the identification of the endogenous p63 isoforms, PC12 cells were transfected using Lipofectamine 2000 (Invitrogen Corp.) with 8 μg pcDNA3.1- $\Delta\text{Np63}\alpha$, $-\Delta\text{Np63}\gamma$, TAp63 α or TAp63 γ expression plasmids (kind gift from Dr. Kurt Engeland, University of Leipzig). In subsequent experiments, 4 μg pSG5-c-Jun expression plasmid (kind gift from Dr. Imakawa, University of Tokyo), 2 μg pcDNA3.1- $\Delta\text{Np63}\gamma$, or 100 nM c-Jun siRNA (Dharmacon, Waltham, MA, USA) were used. As controls, cells were transfected with the corresponding empty vector plasmids, or a control siRNA (Dharmacon) containing a scrambled sequence that does not lead to the specific degradation of any known cellular mRNA. Total amount of transfected nucleic acids was equalized with appropriate amounts of empty vector in all cases. Cells were collected 48 h after transfection for immunoblot analyses. In experiments with the protein synthesis inhibitor cycloheximide (CHX), cells were transfected with pSG5-c-Jun and pcDNA3.1- $\Delta\text{Np63}\gamma$ plasmids 48 h prior to addition of CHX (50 $\mu\text{g}/\text{mL}$; Sigma-Aldrich), and maintained for the indicated time points. In addition, c-Jun siRNA was transfected 48 h prior to addition of $\text{A}\beta_{25-35}$ and maintained throughout the 24 h of $\text{A}\beta$ incubation. Floating and attached cells were harvested, and total protein extracts were prepared for Western blot analysis.

3.3.5. Western blot

Protein levels of TAp63, ΔNp63 and c-Jun in PC12 neuronal-like cells and primary cortical neurons were determined by Western blot analysis. Briefly, 100 μg of total proteins were separated by 8% sodium dodecyl-polyacrylamide gel electrophoresis. After electrophoretic transfer onto nitrocellulose membranes, and blocking with a 5% milk solution, membranes were incubated overnight at 4°C with a primary mouse monoclonal antibody reactive to p63 (4A4; Santa Cruz Biotechnology, Santa Cruz, CA, USA), which detects both TAp63 and ΔNp63 isoforms, and a primary rabbit monoclonal antibody reactive to c-Jun (60A8; Cell Signaling Technology, Inc., Danvers, MA, USA). Finally, secondary goat anti-mouse or anti-rabbit IgG antibody conjugated with horseradish peroxidase (BioRad Laboratories, Hercules, CA, USA) was added for 3 h at room temperature. The membranes were processed for protein detection using the SuperSignal substrate (Pierce Biotechnology, Rockford, IL, USA). β -Actin (AC-15; Sigma-Aldrich) was used as

loading control. Protein concentrations were determined using the Bio-Rad protein assay kit (Bio-Rad Laboratories), according to the manufacturer's specifications.

2.3.6. Statistical analysis

The relative intensities of protein bands were analyzed using the QuantityOne Version 4.6 densitometric analysis program (Bio-Rad Laboratories) and normalized to the respective loading controls. Statistical analysis was performed using GraphPad InStat version 3.00 (Graph-Pad Software) for the analysis of variance and Bonferroni's multiple comparison tests. Values of $p < 0.05$ were considered significant.

2.4. Results

2.4.1. A β -induced cell stress is associated with decreased Δ Np63 and increased c-Jun protein levels

Expression of p63 isoforms was first confirmed in PC12 neuronal-like cells after overexpression of either TAp63 α , TAp63 γ , Δ Np63 α , or Δ Np63 γ . Endogenous TAp63 γ (~ 57 kDa) and Δ Np63 γ (~ 54 kDa) were detected from a group of at least six different isoforms encoded by p63 (Fig. 2.1A). In addition, endogenous expression of Δ Np63 γ was more than 5-fold greater than that of TAp63 γ .

Genotoxic signals are known to regulate p63 (Kirschner et al., 2008; Liefer et al., 2000; Papoutsaki et al., 2005; Yao et al., 2010a). In fact, exposure of PC12 neuronal-like cells to classic genotoxic insults, such as doxorubicin and cisplatin resulted in increased TAp63 levels, concurrent with the reduction of Δ Np63 abundance (Fig. 2.1B). To determine whether p63 levels are also controlled by A β -induced stress, we performed a time-course analysis of A β ₂₅₋₃₅ treatment in PC12 neuronal-like cells. Our results show that A β treatment resulted in stabilization of TAp63 and, most importantly, reduction of Δ Np63 (Fig. 2.2A). These effects were more evident after 24 h of A β treatment. c-Jun, a key regulator of stress-mediated cell death has been shown to modulate the abundance of TAp63 (Yao et al., 2010a). We therefore investigated if c-Jun would have any role in the A β -mediated regulation of p63 levels. Time-course analysis of A β ₂₅₋₃₅ treatment revealed that c-Jun protein levels increased with time, peaking at 24 h after A β treatment (Fig. 2.2A). Similarly, exposure of PC12 neuronal-like cells to classic genotoxic insults resulted in c-Jun upregulation (Fig. 2.1B). Finally, to confirm A β role on the regulation of p63 levels,

PC12 cells were incubated with the full-length soluble A β_{1-40} and fibrillar A β_{1-42} peptides. As predicted, similarly to A β_{25-35} , both A β_{1-40} and A β_{1-42} decreased Δ Np63 levels while increasing TAp63 and c-Jun levels (Fig. 2.2B). These results suggest the existence of an inverse relationship between Δ Np63 and c-Jun levels following A β treatment.

To investigate if A β -mediated reduction of Δ Np63 protein levels is influenced by the mitogen activated protein kinase (MAPK) pathway, PC12 neuronal-like cells were treated with MAPK inhibitors for 1 h before A β incubation, and p63 levels were examined by Western blot analysis. Treatment with the JNK inhibitor SP600125, ERK inhibitor PD98059 and p38 inhibitor SB202190 rescued the reduction of Δ Np63 levels observed after A β treatment (Fig. 2.2C).

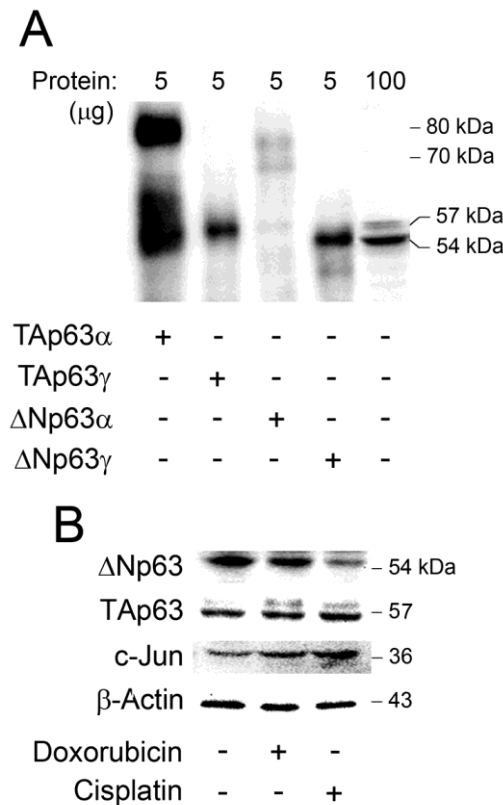


Figure 2.1. Expression of endogenous p63 isoforms and genotoxic stress-induced regulation of p63 and c-Jun protein levels in PC12 neuronal-like cells. A) Detection of p63 isoforms in cells transfected with the overexpression plasmid TAp63 α , TAp63 γ , Δ Np63 α , or Δ Np63 γ for 48 h, compared with untransfected cells. Total proteins were extracted from transfected and untransfected cells and used for Western blot analysis of 5 and 100 μ g, respectively. p63 protein isoforms were identified using the pan-p63 monoclonal antibody 4A4, as described in Materials and Methods. B) Protein levels of Δ Np63, TAp63 and c-Jun in cells incubated with 5 μ M doxorubicin or 20 μ M cisplatin for 6 h, or no addition (control).

β -actin was used as loading control. Immunoblots are representative of at least three different experiments.

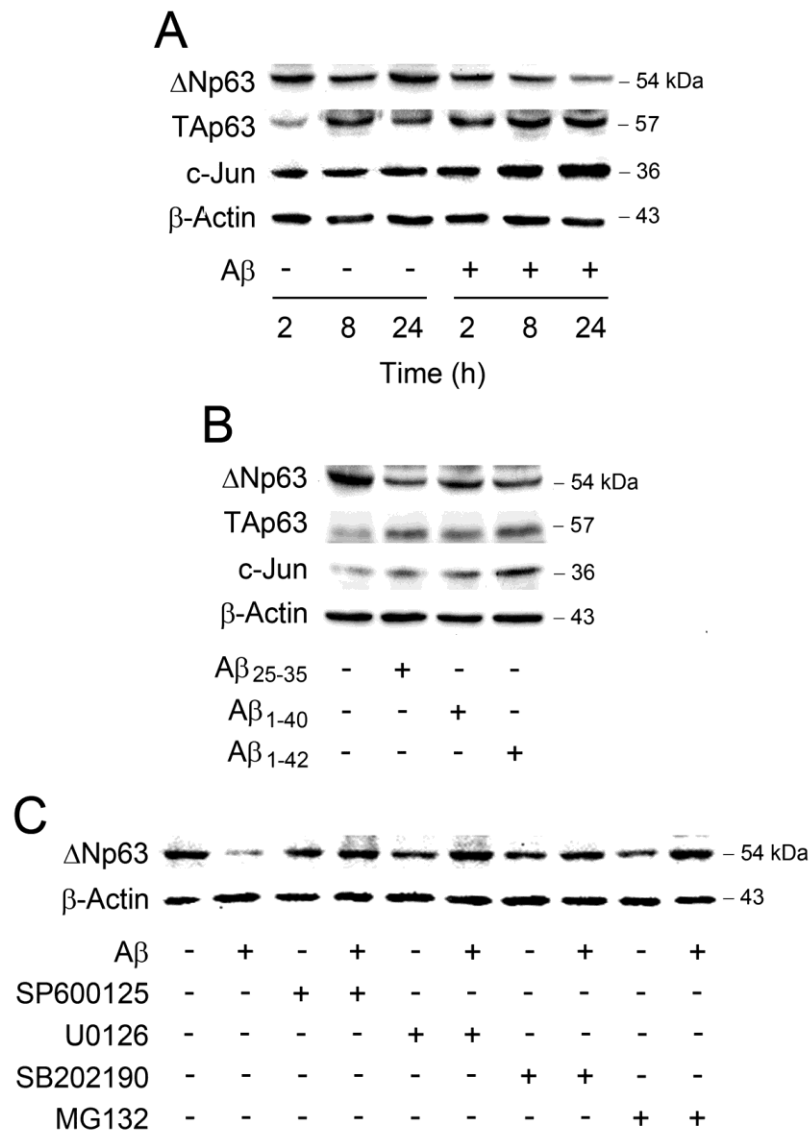


Figure 2.2. $A\beta$ -induced cell stress is associated with decreased Δ Np63 and increased TAp63 and c-Jun protein levels in PC12 neuronal-like cells. Cells were incubated with 25 μ M soluble $A\beta_{25-35}$ or no addition (control). Total proteins were extracted for Western blot analysis as described in Materials and Methods. β -actin was used as loading control. A) Protein levels of Δ Np63, TAp63 and c-Jun in cells incubated with $A\beta_{25-35}$ for 2, 8, and 24 h. B) Protein levels of Δ Np63, TAp63 and c-Jun in cells incubated with $A\beta_{25-35}$, 10 μ M soluble $A\beta_{1-40}$, or 20 μ M fibrillar $A\beta_{1-42}$ for 24 h. C) Protein levels of Δ Np63 in cells incubated with the JNK inhibitor (SP600125), ERK inhibitor (U0126), p38 inhibitor (SB202190) or proteasome inhibitor MG132 for 1 h, in the presence or absence of $A\beta_{25-35}$ incubated for 24 h. β -actin was used as loading control. Immunoblots are representative of at least three different experiments.

We also investigated the effect of directly inhibiting the proteasome by treating cells with the proteasome inhibitor MG132.

Treatment with the proteasome inhibitor abolished the A β -dependent reduction of Δ Np63 levels (Fig. 2.2C), indicating that Δ Np63 degradation occurs via the proteasome. These results suggest that the decrease in Δ Np63 protein levels in cells exposed to A β is MAPK pathway- and proteasome-dependent.

2.4.2. TUDCA modulates A β -induced changes in Δ Np63 and c-Jun protein levels

It has been previously shown that soluble A β_{25-35} fragment induces apoptosis in PC12 neuronal-like cells and cortical neurons, which is abrogated by TUDCA pretreatment (Ramalho et al., 2004; Solá et al., 2003a; Viana et al., 2010). In this study, rat PC12 neuronal-like cells and primary cortical neurons were incubated with A β_{25-35} , with or without pre-treatment with the anti-apoptotic bile acid TUDCA, and assessed for cell death as well as Δ Np63 and c-Jun protein levels. Incubation with A β_{25-35} for 24 h induced apoptosis in ~ 13 and 40% of PC12 cells and cortical neurons, respectively ($p < 0.01$) (Fig. 2.3A). Pre-treatment with TUDCA markedly reduced A β -induced apoptosis ($p < 0.05$). Notably, TUDCA prevented A β -induced Δ Np63 degradation in both PC12 cells and cortical neurons, possibly by restoring c-Jun protein levels to almost control values ($p < 0.01$ in PC12 cells, and $p < 0.05$ in cortical neurons). These results suggest that inhibition of Δ Np63 degradation through modulation of c-Jun levels may also account for TUDCA neuroprotective mechanism.

2.4.3. c-Jun is required for Δ Np63 degradation after A β treatment

To clarify whether c-Jun could directly lead to Δ Np63 degradation, c-Jun was overexpressed in PC12 cells. c-Jun overexpression led to a reduction of endogenous Δ Np63, compared with cells transfected with the empty vector pSG5 (Fig. 2.4A). Additionally, transient co-expression of c-Jun and Δ Np63 caused a marked decrease of exogenous Δ Np63 ($p < 0.01$) (Fig. 2.4B), even with high level expression reached after transfection, suggesting that c-Jun may be a potent negative regulator of Δ Np63 abundance.

To further investigate the role of c-Jun in regulating Δ Np63 abundance, we then examined whether Δ Np63 protein levels were altered by silencing endogenous c-Jun. Immunoblotting analysis revealed that knockdown of c-Jun by specific c-Jun siRNA abrogated the reduction of Δ Np63 levels following A β stress, when compared with control siRNA-transfected cells ($p < 0.05$) (Fig. 2.5A).

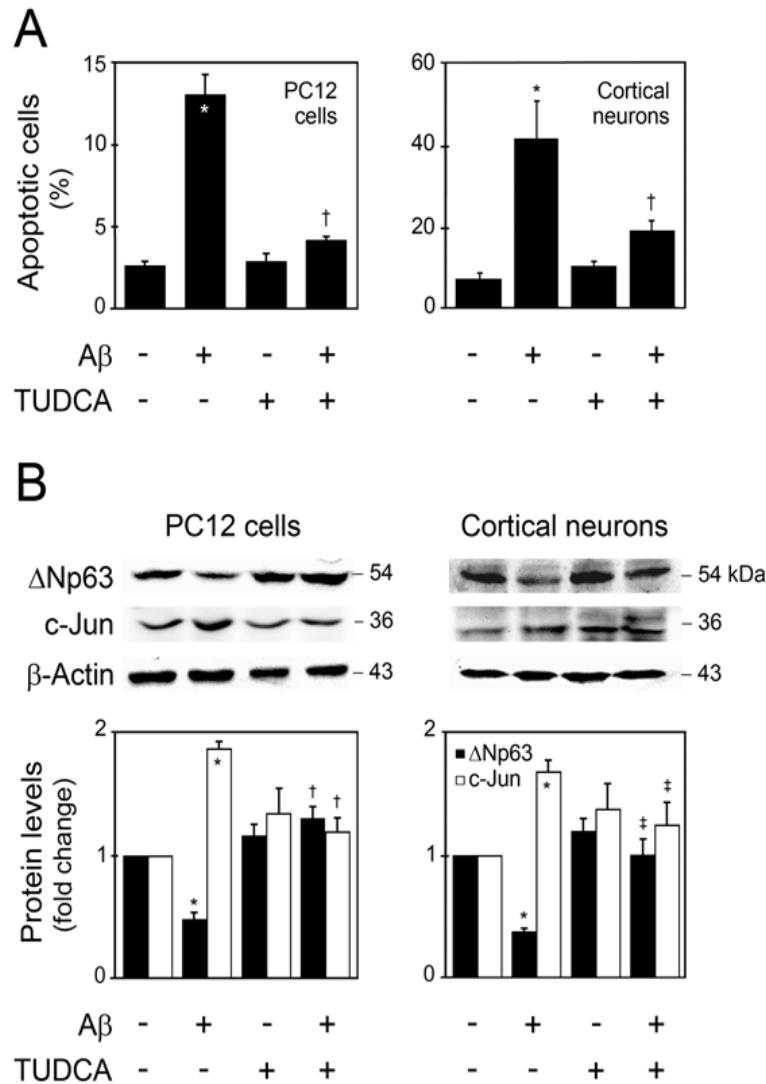


Figure 2.3. TUDCA modulates A β -induced apoptotic changes in Δ Np63 and c-Jun protein levels in PC12 neuronal-like cells and cortical neurons. Cells were incubated for 24 h with 25 μ M soluble A β_{25-35} , or no addition (control), in the presence or absence of 100 μ M TUDCA. In co-incubation experiments, TUDCA was added 12 h prior to incubation with A β . Cells were fixed and stained for microscopic assessment of apoptosis and total proteins were extracted for Western blot analysis as described in Materials and Methods. A) Percentage of apoptosis after Hoechst staining in cells exposed to A β with or without TUDCA pretreatment. Results are expressed as mean \pm SEM for at least three different experiments. * $p < 0.01$ from control and † $p < 0.05$ from A β alone. B) Protein levels of Δ Np63 and c-Jun in cells exposed to A β with or without TUDCA pre-treatment. Representative immunoblot of Δ Np63 and c-Jun (top) and respective protein levels (bottom). Results were normalized to endogenous β -Actin protein levels and expressed as mean \pm SEM for at least four different experiments. * $p < 0.01$ from control; † $p < 0.01$ and ‡ $p < 0.05$ from A β alone.

These results strongly suggest that A β -mediated Δ Np63 degradation occurs in a c-Jun-dependent manner. Furthermore, knockdown of endogenous c-Jun in cells transfected with Δ Np63 plasmid resulted in increased expression of exogenous

Δ Np63 ($p < 0.01$) (Fig. 2.5B). These results further corroborate the hypothesis that c-Jun plays an important role in regulating Δ Np63 abundance.

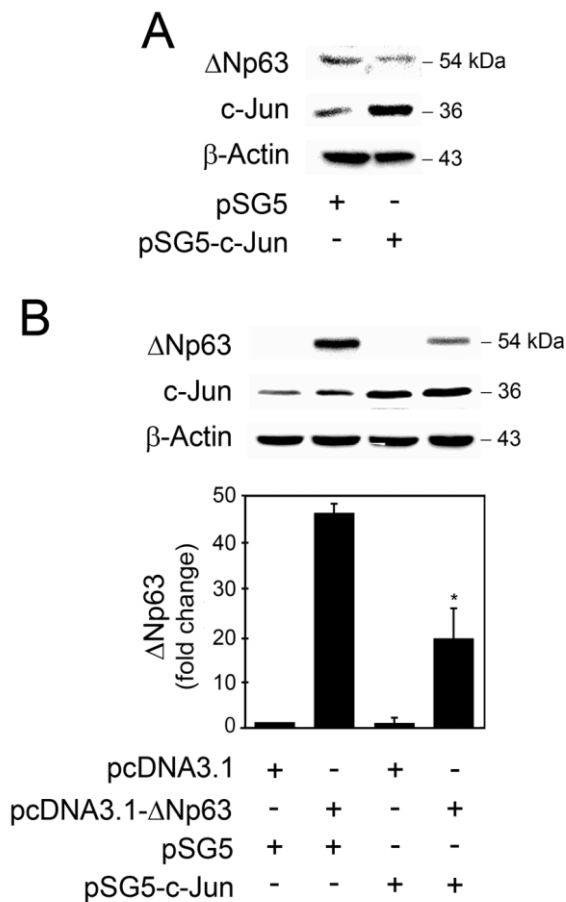


Figure 2.4. Overexpression of c-Jun downregulates both endogenous and exogenous levels of Δ Np63 in PC12 neuronal-like cells. Cells were transfected with c-Jun overexpression plasmid in the presence or absence of Δ Np63 γ overexpression plasmid. After 48 h of transfection, total proteins were extracted for Western blot analysis as described in Materials and Methods. A) Protein levels of Δ Np63 and c-Jun in cells transfected with c-Jun overexpression plasmid (pSG5-c-Jun) or its corresponding empty vector (pSG5). B) Protein levels of Δ Np63 and c-Jun in cells co-transfected with c-Jun overexpression plasmid (pSG5-c-Jun), or its corresponding empty vector (pSG5), and Δ Np63 γ overexpression plasmid (pcDNA3.1- Δ Np63), or its corresponding empty vector (pcDNA3.1). Representative immunoblot of Δ Np63 and c-Jun (top) and respective protein levels (bottom). Results were normalized to endogenous β -Actin protein levels and expressed as mean \pm SEM for at least four different experiments. * $p < 0.01$ from Δ Np63 overexpressing cells.

Finally, to better understand c-Jun contribution to Δ Np63 degradation, we investigated Δ Np63 half-life in the presence of c-Jun. For this purpose, PC12 cells transfected with Δ Np63 alone or together with c-Jun were treated with the protein synthesis inhibitor CHX.

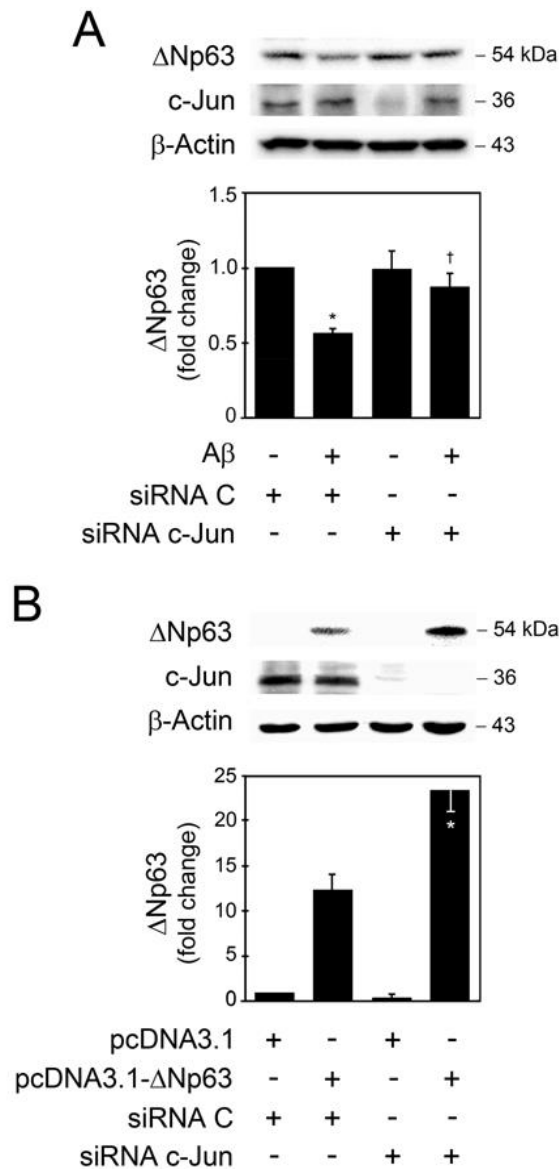


Figure 2.5. Silencing of endogenous c-Jun abrogates Aβ-induced ΔNp63 degradation and increases exogenous ΔNp63 levels in PC12 neuronal-like cells. Cells were transfected with 100 nM of either c-Jun siRNA or control siRNA (siRNA C) for 48 h. A) After 48 h of siRNA transfections, cells were challenged with 25 μM soluble Aβ₂₅₋₃₅, or no addition (control), for 24 h. **p* < 0.01 from control cells transfected with siRNA control (siRNA C); †*p* < 0.05 from Aβ-incubated cells transfected with siRNA control. B) ΔNp63γ overexpression plasmid (pcDNA3.1-ΔNp63) and its corresponding empty vector (pcDNA3.1) were co-transfected with c-Jun and control siRNAs. Total proteins were extracted for Western blot analysis as described in Materials and Methods. Representative immunoblots of ΔNp63 and c-Jun (top) and respective protein levels (bottom). Results were normalized to endogenous β-Actin protein levels and expressed as mean ± SEM for at least three different experiments. **p* < 0.01 from ΔNp63 overexpressing cells transfected with siRNA control (siRNA C).

Results demonstrate that the highly stable ΔNp63 half-life was reduced to less than 8 h in the presence of c-Jun (*p* < 0.01) (Fig. 2.6), confirming that c-Jun indeed regulates the stability of ΔNp63.

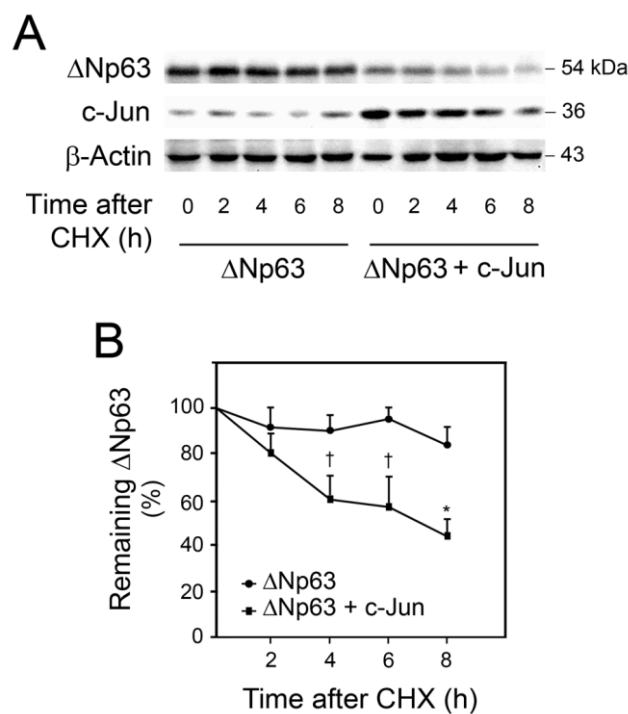


Figure 2.6. *c-Jun* decreases Δ Np63 half-life in PC12 neuronal-like cells. Cells transfected with Δ Np63 γ alone (Δ Np63) or with *c-Jun* (Δ Np63 + *c-Jun*) were untreated (0 h) or treated with 50 μ g/mL CHX for 2, 4, 6, and 8 h. At the indicated time points, total proteins were extracted for immunoblot analysis as described in Materials and Methods. A) Representative immunoblots of Δ Np63 and *c-Jun* after CHX treatment. B) Percentage of remaining Δ Np63 after CHX treatment. Results were normalized to endogenous β -Actin protein levels and expressed as mean \pm SEM for at least four different experiments. * $p < 0.01$ and $^{\dagger}p < 0.05$ from Δ Np63 overexpressing cells.

2.5. Discussion

A β -induced toxicity is a multifactorial process that ultimately leads to apoptotic neuronal death. In the present study, we show that A β induces an antagonistic effect in the regulation of p63 isoform abundance in PC12 neuronal-like cells, with upregulation of the pro-apoptotic isoform TAp63 γ and downregulation of the anti-apoptotic isoform Δ Np63 γ . A similar effect was observed by incubation of PC12 neuronal-like cells with the genotoxic drugs doxorubicin and cisplatin. Previous studies have already shown that treatment of cells with various DNA-damaging agents resulted in increased expression of TAp63 isoforms (Hershkovitz Rokah et al., 2010; Kirschner et al., 2008; Sayan et al., 2007a; Yao et al., 2010a). A downregulation of Δ Np63 in response to UV irradiation or genotoxic drugs was only reported for the α isoform (Chatterjee et al., 2008; Lazzari et al., 2011; Liefer et al., 2000; Papoutsaki et al., 2005; Westfall et al., 2005). Further, we show that A β

induces apoptosis in rat cortical neurons by regulating the abundance of both antagonistic isoforms of p63, TAp63 γ and Δ Np63 γ .

The many isoforms generated from the p63 gene provide the molecular flexibility to play very different, and even functionally antagonistic roles, depending on the cellular context. Indeed, TAp63 isoforms are often upregulated after exposure to cellular insults, contributing to cell death (HersHKovitz Rokah et al., 2010; Kirschner et al., 2008; Sayan et al., 2007a; Yao et al., 2010a), as TAp63 can activate both death receptor- and mitochondrial-mediated apoptotic pathways (Gressner et al., 2005). Similarly, stress signals trigger the reduction of Δ Np63 levels (Chatterjee et al., 2008; Lazzari et al., 2011; Liefer et al., 2000; Papoutsaki et al., 2005; Westfall et al., 2005), which will allow the manifestation of apoptosis. The balance between these two major p63 isoforms dictates cell fate (Vanbokhoven et al., 2011). Because both isoforms have profoundly distinct biological effects, it is not surprising that they are differently regulated by A β -induced stress signaling. As shown here, exposure of both PC12 neuronal-like cells and cortical neurons to A β active fragment A β ₂₅₋₃₅ resulted in apoptotic cell death. In addition, A β ₂₅₋₃₅ and the full-length A β peptides, A β ₁₋₄₀ and A β ₁₋₄₂, increased TAp63 and decreased Δ Np63 levels. Importantly, the anti-apoptotic bile acid TUDCA strongly modulated A β -induced apoptosis while preventing the changes in p63 levels, further suggesting that the reduction of Δ Np63 levels is important for apoptosis to occur.

c-Jun transcriptionally activates the TAp63 promotor (Yao et al., 2010a), possibly contributing to some forms of c-Jun-mediated cell death. Furthermore, c-Jun is increased after A β exposure and in AD brains (Anderson et al., 1994; Anderson et al., 1996; Estus et al., 1997) suggesting a role for c-Jun in A β -induced toxicity. We have recently shown that JNK is the proximal stress sensor for A β -induced toxicity, and that it translocates to the nucleus and activates caspase-2 in PC12 neuronal cells (Viana et al., 2010). Caspase-2 in turn induces cleavage of golgin-160, suggesting a unique transduction mechanism of A β apoptotic signaling through the Golgi complex. This led us to hypothesize that c-Jun could be responsible for A β -dependent decrease in Δ Np63 protein levels. Here, we demonstrate that Δ Np63 reduction was associated with increased c-Jun protein levels after A β treatment of PC12 neuronal-like cells and cortical neurons. Moreover, TUDCA rescued A β -induced decrease of Δ Np63 levels and prevented the increase in c-Jun levels. Importantly, c-Jun overexpression led to Δ Np63 degradation, whereas knockdown of c-Jun by specific c-Jun siRNA abrogated

the reduction of Δ Np63 following A β stress. Finally, the highly stable Δ Np63 half-life was reduced in the presence of c-Jun. These results clearly show that A β -mediated Δ Np63 degradation occurs in a c-Jun-dependent manner, and highlight the existence of distinct pathways that have probably evolved for the reciprocal regulation of the abundance of functionally different but highly homologous proteins TAp63 and Δ Np63 under A β stress.

c-Jun is one of the components of the transcription factor AP-1 and its expression is regulated by a variety of signals in different cell types (Hess et al., 2004). Despite the extensive knowledge regarding c-Jun activation, downstream cell signaling events remain unclear in A β -induced cell stress. Here we demonstrate that Δ Np63 γ is a downstream target of c-Jun in A β -induced apoptosis. In fact, after depleting cells of c-Jun by specific siRNA, A β failed to decrease Δ Np63 protein levels. c-Jun is a major target of the MAPK pathway as it contributes to the cellular stress response and is believed to mediate neuronal apoptosis (Behrens et al., 1999; Saganuma et al., 2010). We therefore explored whether A β -mediated Δ Np63 γ reduction was influenced by the MAPK pathway. Our results show that in the presence of the JNK, ERK or p38 inhibitors, A β no longer resulted in decreased Δ Np63. The same was true for the incubation with the proteasome inhibitor, suggesting that the decrease in Δ Np63 protein levels in cells exposed to A β was MAPK pathway- and proteasome-dependent. In the past few years, some Δ Np63 α -modifying enzymes have been identified and reported to regulate Δ Np63 α stability (Bakkers et al., 2005). These proteins bind to sites in the C-terminal region of Δ Np63 α , which are absent in the shorter and more stable Δ Np63 γ isoform. Future studies are needed to clarify the exact mechanism by which c-Jun targets Δ Np63 γ isoform to proteasomal-dependent degradation. Despite the fact that A β may inhibit the proteasome [39, 40], our results are in accordance with others demonstrating that important mediators of AD are degraded in a proteasome-dependent fashion [41, 42], thus contributing to AD pathogenesis.

In conclusion, this study clearly shows that A β exposure differently regulates TAp63 and Δ Np63 isoforms to allow the manifestation of apoptosis. This suggests that the selective regulation of the two antagonistic isoforms of p63 is crucial in maintaining the homeostatic balance between life and death of a cell that is undergoing A β -induced cell stress. The present study also convincingly shows that c-Jun is required for A β -mediated degradation of Δ Np63, which occurs via MAPK

pathway and proteasome activation. Thus, c-Jun appears to be a stress sensor for A β -induced apoptosis, which in turn is strongly modulated by TUDCA. These results provide novel insights into the specific cellular mechanism of A β -induced neuronal apoptosis and suggest novel targets for potential therapeutic intervention.

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TAp63 γ Demethylation Regulates Protein Stability and Cellular Distribution during Neural Stem Cell Differentiation

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Reprinted from *PLoS ONE* vol 7, Issue 12, Maria B. Fonseca, Ana F. Nunes, Ana L. Morgado Susana Solá, Cecília M. P. Rodrigues. TAp63 γ Demethylation regulates protein stability and cellular distribution during neural stem cell differentiation, page e52417, Copyright 2012, Fonseca *et al.* All rights reserved.

3.1. Abstract

p63 is a close relative of the p53 tumor suppressor and transcription factor that modulates cell fate. The full-length isoform of p63, containing a transactivation (TA) domain (TAp63) is an essential proapoptotic protein in neural development. The role of p63 in epithelial development is also well established; however, its precise function during neural differentiation remains largely controversial. Recently, it has been demonstrated that several conserved elements of apoptosis are also integral components of cellular differentiation; p53 directly interacts with key regulators of neurogenesis. The aim of this study was to evaluate the role of p63 during mouse neural stem cell (NSC) differentiation and test whether the histone H3 lysine 27-specific demethylase JMJD3 interacts with p63 to redirect NSCs to neurogenesis. Our results showed that JMJD3 and TAp63 γ are coordinately regulated to establish neural-specific gene expression programs in NSCs undergoing differentiation. JMJD3 overexpression increased TAp63 γ levels in a demethylase activity-dependent manner. Importantly, overexpression of TAp63 γ increased β -III tubulin whereas downregulation of TAp63 γ by specific p63 siRNA decreased β -III tubulin. Immunoprecipitation assays demonstrated direct interaction between TAp63 γ and JMJD3, and modulation of TAp63 γ methylation status by JMJD3-demethylase activity. Importantly, the demethylase activity of JMJD3 influenced TAp63 γ protein stabilization and cellular distribution, as well as TAp63 γ -regulated neurogenesis. These findings clarify the role of p63 in adult neural progenitor cells and reveal TAp63 γ as a direct target for JMJD3-mediated neuronal commitment.

Keywords: Differentiation; JMJD3; Neural stem cells; p63 post-translation modifications

3.2. Introduction

The transcription factor p63, member of the p53 family, can be expressed as a full-length isoform containing a transactivation (TA) domain, termed TAp63, or as a truncated isoform that lacks the TA domain, termed Δ Np63. This isoform functions, at least in part, as naturally occurring dominant-inhibitor of full-length p53 family members. Additionally, both TAp63 and Δ Np63 undergo C-terminal alternative splicing giving rise to at least 6 different isoforms, which along with post-translational modifications (PTM), accounts for molecular and regulatory complexity (Fonseca et al., 2012; Nicotera and Melino, 2005; Yang et al., 1998). Full-length p53 family members show structural and functional similarities, including a comparable domain structure of an N-terminal TA domain, an invariant DNA-binding domain, and an oligomerization domain (Courtois et al., 2004). p63 has been well-established as an important regulator of cell survival and cell death in the nervous system, primarily by acting through the apoptosis machinery (Fonseca et al., 2012; Jacobs et al., 2005; Nicotera and Melino, 2005). In this respect, we have shown that both TA and Δ Np63 isoforms are involved in molecular mechanisms associated with Alzheimer's disease (Fonseca et al., 2012).

Recently, it has been suggested that cell death-relevant proteins, especially those involved in the core of the executing apoptosis machinery, may play a dual function in differentiation and cell death (Fernando and Megeney, 2007). Restrictive activation and careful regulation will assure differentiation efficiency and thus avoid cell loss. In this regard, we have previously demonstrated the involvement of specific apoptosis-related microRNAs and proteins, including p53, caspases and calpains, in mouse neural stem cell (NSC) differentiation, by mechanisms that do not result in cell death (Aranha et al., 2011; Aranha et al., 2010; Aranha et al., 2009; Santos et al., 2012b; Solá et al., 2011b). Several studies have shown that inactivation of p53 sustains the undifferentiated state of neural precursor cells (Armesilla-Diaz et al., 2009; Meletis et al., 2006; Zheng et al., 2008), and that p53 is required for both neurite outgrowth and axonal regeneration in mice primary neurons (Di Giovanni et al., 2006). We have further dissected the role of p53 during NSC differentiation by showing that this proapoptotic protein cross-talks with key regulators of neurogenesis, such as the histone H3 lysine 27-specific demethylase JMJD3 (Solá et al., 2011b). In fact, PTM of apoptosis-related proteins may redirect stem cells to differentiation, as

an alternative to cell death, and establish tissue-specific programs of gene expression throughout differentiation. A strong interplay between p53, p63 and p73 isoforms has been recently demonstrated, which orchestrates cell fate decisions (Jost et al., 1997; Marcel et al., 2012). In addition, similar to p53, TAp63 can oligomerize, bind to DNA, transactivate p53 target genes, and induce cell cycle arrest and apoptosis (Fonseca et al., 2012; Jost et al., 1997; Yang et al., 1998).

The pivotal role of p63 during epithelial development has been well recognized. Mice lacking all p63 isoforms die at birth and show severe developmental abnormalities, including limb truncation, and defects in the epidermis and its appendages (Yang et al., 1999). However, although TAp63 critical function in sympathetic neuronal development is firmly established (Jacobs et al., 2005), two independent studies have recently reported that p63 is not essential for central nervous system development (Hernández-Acosta et al., 2011; Holembowski et al., 2011). Nevertheless, in contrast to p63-restricted expression observed during mice and human brain development, high levels of p63 protein and mRNA were observed in adult human cerebral cortex and hippocampus (Hernández-Acosta et al., 2011), suggesting a role for p63 in the adult brain. Furthermore, in postnatal mice, p63 was shown to be expressed in neurogenic niches, such as the subventricular zone of the lateral ventricle (Hernández-Acosta et al., 2011). Together, this evidence supports the idea that p63 may have a key role during adult neurogenesis.

Here, we investigated p63 involvement during adult mouse NSC differentiation and explored the potential cross-talk between p63 and JMJD3 in this cellular context. Our results demonstrated that TAp63 γ and JMJD3 are coordinately regulated during NSC differentiation to establish a neuronal-specific gene expression program. In addition, TAp63 γ subcellular distribution and neurogenic functions may be regulated by direct JMJD3-dependent demethylation of TAp63 γ .

3.3. Material and methods

3.3.1. Ethics statement

The mouse NSC line used in this study was obtained from Dr. Smith's Laboratory, University of Cambridge, Cambridge, UK (Pratt et al., 2000; Silva et al., 2006; Solá et al., 2011b), and provided by Dr. Henrique, University of Lisbon, Lisbon, Portugal. The Animal Ethical Committee at the Faculty of Pharmacy, University of Lisbon, Portugal waived the need for approval.

3.3.2. Cell culture and differentiation

A mouse NSC line was derived from day 14.5 post-coitum mouse fetal forebrain (Pratt et al., 2000; Silva et al., 2006; Solá et al., 2011b). This cell line was established using a method that produces pure cultures of adherent NSCs, which continuously expand by symmetrical division, and are capable of tripotential differentiation (Conti et al., 2005; Glaser et al., 2007; Pollard et al., 2006). Cells were grown in monolayer as previously described (Santos et al., 2012b; Spiliotopoulos et al., 2009) and routinely maintained in undifferentiation medium, Euromed-N medium (EuroClone S.p.A., Pavia, Italy), supplemented with 1% N-2 supplement (Invitrogen Corp., Grand Island, NY), 20 ng/mL epidermal growth factor (EGF; PeproTech EC, London, UK), 20 ng/mL basic fibroblast growth factor (bFGF; PeproTech EC) and 1% penicillin-streptomycin (Invitrogen Corp.), in uncoated tissue culture plastic flasks at 37°C in a humidified atmosphere of 5% CO₂. Medium was changed every 3 days and cells collected with accutase (Sigma-Aldrich Co., St. Louis, MO) when confluent. Differentiation of NSCs was performed by first plating cells in undifferentiation medium onto uncoated tissue culture plastic dishes at 1 x 10⁶ cells/cm² for 24 h, and changing the culture medium to differentiation medium, Euromed-N medium supplemented with 10 ng/mL bFGF, 0.5% N-2 supplement, 1% B27 supplement and 1% penicillin-streptomycin. Cells were collected before medium change (time 0), or cultured for additional 6, 12, 24 or 48 h, and then fixed for immunocytochemistry analysis or collected for protein extraction.

3.3.3. siRNAs and plasmid transfections

The NSC cell line was transfected with Flag-JMJD3 or Flag-JMJD3 mutant overexpression plasmids to amplify JMJD3 expression. The expression plasmids were kindly provided by Dr. Kristen Jepsen (University of California, San Diego, USA). The Flag-JMJD3 construct was cloned by inserting full-length mouse JMJD3 cDNA in frame into p3xFLAG CMV-10 (Sigma-Aldrich Co.) vector within HindIII and BamHI sites. The Flag-JMJD3 mutant was generated by removing the carboxy-terminus 410 amino acids, which include the jumonji C domain. Briefly, NSCs were first cultured in uncoated dishes in undifferentiation medium without penicillin-streptomycin. Twenty-four hours after plating, cells were transfected using Lipofectamine 2000 (Invitrogen Corp.), according to the manufacturer's instructions, the medium was changed to differentiation medium, and cells were cultured for

additional 24 h. The cDNAs for TAp63 γ were ligated as BamHI/XhoI fragments into the pcDNA3.1/His C vector (Invitrogen Corp.). Mutant TAp63 γ carries a R304H exchange to yield a mutation in the DNA binding domain, as previously described (Dietz et al., 2002). Briefly, the mutant expression vector includes a His at the equivalent Arg position, which is transcriptionally impaired. As a control (mock), cells were incubated with the transfection agent at the same concentration and time, in the absence of any plasmid. Attached cells were either harvested for immunoblotting or fixed for immunocytochemistry and apoptosis assays using Hoechst staining. p63 manipulation was achieved by transfecting cells with the overexpression plasmids TAp63 γ and TAp63 γ mutant that lack p63 transactivation activity (kind gift from Dr. Kurt Engeland, University of Leipzig), or 100 nM of siRNA designed to knockdown mouse p63 expression (M-040654-01, Dharmacon, Waltham, MA, USA). As a control, cells were transfected with the corresponding empty vector plasmid (pcDNA3.1), or control siRNA containing a scrambled sequence that does not lead to specific degradation of any known cellular mRNA. Transfection efficiencies were assessed by immunoblotting analyses and found to be ~70% for JMJD3 and 80% for TAp63 γ overexpression plasmids. p63 protein levels, in turn, decreased by ~ 60% after transfection with siRNAs. In experiments using the protein synthesis inhibitor CHX, cells were previously transfected with TAp63 γ and either Flag-JMJD3 or Flag-JMJD3 mutant plasmids 24 h prior to addition of 50 μ g/mL CHX (Sigma-Aldrich Co.), and maintained for 4, 6 and 8 h.

3.3.4. Total, cytosolic and nuclear protein extraction

For total protein extracts, NSCs were lysed in ice-cold buffer (10 mM Tris-HCl, pH 7.6, 5 mM MgCl₂, 1.5 mM potassium acetate, 1% Nonidet P-40, 2 mM dithiothreitol) and protease inhibitor cocktail tablets Complete (Roche Applied Science, Mannheim, Germany) for 30 min, and then sonicated. The lysate was centrifuged at 3,200 g for 10 minutes at 4°C, and the supernatant recovered. For nuclear and cytosolic extracts, cells were lysed with hypotonic buffer (10 mM Tris-HCl, pH 7.6, 5 mM MgCl₂, 1.5 mM potassium acetate, 2 mM dithiothreitol) and protease inhibitors, homogenized with 40 strokes in a loose fitting Dounce, and centrifuged at 500 g for 10 min at 4°C. Cytosolic proteins were recovered in the supernatant, while the nuclear pellet was washed in buffer containing 10 mM Tris-HCl, pH 7.6, 5 mM MgCl₂, 0.25 M sucrose, 0.5% Triton X-100 and protease

inhibitors, then resuspended and sonicated in buffer containing 10 mM Tris-HCl, pH 7.6, 0.25 M sucrose with protease inhibitors. Finally, the suspension was centrifuged through 0.88 M sucrose at 2,000 g for 20 min at 4°C, and nuclear proteins were recovered in the supernatant.

3.3.5. Immunoblotting

Protein levels of p63, JMJD3, Flag, β -III tubulin, NeuN, MAP2 and H3K27me3 were determined by Western blot analysis in 8 or 12% sodium dodecyl sulphate polyacrylamide gel electrophoresis, using either primary mouse monoclonal antibodies reactive to p63 (4A4; Santa Cruz Biotechnology, Santa Cruz, CA), NeuN (MAB377; Chemicon International, Temecula, CA), Flag (M2; Sigma-Aldrich Co.), and β -III tubulin (Tuj1; Covance, Princeton, New Jersey), or primary polyclonal antibodies reactive to MAP2 (AB5622, Chemicon International) H3K27me3 (Abcam plc, Cambridge, UK) and JMJD3 (RB10082; Abgent Inc, San Diego, CA), as well as corresponding secondary antibodies conjugated with horseradish peroxidase (Bio-Rad Laboratories, Hercules, CA, USA). Membranes were processed for protein detection using Super SignalTM substrate (Pierce, Rockford, IL, USA). β -Actin (AC-15; Sigma-Aldrich Co.) was used as loading control. GAPDH (6C5; Santa Cruz Biotechnology) and total histone H3 (Millipore Corporation, Temecula, CA, USA) were used as markers for cytoplasmic and nuclear protein extraction, respectively. Protein concentrations were determined using the Bio-Rad protein assay kit (Bio-Rad Laboratories), according to the manufacturer's specification.

3.3.6. Immunocytochemistry

NSCs undergoing differentiation were fixed with 4% paraformaldehyde in phosphate-buffered saline (PBS) for 30 min. Cells were then blocked for 1 h at room temperature in PBS containing 0.1% Triton-X-100, 1% fetal bovine serum and 10% normal donkey serum (Jackson Immuno Research Laboratories, Inc., West Grove, PA). Subsequently, cells were incubated with either primary monoclonal antibody reactive to p63 (4A4; 1:50) or primary polyclonal antibody reactive to JMJD3 (KDM6B; 1:50) in blocking solution, overnight at 4°C. After three washes with PBS, cells were incubated with anti-rabbit Alexa Fluor 594- or anti-mouse Alexa Fluor 568-conjugated secondary antibodies (Invitrogen Corp.; 1:200) for 2 h at room

temperature. In control samples, the primary antibody was replaced by blocking buffer. Cells were incubated with Hoechst dye for nuclear staining. Images were acquired with an Axioskop fluorescence microscope (Carl Zeiss GmbH, Hamburg, Germany).

3.3.7. Immunoprecipitation assay

The physical association between p63 and JMJD3 was evaluated by immunoprecipitation analysis. In brief, whole-cell extracts were prepared by lysing cells by means of sonication in lysis buffer (50 mM Tris-HCl pH 7.4, 180 mM NaCl, 1 mM EDTA, 0,5% Triton X-100) and protease inhibitors (Roche Applied Science). Immunoprecipitation experiments were carried out using the monoclonal antibody reactive to p63 (4A4) and the Ezview Red Protein G Affinity Gel (Sigma-Aldrich Co.). Typically, 500 µg of lysate was incubated with 1 µg of p63-specific antibody overnight at 4°C. Immunoblots were then probed with the rabbit polyclonal antibody reactive to JMJD3 (KDM6B). p63 protein levels were determined in the same membrane after stripping off the immune complex for the detection of JMJD3. Immunoprecipitation assays using mouse monoclonal antibodies reactive to IgG showed neglectable binding with either JMJD3 or p63. Methylated levels of p63 were detected by immunoprecipitation analysis in denaturing conditions. In brief, whole-cell extracts were prepared by lysing cells by means of sonication in lysis buffer (50 mM Tris-HCl pH 7.4, 180 mM NaCl, 1 mM EDTA, 1% Triton X-100, 10 mM dithiothreitol) and protease inhibitors (Roche Applied Science). Immunoprecipitation experiments were carried out using the monoclonal antibody reactive to p63 and the Ezview Red Protein G Affinity Gel (Sigma-Aldrich Co.). Typically, 500 µg of lysate was incubated with 1 µg of p63-specific antibody overnight at 4°C. Immunoblots were then probed with the rabbit polyclonal methylated lysine (MeK) (Abcam plc) antibody. p63 expression was determined in the same membrane after stripping off the immune complex for the detection of MeK. Finally, the results of MeK after p63 immunoprecipitation were normalized with those obtained using mouse monoclonal antibodies reactive to IgG immunoprecipitation assays as well as with p63 total levels.

3.3.8. Evaluation of apoptosis

Hoechst labeling of NSCs were used to detect apoptotic nuclei. In brief, for morphologic evaluation of apoptosis, medium was gently removed to minimize detachment of cells. Attached cells were fixed with 4% paraformaldehyde in PBS, pH 7.4, for 10 minutes at room temperature, incubated with Hoechst dye 33258 (Sigma-Aldrich Co.) at 5 µg/ml in PBS for 5 minutes, washed with PBS and mounted using Fluoromount. Fluorescent nuclei were scored blindly and categorized according to the condensation and staining characteristics of chromatin. Normal nuclei showed noncondensed chromatin dispersed over the entire nucleus. Apoptotic nuclei were identified by condensed chromatin, contiguous to the nuclear membrane, as well as nuclear fragmentation of condensed chromatin.

3.3.9. Densitometry and statistical analysis

The relative intensities of protein bands were analyzed using the QuantityOne Version 4.6 densitometric analysis program (Bio-Rad Laboratories) and normalized to the respective loading controls. Statistical analysis was performed using GraphPad InStat version 3.00 (Graph-Pad Software, San Diego, CA, USA) for the analysis of variance and Bonferroni's multiple comparison tests. Values of $p < 0.05$ were considered significant.

3.4. Results

3.4.1. TAp63 γ and JMJD3 levels increase throughout mouse NSC differentiation

Several lines of evidence point toward the involvement of classical apoptotic molecules in neural differentiation, including p53, caspases and Bcl-2 family members. To investigate p63 involvement in neurogenesis, we first evaluated endogenous p63 levels throughout neural differentiation of NSCs. Comparing with the exogenous overexpression of several p63 isoforms (Fonseca et al., 2012), TAp63 γ (57 kDa) was the only endogenous isoform detected by Western blot analysis in NSCs. Importantly, TAp63 γ levels increased by 7-fold at 24 h of NSC differentiation (Fig. 3.1A). JMJD3 upregulation was observed as early as at 6 h of differentiation, peaking at 24 h (Fig. 3.1A), in agreement with previous studies (Fernando et al., 2005). Accordingly, JMJD3 activity was also increased during differentiation, as

demonstrated by the reduced levels of H3K27 trimethylation throughout time (Fig. 3.1A). The neuronal marker β -III tubulin increased throughout differentiation, peaking at 24 h (Fig. 3.1A), as previously described (Santos et al., 2012b).

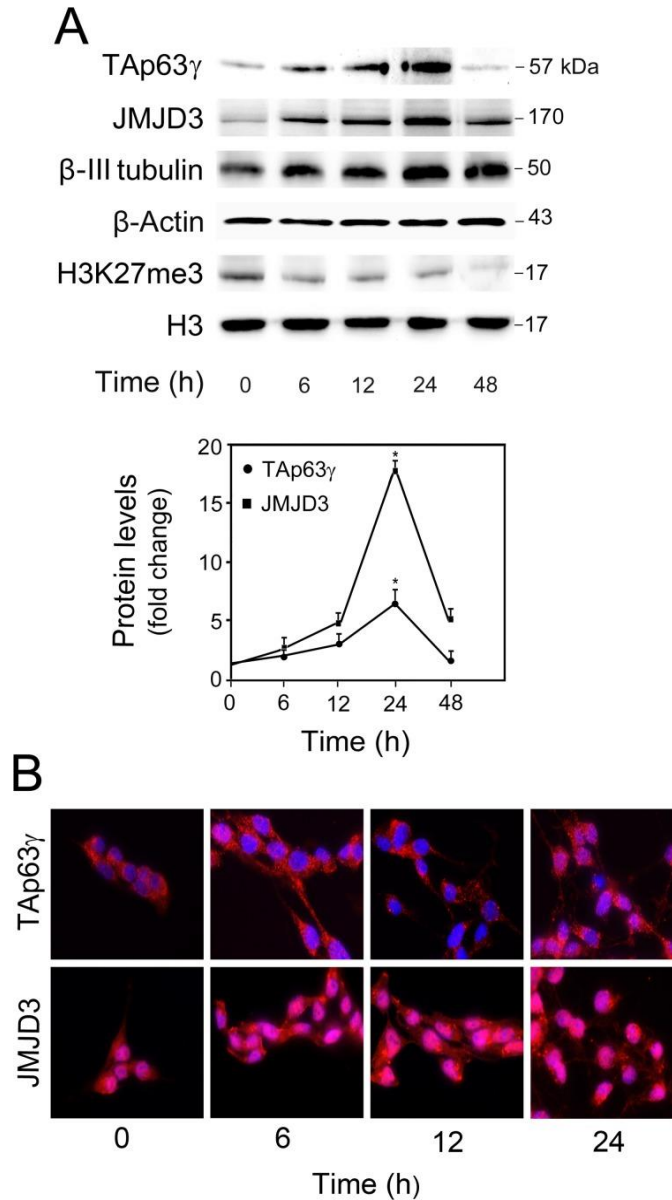


Figure 3.1. Endogenous TAp63 γ protein levels increase at early stages of neural differentiation. Undifferentiated (0 h) and differentiated mouse NSCs were collected for Western blot analysis or fixed for immunostaining at indicated time-points, as described in Materials and Methods. (A) Protein levels of TAp63 γ , JMJD3, β -III tubulin, and H3K27me3 throughout NSC differentiation. Representative immunoblots (top), and TAp63 γ and JMJD3 protein levels (bottom). β -Actin and H3 were used as loading controls. Immunoblots are representative of at least three different experiments. TAp63 γ and JMJD3 protein levels were normalized to endogenous β -Actin protein levels and expressed as mean \pm SEM for at least three different experiments. * $p < 0.01$ from control, undifferentiated. (B) Fluorescence staining of TAp63 γ and JMJD3 throughout NSC differentiation. Hoechst dye was used for

nuclear staining. Images are representative of at least 3 different experiments. Scale bar = 10 μ m

Other markers, including mouse achaete scute homolog-1 (Mash1) and neuronal differentiation 1 (NeuroD1) were also markedly increased (data not shown). Immunocytochemistry analysis corroborated Western blot data by showing upregulation and nuclear distribution of TAp63 γ and JMJD3 at 24 h of differentiation (Fig. 3.1B). These results suggest that JMJD3 and TAp63 γ are coordinately regulated to influence neural-specific gene expression programs.

3.4.2. JMJD3 regulates TAp63 γ protein in a demethylase activity-dependent manner

To clarify whether JMJD3 regulates TAp63 γ during neurogenesis, we overexpressed JMJD3 by transfecting NSCs with a Flag-JMJD3 plasmid and evaluated TAp63 γ protein levels 24 h after transfection. In control experiments, cells were transfected with either a Flag-JMJD3 mutant plasmid that does not contain the C-terminal region associated with JMJD3 demethylase activity, or no plasmid (mock). Overexpression of JMJD3 markedly increased TAp63 γ protein levels when compared with control (mock) cells ($p < 0.01$) (Fig. 3.2).

To better distinguish endogenous JMJD3 protein from the transfected versions, we have also detected Flag using a Flag antibody. Of note, overexpressing the mutant form of JMJD3 had no effect on TAp63 γ protein levels, indicating that JMJD3-induced increase of TAp63 γ is dependent on its demethylase activity. Consistent with a role for JMJD3 as H3K27 demethylase, JMJD3 overexpression resulted in ~ 50% decreased levels of trimethylated H3K27 when compared with mock or cells transfected with JMJD3 mutant plasmid ($p < 0.05$) (Fig. 3.2). As expected, JMJD3 overexpression significantly enhanced the neuronal marker β -III tubulin by ~2-fold when compared with mock- and JMJD3 mutant plasmid-transfected cells ($p < 0.05$) (Fig. 3.2). These results are consistent with a role for JMJD3-dependent demethylation in neurogenesis progression. Moreover, the data here presented suggest that JMJD3-demethylase activity modulates TAp63 γ protein levels and this may account, at least in part, for the neuronal commitment of NSCs.

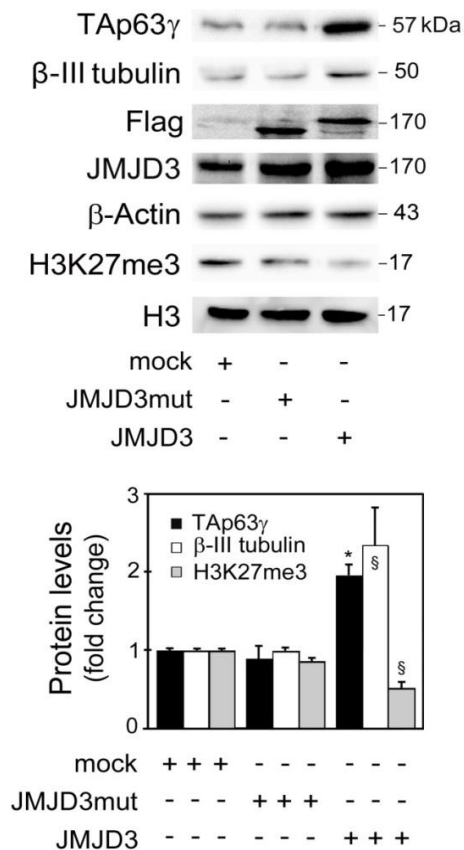


Figure 3.2. JMJD3 modulates TAp63γ levels during neural differentiation. Mouse NSCs undergoing differentiation were transfected with JMJD3 or JMJD3 mutant (JMJD3mut), overexpression plasmids or no plasmid (mock), and collected for Western blot analysis as described in Material and Methods. Representative immunoblots of TAp63γ, β-III tubulin, Flag, JMJD3 and H3K27me3, in control (mock), JMJD3mut- and JMJD3-overexpressing cells (top) and respective protein levels (bottom). β-Actin and H3 were used as loading controls. Immunoblots are representative of at least three different experiments. TAp63γ and β-III tubulin protein levels were normalized to endogenous β-Actin whereas H3K27me3 protein levels were normalized to endogenous total H3, when compared with mock cells. Results were expressed as mean ± SEM for at least three different experiments. \$p < 0.05 and *p < 0.01 from control.

3.4.3. TAp63γ manipulation influences neuronal differentiation

To substantiate a role for TAp63γ in non-embryonic neuronal differentiation, we tested the functional relevance of TAp63γ in regulating β-III tubulin abundance in NSCs undergoing differentiation by short-interference RNA (siRNA)-mediated gene knockdown of p63. Immunoblot analysis revealed that knockdown of TAp63γ by specific p63 siRNA resulted in a ~ 50% reduction in β-III tubulin levels when compared with control siRNA-transfected cells (Fig. 3.3A and B). Other neural

markers, including the neuronal nuclei (NeuN) and microtubule-associated protein 2 (MAP2) were also markedly reduced (Fig. 3.3A).

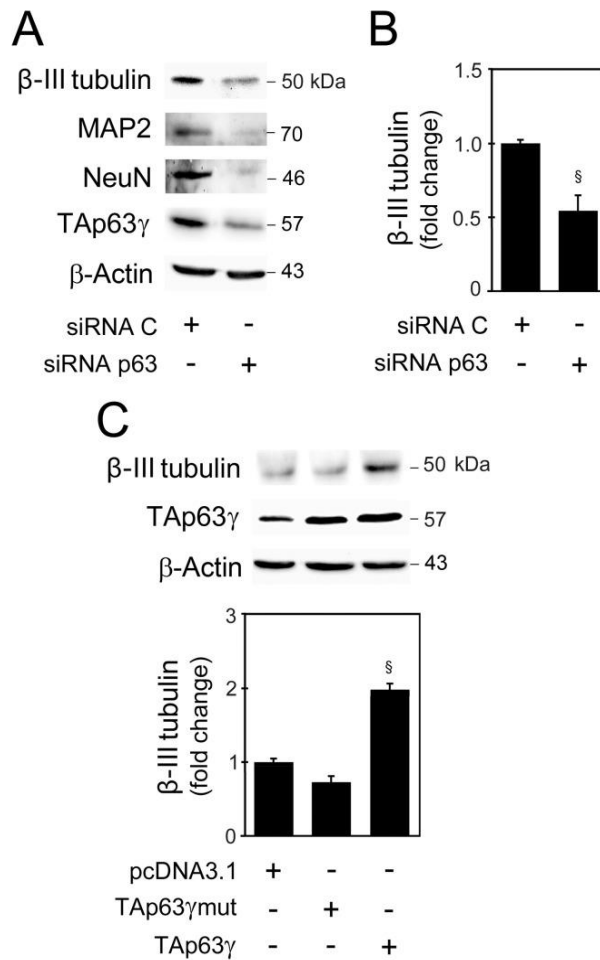


Figure 3.3. Modulation of TAp63γ levels in mouse NSCs affects neuronal differentiation. Mouse NSCs undergoing differentiation were transfected with p63 siRNA or TAp63γ overexpression plasmids and collected for Western blot analysis as described in Material and Methods. (A) Representative immunoblot of β-III tubulin, NeuN, MAP2 and TAp63γ in cells transfected with 100 nM of either p63 siRNA or control siRNA (siRNA C) for 24 h. (B) Respective β-III tubulin protein levels. (C) Protein levels of β-III tubulin and TAp63γ in cells transfected with overexpression plasmids TAp63γ, TAp63γ mutant (TAp63γmut) or its corresponding empty vector (pcDNA3.1). Representative immunoblot of β-III tubulin and TAp63γ (top) and respective β-III tubulin protein levels (bottom). Results were normalized to endogenous β-Actin protein levels and expressed as mean ± SEM for at least three different experiments. §p < 0.05 from control.

These results were corroborated by immunofluorescence analysis (data not shown) and indicate that the increase in TAp63γ throughout NSC differentiation is important for neuronal fate specification. In addition, overexpression of TAp63γ significantly increased β-III tubulin protein levels by ~2-fold when compared with

cells transfected with the corresponding empty vector ($p < 0.01$) (Fig. 3.3C). Importantly, overexpression with the mutant form of TAp63 γ that lacks p63 transactivation activity had no effect on β -III tubulin protein levels (Fig. 3.3C), indicating that TAp63 γ -mediated increase of β -III tubulin is dependent on its transactivation activity.

3.4.4. TAp63 γ is directly demethylated by JMJD3 during neural differentiation

Since JMJD3 also demethylates non-histone proteins, including p53 (Solá et al., 2011b), we hypothesized that JMJD3 may possibly demethylate TAp63 γ during neurogenesis. Thus, the interaction between JMJD3 and TAp63 γ , as well as JMJD3-mediated TAp63 γ demethylation were investigated by immunoprecipitation assays. Specifically, to evaluate TAp63 γ and JMJD3 endogenous association during differentiation of NSCs, we immunoprecipitated TAp63 γ from total protein extracts with p63 antibody, and immunoblots were probed with JMJD3 antibody. As depicted in Fig. 3.4A, JMJD3 directly binds to TAp63 γ during NSC differentiation ($p < 0.01$).

To investigate whether TAp63 γ /JMJD3 association is dependent on JMJD3-demethylase activity, TAp63 γ immunoprecipitation was performed in NSCs overexpressing either JMJD3 wild-type or JMJD3 mutant plasmids. Western blot analysis revealed a significant increase in TAp63 γ /JMJD3 association in cells overexpressing JMJD3 wild-type when compared with mock ($p < 0.05$) (Fig. 3.4B). Importantly, the association between TAp63 γ and JMJD3 was not increased in cells transfected with mutant JMJD3, suggesting that the interaction between TAp63 γ and JMJD3 is dependent on the catalytic JmjC domain of JMJD3. To investigate whether TAp63 γ /JMJD3 association results in modification of TAp63 γ methylation status, TAp63 γ immunoprecipitation under denaturing conditions was performed in NSCs transfected with JMJD3 wild-type or JMJD3 mutant overexpression plasmids. Subsequent detection of methylated TAp63 γ was performed by probing immunoblots with a pan-methylated lysine antibody. Notably, TAp63 γ was significantly less methylated in cells overexpressing JMJD3 wild-type, as compared to cells transfected with the C-terminal mutant form of JMJD3 or control (mock) cells ($p < 0.01$) (Fig. 3.4C). These results suggest that the proneuronal effects of TAp63 γ during differentiation of NSCs might involve direct JMJD3-dependent demethylation.

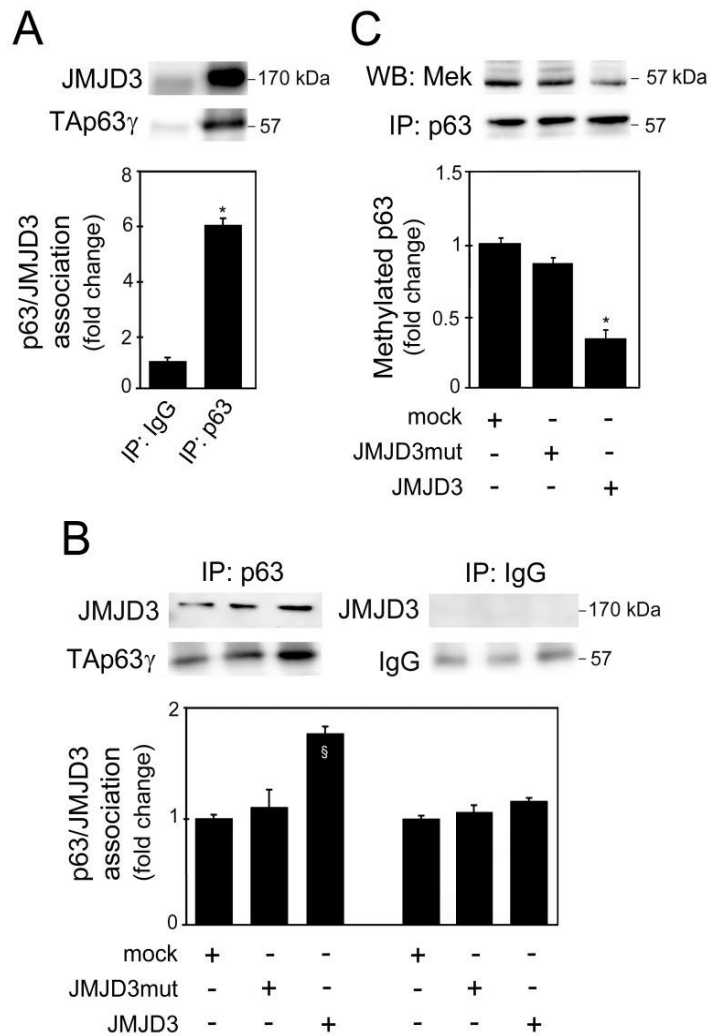


Figure 3.4. TAp63 γ and JMJD3 directly associate during neural differentiation. Mouse NSCs undergoing differentiation were collected and processed for immunoprecipitation assays with either p63 antibody or mouse IgG as control, as described in Material and Methods. (A) Representative immunoblot of JMJD3 and TAp63 γ (top) and histogram of TAp63 γ /JMJD3 endogenous association (bottom). (B) Representative immunoblot of JMJD3 and TAp63 γ (top) and histogram of TAp63 γ /JMJD3 association (bottom) in cells transfected with JMJD3 or JMJD3 mutant (JMJD3mut) overexpression plasmids, or no plasmid (mock). (C) Representative immunoblot of methylated lysine (MeK) and TAp63 γ (top), and histogram of TAp63 γ methylated levels (bottom). All densitometry values for JMJD3 and methylated lysines were normalized to the respective p63 expression, and the results expressed as mean \pm SEM for at least three different experiments. $\S p < 0.05$ and $*p < 0.01$ from controls. IP, Immunoprecipitation; WB, Western blot; MeK, Methyl K pan.

3.4.5. TAp63 γ is stabilized by JMJD3-demethylase activity and accumulates in the nucleus

p63 activity is controlled by an intricate network of PTM that targets and modulates its transcriptional activity, stability or subcellular trafficking (Stehmeier

and Muller, 2009). These PTM are catalyzed by a large number of enzymes that contribute to the activation of p63 through a variety of mechanisms. To investigate the effect of JMJD3-mediated TAp63 γ demethylation on TAp63 γ protein stability, we evaluated TAp63 γ half-life in the presence and absence of JMJD3-demethylase activity. For this purpose, NSCs co-transfected with TAp63 γ and either Flag-JMJD3, Flag-JMJD3 mutant or no plasmid (mock) were treated with the protein synthesis inhibitor CHX (Fig. 3.5).

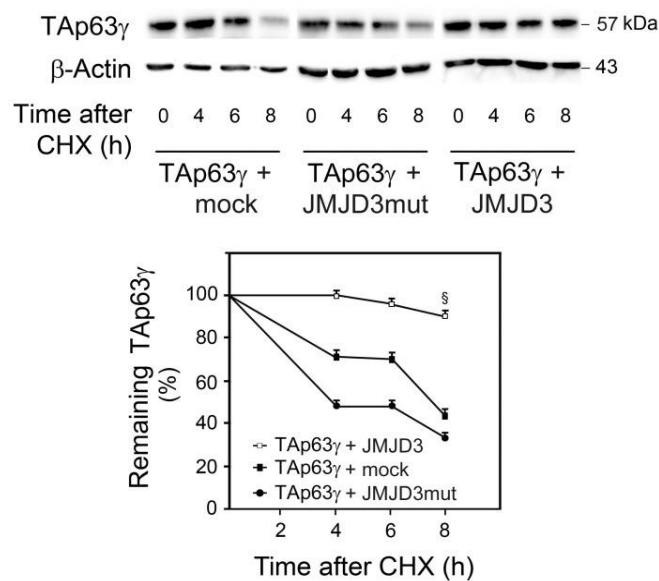


Figure 3.5. TAp63 γ is stabilized by JMJD3 during mouse NSC differentiation. Cells co-transfected with TAp63 γ and with the overexpression plasmids JMJD3 (TAp63 + JMJD3), JMJD3 mutant (TAp63 + JMJD3mut), or no plasmid (TAp63 + mock) were untreated (0 h) or treated with 50 μ g/mL CHX for 2, 4, 6, and 8 h. At the indicated time-points, total proteins were extracted for immunoblot analysis as described in Materials and Methods. Representative immunoblots of TAp63 γ after CHX treatment (top) and percentage of remaining TAp63 γ after CHX treatment (bottom). Results were normalized to endogenous β -Actin protein levels and expressed as mean \pm SEM for at least three different experiments. $\$p < 0.05$ from control.

Our results demonstrate that TAp63 γ half-life was reduced to less than 8 and 4 h, respectively in control (mock)- and mutant JMJD3-transfected cells ($p < 0.05$). In contrast, TAp63 γ protein levels only slightly decreased in the presence of JMJD3 wild-type, showing that JMJD3-demethylase activity indeed regulates the stability of TAp63 γ .

We next investigated the effect of JMJD3-mediated TAp63 γ demethylation on TAp63 γ subcellular distribution (Fig. 3.6).

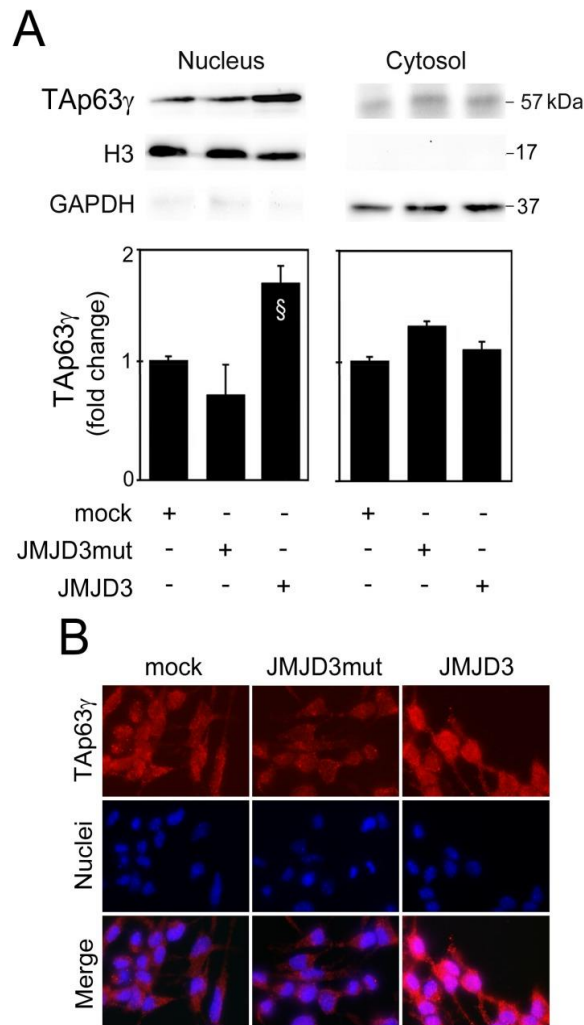


Figure 3.6. TAp63 γ is translocated to the nucleus in a demethylase activity-dependent manner. Mouse NSCs undergoing differentiation were transfected with JMJD3 or JMJD3 mutant (JMJD3mut) overexpression plasmids, or no plasmid (mock), and collected for Western blot analysis, immunocytochemistry and apoptosis assays as described in Material and Methods. (A) Representative immunoblots of nuclear and cytosolic TAp63 γ (top) and respective protein levels (bottom). GAPDH and H3 were used as loading controls for cytosolic and nuclear fractions, respectively. Results were normalized to the respective endogenous controls and expressed as mean \pm SEM for at least three different experiments. $\S p < 0.05$ from control. (B) Subcellular localization of TAp63 γ in transfected mouse NSCs. Hoechst dye was used for nuclear staining and morphologic evaluation of apoptosis. Images are representative of at least 3 different experiments. Scale bar = 10 μ m.

Increased nuclear localization of TAp63 γ was observed in NSCs overexpressing wild-type JMJD3 compared with control (mock)- and mutant JMJD3-transfected cells ($p < 0.05$) (Fig. 3.6A). Immunocytochemistry analysis confirmed Western blot data by showing TAp63 γ accumulation in the nucleus of JMJD3-

transfected cells compared to cells overexpressing either the mutant form of JMJD3 or control (mock) cells (Fig. 3.6B).

Together, these results suggest that TAp63 γ demethylation by JMJD3 is crucial for its stabilization and accumulation in the nucleus. Moreover, these data support the hypothesis that JMJD3-induced TAp63 γ nuclear translocation might direct NSCs to a neuronal fate specification, through the transcriptional activation of proneuronal genes. Importantly, TAp63 γ nuclear accumulation was not associated with an increase in apoptotic cell death, as confirmed by Hoechst staining (Fig. 3.6B).

3.5. Discussion

This study demonstrates for the first time a role for p63 in adult neural progenitors, directing NSCs to a neuronal phenotype. Our findings are in accordance with postnatal p63 expression in the subventricular zone of the lateral ventricle (Hernández-Acosta et al., 2011), a region for continued adult neurogenesis. In contrast with the lack of p63 effect on central nervous system development (Hernández-Acosta et al., 2011; Holembowski et al., 2011), our results point toward an age-dependent p63 involvement in the regulation of neural differentiation. Furthermore, we demonstrate that, during neural differentiation, p63 interacts with JMJD3, a key regulator of neurogenesis (Burgold et al., 2008), which results in the modulation of p63 methylation status. Finally, our results demonstrate that JMJD3-demethylase activity regulates p63 half-life and nuclear accumulation during mouse NSC differentiation.

Much attention has been centered on p63 regulatory pathways in epidermal differentiation, due to the severe epithelial phenotype of p63 null mice (Yang et al., 1999). Recently, a role for p63 on cardiac differentiation of embryonic stem cells has also been reported (Paris et al., 2012). However, the precise function for p63 during neural differentiation remains largely unknown, when compared with other members of the p53 family. In fact, p53 and p73 are well-established key regulators of both embryonic and adult neurogenesis. Mice lacking p53 display elevated proliferation rate in the neurogenic niche of the adult lateral ventricle wall, as well as increased self-renewal of *in vitro* propagated p53^{-/-} NSCs (Meletis et al., 2006). Moreover, a relevant role for p53 in the biology of NSCs derived from the embryo olfactory bulb has been identified, where lack of p53 increases neurosphere-forming potential of precursor cells by favoring self-renewal capacity (Armesilla-Diaz et al., 2009).

TAp73, in turn, is an essential regulator of stemness in NSCs, which maintains an adequate neurogenic pool by promoting self-renewal and proliferation and inhibiting premature senescence of NSC and early progenitor cells, in both embryonic and adult neurogenesis (Talos et al., 2010). In addition, the width of neurogenic areas appears to be significantly reduced in brains of embryonic and adult p73 knockout mice (Agostini et al., 2010). Curiously, TAp73 acts via the basic helix-loop-helix Hey2 to promote long-term maintenance of neural precursors (Fujitani et al., 2010). p73 deficiency results in impaired self-renewal and premature neuronal differentiation of mouse neural progenitors independently of p53 (Gonzalez-Cano et al., 2010).

In contrast with p53 and p73, there is still a breach in the literature regarding p63 potential involvement in adult neurogenesis by cell death-independent mechanisms. Further, emerging knowledge suggests that a number of apoptosis-associated factors, including p53, regulate neural differentiation (Paris et al., 2012; Yang et al., 1999). This led us to explore p63 involvement in adult mouse NSC differentiation, which are capable of tripotential differentiation in neurons, glial cells and oligodendrocytes (Glaser et al., 2007), resembling adult neurogenesis. Several studies have claimed that p63 is dispensable for embryonic neurogenesis. However, since p63 knockout mice do not survive into postnatal life, a role for p63 in the adult brain cannot be excluded.

In this study, a detailed characterization of p63 isoform expression (Fonseca et al., 2012) revealed that only one isoform with ~57 kDa was detected and subsequently confirmed as TAp63 γ by comparison with exogenous p63 isoform overexpression (Jacobs et al., 2005). Time-course analysis of TAp63 γ protein levels throughout NSC differentiation demonstrated an increase of TAp63 γ at early stages of neural differentiation, when JMJD3 protein levels and activity were already significantly increased. Accordingly, we have previously demonstrated that JMJD3 expression and activity at the Hoxc8 promoter increased early in mouse NSC differentiation (Solá et al., 2011b). Importantly, overexpression of JMJD3 in NSCs undergoing differentiation resulted in increased levels of TAp63 γ protein, accompanied by increased neuronal marker β -III tubulin. We have previously reported a similar effect of JMJD3 on the neural precursor Pax6 in JMJD3-transfected mouse NSCs (Solá et al., 2011b). All together, these results suggest that JMJD3 modulates TAp63 γ levels during neural differentiation, which might contribute to the neuronal fate specification of NSCs. In accordance with this hypothesis, overexpression of TAp63 γ during early

differentiation of NSCs resulted in increased β -III tubulin levels, whereas downregulation of TAp63 γ expression by specific p63 siRNA abrogated the increase in β -III tubulin.

Interestingly, in NSCs undergoing differentiation, both TAp63 γ and β -III tubulin were modulated by JMJD3 in a demethylase activity-dependent manner. While not excluding an effect of H3K27 demethylation on NSC neuronal differentiation, our results also suggest that TAp63 γ -mediated neuronal differentiation essentially relies on TAp63 γ direct demethylation by JMJD3. In this respect, JMJD3 was reported to bind non-histone proteins, including p53 (Solá et al., 2011b), much like other demethylases (Tsai et al., 2008). Our results demonstrate a direct interaction between TAp63 γ and JMJD3, dependent of the C-terminal region of JMJD3, and modulation of TAp63 γ methylation levels by JMJD3. Importantly, JMJD3-demethylase activity appears to be relevant in regulating TAp63 γ protein half-life. Cycloheximide experiments demonstrated that modulation of TAp63 γ levels by JMJD3 during differentiation of NSCs occurs through protein stabilization and not by transcriptional regulatory mechanisms. Supporting this idea, it has recently been shown that among several genes involved in neurogenesis and neuronal differentiation that are up-regulated by H3K27 demethylation, p63 is not included (Pereira et al.). This suggests that JMJD3-mediated regulation of TAp63 γ in NSCs does not occur at the transcriptional level. In addition to TAp63 γ stabilization, we here show that JMJD3-demethylase activity increases TAp63 γ nuclear accumulation during NSC differentiation. These results are in agreement with those previously obtained for JMJD3 and p53 in mouse NSCs (Solá et al., 2011b), reinforcing the similarities in structural and function properties of p53 family members. Noteworthy, TAp63 γ cellular distribution concurs with a role for this protein as a transcriptional activator of pro-neuronal gene expression. Accordingly, NSCs cells transfected with the mutant form of TAp63 γ that lacks p63 transactivation activity failed to differentiate in β -III tubulin-positive cells, indicating that TAp63 γ -mediated neuronal differentiation might be dependent on its transactivation activity. This study constitutes the first to show that TAp63 γ demethylation affects its stability and subcellular localization. Similar effects were already described for p63 phosphorylation and acetylation, the best characterized p63 PTM (Collavin et al., 2010) resulting in different cellular outcomes. A deeper knowledge of these regulatory modifications of p63 protein will improve our understanding of p63

function during adult neural differentiation. In this respect, future studies are warranted to determine the specific residues demethylated by JMJD3 and to address the importance of TAp63 γ demethylation in neurogenesis by modification of the identified residues. Since most mutated p63 proteins found in patients suffering from ectodermal dysplasia syndromes (Ying et al., 2005) are more stable than wild-type peptides, it would be interesting to clarify whether the mutated residues are sites of methylation. We also anticipate TAp63 γ protein demethylation to be highlighted as a PTM crucial for the neurogenic process.

In conclusion, our results clearly demonstrate that TAp63 γ and JMJD3 directly interact during NSC differentiation, in a JMJD3 C-terminal region-dependent manner. In addition, both TAp63 γ protein stability and nuclear accumulation appear to be modulated by JMJD3-demethylase activity during neural differentiation. These findings suggest that JMJD3 is a regulator of TAp63 γ during NSC differentiation, and JMJD3-mediated TAp63 γ demethylation plays a role in proneural gene expression.

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Amyloid β Peptides Promote Autophagy-dependent Differentiation of Mouse Neural Stem Cells

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4.1. Abstract

Although regarded as neurotoxic, amyloid β ($A\beta$) peptides may also mediate a wide range of non-pathogenic processes. Autophagy has been implicated in $A\beta$ -mediated effects, although its precise function in neural differentiation remains unknown. Here, we addressed the role of different $A\beta$ fragments in neural stem cell (NSC) proliferation and differentiation, and investigated whether autophagy is involved in $A\beta$ -induced alterations of neural fate. Our results demonstrate that neuronal and glial-specific protein markers are significantly induced by both $A\beta_{1-40}$ and $A\beta_{1-42}$. However, $A\beta_{1-40}$ preferentially enhances neurogenesis of NSCs, as determined by β III-tubulin, NeuN and MAP2 neuronal marker immunoreactivity, while $A\beta_{1-42}$ appears to favor gliogenesis. In contrast, $A\beta_{25-35}$ does not influence NSC fate. The effect of $A\beta_{1-40}$ on neurogenesis is partially dependent on its role in NSC self-renewal as both S-phase of the cell cycle and BrdU labeling were markedly increased. Nevertheless, $A\beta_{1-40}$ resulted also in increased Tuj1 promoter activity. Autophagy, assessed by conversion of endogenous LC3-I/-II, fluorescence of pGFP-LC3 transfected cells, and Atg9 protein levels was evident in both $A\beta_{1-40}$ - and $A\beta_{1-42}$ -treated NSCs, independently of reactive oxygen species production and apoptosis. Finally, inhibition of autophagy by pharmacologic means abrogated $A\beta$ -induced lineage-specific protein markers. These results support distinct roles for different $A\beta$ peptides in NSC fate decision and underline the importance of autophagy control of this process.

Keywords: Alzheimer's disease; Gliogenesis; Neural stem cell fate; Neurogenesis; Proliferation

4.2. Introduction

Over the past years, neural differentiation in mammals has significantly impacted on our understanding of brain physiology, holding great promise for neuro-replacement therapies (Alvarez-Buylla and Garcia-Verdugo, 2002; Bernal and Peterson, 2004; Gage, 2000; Kempermann and Gage, 2000). Neural stem cells (NSCs) are self-renewing, multipotent cells that have the ability to differentiate into the three major cell types of the central nervous system (CNS) including, neurons, astrocytes and oligodendrocytes (Reynolds and Weiss, 1996). The dimension of the NSC pool and its ability to restore damaged neural tissue in the brain results from tightly regulated cellular processes, including self-renewal, differentiation and cell death. Thus, a better understanding of the molecular mechanisms responsible for neural differentiation, as an alternative to cell death will surely advance neuronal repair strategies.

Amyloid- β ($A\beta$) peptide is the main component of deposits found in the brains of patients with Alzheimer's disease (AD) (Selkoe, 2001b). It is processed from the amyloid precursor protein (APP), through β - and γ -secretases, originating $A\beta_{1-40}$, the major species under physiological conditions, and a number of minor and more toxic species, such as $A\beta_{1-42}$ (Steiner and Haass, 2000). While best known as components responsible for neuronal death in AD, evidence has suggested that $A\beta$ species are highly multifunctional peptides with significant non-pathological activities. In fact, under deprived conditions, $A\beta$ exhibits neurotrophic and neuroprotective properties at physiological concentrations in neonatal cells (Kontush et al., 2001; Whitson et al., 1989; Yankner et al., 1990). $A\beta_{1-40}$ might have a beneficial role in reducing the amyloid burden, while $A\beta_{1-42}$ is the major component of amyloid deposits, responsible for many neurodegenerative phenotypes and learning deficits (McGowan et al., 2005). Indeed, studies in human brain, cerebrospinal fluid and plasma, as well as in transgenic animals and cellular systems modeling familial AD mutations have demonstrated that the $A\beta_{42}/A\beta_{40}$ ratio is consistently elevated (Bentahir et al., 2006; Kumar-Singh et al., 2006). Recently, it has been demonstrated that $A\beta_{1-40}$ may also have neurogenic properties (Chen and Dong, 2009). However, the precise molecular pathways underlying the regulation of NSC proliferation and differentiation by different $A\beta$ peptides species are still not fully defined, and may implicate survival among other processes.

Autophagy as a dynamic process of protein degradation fulfills multiple functions in mammalian cells, and is essential for cellular survival and differentiation,

development and homeostasis (Asanuma et al., 2003; Levine and Klionsky, 2004; Pua et al., 2007; Zeng and Zhou, 2008; Zhao et al., 2010; Zhuang et al., 2011). It is regulated by a complex signal transduction machinery involving autophagy-related (Atg) gene products and other proteins that sense the intracellular energy status. As most neurons survive for the lifetime of the organism, maintenance of organelle function and clearance of aberrant or damaged proteins are critical processes regulated by autophagy. In fact, a growing number of studies support the idea that autophagy is highly active during differentiation and development (Asanuma et al., 2003; Vessoni et al., 2012), including neural differentiation (Zhao et al., 2010). In addition, autophagy has recently been reported as a mechanism of neuronal protection from A β -induced cytotoxicity (Cheung et al., 2011; Hung et al., 2009; Moreira et al., 2010; Wang et al., 2010). Although A β -induced cell death via an autophagic degradation pathway has also been reported, the correlation between pro-neurogenic effects of A β peptides and autophagic activity has not been explored before.

Reactive oxygen species (ROS) may be generated by A β species. Further, ROS are important signaling molecules for autophagy (He et al., 2011), during periods of nutrient deprivation, hypoxia, ischemia, reperfusion injury, and general cell stress (Chen et al., 2009; Gurusamy and Das, 2009), and have been implicated in differentiation in certain developmental programs such as neurogenesis (Essick and Sam, 2010). In fact, the correct balance of ROS production and utilization is critical to the regulation of self-renewal and differentiation in pluripotent cells (Ray et al., 2012; Santos et al., 2012a).

In the present study, we elucidated the role of different A β peptides during NSC fate decision. Our results demonstrate that, in contrast with their conventional effects in cell death, lower levels of A β ₁₋₄₀ and A β ₁₋₄₂ mediate neural differentiation. A β ₁₋₄₀ strongly promotes NSC proliferation and neurogenesis, while A β ₁₋₄₂ facilitates glial fate decision. Moreover, A β active fragments increase neural-lineage markers possibly by enhancing the autophagy survival response in differentiating NSC, independently of ROS production and apoptosis.

4.3. Material and methods

4.3.1. Cell culture

A mouse NSC line was derived from day 14.5 post-coitum mouse fetal forebrain. This cell line was established using a method that produces pure cultures of adherent NSCs, which continuously expand by symmetrical division and are capable of

tripotential differentiation (Ezashi et al., 2005; Smith et al., 2000). NSCs were grown in monolayer as previously described (Conti et al., 2005; Glaser et al., 2007; Pollard et al., 2006), and routinely maintained in undifferentiation medium, Euromed-N medium (EuroClone S.p.A., Pavia, Italy), supplemented with 1% N-2 supplement (Invitrogen Corp., Grand Island, NY, USA), 20 ng/mL epidermal growth factor (EGF; PeproTech EC, London, UK), 20 ng/mL basic fibroblast growth factor (bFGF; PeproTech EC) and 1% penicillin-streptomycin (Invitrogen Corp.), in uncoated tissue culture plastic flasks at 37°C, in a humidified atmosphere of 5% CO₂. Medium was changed every 3 days and cells collected with accutase (Sigma-Aldrich Co., St. Louis, MO) when confluent. Differentiation of NSCs was performed by first plating cells in undifferentiation medium onto uncoated tissue culture plastic dishes at 1x10⁶ cells/cm² for 24 h, and changing the culture medium to differentiation medium, Euromed-N medium supplemented with 10 ng/mL bFGF, 0.5% N-2 supplement, 1% B27 supplement and 1% penicillin-streptomycin.

4.3.2. Cell treatments

Twenty-four hours after induction of differentiation, 1.5 µM of peptide active fragments Aβ₂₅₋₃₅, Aβ₁₋₄₀, or Aβ₁₋₄₂ (American Peptide Company, Sunnyvale, CA, USA) were added to the culture medium for 48 h. In selected experiments, undifferentiated cells were also incubated with Aβ peptide fragments for different time periods, up to 24 h. Aβ-treated cells were then collected for luciferase and lactate dehydrogenase (LDH) assays, immunoblotting, flow cytometry, and immunocytochemistry analysis. To inhibit autophagy, 10 mM of 3-methyladenine (3-MA) (Sigma-Aldrich Co.) was added to the culture medium for 48 h.

4.3.3. Plasmid transfections

For the luciferase reporter assay, cells were transfected 24 h after plating into 35 mm dishes with the murine Tuj1-promoter plasmid (1 µg per dish) and the *Renilla luciferase* reporter as internal control for transfection efficiency (1 ng per dish) (CMV-PRL; Promega, Fitchburg, WI, USA) using lipofectamine 2000 (Invitrogen Corp.). The Tuj1-promoter, kindly provided by Fred Gage, was cloned by PCR from genomic DNA and inserted into pNeoLuci (Spiliotopoulos et al., 2009). To analyze the intracellular localization and processing of the microtubule-associated protein 1 light chain 3 (LC3), a reliable autophagy marker, cells were transfected with a pGFP-LC3 plasmid for 24 h.

The pGFP-LC3 construct was kindly provided by Dr. Tamotsu Yoshimori and generated by inserting LC3 cDNA into the *Bgl*III and *Eco*RI sites of pEGFP-C1, a GFP fusion protein expression vector (Clontech Laboratories Inc., Mountain View, CA, USA) (Kuwabara et al., 2004). GFP intensity was evaluated by immunocytochemistry.

4.3.4. Dual luciferase assay

Twenty-four hours after transfection with the murine Tuj1-promoter plasmid, cells were treated with A β peptides in fresh culture medium for 48 h before harvest. Firefly and *Renilla luciferase* activities were measured using the Dual-Luciferase® Reporter Assay System (Promega) according to the manufacturer's recommendation. The luminescence signal of the specific luciferase reporter plasmid was normalized to the internal control *Renilla luciferase* reporter intensity.

4.3.5. Immunoblotting

Steady-state levels of β III-tubulin, GFAP, NeuN, MAP2, Atg9 and LC3 in NSCs were determined by Western blot analysis. Cells were collected and lysed for isolation of total protein extracts using ice-cold lysis buffer (10 mM Tris-HCl, pH 7.6, 5 mM MgCl₂, 1.5 mM potassium acetate, 1% Nonidet P-40, 2 mM dithiothreitol) and protease inhibitor cocktail tablets Complete (Roche Applied Science, Mannheim, Germany) for 30 min. Samples were then sonicated and centrifuged at 3,200g at 4°C for 10 min. Protein content was measured by the Bio-Rad protein assay kit (Bio-Rad Laboratories, Hercules, CA, USA) according to the manufacturer's specifications. One hundred μ g of protein extracts were separated on 8 and 12% sodium dodecyl sulphate polyacrylamide electrophoresis gels. After electrophoretic transfer onto nitrocellulose membranes, and blocking with a 5% milk solution, membranes were incubated overnight at 4°C with either primary mouse monoclonal antibodies reactive to β III-tubulin (Tuj1 clone; Covance, Princeton, New Jersey), GFAP and NeuN (MAB360 and MAB377, respectively; Chemicon International, Temecula, CA, USA), primary rabbit polyclonal antibodies reactive to MAP2 (AB5622; Chemicon International) and LC3 (PA1-16931; Affinity Bioreagents, Golden, Colorado, USA), or primary goat polyclonal antibody reactive to Atg9a (sc-70141; Santa Cruz Biotechnology, Inc., Santa Cruz, CA, USA). Blots were subsequently incubated with secondary antibodies conjugated with horseradish peroxidase (Bio-Rad Laboratories) for 3 h at room temperature. Membranes were processed for protein detection using Super Signal™ substrate

(Pierce, Rockford, IL, USA). β -Actin (AC-15; Sigma-Aldrich Co.) was used as loading control.

4.3.6. Immunocytochemistry

For detection of proliferating cells, S-phase nuclei were stained in undifferentiated cells using the bromodeoxyuridine (BrdU) *in-situ* detection kit (BD Biosciences Pharmingen, San Diego, CA, USA). BrdU was added to the culture medium 18 h after A β treatments, and cells were re-incubated for additional 6 h and processed according to manufacturer's instructions. For fluorescence microscopy, NSCs cells were maintain in differentiation medium for 6 days, fixed with 4% paraformaldehyde (w/v) in phosphate buffer saline (PBS) and blocked for 1 h at room temperature in PBS, containing 0.1% Triton X-100, 1% fetal bovine serum (FBS), and 10% normal donkey serum (Jackson ImmunoResearch Laboratories, Inc., West Grove, PA, USA). Cells were then incubated with either anti- β III-tubulin antibody at a dilution of 1:500 in blocking solution, with anti-MAP2 (AB5622, Millipore Corporation, Darmstadt, Germany), anti-Nestin (MAB353; Chemicon International), anti-NG2 (neuronal/glial 2 AB5320; Millipore) and anti-GFAP antibodies at a dilution of 1:200 in blocking solution, or with anti-GFP (B-2) antibody (sc-9998; Santa Cruz Biotechnology, Inc.) at a dilution of 1:50 in blocking solution, overnight at 4°C. At the end of the incubation with primary antibodies and after washing in PBS, cells were incubated with appropriate secondary antibodies, mouse antibodies conjugated to either Alexa 568 (Life Technologies Ltd., Carlsbad, CA, USA) at a dilution of 1:200 or Dylight 488 (Jackson ImmunoResearch Laboratories, Inc.) at a dilution 1: 100, and Alexa 594-conjugated anti-rabbit antibody (Life Technologies Ltd) at a dilution of 1:200, for 2 h at room temperature. Finally, nuclei were counterstained with Hoechst 33258 (Sigma-Aldrich Co.) at 50 μ g/ml in PBS, for 5 min at room temperature. Samples were mounted using Fluoromount-GTM (Beckman Coulter, Inc., Brea, CA, USA). Fluorescence microscopy assessments were performed with a Zeiss AX10 microscope (Carl Zeiss, Jena, Germany) equipped with a Leica DFC490 camera (Leica Wetzlar, Germany) or with a Zeiss LSM 510 META confocal microscope (Carl Zeiss).

4.3.7. Flow cytometry analysis

For detection of β III-tubulin and GFAP expression levels, cells were fixed with 4% paraformaldehyde in PBS for 20 min at 4°C, washed twice with washing solution

0.1% saponin (Fluka, Biochemika, Switzerland) in PBS, and blocked for 20 min in blocking solution 0.25% saponin and 5% FBS in PBS. Subsequently, cells were washed and incubated with antibodies reactive to β III-tubulin or GFAP at a dilution of 1:500 and 1:200, respectively, in antibody blocking solution 0.1% saponin and 5% FBS in PBS, for 30 min. Cells were then washed twice and incubated with anti-mouse antibody conjugated to Dylight 488, at a dilution of 1:100 for 30 min. Cells were washed twice, resuspended in PBS with 2% FBS and analyzed using the Guava EasyCyte 5HT® Cytometry system (Millipore). For ROS quantification, 10 μ M 2',7'-dichlorodihydrofluorescein diacetate (H2DCFDA; Molecular Probes, Invitrogen, Eugene, OR, USA) was added to the culture medium 30 min prior to cell collection. Then, cells were resuspended in PBS with 2% FBS, and emission of green fluorescence was analyzed in the Guava EasyCyte 5HT® Cytometry system after 20 min. Proliferation levels were determined by BrdU incorporation analysis using the APC BrdU Flow Kit (BD Biosciences Pharmingen). BrdU was added to the culture medium 18 h after cell treatments, and cells were re-incubated for additional 6 h and later analyzed by flow cytometry using the LSR Fortessa™ system (Becton Dickinson, Mountain View, CA). The percentage of cells in the S-phase of the cell cycle was also evaluated by the LSR Fortessa™ system. First, cells were synchronized by double-thymidine block. Twelve hours after plating, 2 mM thymidine (Sigma-Aldrich Co.) was added to the culture media for additional 12 h. Cells were then released from first thymidine block by removing culture media, washing 3 times with PBS and by adding fresh undifferentiation medium, without thymidine. Twelve hours later, cells were submitted to a second thymidine block. A β s were added to the medium without thymidine at the end of second block. Cells were grown for additional 48 h, prior to cell collection with accutase. Subsequently, cells were washed with PBS, fixed in 80% ethanol at 4°C overnight, and then stained with 5 μ g/mL propidium iodide (PI) (Sigma-Aldrich Co.) for DNA contents. Data were statistically evaluated using FlowJo software (Tree Star, Inc, Ashland, OR, USA).

4.3.8. Evaluation of cell death

Hoechst labeling of NSC was used to detect apoptotic nuclei. In brief, for morphologic evaluation of apoptosis, medium was gently removed to minimize detachment of cells. Attached cells were fixed with 4% paraformaldehyde in PBS, pH 7.4, for 10 min at room temperature, incubated with Hoechst dye 33258 (Sigma-Aldrich

Co.) at 5 µg/ml in PBS for 5 min, washed with PBS and mounted using Fluoromount. Fluorescent nuclei were scored blindly and categorized according to the condensation and staining characteristics of chromatin. Normal nuclei showed noncondensed chromatin dispersed over the entire nucleus. Apoptotic nuclei were identified by condensed chromatin, contiguous to the nuclear membrane, as well as nuclear fragmentation of condensed chromatin. Cell viability was quantified by the LDH assay (Sigma-Aldrich Co.). The absorbance was measured spectrophotometrically at 490 nm wavelength, using a 96-well plate reader (Bio-Rad Laboratories).

4.3.9. Densitometry and statistical analysis

The relative intensities of protein bands were analyzed using the QuantityOne Version 4.6 densitometric analysis program (Bio-Rad Laboratories) and normalized to the respective loading controls. Statistical analysis was performed using GraphPad InStat version 3.00 (Graph-Pad Software, San Diego, CA, USA) for the analysis of variance and Bonferroni's multiple comparison tests. Values of $p < 0.05$ were considered significant.

4.4. Results

4.4.1. Characterization of NSCs isolated from mouse fetal forebrain under differentiating conditions

Monolayer culturing systems of NSCs can be generated from embryonic stem cells, induced pluripotent stem cells (derived from reprogrammed somatic cells), as well as from fetal and adult brain (Kabeya et al., 2000). These systems have the potential to give rise to neurons, astrocytes and oligodendrocytes. The different cellular compositions of the monolayer cultures, with homogeneous composition, result in high neurogenic potential. In this study, we used NSCs derived from 14.5-days post coitum mouse fetal forebrain. This cell line was established using a method that produces pure cultures of adherent NSCs, which continuously expand by symmetrical division and are capable of tripotential differentiation (Conti and Cattaneo, 2010). NSCs were grown in monolayer as previously described (Conti et al., 2005; Glaser et al., 2007; Pollard et al., 2006) and routinely maintained in undifferentiating medium (Fig. 4.1A). Under these conditions, ~ 90% of the cells were positive for proliferative marker Nestin.

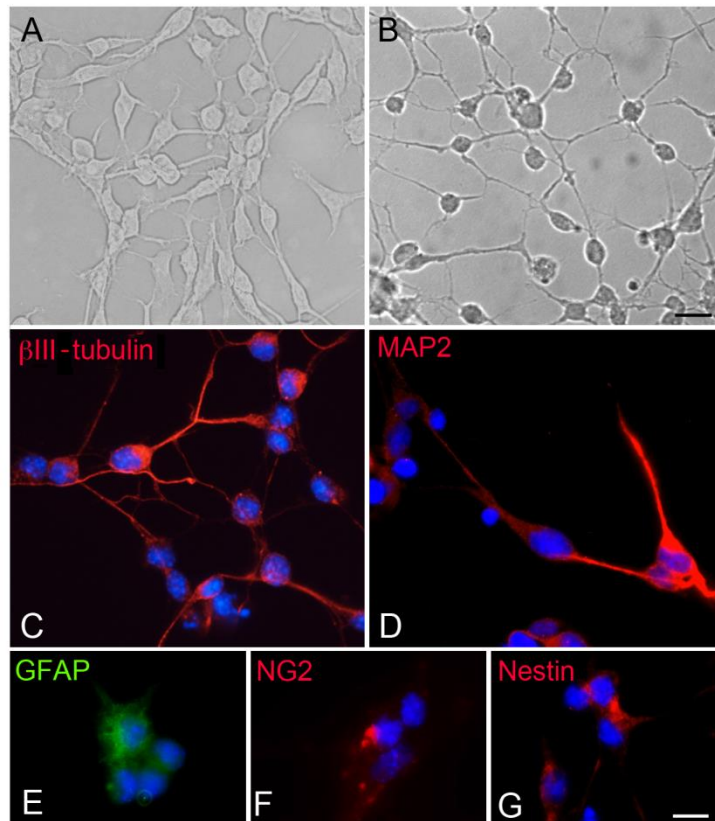


Figure 4.1. Monolayer culture system of NSCs and differentiation into major CNS cell types. Mouse NSCs were expanded and induced to differentiate as described in Materials and Methods. Undifferentiated (A) and differentiated (B) NSCs. Fluorescence staining of β III-tubulin (C), MAP2 (D), GFAP (E), NG2 (F) and Nestin (G) throughout NSC differentiation. Nuclei were stained with Hoechst. Scale bar, 10 μ m.

Following incubation in differentiation medium, cells displayed a sharp increase in markers for neurons and neural precursors. In fact, at 3 days of differentiation, 15-20% of cells were positive for β III-tubulin or GFAP, and \sim 50% were positive for Nestin. After 3 days in differentiating conditions, cells were gently dissociated, replated on a laminine-coated surface, and exposed to a FGF-2 and BDNF containing medium for terminal differentiation for additional 3 days (Spiliotopoulos et al., 2009). When exposed to these conditions, NSCs gradually adhered and progressively developed a neuronal morphology as indicated by the appearance of neurites outgrowth, and establishment of complex branched morphology and cell-cell contacts (Fig. 4.1B). A significant fraction of cells in culture showed increased immunoreactivity for the immature neuronal marker β III-tubulin, in addition to acquiring immunoreactive signal for the mature neuronal marker MAP2, and showing a more complex and branched neuronal morphology (Fig. 4.1C and D). Finally, only a small portion of the total cell population became GFAP-positive astrocytes and NG2-positive oligodendrocytes (Fig.

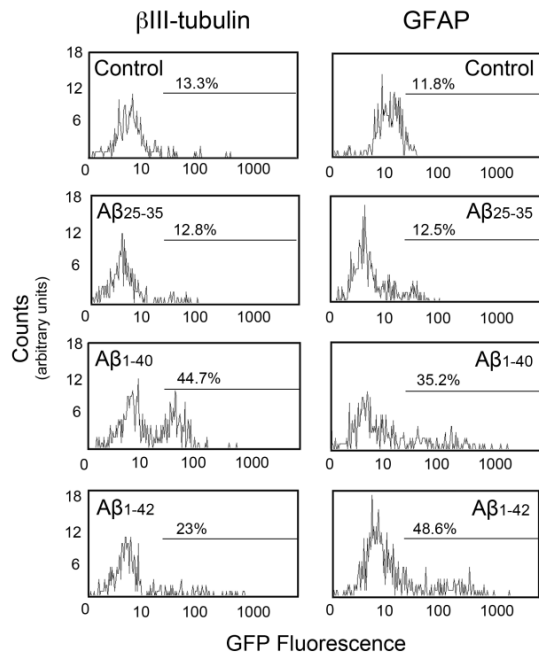
4.1E and F), indicating that the culture conditions do not favor conversion into the astroglial and oligodendroglial lineages. Differentiated cells also appear to have cell type-specific morphologies. Consistent with induction of differentiation, Nestin immunoreactivity in NSC cultures showed a few number of cells expressing this immature marker (Fig. 4.1G).

4.4.2. Distinct roles of A β ₁₋₄₀ and A β ₁₋₄₂ in modulating lineage-specific markers of NSCs

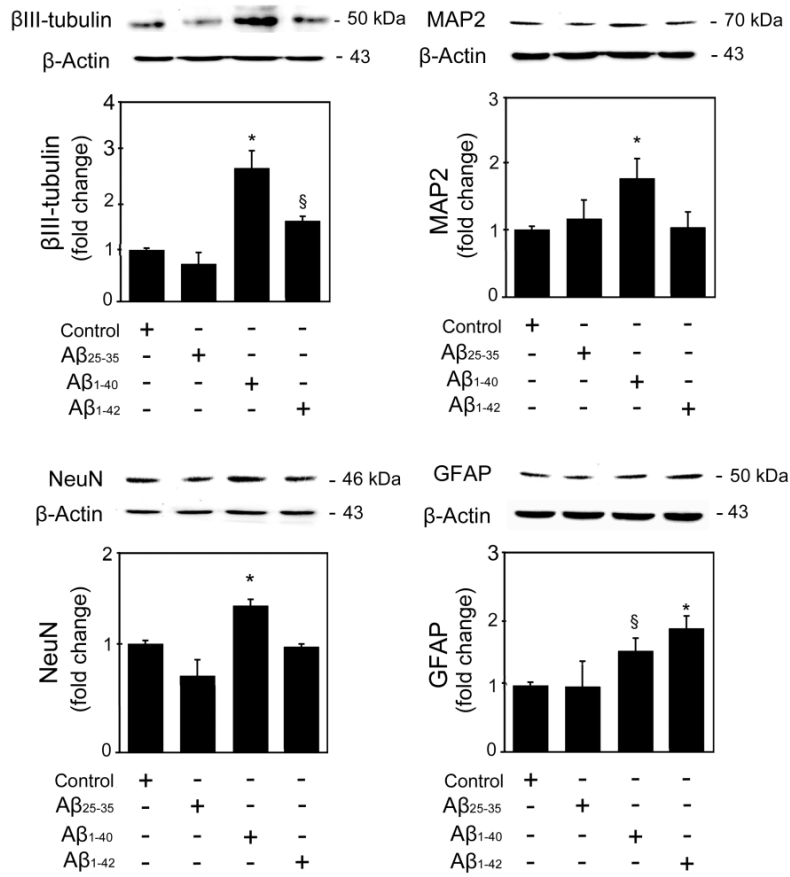
Several lines of evidence point toward the involvement of A β in neurogenesis (Spiliotopoulos et al., 2009). However, the effects of A β in neural differentiation have not reached a consensual agreement. To address the role of A β during neural differentiation *in vitro*, the expression levels of β III-tubulin, MAP2, NeuN and GFAP were investigated in NSCs incubated with A β ₁₋₄₀, A β ₁₋₄₂ or A β ₂₅₋₃₅ for 48 h. Flow cytometry analysis showed that A β ₁₋₄₀ and A β ₁₋₄₂ induced a marked increase of both β III-tubulin- and GFAP-positive cells ($p < 0.01$). However, while A β ₁₋₄₀ appeared to preferentially increase neuronal markers, A β ₁₋₄₂ exhibited a stronger effect on astrocytic differentiation (Fig. 4.2A). In addition, A β ₂₅₋₃₅ elicited no significant alterations in neuronal and astrocytic-specific protein markers. Accordingly, Western blot data revealed that, although increasing GFAP levels ($p < 0.05$), A β ₁₋₄₀ markedly augmented β III-tubulin, MAP2 and NeuN ($p < 0.01$) throughout differentiation (Fig. 4.2B).

A β ₁₋₄₂, in turn, induced β III-tubulin levels ($p < 0.05$); however, the strongest effect was observed in GFAP protein levels, which doubled in A β ₁₋₄₂-treated cells ($p < 0.01$). Finally, immunocytochemistry analysis of the β III-tubulin and MAP2 markers corroborated the effects of A β ₁₋₄₀ and A β ₁₋₄₂ in regulating neuronal lineage of NSCs (Fig. 4.2C). While A β ₁₋₄₂ slightly increased the expression of β III-tubulin and did not alter MAP2, A β ₁₋₄₀ significantly increased both markers, when compared with untreated cells. These results reinforce a stronger effect of A β ₁₋₄₀ in enhancing the neuronal lineage of NSCs when compared with A β ₁₋₄₂, and demonstrate distinct effects for different A β active fragments in NSC-fate determination.

A



B



C

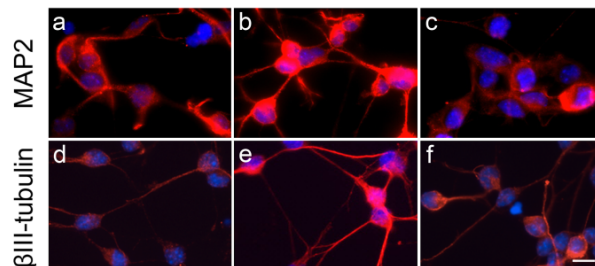


Figure 4.2. A β 1-40 preferentially promotes neuronal differentiation of NSCs. Cells were induced to differentiate, treated with either A β ₂₅₋₃₅, A β ₁₋₄₀ or A β ₁₋₄₂ for 48 h, and labeled for neural marker detection by flow cytometry as described in Materials and Methods. (A) Representative histograms of β III-tubulin-positive cells (left) and GFAP-positive cells (right). (B) Representative immunoblot of β III-tubulin and MAP2 (top), and NeuN and GFAP (bottom), and respective protein levels. Results were normalized to endogenous β -Actin protein levels and expressed as mean \pm SEM for at least three different experiments. (C) Immunostaining of neuronal markers β III-tubulin and MAP2 in control untreated cells (a and d), and in cells treated with A β ₁₋₄₀ (b and e) and A β ₁₋₄₂ (c and f). Nuclei were stained with Hoescht. Scale bar, 10 μ m. * $p < 0.01$ and § $p < 0.05$ from controls.

4.4.3. A β ₁₋₄₀ increases proliferation and neuronal-promoter activity of NSCs

It has been suggested that A β peptides may also alter NSC proliferation depending on the time and type of animal models used (Chen and Dong, 2009). We next investigated whether the effects of A β ₁₋₄₀ and A β ₁₋₄₂ in enhancing lineage-specific markers were due to proliferative effects. Undifferentiated cells were preincubated with A β ₁₋₄₀ and A β ₁₋₄₂ for 24 h and pulse-labeled for 6 h with BrdU to mark S-phase cells. Immunocytochemistry analysis revealed that treatment with A β ₁₋₄₀ significantly increased BrdU incorporation, when compared with untreated cells (Fig. 4.3A). Surprisingly, no significant changes were observed in the percentage of BrdU-positive cells upon A β ₁₋₄₂ treatment. The percentage of BrdU incorporated in A β -treated NSCs was also determined by flow cytometry analysis. Our results confirmed that ~ 80% of the untreated cells incorporated BrdU, indicating that the majority of NSCs are in S-phase and proliferating. Interestingly, > 90% of the cells treated with A β ₁₋₄₀ were BrdU-positive, while treatment with A β ₁₋₄₂ had no effect in BrdU incorporation, when compared with untreated cells ($p < 0.05$) (Fig.4.3B). To validate our results, the DNA content distribution of NSCs was also analyzed by flow cytometry.

In these experiments cells were stained with PI for determining DNA content after treatment with A β peptides. As shown in Fig.4.3C, the percentage of cells in S-phase raised ~ 15% after A β ₁₋₄₀ treatment ($p < 0.05$). As expected, no significant increase in proliferation was observed following treatment with A β ₁₋₄₂. Thus, our results suggest that A β ₁₋₄₀ and A β ₁₋₄₂ have distinct functions in mediating NSC proliferation. While the effect of A β ₁₋₄₀ on neuronal-specific lineage may be partially the ultimate result of increased number of neural progenitors, A β ₁₋₄₂ appears to favor glial differentiation by a mechanism independent of NSC proliferation.

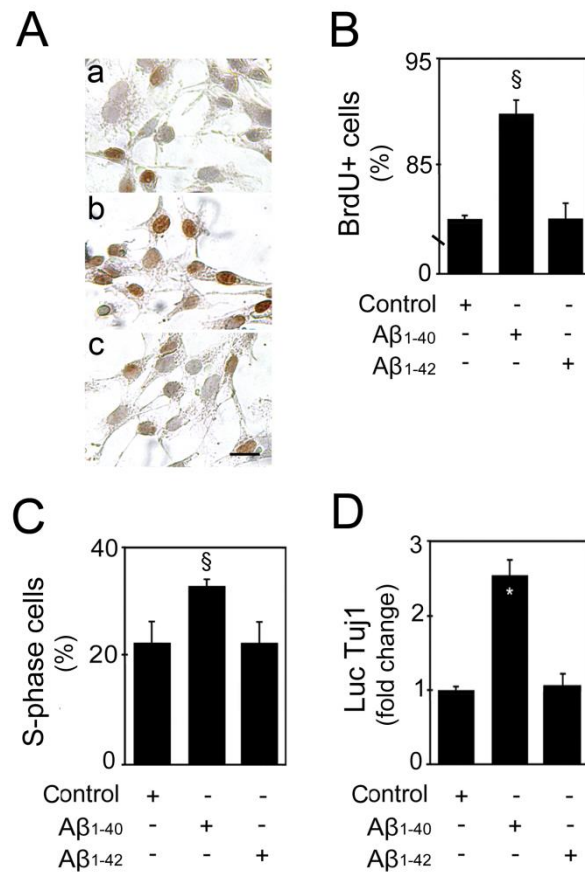


Figure 4.3. Aβ₁₋₄₀ increases the S-phase of the cell cycle and neuronal-promoter activity in NSCs. Undifferentiated cells were preincubated with Aβ₁₋₄₀ and Aβ₁₋₄₂ for 24 h and pulse-labeled for 6 h with BrdU to mark S-phase cells as described in Materials and Methods. (A) Immunostaining with rabbit anti-BrdU in control untreated cells (a), and in cells exposed to either Aβ₁₋₄₀ (b) or Aβ₁₋₄₂ (c). Scale bar, 10 μm. (B) Percentage of BrdU-positive cells analyzed by flow cytometry. (C) S-phase cells analyzed by flow cytometry. (D) Neuronal lineage-specific promoter activity. NSCs were transfected with a βIII-tubulin (Tuj1) promoter-driven luciferase construct, 24 h before Aβ₁₋₄₀ incubation. After 48 h of Aβ₁₋₄₀ treatment, luciferase activity was measured in cell lysates. Aβ₁₋₄₀ significantly increased BrdU-positive and S-phase cells as well as Tuj1 promoter activity. Results were expressed as mean ± SEM for at least three different experiments. **p* < 0.01 and §*p* < 0.05 from controls.

To further dissect the mechanism by which Aβ₁₋₄₀ modulates increased neuronal fate, NSCs were transfected with a βIII-tubulin (Tuj1) promoter-driven luciferase construct, 24 h before Aβ₁₋₄₀ incubation. After 48 h of Aβ₁₋₄₀ treatment, luciferase activity was measured in cell lysates. Notably, Tuj1-promoter activity was markedly induced in Aβ₁₋₄₀ treated cells, when compared with untreated NSCs (*p* < 0.01), validating data on the role of Aβ₁₋₄₀ in the neurogenesis process (Fig. 4.3D). Aβ₁₋₄₂ had no major effect on Tuj1 promoter induction. Thus, our results indicate that the pro-neurogenic effect of Aβ₁₋₄₀ results from its ability in maintaining a proliferative NSC

pool, and activating the β III-tubulin promoter.

4.4.4. $A\beta_{1-40}$ and $A\beta_{1-42}$ increase autophagy during differentiation of NSCs

Autophagy is characterized by sequestration of cytoplasmic constituents in double or multimembrane autophagic vesicles, and their delivery to and subsequent degradation by the cell own lysosomal system (Chevallier et al., 2005; Jin et al., 2004; Wang et al., 2004; Wen et al., 2004). LC3 was originally identified as a small subunit of microtubule-associated protein 1A and 1B from rat brain (Gozuacik and Kimchi, 2004), and is usually associated to autophagosome membranes during the autophagic process (Mann and Hammarback, 1994). Therefore, LC3 has been recently proposed as a marker for autophagic vesicles and autophagic activity (Kabeya et al., 2000). A growing body of evidence points to a critical role for autophagy during proliferation and differentiation, as a response-survival mechanism to limit oxidative stress associated with these processes (Asanuma et al., 2003; Kamada et al., 2000). However, the specific role of $A\beta$ species in mediating autophagy is largely unknown. To elucidate the role of autophagy and potential modulation by $A\beta$ peptides in neural differentiation, we undertook various screening approaches. We investigated the LC3-I/II conversion and used the autophagic marker GFP-LC3 in differentiating NSCs undergoing differentiation after $A\beta_{1-40}$ and $A\beta_{1-42}$ treatments. Immediately after the synthesis, LC3 carboxyl terminal region is cleaved by a protease to form LC3-I peptide (18 kDa) in the cytosol (Pua et al., 2007; Zhao et al., 2010; Zhuang et al., 2011). For autophagosomal membrane localization, LC3 must be processed, by E1 and E2 enzymes, to a membrane-bound form LC3-II (16 kDa), being subsequently conjugated to the preautophagosomal membrane (Kabeya et al., 2000). Importantly, our results revealed that both $A\beta_{1-40}$ and $A\beta_{1-42}$ further increase LC3-I to -II conversion, when compared with non-treated cells (Fig. 4.4A) ($p < 0.01$). $A\beta$ -induced autophagy during NSC differentiation was confirmed by monitoring the accumulation of LC3 by immunofluorescence. In fact, both $A\beta_{1-40}$ and $A\beta_{1-42}$ increased GFP-LC3 puncta in NSCs undergoing differentiation (Fig. 4.4B). Moreover, the autophagy-related protein 9 (Atg9), a multi-pass membrane protein that localizes to the pre-autophagosomal structure, markedly augmented throughout differentiation in cells treated with $A\beta_{1-40}$ or $A\beta_{1-42}$ ($p < 0.01$) (Fig. r.4C).

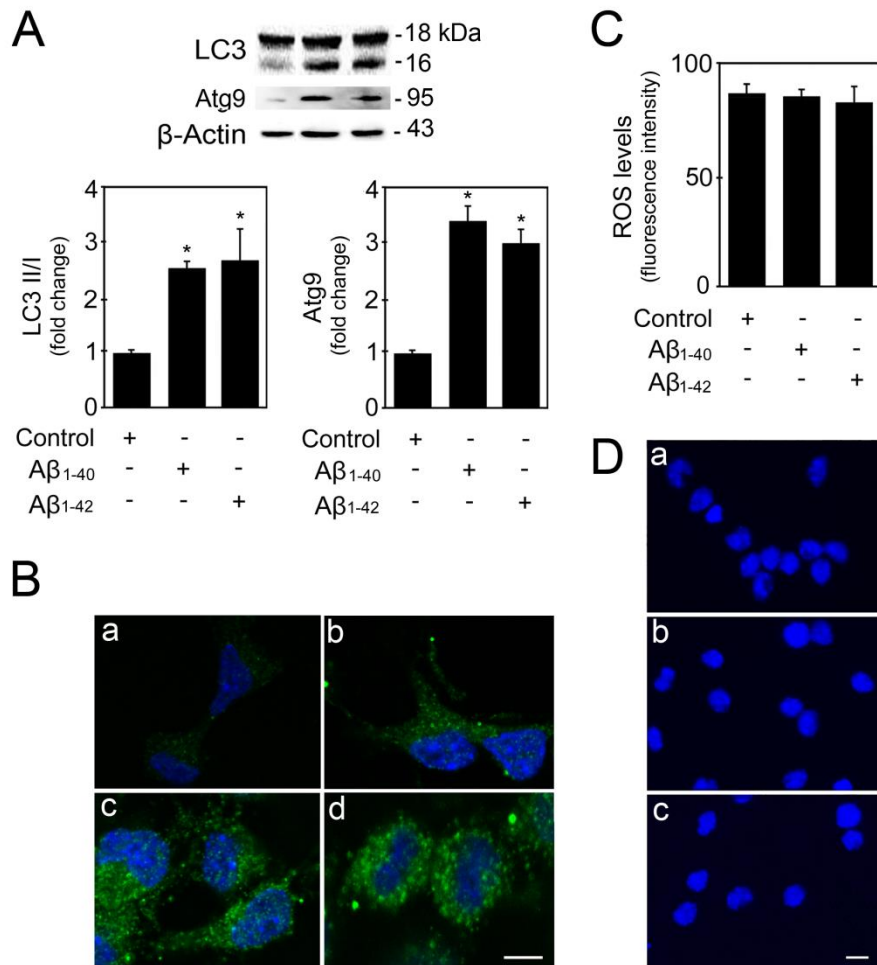


Figure 4.4. Autophagy is increased in A β ₁₋₄₀- and A β ₁₋₄₂-treated NSCs. Cells were induced to differentiate, treated with either A β ₁₋₄₀ or A β ₁₋₄₂ for 24 h, and then collected for Western blot, apoptosis, confocal microscopy and flow cytometry analyses as described in Material and Methods. (A) Representative immunoblots of LC3-I, LC3-II and Atg9 (top) and respective protein levels (bottom). β -Actin was used as loading control. (B) Representative confocal images of GFP-LC3 puncta in undifferentiated (a) or differentiated (b) conditions, and treated with A β ₁₋₄₀ (c) or A β ₁₋₄₂ (d). Scale bar, 5 μ m. (C) Intracellular ROS quantification of fluorescent DCF by flow cytometry. (D) Representative images of Hoechst staining in control cells (a), or cells treated with A β ₁₋₄₀ (b) or A β ₁₋₄₂ (c). Scale bar, 10 μ m. Autophagy is increased after A β treatment; however, ROS levels and apoptosis were not altered. Results were expressed as mean \pm SEM for at least three different experiments. * p < 0.01 from controls.

Finally, in the concentrations used, A β peptides did not increase redox status (Fig. 4.4C) nor induced cell death throughout NSC differentiation, as detected by Hoechst (Fig. 4.4D) and PI and Annexin-V staining. These data suggest that the protective mechanism of autophagy is potentially modulated by A β peptides to promote neural differentiation.

4.4.5. Inhibition of autophagy reverts the effects of A β ₁₋₄₀ and A β ₁₋₄₂ in enhancing lineage-specific markers in NSCs

To clarify the contribution of autophagy in A β -regulated NSC fate, we tested the effects of autophagy inhibition on the ability of both A β ₁₋₄₀ and A β ₁₋₄₂ to increase lineage-specific markers. We used the autophagy inhibitor 3-MA and re-evaluated the effects of A β ₁₋₄₀ and A β ₁₋₄₂ in neuronal and astrocytic differentiation, respectively. Confocal microscopy confirmed that treatment of NSCs with 3-MA markedly decreased the number of GFP-LC3-labeled puncta (Fig. 4.5A). Similar results were obtained after treatment with a second autophagy inhibitor, wortmannin (data not shown). Cell death increased in the presence of 3-MA in both A β -treated and untreated cells, as determined by the LDH assay (Fig. 4.5B) ($p < 0.01$) and PI and Annexin-V staining (data not shown). In addition, flow cytometry analysis revealed that the effects of A β ₁₋₄₀ and A β ₁₋₄₂ in NSC fate were completely reverted after incubation with 3-MA. Notably, the inhibition of autophagy diminished the number of β III-tubulin- and GFAP-positive cells in NSCs incubated with A β ₁₋₄₀ and A β ₁₋₄₂, when compared with control (Fig. 4.5C) ($p < 0.01$). Finally, immunocytochemistry analysis of both β III-tubulin and GFAP confirmed the inhibitory effects of 3-MA in A β ₁₋₄₀ and A β ₁₋₄₂-induced neuronal and astrocytic-specific protein markers, respectively (Fig. 4.5D). These results indicate that A β ₁₋₄₀ and A β ₁₋₄₂ may be important regulators of neural differentiation through an autophagy-dependent manner.

4.5. Discussion

A β peptides have important physiological functions before they aggregate and form amyloid fibrils (Tanida et al., 2002; Tanida et al., 2001). However, our understanding of A β signals controlling these processes is limited. In this study, we demonstrate that active fragments of A β ₁₋₄₀ and A β ₁₋₄₂ peptides, but not A β ₂₅₋₃₅ peptide, significantly stimulate neural-lineage in NSCs, through a mechanism at least in part dependent on autophagy signaling mechanisms.

Much attention has been centered on toxic effects of A β peptides (Parihar and Brewer, 2010; Pearson and Peers, 2006; Plant et al., 2003; Ramsden et al., 2002). In fact, A β peptides are strongly implicated in AD, promoting synaptic dysfunction and neuronal cell death by a mechanism involving increased oxidative stress and disruption of cellular calcium homeostasis (Klein, 2002; Pike et al., 1993). However, A β peptides may also activate kinase enzymes, protect against oxidative stress (Mattson, 1997),

regulate cholesterol transport and function as transcription factors (Baruch-Suchodolsky and Fischer, 2009).

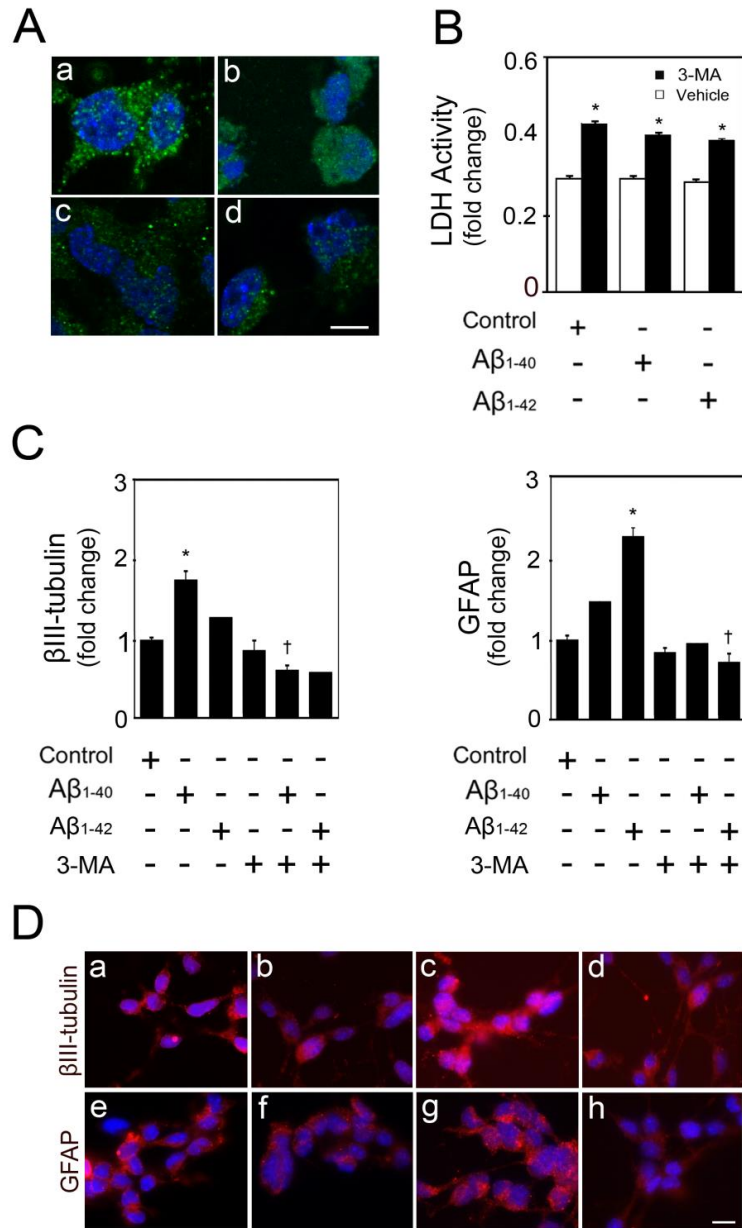


Figure 4.5. The autophagy inhibitor 3-MA abrogated the effects of Aβ₁₋₄₀ and Aβ₁₋₄₂ in neuronal and astrocytic differentiation of NSCs. Mouse NSCs were induced to differentiate and treated with either 3-MA (5 mM), Aβ₁₋₄₀ or Aβ₁₋₄₂ for 24 h. Cells were collected for LDH, flow cytometry, confocal and immunocytochemistry analysis as described in Material and Methods. (A) Representative confocal images of GFP-LC3 puncta in control cells (a), or in cells treated with either 3-MA (b), Aβ₁₋₄₀ + 3-MA (c), Aβ₁₋₄₂ + 3-MA (d) for 24 h. Scale bar, 5 μm. (B) LDH release. (C) Percentage of βIII-tubulin- and GFAP-positive assessed by flow cytometry analysis. (D) Representative images of βIII-tubulin- and GFAP-positive cells in controls (a and e), and in cells treated with either 3-MA (b and f), Aβ₁₋₄₀ + 3-MA (c and g), Aβ₁₋₄₂ + 3-MA (d and h) for 24 h. Results were expressed as mean ± SEM for at least three different experiments. **p* < 0.01 from controls; †*p* < 0.01 from Aβ alone.

The beneficial role for A β ₁₋₄₀ peptide in neurons has previously been reported *in vivo*, where A β ₁₋₄₀ was shown to inhibit amyloid deposition (Chen and Dong, 2009). Here, we first determined the effects of A β ₁₋₄₀, A β ₁₋₄₂ and A β ₂₅₋₃₅ in expression levels of neural markers during differentiation of mouse NSC. Soluble A β ₁₋₄₀ and A β ₁₋₄₂ increased both β III-tubulin and GFAP levels; however, A β ₁₋₄₀ was preferentially pro-neurogenic, while A β ₁₋₄₂ was pro-astrocytic. In addition, we have shown that A β ₁₋₄₀ not only promotes NSC self-renewal but also enhances the activity of neuronal differentiation. In fact, after A β ₁₋₄₀ treatment of NSCs, the S-phase of the cell cycle and BrdU labeling were markedly enhanced. A potential direct effect of A β ₁₋₄₀ on β III-tubulin promoter activity and its influence on neurogenesis may be further clarified in knockdown experiments of β III-tubulin after A β ₁₋₄₀ treatment.

Our findings are in accordance with a previous report showing that non-aggregated A β ₁₋₄₀ and A β ₁₋₄₂ promote neuronal and astrocytic cell fate in neural progenitor cells (Kim et al., 2007). However, in that study, A β ₁₋₄₂ also increases NSC proliferation, while we did not observed significant alterations in self-renewal after A β ₁₋₄₂ incubation. Distinct cellular models and experimental conditions in both studies could account for this apparently discrepant result. The authors have used NSCs derived from 18-dpc rat fetal brain, while we used NSC derived from 14.5-dpc mouse fetal brain. Moreover, others have demonstrated a predominant effect of A β ₁₋₄₂ in neurogenesis (Chen and Dong, 2009). In fact, the number of β III-tubulin-positive neurons was increased by A β ₁₋₄₂ in one study (Calafiore et al., 2012; Heo et al., 2007; Lopez-Toledano and Shelanski, 2004), while others reported that low concentrations of oligomeric A β ₁₋₄₂ peptides enhance proliferation and neuronal differentiation of NSCs (Lopez-Toledano and Shelanski, 2004). Hence, although the absence of A β ₂₅₋₃₅ effect in eliciting either self-renewal or neural differentiation appears to be consensual in the literature, the debate is still ongoing as to the role of different forms of A β on the neurogenesis process.

On the other hand, studies using animal models of AD have proposed the opposite effect of A β peptides in neurogenesis (Heo et al., 2007). However, these results appear to be correlated with the decreased levels of soluble A β peptide observed in AD. In fact, A β peptide has already been reported to have differential effects on human embryonic stem cell proliferation depending on its aggregation level (Haughey et al., 2002a; Haughey et al., 2002b); the neurogenic functions of A β were greatly

reduced when this active peptide was in aggregated forms. Consistent with this, others have demonstrated that higher levels of A β monomers, oligomers, and fibrils in the brain microenvironment in individuals with amyloidosis- β induce oxidative stress and have a negative effect on endogenous neurogenesis (Porayette et al., 2009). AD is a dynamic disease process, and it is plausible that an increase in neuronal differentiation is followed by an overall decline as A β aggregates and loses its neurogenic functions.

By evaluating the lipidated LC3-II and Atg9 markers of autophagy, our results have also shown that low μ M levels of soluble A β_{1-40} and A β_{1-42} markedly increase autophagy throughout NSC differentiation. In fact, autophagy has been shown to play a critical role in stem cell maintenance and in a variety of cell differentiation processes (Mazur-Kolecka et al., 2006). Recently, it has been revealed that NSCs may activate autophagy to also fulfill their high energy demands (Asanuma et al., 2003; Vessoni et al., 2012; Zhao et al., 2010). The link between A β peptides and autophagy has also previously been described. Autophagy protects neurons from A β -induced toxicity (Vázquez et al., 2012) and serves as a mechanism that mediates clearance of ubiquitinated A β to clear molecular debris and restore neurotransmitter balance (Hung et al., 2009). Nevertheless, the majority of studies relating A β peptide with autophagy have demonstrated that A β peptide triggers autophagic cell death by inducing ROS accumulation (Khandelwal et al., 2011; Zheng et al., 2006a). However, although ROS play an important role in the induction of autophagy (Lipinski et al., 2010; Wang et al., 2010; Yang et al., 2012), our results showed that autophagy induced by A β peptides during neural differentiation was not associated with increased levels of oxidative stress, and other A β -mediated events may account for this cellular outcome. In addition, the autophagy inhibitor 3-MA significantly increased cell death, indicating that autophagy triggered by soluble low levels of A β might operate as a NSC survival response. Indeed, autophagy was shown to inhibit apoptosis by several mechanisms (Gurusamy and Das, 2009). Remarkably, 3-MA inhibited A β -mediated effects throughout differentiation, showing that neurogenesis and gliogenesis are favored in A β_{1-40} - and A β_{1-42} -treated NSC as the result of increased autophagy activity. It would be interesting to dissect the molecular mechanisms by which soluble A β species promote neural differentiation, and to further understand how A β may induce autophagy through a ROS-independent manner. In fact, A β peptide was already found in the nucleus to activate p53 promoter activity (Yang and Klionsky, 2010), possibly directly regulating the expression of many other genes.

Together, our results corroborate the beneficial role of soluble A β ₁₋₄₀ and A β ₁₋₄₂ in mediating neurogenesis and astrogliogenesis, respectively, and identify autophagy as an essential mechanism of A β -induced neural differentiation.

Acknowledgments

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5. General Discussion and Concluding Remarks

The studies presented in this thesis contribute to a better understanding of the apoptotic mechanisms implicated in AD and extend our knowledge on the role of apoptosis-related molecules and A β peptides as components of neural proliferation and differentiation processes.

In brief, we demonstrated a role for p63 during A β -induced apoptosis and the existence of a c-Jun-dependent mechanism regulating the abundance of anti-apoptotic Δ Np63 in the context of A β -induced stress. Importantly, the anti-apoptotic bile acid TUDCA was efficient in partially modulating these effects. Next, we implicated p63 in regulating neural differentiation by demonstrating that the TAp63 γ isoform cross-talks with key regulators of neurogenesis, specifically with the histone H3 lysine 27-specific demethylase JMJD3. Finally, we explored the effect of soluble A β fragments in modulating NSC fate, and identified autophagy as an essential mechanism of A β -induced neural differentiation (Fig. 5.1). The data presented here provide new insights into the regulation of A β -induced cell death and neural differentiation by apoptosis-associated molecules, and represents a step forward in understanding the molecular mechanisms by which A β peptides mediate neural differentiation. In this last concluding chapter, we integrate our findings, and address future perspectives arising from these studies.

The p63 protein is a multi-isoform p53 family member that is involved in cell death (Gressner et al., 2005). In the present work, we evaluated the effect of A β -induced apoptosis in the regulation of p63 abundance. A β treatment of PC12 neuronal-like cells and rat cortical neurons caused an upregulation of the pro-apoptotic isoform TAp63 γ and downregulation of the anti-apoptotic isoform Δ Np63 γ , which allowed the manifestation of apoptosis. In parallel, we showed that genotoxic drugs such as doxorubicin and cisplatin increased TAp63 γ levels, concurrent with the reduction of Δ Np63 γ abundance in PC12 cells. In fact, it is well documented that genotoxic signals regulate p63 protein levels, promoting phosphorylation-induced, proteasome-mediated degradation of the pro-survival isoform Δ Np63 (Chatterjee et al., 2008; Lazzari et al., 2011). However, this evidence was only reported for α isoforms. Importantly, the bile acid TUDCA, a well characterized endogenous potent inhibitor of apoptosis in different cell types (Ramalho et al., 2004; Solá et al., 2006; Viana et al., 2010), strongly modulated A β -induced apoptosis, while preventing the changes in p63 levels, further suggesting that the reduction of Δ Np63 levels is important for apoptosis to occur.

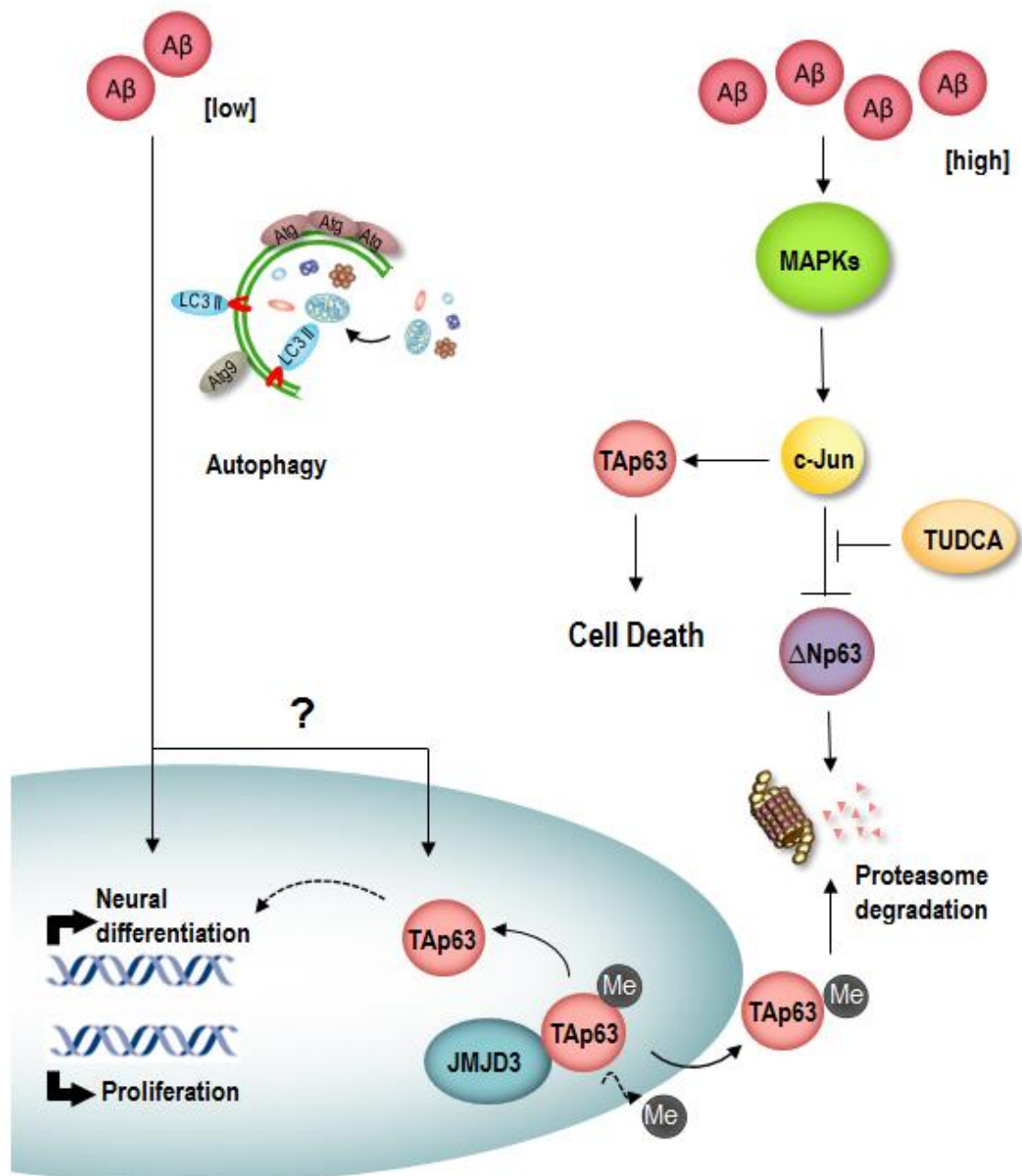


Figure 5.1. Graphical abstract. In the context of $A\beta$ -induced stress, the abundance of $\Delta Np63$ and $TAp63$ is regulated by a $c-Jun$ -dependent mechanism. Importantly, the bile acid TUDCA partially modulates these effects. $A\beta$ -mediated reduction of $\Delta Np63$ protein levels may be influenced by the MAPK pathway and occurs in a proteasome-dependent manner. The $TAp63\gamma$ isoform cross-talks with key regulators of neurogenesis, namely the histone demethylase JMJD3, to redirect stem cells to differentiation, as an alternative to cell death. Finally, low levels of soluble $A\beta$ peptides may also modulate neural differentiation. Autophagy appears to be an essential player in $A\beta$ -induced neural differentiation. Interactions that were suggested or shown indirectly are represented by dashed lines.

$c-Jun$, a key regulator of stress-mediated cell death has been shown to play a role in $A\beta$ -induced toxicity (Estus et al., 1997; Viana et al., 2010). In addition, it has been

reported that this member of the AP-1 family of transcription factors modulates the abundance of TAp63 (Yao et al., 2010b). Indeed, here we demonstrated that Δ Np63 reduction was associated with increased c-Jun protein levels after A β treatment in PC12 neuronal-like cells and cortical neurons. Further, A β -mediated reduction of Δ Np63 protein levels appeared to be influenced by the MAPK pathway and occur in a proteasome-dependent manner. In fact, it has been reported that A β may inhibit the proteasome (Gregori et al., 1995; Tseng et al., 2008). Nevertheless, our results are in accordance with other studies demonstrating that important mediators of AD are degraded in a proteasome-dependent fashion (Lanni et al., 2010; Roselli et al., 2005), thus contributing to AD pathogenesis. Therefore, the use of distinct cell model systems and A β exposure conditions may help reconcile data from different studies. Of note, while TUDCA rescued A β -induced decrease of Δ Np63 levels, it also prevented the increase in c-Jun levels promoted by the peptide. Together, these findings demonstrate that the abundance of Δ Np63 and TAp63 in response to A β -induced cell stress is coordinately regulated by a c-Jun-dependent mechanism, and highlight the importance of discovering novel targets for potential therapeutic intervention. Since TUDCA is a cholesterol-derived molecule and presents high affinity to lipid membranes (Solá et al., 2006), it would be interesting to further explore in the future, whether this bile acid may also interfere with A β load (Nunes et al., 2012) and entrance in the cells.

Curiously, it has been recently suggested that molecules involved in the core of the executing apoptosis machinery play a dual role in differentiation and cell death. We have previously demonstrated the involvement of specific apoptosis-related miRNAs and proteins, including p53, caspases and calpains, in mouse NSC differentiation, and also showed that p53 interacts with key regulators of neurogenesis, such as JMJD3, to redirect stem cells to differentiation, as an alternative to cell death (Aranha et al., 2009; Santos et al., 2012b; Solá et al., 2011; Solá et al., 2012). Given the functional and structural similarities of p63 and p53, we next investigated the role of p63 during mouse NSC differentiation and evaluated whether p63 interacts with JMJD3 in this cellular context. In fact, in contrast with p53 and p73, there is still a breach in the literature regarding p63 potential involvement in neurogenesis by cell death-independent mechanisms. In spite of other studies claiming that p63 is dispensable for neurogenesis, p63 was shown to be expressed in neurogenic niches, such as the SVZ of the lateral ventricle in postnatal mice, supporting the idea that p63 may have a key role during neurogenesis (Hernández-Acosta et al., 2011). Our results reveal for the first time a role

for p63 in neural progenitors, directing NSCs to a neuronal phenotype. In fact, our data support the hypothesis that JMJD3-induced TAp63 γ nuclear translocation might direct NSCs to a neuronal fate specification, through the transcriptional activation of pro-neuronal genes. Overexpression of TAp63 γ during early differentiation of NSCs resulted in increased β -III tubulin levels, whereas downregulation of TAp63 γ expression by specific p63 siRNA abrogated the increase in β -III tubulin. Interestingly, we showed that JMJD3 directly interacts with p63 to induce p63 demethylation and subsequent p63 stabilization during mouse neural differentiation. A deeper knowledge of the regulatory modifications of p63 protein will certainly improve our understanding of p63 function during neural differentiation. In this respect, future studies are warranted to determine the specific p63 residues demethylated by JMJD3 and to address the importance of TAp63 γ demethylation in neurogenesis by modification of the identified residues. On the other hand, since TUDCA modulates p63 during apoptosis, it would be interesting to also clarify whether this bile acid regulates p63 in this cellular context, also affecting NSC fate.

At last, we investigated whether low levels of soluble A β peptides may also modulate neural differentiation. In fact, several studies have shown that classical triggers of apoptosis may positively influence neural differentiation (Solá et al., 2012). In addition, A β species are highly multifunctional peptides with significant non-pathological activities. However, the precise molecular pathways underlying the regulation of NSC proliferation and differentiation by different A β peptides are still not fully defined. Our results demonstrate that A β ₁₋₄₀ promotes NSC self-renewal and enhances mostly neuronal differentiation. In fact, after A β ₁₋₄₀ treatment of NSCs, S-phase of the cell cycle, BrdU labeling, and β III-tubulin promoter-driven luciferase activity were markedly enhanced. In contrast, A β ₁₋₄₂ promoted mostly astrocytic cell fate in NSCs, having no effect in NSC proliferation. These results are in part in discordance with other previous reports (Chen and Dong, 2009; Heo et al., 2007; López-Toledano and Shelanski, 2004). Indeed, there is variance in the literature regarding the experimental conditions used to address the neurogenic effects of A β , which can apparently explain these discrepancies in the results.

Due to the involvement of autophagy in cellular survival and differentiation, development and homeostasis (Aburto et al., 2012; Levine and Kroemer, 2008; Mizushima and Levine, 2010; Vessoni et al., 2012), and since autophagy is involved in A β -mediated effects (Hung et al., 2009), we explored the role of autophagy in A β -

induced alterations of neural fate. In fact, the correlation between pro-neurogenic effects of A β peptides and autophagy has not been explored before. Our results demonstrated that low levels of soluble A β_{1-40} and A β_{1-42} markedly increase autophagy throughout NSC differentiation. Surprisingly, neurogenesis and gliogenesis were favored in A β_{1-40} - and A β_{1-42} -treated NSCs as the result of enhanced autophagy activity, without increased levels of oxidative stress and apoptosis. The inhibition of autophagy in this cellular context significantly increased cell death, indicating that autophagy triggered by soluble low levels of A β might operate as a NSC survival response.

As a final note, it is important to look beyond the role A β peptides during neural differentiation and to further dissect the precise molecular targets of soluble A β species during this process. Taking into account the role of apoptosis-related proteins during neural differentiation, namely the p63 protein, it is tempting to think that A β -induced effect on NSCs might be partially dependent on p63 and c-Jun. Finally, it would be interesting to explore how low levels of A β regulate p63 expression in neural differentiation; how A β may induce autophagy through a ROS-independent manner; and whether TUDCA regulates the survival process of autophagy in both apoptotic and differentiation contexts.

The poor survival and differentiation levels of stem cells after either transplantation or neural injury have been one of the major problems of stem cell-based therapy. With the growing identification of the regulatory networks between neural apoptosis and differentiation, it is likely that we will witness relevant advances in potential therapeutic tools that contribute to a more efficient use of stem cells in neural-replacement therapies.

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