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**Participación de mTOR en el transporte de aminoácidos
involucrados en la síntesis de glutatión en el sistema nervioso del
ratón**

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ABREVIATURAS

4EBP-1, la proteína de unión al factor de inicio de la traducción eucariota eIF-4E
4F2hc, proteína de unión a membrana la cadena pesada de antígeno 4F2
γGT, γ-glutamyl transpeptidasa
AMPK, proteína cinasa activada por AMP
AKT o PKB, el nombre viene de un retrovirus aislado de la cepa Ak llamado "Akt-8". El oncogen codificado en este virus se denominó v-Akt. Proteína cinasa B
ARE, elementos de respuesta antioxidante
ASK1, cinasa reguladora de la señal de apoptosis
ATF4, factor de transcripción 4
ATP, adenosín trifosfato
BCA, ácido bicinconínico
BCH, 2-aminobiciclo-(2,2,1)-heptano-2-ácido carboxílico
BHE, barrera hematoencefálica
BSA, albúmina de suero bovino
BSO, L-butionina-S-R-sulfoximina
CAT, catalasa
COX2, subunidad 2 de la citocromo c oxidasa
CPT-1, carnitina palmitoiltransferasa 1
Cu²⁺, 3+, iones de cobre
Cys, cisteína
Cys2, cistina
DAPI, 4',6-diamino-2-fenilindol
DEPTOR, proteína de interacción con mTOR
DMEM/F-12, Dulbecco's Modified Eagle Medium: Nutrient Mixture F- 12
DTPA, pentaacetato de dietilentriamina
EAAT1/2, transportadores de aminoácidos excitadores 1 y 2
EAAT3, transportador de aminoácidos excitadores 3
EEF2K, cinasa del factor de elongación eEF2
eIF4E, factor de iniciación de traducción 4
ERK, cinasa regulada por señales extracelulares
Fe²⁺, 3+, iones de hierro
FOXO1/3a, proteína forkhead box O1/3a
G6P-D, glucosa 6-fosfato deshidrogenasa
GAP, GTPasa
GCL, cisteína-glutamato ligasa
GCLc, subunidad catalítica
GCLm, subunidad moduladora
Glu, glutamato
Gly, glicina
GPCR, receptores asociados a proteínas G
GR, glutatión reductasa
GRB2, proteína 2 de unión al receptor de factores de crecimiento
GS, glutatión sintetasa
GSH, glutatión
GSK3, glucógeno sintasa cinasa 3
GSSG, glutatión disulfuro
GST, GSH S-transferasas
H₂O₂, peróxido de hidrógeno
HIF1α, factor inducible de hipoxia 1-alfa
iNOS, NOS inducible

I κ B, inhibidor de kappa B
IKK, cinasa de I κ B
ip, intraperitoneal
IRAK, cinasa asociada al receptor de interleucina 1
JNK, cinasa c-jun N-terminal
LAT1, transportador 1 de aminoácidos de tipo-L
MAPK, cinasas activadas por mitógenos
mBCI, monoclorobimano
Mg²⁺, ión de magnesio
mGluR, receptores de glutamato metabotrópicos
MK571, ácido 5-(3-(2-(7-cloroquinolina-2-il) etenil) fenil)-8-dimetilcarbamil-4,6-ditiaoctanoico
mLST8, proteína letal 8 de mamífero con Sec13, también conocida como GbL
mRNA, ácido ribonucleico mensajero
MRP1, proteína 1 de resistencia a multidroga
mSINI, proteína interactiva de la cinasa de mamífero activada por estrés
mTOR, blanco funcional de la rapamicina
mtTFA; factor de transcripción mitocondrial
Na⁺, ión sodio
NADPH; nicotinamida-adenina-dinucleótido-fosfato
NeuN, núcleos neuronales
NF κ B, factor nuclear potenciador de las cadenas ligeras kappa de las células B activadas
NGF, factor de crecimiento neuronal
NMDA, N-metil-D-aspartato
NO[•], óxido nítrico
NO₂[•], radical dióxido de nitrógeno
NOS, NO sintasa
Nrf2, factor nuclear 2 derivado del factor eritroide 2
NOX, NADPH oxidasas
O₂, oxígeno molecular
O₂^{-•}, superóxido
OD; densidad óptica
OH[•], radical hidroxilo
OONO[•], peroxinitrito
OPA, O-ftalaldehído
p, fosforilado
PB, amortiguador de fosfatos
PBT, PB + 0.3% Triton X-100
PC12, línea celular de tumores de médula adrenal de ratón
PDC, pirrolidina-2,4-ácido dicarboxílico
PDK1, piruvato deshidrogenasa cinasa
PI, yoduro de propidio
PI3K, fosfatidilinositol 3-cinasa
PIKK, cinasas relacionadas a PI3K
PKC, proteína cinasa c
PLC γ , fosfolipasa C gamma
PRAS40, sustrato de Akt rico en prolinas de 40 kDa
Protor-1, proteína observada con rictor-1
Prx, peroxiredoxina
Raptor, proteína reguladora asociada a mTOR

Rheb, homólogo de Ras enriquecido en el cerebro
Rictor, proteína asociada a mTOR insensible a rapamicina
RIPA, radioinmunoprecipitación
RNS, especies reactivas del nitrógeno
roGFP, proteína verde fluorescente redox sensible
ROS, especies reactivas del oxígeno
RPE, células epiteliales de pigmento retinal
RSK, familia de cinasas ribosomales S6
RTK, receptores tirosina cinasa
S6K, proteína ribosomal S6 cinasa beta-1
SAS, sulfasalazina
SBF, suero bovino fetal
SE, error estándar
Ser, serina
-SH, tiol
Shc, proteína adaptadora 1 Shc
Sistema xc-, sistema de transporte de cistina y glutamato sodio-independiente
SNAT2, transportador del sistema A tipo 2
SNC, sistema nervioso central
SOD, superóxido dismutasa
Sos, hijo de las proteínas sevenless
SREBP, elementos reguladores de esteroides
TCA, ácidos tricarbónicos
Thr, treonina
TNF, factor de necrosis tumoral
TrkA, receptor de tropomiosina tipo cinasa A
Trx, tiorredoxina
TR, Trx reductasa
TRAFs, factores asociados al receptor TNF
TSC1/2, complejo de esclerosis tuberosa
Tyr, tirosina
UCPH, 2-Amino-5,6,7,8-tetrahidro-4-(4-metoxifenil)-7-(naftaleno-1-yl)-5-oxo-4H-cromeno-3-carbonitrilo
ULK1, cinasa 1 activadora de la autofagia similar a unc-51
UK5099, mitocondrial 2-ciano-3-(1-fenil-1H-indol-3-il)-2-ácido propenóico
UV, ultravioleta
xCT, subunidad catalítica del sistema xc-

RESUMEN

El glutatión (GSH) es un antioxidante que juega un papel primordial en la protección de las células contra el estrés oxidante, mantiene la homeostasis redox y además participa en la desintoxicación de xenobióticos. En el cerebro la síntesis de GSH está limitada por la disponibilidad de cisteína y glutamato. La cistina y la cisteína son transportadas a través de la barrera hematoencefálica (BHE) y hacia los astrocitos y neuronas vía el sistema de transporte de cistina y glutamato sodio (Na^+)- independiente (sistema xc-), compuesto por la subunidad catalítica (xCT) y la de unión a membrana, la cadena pesada de antígeno 4F2 (4F2hc), el transportador de aminoácidos tipo L (LAT1) y el transportador de aminoácidos excitadores 3 (EAAT3). Las vías de señalización del blanco funcional de la rapamicina (mTOR) y de las neurotrofinas pueden estar involucradas en la regulación de los transportadores de aminoácidos para la síntesis de GSH. En este trabajo se encontró que la administración sistémica de L-butionina-S-R-sulfoximina (BSO) altera la homeostasis de GSH en el cerebelo una región del cerebro de ratón, y en un modelo *in vitro* de cultivo primario de astrocitos. La inyección ip de 6 mmol/kg de BSO disminuyó los niveles de GSH en el hígado. De las regiones de cerebro evaluadas, el cerebelo fue el único que presentó una respuesta redox, activando las vías de mTOR y del factor de crecimiento neuronal (NGF) y su receptor de tropomiosina tipo cinasa A (TrkA), llevando a un incremento en el transportador EAAT3 y en la concentración de GSH. Por otro lado, en astrocitos la disminución de GSH fue reversible 12 h después de retirar el BSO. La recuperación de los niveles de GSH se previno al inhibir simultáneamente a xCT, LAT1 y EAAT3. La inhibición del transporte de piruvato mitocondrial y la oxidación de ácidos grasos, así como la inhibición de mTOR disminuyeron los niveles de GSH y previnieron la recuperación después del tratamiento con BSO. Además, la inhibición de mTOR exacerbó los niveles de estrés oxidante y participó en la regulación bioenergética celular. Estos resultados sugieren que mTOR y el metabolismo mitocondrial regulan la homeostasis de GSH en los astrocitos.

ABSTRACT

Glutathione (GSH) is an essential component of intracellular antioxidant systems that plays a primordial role in the protection of cells against oxidative stress, maintaining redox homeostasis and xenobiotic detoxification. GSH synthesis in the brain is limited by the availability of cysteine and glutamate. Cystine/cysteine are transported through the endothelial cells of the blood-brain barrier (BBB) and into the astrocytes and neurons via the system xc⁻, which is composed of the catalytic subunit xCT and the heavy chain of 4F2 cell surface antigen (4F2hc), the L-type amino acid transporter 1 (LAT1) and the excitatory amino acid transporter 3 (EAAT3). The mammalian target of rapamycin (mTOR) and neurotrophins can activate signaling pathways that modulate amino acid transporters for GSH synthesis. The present study found that systemic L-buthionine-S-R-sulfoximine (BSO) administration selectively altered GSH homeostasis in the mice cerebellum and in an *in vitro* model of primary cortical astrocytes. Intraperitoneal treatment of mice with 6 mmol/kg of BSO depleted GSH in the liver. The cerebellum, but not other brain regions, exhibited a redox response, activating mTOR and the neuronal growth factor (NGF)/tropomyosin receptor kinase A (TrkA) signaling pathways that lead to an increase in the protein levels of the EAAT3 transporter, and an increase of the GSH concentration. Furthermore, inhibition of *de novo* GSH synthesis with BSO (500 μ M) induced GSH depletion in astrocytes. This depletion was reversible after 12 h of BSO withdrawal. Replenishment of the intracellular GSH pool was prevented by the simultaneous inhibition of xCT, EAAT3 and LAT1. Inhibition of mitochondrial pyruvate transport and free fatty acid oxidation as well as the mTOR signaling depleted GSH and prevented the recovery of the intracellular GSH pool after BSO withdrawal. Moreover, mTOR inhibition exacerbated oxidative stress and was found to regulate bioenergetics in astrocytes after BSO withdrawal. Our results suggest that mTOR signaling and mitochondrial metabolism regulate GSH homeostasis in astrocytes.

INTRODUCCIÓN

Estrés oxidante y homeostasis redox

Las especies reactivas del oxígeno (ROS) son compuestos derivados del oxígeno que pueden recibir o donar electrones participando en reacciones nucleofílicas, electrofílicas y/o redox (Circu y Aw, 2010; Halliwell y Cross, 1994; Trachootham et al., 2008). Las ROS comprenden radicales libres y no radicales, como el radical hidroxilo (OH^\bullet), el anión superóxido ($\text{O}_2^{\bullet-}$) y el peróxido de hidrógeno (H_2O_2) (Olsen et al., 2013). Por otro lado, las especies reactivas del nitrógeno (RNS) derivan de nitrógeno y oxígeno e incluyen al óxido nítrico (NO^\bullet), al radical dióxido de nitrógeno (NO_2^\bullet) y el peroxinitrito (OONO^\bullet) (Olsen et al., 2013; Ye et al., 2015).

La reducción del oxígeno molecular (O_2) es el principal mecanismo para la formación de ROS. En la célula, la mitocondria es la principal fuente generadora de ROS a través de la cadena transportadora de electrones, principalmente con la reducción de O_2 a $\text{O}_2^{\bullet-}$ (Olsen et al., 2013). El $\text{O}_2^{\bullet-}$ generado puede ser dismutado generando H_2O_2 a través de la acción de las superóxido dismutasas (SOD) (Finkel, 2011). Además, el $\text{O}_2^{\bullet-}$ y el H_2O_2 fomentan la formación del OH^\bullet a través de las reacciones de Fenton/Haber-Weiss. La reacción de Fenton es un proceso de reducción a partir de H_2O_2 y iones metálicos de hierro o cobre (Fe^{2+} y Cu^{2+}); posteriormente en la reacción de Haber-Weiss se genera OH^\bullet a partir de H_2O_2 y $\text{O}_2^{\bullet-}$, la reacción es catalizada por Fe^{3+} y Cu^{3+} (Forman, 2016; Halliwell y Cross, 1994). Las enzimas nicotinamida-adenina-dinucleótido-fosfato (NADPH) oxidasas (NOX) son las únicas enzimas cuya función es la de generar ROS ($\text{O}_2^{\bullet-}$ o H_2O_2), a diferencia de las otras fuentes que generan ROS como subproductos, estas enzimas tienen como función primaria la producción de ROS que participan en procesos fisiológicos, éstas representan la segunda fuente importante de formación de ROS en la célula (Coyoy y Moran, 2012; Ye et al., 2015).

Otras fuentes intracelulares de ROS incluyen a la xantina oxidasa, las ciclooxigenasas, las enzimas citocromo p450, y las lipooxigenasas. Los microsomas y peroxisomas también son fuentes de ROS, junto con los neutrófilos y macrófagos que poseen mecanismos dependientes del oxígeno como defensa en contra de microorganismos patógenos (Finkel, 2011; Schrader y Fahimi, 2006; Ye et al., 2015).

La formación de RNS comienza con la síntesis de NO^\bullet , a partir de arginina, oxígeno y NADPH, catalizada por la NO^\bullet sintasa (NOS). En la presencia de $\text{O}_2^{\bullet-}$, el NO^\bullet se transforma en OONO^- , un potente agente oxidante. La mayoría del OONO^- se sintetiza dentro de las células fagocíticas del sistema inmune, a través de la NOS inducible (iNOS) y las NOX (Olsen et al., 2013).

Las ROS/RNS pueden actuar como moléculas de señalización teniendo efecto en la estabilidad, la expresión, función y actividad de múltiples proteínas controlando procesos celulares (Finkel, 2011; Reczek y Chandel, 2015). En condiciones fisiológicas el balance entre la generación y la eliminación de las ROS/RNS mantiene un funcionamiento adecuado dentro de la célula (Trachootham et al., 2008). Sin embargo, el desbalance entre el incremento de los niveles de ROS/RNS y la habilidad de la célula de metabolizar/desintoxicarlas genera un estado en el cual se pierde la homeostasis llamado estrés oxidante. Las ROS/RNS a altas concentraciones son deletéreas generando daño oxidante en las biomoléculas como DNA, lípidos, proteínas, etc. (Circu y Aw, 2010; Ye et al., 2015). La generación de estrés oxidante resulta en modificaciones oxidantes que pueden llevar a la pérdida de función, envejecimiento y hasta muerte celular (Forman, 2016; Olsen et al., 2013).

Para contrarrestar la producción excesiva de ROS/RNS y mantener la homeostasis redox celular, los organismos poseen sistemas antioxidantes que se dividen en enzimáticos y no enzimáticos (Durackova, 2010; Trachootham et al., 2008). Los antioxidantes incluyen

moléculas de bajo peso molecular como el glutatión o γ -L-glutamyl-L-cisteinilglicina (GSH), así como diversas proteínas antioxidantes con ubicaciones subcelulares distintas (Finkel, 2011). El sistema de la tiorredoxina (Trx) es otro antioxidante importante compuesto por la Trx y la Trx reductasa (TR), que participan en la reducción de proteínas oxidadas (Trachootham et al., 2008). Las enzimas catalasa (CAT) y las peroxiredoxinas (Prx) se encargan de la desintoxicación de peróxidos, mientras que las SOD catalizan la dismutación del $O_2^{\bullet -}$ (Holmstrom y Finkel, 2014). Otros antioxidantes endógenos son: el ácido úrico, el ácido lipico y el ubiquinol, así como los que se obtienen de la dieta, entre los que se incluyen las vitaminas C y E, los carotenoides y los flavonoides (Durackova, 2010; Ye et al., 2015). El factor nuclear 2 derivado del factor eritroide 2 (Nrf2) es un factor transcripcional activado por estrés oxidante y electrófilos. Una vez en el núcleo se une a los elementos de respuesta antioxidante (ARE) activando la transcripción de genes que funcionan como antioxidantes, de enzimas de desintoxicación de fase II, así como enzimas involucradas en la síntesis de GSH, todas estas proteínas juegan papeles primordiales en la defensa celular contra el estrés oxidante (Trachootham et al., 2008).

El sistema nervioso central (SNC) es especialmente susceptible al daño oxidante, siendo las neuronas y los oligodendrocitos más sensibles que los astrocitos y la microglía. Esto se debe al alto consumo de O_2 , a que tiene una alta concentración de lípidos que pueden ser susceptibles a la lipoperoxidación y a que presentan menores niveles de defensas antioxidantes en comparación con otros órganos (Patel, 2016; Salim, 2017).

Glutatión (GSH)

El GSH es el tiol (-SH) de bajo peso molecular predominante en los tejidos de los mamíferos con concentraciones que van de 1 a 10 mM, siendo el hígado el órgano con mayor concentración (Janssen-Heininger et al., 2013). Este antioxidante se encarga del mantenimiento de la homeostasis redox en la célula, almacén de cisteína y glutamato,

desintoxicación de xenobióticos y metabolitos a través de las GSH S-transferasas (GST) y de la formación de puentes disulfuro, así como la protección de residuos de cisteína para evitar la oxidación de proteínas. Estos mecanismos son importantes en la regulación de diversas funciones celulares tales como la proliferación y la apoptosis (Aquilano et al., 2014; Lu, 2013; Meister, 1981; Wu et al., 2004).

Dentro de la célula, este -SH es mantenido en su forma reducida por la enzima GSH reductasa (GR) la cual reduce el grupo disulfuro del GSH disulfuro (GSSG) a través de una reacción dependiente de la donación de electrones provenientes del NADPH iniciando un ciclo redox (Lu, 2009; Meister, 1981). El cociente GSH/GSSG es un indicador del ambiente redox, estos dos compuestos son la pareja redox más abundante dentro de la célula (Schafer y Buettner, 2001).

El GSH se sintetiza a partir de los aminoácidos glutamato, cisteína y glicina, en dos reacciones dependientes de adenosín trifosfato (ATP). En la primera, la enzima cisteína-glutamato ligasa (GCL), cataliza la formación del L- γ -glutamil-L-cisteína, mientras que en la segunda reacción la glutatión sintetasa (GS) agrega el aminoácido glicina (Lu, 2013). Bajo condiciones fisiológicas la GCL es regulada por la unión competitiva de GSH, generando un proceso de retroalimentación negativa cuando hay incremento en la concentración de GSH (Richman y Meister, 1975). Además, la cisteína es el aminoácido limitante para la síntesis de GSH. Ésta puede ser obtenida de la ruptura de proteínas obtenidas de la dieta y a partir de la vía de la transsulfuración. También, la actividad de la GCL es un paso limitante en el proceso (Lu, 2013; Vitvitsky et al., 2006). Una vez sintetizado el GSH se exporta al medio extracelular a través de transportadores de membrana. En la porción extracelular de la membrana existen peptidasas como la γ -glutamil transpeptidasa (γ GT) que generan γ -glutamil y el dipéptido CysGly que posteriormente es hidrolizado para que

los aminoácidos puedan ser importados nuevamente por las células para continuar el ciclo de síntesis de GSH y/o proteínas (Dringen et al., 1999; Dringen et al., 2001).

Dada la importancia del GSH se han desarrollado diferentes estrategias para modelar la falta de éste y conocer las vías de señalización que participan en su regulación. La más utilizada, es el uso de L-butionina-S-R-sulfoximina (BSO), el inhibidor específico de la GCL más efectivo que bloquea la síntesis *de novo* de GSH. BSO se une reversiblemente a la GCL como un análogo del primer producto de la síntesis. Por acción del BSO, la poza preexistente de GSH es consumida gradualmente, ya sea por reacciones enzimáticas o por su exportación fuera de la célula (Limón-Pacheco y Gonsebatt, 2007).

Glutión en el SNC

El cerebro contiene diferentes concentraciones de GSH (2-3 mM), las regiones con mayores niveles son la corteza y el cerebelo (Kang et al., 1999). El GSH realiza funciones específicas en el SNC; este tripéptido es considerado un neuromodulador/neurotransmisor que puede regular los receptores de glutamato del tipo N-metil-D-aspartato (NMDA) y también participa en la proliferación y diferenciación neuronal (Aoyama et al., 2008; Dringen, 2000; Janaky et al., 1999).

El contenido de GSH varía en los diferentes tipos celulares. Las neuronas tienen menor concentración comparada con los astrocitos (Rice y Russo-Menna, 1998). Los astrocitos participan en el metabolismo antioxidante y la desintoxicación de xenobióticos en el cerebro, además, liberan GSH a través de la proteína 1 de resistencia a multidroga (MRP1) para proveer los precursores necesarios para la síntesis de GSH en neuronas (Dringen et al., 1997; Hirrlinger y Dringen, 2005). Como se mencionó anteriormente, el GSH liberado es procesado vía la γ GT generando γ -glutamil y el dipéptido CysGly que es hidrolizado por la dipeptidasa neuronal para transportar cisteína a la neurona y ésta pueda sintetizar su propio GSH (Fig. 1) (Dringen et al., 1999; Dringen et al., 2001).

La exposición a metales, pesticidas, radiación ionizante, luz UV y a fármacos puede afectar los niveles de GSH (Limón-Pacheco y Gonsebatt, 2009). Las alteraciones en el metabolismo de GSH son comunes en el envejecimiento, en desórdenes neuropsiquiátricos y en las enfermedades neurodegenerativas. Los niveles bajos de GSH, alteraciones en las enzimas GSH-dependientes y la alta producción de ROS, han sido asociados a neuropatías provocadas por exposición a tóxicos ambientales y a enfermedades tales como Parkinson, Huntington, Alzheimer y la degeneración cerebelar. Sin embargo, la participación del GSH en el desarrollo de estas enfermedades neurodegenerativas todavía sigue siendo estudiada (Aoyama et al., 2008; Aoyama y Nakaki, 2013; Gu et al., 2015; Johnson et al., 2012). Debido a que el BSO no es capaz de cruzar la barrera hematoencefálica (BHE) fácilmente, su uso constituye un acercamiento para estudiar los efectos en el cerebro ante una depleción sistémica de GSH (Limón-Pacheco y Gonsebatt, 2007).

Transportadores de aminoácidos asociados a la síntesis de GSH

Debido a que los aminoácidos no pueden cruzar la membrana plasmática, el transporte de aminoácidos, principalmente cisteína y cistina (su forma oxidada), también es muy importante en la síntesis de GSH (Lu, 2009; Wu et al., 2004). Además, el GSH y la cisteína no pueden atravesar la BHE y llegar al SNC. La cistina es transportada del torrente sanguíneo a las células endoteliales de la BHE vía el sistema de transporte de cistina y glutamato sodio (Na^+)- independiente (sistema xc-), compuesto por dos subunidades la subunidad catalítica (xCT) y la de unión a membrana, la cadena pesada de antígeno 4F2 (4F2hc) (Sato et al., 1999; Shih et al., 2006). Posteriormente la cistina es reducida dentro de la célula y la cisteína transportada al cerebro a través del transportador 1 de aminoácidos de tipo-L (LAT1), este transportador también transporta metionina que puede llevar a la síntesis de cisteína a través de la vía de transulfuración (Killian y Chikhale, 2001; Wade y Brady, 1981). Una vez dentro del cerebro la cistina es transportada a los astrocitos a través

del intercambiador xCT. Debido a la característica excitotóxica del glutamato, los transportadores de aminoácidos excitadores 1 y 2 (EAAT1 y EAAT2) del sistema $x\text{-AG Na}^+$ -dependientes, se encargan de remover el glutamato que libera el xCT (Valdovinos-Flores y Gonsebatt, 2012). Las neuronas dependen de la cisteína que le proveen los astrocitos y la transportan a través del transportador EAAT3 también conocido como el acarreador de aminoácidos excitadores 1 (EAAC1) (Fig. 1) (Himi et al., 2003; Zerangue y Kavanaugh, 1996).

Los transportadores de aminoácidos tienen papeles cruciales, no sólo proveen los precursores para la síntesis de GSH sino que también regulan el crecimiento y la proliferación celular por lo tanto, las vías de señalización que regulan estos procesos tienen una importante relación con la expresión de los transportadores de nutrientes (McCracken y Edinger, 2013).

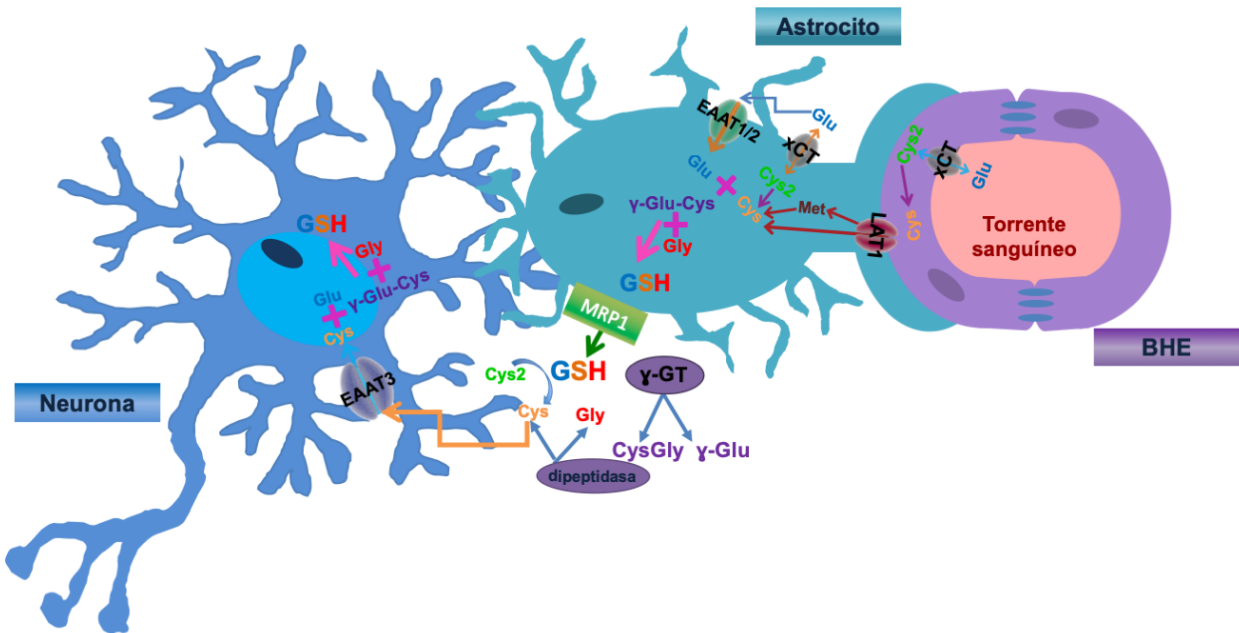


Figura 1. Transporte de aminoácidos en el astrocito y la neurona para la síntesis de GSH. La Cys2 es transportada del torrente sanguíneo a las células endoteliales de la BHE vía xCT. La Cys2 es reducida dentro de la célula y la Cys transportada al cerebro a través del transportador LAT1, este transportador también transporta Met que puede llevar a la síntesis de Cys a través de la vía de la transulfuración. Una vez dentro del cerebro la Cys2 es transportada a los astrocitos a través del intercambiador xCT. Los transportadores EAAT1 y EAAT2 transportan el glutamato que libera el xCT. (continúa)

Posteriormente, los astrocitos liberan GSH a través de la MRP1, éste es procesado vía la γ GT generando γ -glutamil y CysGly que es hidrolizado por la dipeptidasa neuronal para que la neurona transporte Cys a través del transportador EAAT3 y pueda sintetizar su propio GSH. Abreviaturas: γ GT, γ -glutamil transpeptidasa; BHE, barrera hematoencefálica; Cys, cisteína; Cys2, cistina; EAAT1/2, transportadores de aminoácidos excitadores 1 y 2; EAAT3, transportador de aminoácidos excitadores 3; Glu; glutamato Gly; glicina GSH, glutatión; Met, metionina; MRP1, proteína 1 de resistencia a multidroga; LAT1, transportador 1 de aminoácidos de tipo-L; sistema xc-, sistema de transporte de cistina y glutamato Na^+ - independiente; xCT, subunidad catalítica del sistema xc-.

Vías de señalización

Las células utilizan las vías de señalización para regular su actividad. La mayoría son activadas por estímulos externos que activan receptores presentes en la membrana plasmática como los receptores asociados a proteínas G (GPCRs) y los receptores tirosina cinasas (RTKs). Sin embargo, algunas también responden a información generada dentro de la célula en forma de mensajeros metabólicos. Estas vías de señalización transmiten, procesan, codifican e integran señales, para generar respuestas como por ejemplo cambios en la actividad enzimática, expresión génica o la actividad de canales iónicos (Berridge, 2014; Kholodenko, 2006).

En este trabajo analizamos las vías de señalización que activan al blanco funcional de la rapamicina (mTOR) así como la vía activada por el factor de crecimiento neuronal (NGF).

Blanco funcional de la rapamicina (mTOR)

Los factores de crecimiento a través de sus receptores, activan la vía de señalización de la fosfatidilinositol 3-cinasa (PI3K)/AKT/mTOR y aumentan la expresión de los transportadores de nutrientes, permitiendo la entrada de éstos a la célula para el crecimiento y otras funciones importantes (Edinger, 2007). Estas vías de señalización también responden a la disponibilidad y el requerimiento de nutrientes (McCracken y Edinger, 2013).

mTOR es una cinasa de serina (ser) /treonina (thr) de la familia de las cinasas relacionadas a PI3K (PIKK). Esta proteína se encarga de regular el crecimiento celular (el incremento de masa celular, síntesis de proteínas y la proliferación), así como el metabolismo celular en respuesta a diferentes estímulos como el contenido de aminoácidos, cambios en la

bioenergética celular, factores de crecimiento y estrés oxidante, entre otros (Garza-Lombó et al., 2018b). Forma dos complejos diferentes, el complejo sensible a rapamicina y nutrientes o mTORC1 y el complejo insensible a rapamicina o mTORC2 (Saxton y Sabatini, 2017). El primero está compuesto por 5 proteínas: mTOR, la proteína reguladora asociada a mTOR (Raptor), el sustrato de Akt, rico en prolinas de 40 kDa (PRAS40), la proteína letal 8 de mamífero con Sec13 (mLST8, también conocida como GbL), y la proteína de interacción con mTOR (DEPTOR) (Alayev y Holz, 2013). Mientras que el mTORC2; está compuesto por 6 proteínas: mTOR, la proteína asociada a mTOR insensible a rapamicina (Rictor), la proteína interactiva de la cinasa de mamífero activada por estrés (mSINI), la proteína observada con rictor-1 (Protor-1), mLST8 y DEPTOR (Alayev y Holz, 2013; Kim y Guan, 2011).

La activación de la vía PI3K/AKT a través de los receptores de factores de crecimiento inactiva el complejo de esclerosis tuberosa (TSC), un regulador negativo de mTORC1. TSC es un complejo heterotrimérico compuesto por TSC1/TSC2; TSC2 actúa como una proteína aceleradora de la actividad GTPasa (GAP) e inactiva al homólogo de Ras enriquecido en el cerebro (Rheb) un activador de mTORC1. La activación de mTORC1 también requiere que se encuentre cerca de los lisosomas lo cual es regulado por la presencia de aminoácidos y nutrientes vía las proteínas GTPasas Rag, el mTORC1 fosforila a la proteína ribosomal S6 cinasa beta-1 (S6K) y a la proteína de unión al factor de inicio de la traducción eucariota eIF-4E (4EBP-1), los cuales regulan la traducción de mRNAs, la biogénesis mitocondrial, la glicólisis y al factor inducible de hipoxia 1-alfa (HIF1 α) (Garza-Lombó et al., 2018b; Kim y Guan, 2011). mTORC1 también puede regular la síntesis lipídica y de nucleótidos a través de la proteína de unión a elementos reguladores de esteroides (SREBP) y a través de la activación del factor de transcripción 4 (ATF4) respectivamente, así como inhibir la autofagia al fosforilar la cinasa 1 activadora de la autofagia similar a unc-51 (ULK1) (Garza-

Lombó et al., 2018b). Además, un reporte reciente demostró que mTORC1 controla la actividad y la biogénesis mitocondrial, al promover la traducción de mRNAs de genes mitocondriales a través de 4EBP-1 (Fig. 2) (Morita et al., 2013).

Por otro lado, mTORC2 controla la proliferación y supervivencia vía la activación de las proteínas cinasas de la familia AGC (nombrada por las proteínas cinasas A, G y C) como la proteína cinasa C (PKC) que se encargan de regular el remodelamiento del citoesqueleto y la migración celular. La fosforilación de AKT por mTORC2 incrementa la actividad de AKT induciendo la fosforilación de sustratos específicos como la proteína forkhead box O1/3a (FOXO1/3a) o la glucógeno sintasa cinasa 3 (GSK3). Además, también se ha demostrado que mTORC2 regula el metabolismo de aminoácidos y de glucosa (Fig. 2) (Garza-Lombó et al., 2018b; Saxton y Sabatini, 2017). En este trabajo se estudió el papel de mTOR en la regulación del transporte de aminoácidos.

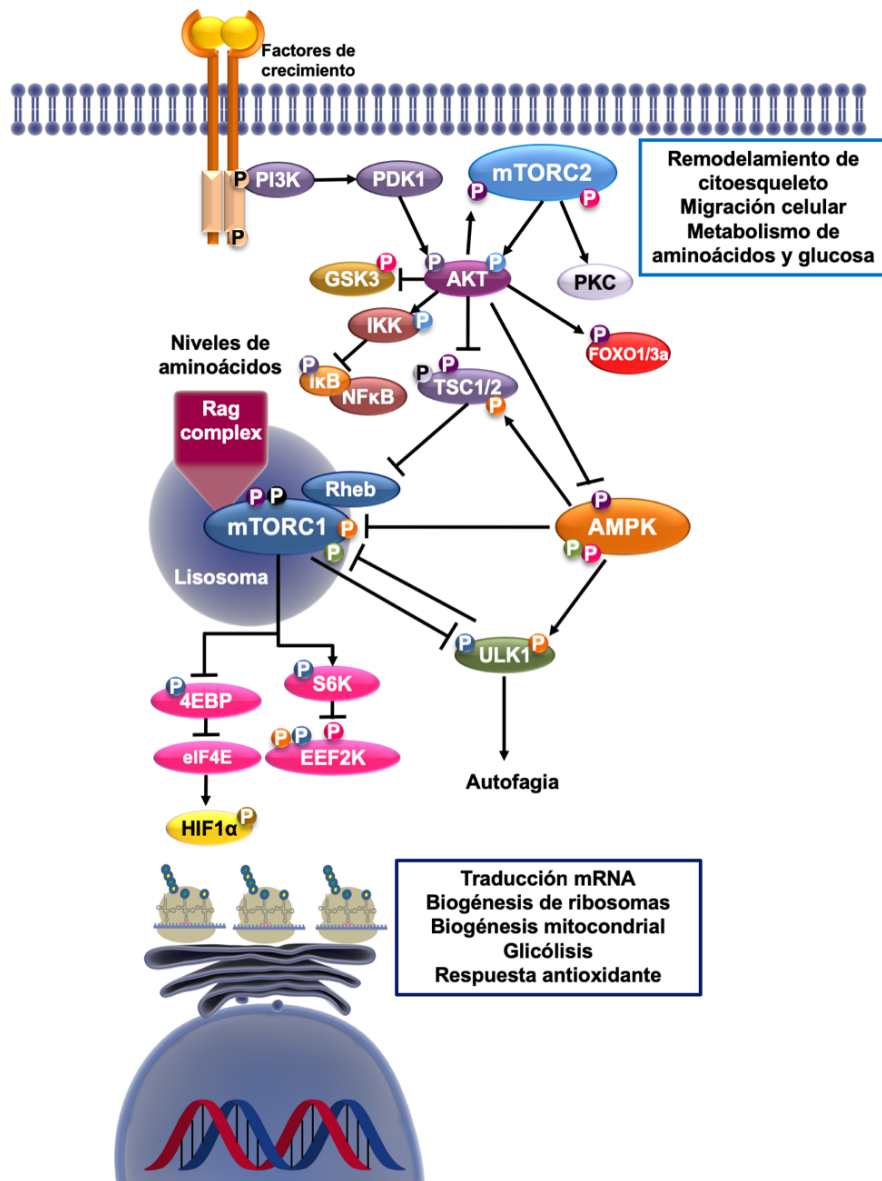


Figura 2. Vía de señalización de mTOR. La activación de la vía PI3K/AKT a través de los receptores de factores de crecimiento inactivan a TSC1/TSC2 que a su vez inactiva al Rheb un activador de mTORC1. La activación de mTORC1 también requiere que se encuentre cerca de los lisosomas regulado por la presencia de aminoácidos y nutrientes vía las proteínas Rag. mTORC1 fosforila a S6K y a 4EBP-1, los cuales regulan HIF1 α , la traducción de mRNAs, la biogénesis mitocondrial, la glicólisis y la respuesta antioxidante. mTORC1 también fosforila a ULK1 inhibiendo la autofagia, que puede ser activada a través de AMPK que activa TSC1/2 y también inhibe a mTORC1. mTORC2 controla la proliferación y supervivencia vía PKC y fosforila a AKT que a su vez fosforila sustratos como FOXO1/3a o GSK3 o a IKK que fosforila I κ B, resultando en la activación de NF κ B; regulando el remodelamiento del citoesqueleto, la migración celular, la supervivencia y el metabolismo de aminoácidos y glucosa. Abreviaturas: 4EBP-1, la proteína de unión al factor de inicio de la traducción eucariota eIF-4E; AMPK, proteína cinasa activada por AMP; EIF2K, cinasa del factor de elongación eEF2; eIF4E, factor de iniciación de traducción 4; FOXO1/3a, proteína forkhead box O1/3a; GSK3, glucógeno sintasa cinasa 3; HIF1 α , factor inducible de hipoxia 1-alfa; I κ B, inhibidor de κ B; IKK, cinasa de I κ B; mTOR, blanco funcional de la rapamicina; NF κ B, factor nuclear potenciador de las cadenas ligeras kappa de las células B activadas; PDK1, piruvato deshidrogenasa cinasa; PI3K, fosfatidilinositol 3-cinasa; PKC, proteína cinasa C; Rheb, homólogo de Ras enriquecido en el cerebro; S6K, proteína ribosomal S6 cinasa beta-1; TSC1/2, complejo de esclerosis tuberosa; ULK1, cinasa 1 activadora de la autofagia similar a unc-51.

mTOR y los transportadores de aminoácidos

El mTORC1 puede ser activado cuando los aminoácidos son abundantes. En ausencia de nutrientes e hipoxia, los niveles de ATP disminuyen rápidamente activando a la cinasa activada por AMP (AMPK), quien a su vez fosforila a TSC2 y Raptor, inactivando a mTORC1 (Fig. 2) (Kim y Guan, 2011; Poncet y Taylor, 2013). Se ha sugerido que los transportadores de aminoácidos pueden influenciar la actividad de mTORC1 regulando la concentración intracelular de aminoácidos o al actuar como sensores llamados “transceptores” que inician vías de señalización. Además, los transportadores proveen la fuente primaria de nitrógeno celular y participan en la síntesis de nucleótidos, carbohidratos, proteínas y GSH (Fuchs y Bode, 2005; Goberdhan et al., 2016; Kim y Guan, 2011). Un aumento en la disponibilidad de aminoácidos esenciales aumenta la expresión de transportadores de aminoácidos como el transportador del sistema A tipo 2 (SNAT2) y LAT1, lo que representa una respuesta adaptativa para mejorar la entrega de aminoácidos y, en consecuencia, aumentar la señal de crecimiento mediada por mTORC1 (Poncet y Taylor, 2013). Además, existen estudios que indican que mTOR puede regular el aumento de los transportadores de aminoácidos (Edinger, 2007). Esta doble regulación hace que sea difícil distinguir entre causa y efecto, si es mTOR quien activa a los transportadores o los transportadores a mTOR (McCracken y Edinger, 2013).

Señalización de mTOR en el SNC

En el cerebro mTORC1 es parte de las vías de señalización activadas por neurotransmisores y neurotrofinas (Garza-Lombó y Gonsebatt, 2016). mTOR está involucrado en numerosos procesos en el SNC incluyendo la regulación del neurodesarrollo, la plasticidad sináptica, la neurogénesis en adultos, así como la memoria y el aprendizaje. Durante el envejecimiento, el mTOR incrementa la neurogénesis, inhibe la autofagia y también regula cambios epigenéticos (Garza-Lombó y Gonsebatt, 2016).

La desregulación de mTOR se ha relacionado a diversos desórdenes cerebrales asociados a la disfunción neuronal y la muerte celular entre ellos, la neurodegeneración, epilepsia, autismo y alteraciones en el comportamiento (Crino, 2016; Garza-Lombó et al., 2018b).

Factor de crecimiento neuronal (NGF)

El NGF es una neurotrofina que se descubrió como una molécula que regula la sobrevivencia y maduración de las neuronas en el desarrollo (Sofroniew et al., 2001). El NGF es sintetizado en la forma de un precursor de 30-35 kDa que debe ser procesado por proteasas para dar origen a la neurotrofina madura de aproximadamente 13 kDa (Friedman y Greene, 1999; Lu et al., 2005).

El NGF puede unirse a dos tipos de receptores transmembranales. El primero es el receptor de tropomiosina tipo cinasa A (TrkA), que es un RTK. Este receptor al unirse con su ligando NGF se dimeriza y transfosforila activando tirosinas (Tyr) dentro y fuera de su dominio de cinasa. Esta transfosforilación genera sitios específicos de unión para proteínas adaptadoras que contienen dominios SH2 como la fosfolipasa C gamma (PLC γ), PI3K y Shc una proteína adaptadora que promueve la activación de Ras a través de la unión del complejo Grb2-Sos. Cuando el NGF se une a su receptor promueve la iniciación de diversas vías de señalización a través de la fosforilación específica de residuos de Tyr (490 y 785) en el receptor. Algunas de las vías de señalización que se activan a través de las fosforilación del residuo Tyr 490, son las cinasas activadas por mitógenos/ cinasa regulada por señales extracelulares (MAPK/ERK) y la de PI3K/AKT que también puede fosforilar a la cinasa de I κ B (IKK) que fosforila al inhibidor de κ B (I κ B), resultando en la activación del factor nuclear potenciador de las cadenas ligeras kappa de las células B activadas (NF κ B); mientras que la Tyr 785 induce la vía de la PLC γ /proteína cinasa C delta (PKC δ) que también puede activar la vía de las MAPKs (Fig. 3) (Huang y Reichardt, 2003; Khwaja, 1999; Reichardt, 2006; Sofroniew et al., 2001). Estas vías están involucradas en las funciones de

sobrevivencia y diferenciación de esta neurotrofina. El segundo tipo son los receptores p75^{NTR} que pertenecen a la superfamilia de receptores del factor de necrosis tumoral (TNF) y son considerados de baja afinidad; su activación está asociada con diferentes vías de señalización (Friedman y Greene, 1999; Lu et al., 2005). La activación de la de la GAP Cdc42 por el receptor, activa a la cinasa reguladora de la señal de apoptosis (ASK1), la cual a su vez activa la cascada de las MAPK/ de la cinasa c-jun N -terminal (JNK) que puede activar una respuesta de muerte celular por apoptosis (Reichardt, 2006). El receptor p75^{NTR} interactúa con los factores asociados al receptor TNF (TRAFs) dando lugar a la activación de NFκB otra vía importante de este receptor. p75^{NTR} se une a TRAF6 que, en un complejo con la cinasa asociada al receptor de interleucina 1 (IRAK) activa a IKK promoviendo la actividad de NFκB el cual activa respuestas de sobrevivencia celular (Reichardt, 2006; Sofroniew et al., 2001) (Fig. 3).

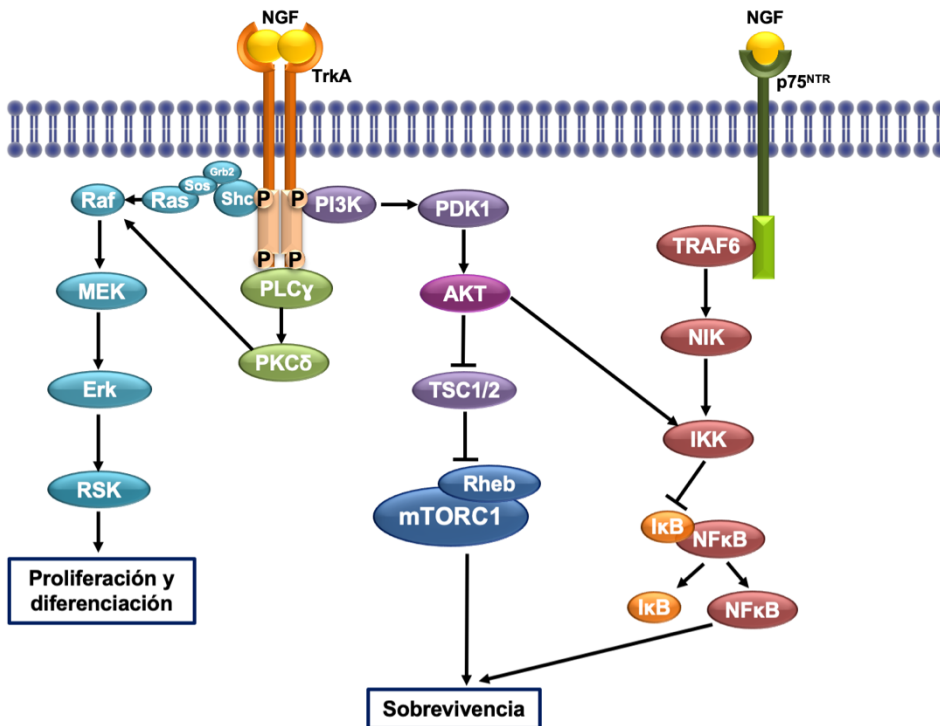


Figura 3. Vía de señalización del NGF. NGF se une a dos tipos de receptores transmembranales, el receptor TrkA el cual se dimeriza y transfosforila, activando las siguientes vías de señalización: MAPK/ERK, PI3K/AKT/TSC1/2/mTOR o PI3K/AKT/IKK/ IκB/NFκB y PLCγ/PKCδ que también puede activar la vía de las MAPKs llevando a respuestas de proliferación, diferenciación y sobrevivencia. (continúa)

Los receptores p75^{NTR}, activan a la GAP Cdc42 que activa a la cinasa ASK1, la cual a su vez activa la cascada de las MAPK/JNK que puede activar una respuesta de muerte celular por apoptosis. p75^{NTR} también se une a TRAF6 que, en un complejo con IRAK activa a IKK que fosforila a I κ B promoviendo la actividad de NF κ B el cual activa respuestas de supervivencia celular. Abreviaturas: ASK1, a la cinasa reguladora de la señal de apoptosis; ERK, cinasa regulada por señales extracelulares; GAP, GTPasa; GRB2, proteína 2 de unión al receptor de factores de crecimiento; I κ B, inhibidor de κ B; IKK, cinasa de I κ B; IRAK, cinasa asociada al receptor de interleucina 1; JNK, cinasa c-jun N-terminal; mTOR, blanco funcional de la rapamicina; NF κ B, factor nuclear potenciador de las cadenas ligeras kappa de las células B activadas; PDK1, piruvato deshidrogenasa cinasa; PI3K, fosfatidilinositol 3-cinasa; PKC δ , proteína cinasa C delta; PLC γ , fosfolipasa C gamma; Rheb, homólogo de Ras enriquecido en el cerebro; RSK, familia de cinasas ribosomales S6; Shc, proteína adaptadora 1 Shc; Sos, hijo de las proteínas sevenless; TRAF6; factor 6 asociado al receptor TNF; TrkA; tropomiosina tipo cinasa A; Tyr, tirosina; TSC1/2, complejo de esclerosis tuberosa.

Señalización de NGF en la respuesta antioxidante

Existe evidencia de que el NGF puede inducir respuestas antioxidantes en diferentes condiciones experimentales, no sólo en el SNC, pero en otros tejidos no neuronales, así como regular el transporte de aminoácidos y la síntesis de GSH.

En la línea celular de tumores de médula adrenal de ratón (PC12) el tratamiento con NGF aumentó el consumo de cisteína y cistina llevando a un incremento en los niveles de GSH (Pan y Perez-Polo, 1996). Del mismo modo el NGF incrementa los niveles de las enzimas antioxidantes CAT y la GPx (Sampath et al., 1994). En células PC12 tratadas con H₂O₂, el NGF estimuló la síntesis de GSH y la actividad de la GCL, la GPx y la glucosa 6-fosfato deshidrogenasa (G6P-D) (Pan y Perez-Polo, 1993). El NGF también protegió a las células del daño inducido por H₂O₂ a través de la inducción de la actividad de la CAT y GPx (Jackson et al., 1990). Todos estos estudios sugieren que esta neurotrofina está involucrada en los procesos de regulación del GSH.

Adicionalmente, en modelos *in vivo*, se ha demostrado que el NGF restaura los niveles de enzimas antioxidantes como la SOD, la GPx y la CAT en diferentes regiones del cerebro de ratas envejecidas (Nistico et al., 1992). En un modelo de Parkinson se demostró que el NGF puede restaurar los niveles de la SOD y la GPx (Ninkovic et al., 2000); en un modelo de Huntington el NGF puede mantener el cociente GSH/GSSG en las regiones del cerebro, estriado e hipocampo (Maksimovic et al., 2001); y en un modelo de Alzheimer el tratamiento con NGF restauró los niveles de la GR y la GPx (Cruz-Aguado et al., 1999). También, los

ratones transgénicos que sobre expresan NGF presentan un incremento en los niveles de GSH en cerebro, hígado y plasma (Arsenijevic et al., 2007). Finalmente, en nuestro grupo de trabajo se demostró que la vía de NGF/TrkA/AKT/IKK/I κ B /NF κ B es activada en el hígado de ratón después del tratamiento con agentes que consumen GSH, induciendo una respuesta antioxidante y de sobrevivencia (Valdovinos-Flores y Gonsebatt, 2013).

Estos resultados revelan la función neuroprotectora del NGF no sólo en enfermedades neurodegenerativas, envejecimiento y contra estrés oxidante en tejidos y células neuronales; sino también en otros tejidos periféricos.

JUSTIFICACIÓN

El estudio de la regulación de la homeostasis de GSH y la respuesta a estrés oxidante en el SNC, es de gran interés por las aplicaciones potenciales que puede tener en los tratamientos para prevenir neuropatías, neurodegeneración y el envejecimiento prematuro. Los resultados de este trabajo ayudarán a entender los mecanismos moleculares que participan en la regulación de la homeostasis de GSH con el fin de diseñar estrategias de neuroprotección y prevención.

Asimismo, el mTOR se ha convertido en un blanco terapéutico para inhibir la proliferación tumoral, por lo que el conocimiento de su participación en la regulación de la homeostasis de GSH puede aportar argumentos para tomar con cautela las terapias que utilizan inhibidores de mTOR en otros padecimientos como las enfermedades neurodegenerativas.

HIPÓTESIS

Los cambios en el estado redox y en la homeostasis de GSH generados por el BSO, inducirán un incremento en el transporte de aminoácidos involucrados en la síntesis de GSH y con las vías de señalización de mTOR y NGF en el SNC.

OBJETIVOS

Objetivo modelo *in vivo*

- Investigar los cambios en la homeostasis de GSH en el SNC inducidos por un tratamiento sistémico con BSO; y su asociación con el transporte de aminoácidos involucrados en la síntesis de GSH y la activación de las vías de señalización de mTOR y NGF.

Objetivo modelo *in vitro*

- Investigar en cultivos primarios de astrocitos corticales, los cambios en la homeostasis de GSH inducidos por el tratamiento con BSO, así como el papel de la vía de señalización de mTOR.

MATERIAL Y MÉTODOS

Reactivos

Los anticuerpos contra fosforilado (p)-p70 S6K (Thr 389, #9234), p-mTOR (Ser 2448, #5536), p-TrkA (Tyr 490, #9141), p70 S6K (#2708), mTOR (#2983), NGF (#2046) p-4EBP1 (Thr 37/46, #2855), 4EBP1 (#9452), p-AKT (Ser 473, #9271), AKT (#9272), el secundario anti-conejo (#7074) y el marcador biotinilado (#7727) se obtuvieron de Cell Signaling Technology (Danvers, MA, EUA). Los anticuerpos contra EAAT3 (ab124802), TrkA (ab76291), xCT (ab37185), NeuN (ab177487) y NGF (ab52918, para inmunofluorescencia) se adquirieron en Abcam (Cambridge, Reino Unido). Los anticuerpos contra LAT1 (sc-134994), mtTFA (sc-376672), GCLc (sc-390811) y GCLm (sc-55586) se obtuvieron de Santa Cruz Biotechnology (Santa Cruz, CA, EUA). El anticuerpo contra β -tubulina (T4026), el BSO, el O-ftalaldehído (OPA, P0657-5G) y las microplacas (Greiner high and medium binding 96 well plates M4686-40EA) fueron comprados en Sigma-Aldrich (Darmstadt, Alemania). El anticuerpo contra β -actina (GT5512) en GeneTex (Irvine, CA, EUA). El anticuerpo secundario anti-ratón (61-6520), el ensayo de cuantificación de proteína Pierce de ácido bicinonínico (BCA), el medio de cultivo Dulbecco's Modified Eagle Medium: Nutrient Mixture F- 12 (DMEM/F-12) y los colorantes para citometría de flujo, yoduro de propidio (PI) y el monoclorobimano (mbCl) se obtuvieron de Thermo Fisher Scientific (Waltham, MA, EUA). Los anticuerpos secundarios para inmunofluorescencia Alexa Fluor 546 anti-conejo, Alexa Fluor 488 anti-ratón y el marcador de núcleos 4',6-diamino-2-fenilindol (DAPI) fueron adquiridos en Invitrogen (Carlsbad, CA, EUA). El kit de quimioluminiscencia para Western blot, ECL (Enhanced Chemiluminescence) Advance Western Blotting y las placas fotográficas Amersham Hyperfilm ECL se compraron en Amersham Biosciences (Little Chalfont, Reino Unido). El suero de caballo y el medio de montaje de fluorescencia se obtuvieron de laboratorios Vector (Burlingame, CA, EUA) y Agilent DAKO (Santa Clara, CA, EUA), respectivamente.

Modelo *in vivo*

Protocolo de tratamiento

Los animales utilizados en este estudio fueron proporcionados por la Unidad de Modelos Biológicos del Instituto de Investigaciones Biomédicas de la UNAM.

En nuestro modelo experimental utilizamos ratones BALB/c de 5 semanas de edad mantenidos a 23-25°C con una humedad relativa de 50-60% y bajo un ciclo de luz/oscuridad de 12 h. Los ratones recibieron una inyección intraperitoneal (ip) de 6 mmol/kg de BSO disuelto en solución salina. Los controles se inyectaron vía ip con solución salina. Los animales se sacrificaron a las 0.5 y 2 h después de la inyección. El sacrificio se realizó por dislocación cervical y los tejidos se procesaron inmediatamente o se guardaron a una temperatura de -70 °C.

Los experimentos descritos en este trabajo se realizaron siguiendo las normas descritas en “Principles of Laboratory Animal Care” (Institutos Nacionales de Salud, NIH) y la Norma Oficial Mexicana de la Secretaría de Agricultura, Ganadería, Desarrollo Rural, Pesca y Alimentación (SAGARPA) titulada “Especificaciones técnicas para la producción, cuidado y uso de los animales de laboratorio” (Clave NOM-062-ZOO-1999, publicado en agosto de 2001).

Determinación de GSH

Las muestras de tejido se homogenizaron en 10 volúmenes de amortiguador A (KCl 154 mM, pentaacetato de dietilentiamina (DTPA) 5 mM y amortiguador de fosfatos (PB) 0.1 M, pH 6.8). Después de homogenizar, se agregó un volumen de amortiguador B (HCl 40 mM, DTPA 10 mM, ácido ascórbico 20 mM y ácido tricloroacético 10%) a un volumen del homogenado. La suspensión se centrifugó a 14,000 g y el sobrenadante se filtró a través de filtros de 0.45 µm. Las muestras pueden ser almacenadas a -70 °C por 4 semanas.

Los niveles de GSH y GSSG se determinaron en las muestras de tejido. El homogenado y

las mediciones se realizaron mediante la metodología descrita por Senft et al., 2000. El ensayo fluorométrico de OPA se adaptó a microplaca. La fluorescencia se determinó con filtros de 365 nm de excitación y 430 nm de emisión en un Multidetector de Elisa DTX 800/880 (Beckman Coulter, Fullerton, CA, EUA). Se usó como referencia una curva estándar de GSH y GSSG.

El método de OPA se basa en la formación de un derivado fluorescente, isoindol, para el caso del GSH. Para la determinación del GSSG en un primer paso se inhibe esta reacción y posteriormente el GSSG es reducido a GSH para la posterior derivación del isoindol con OPA.

Extracción de fracción citoplásmica

Se disectó el cerebelo y las muestras frescas de tejido se homogenizaron con el amortiguador A (HEPES 10 mM pH 7.9, KCl 10 mM, EDTA 10 mM, DTT 1 mM, IGEPAL 0.4%, Na_3VO_4 1 mM, PMSF 1 mM, aprotinina y leupeptina 10 mg/ml), se incubaron 10 minutos en hielo, y se centrifugaron a 4,000 g 15 min a 4 °C. El sobrenadante (fracción citoplásmica) se recolectó y se almacenó a -70 °C (Basaki et al., 2007).

Extracción de proteínas de membrana por ultracentrifugación

También se utilizó un protocolo de extracción de membranas por ultracentrifugación (Schindler et al., 2006). Las muestras de tejido se homogenizaron en 10 volúmenes de amortiguador de extracción BCL (HEPES 10 mM, NaCl 10 mM, KH_2PO_4 1 mM, NaHCO_3 5 mM, EDTA 5 mM, CaCl_2 1 mM, MgCl_2 0.5 mM, PMSF 1 mM, aprotinina y leupeptina 10 mg/ml) que contenía 10% de sacarosa 2.5 M. El homogenado obtenido se centrifugó en dos ocasiones a 6,300 g por 10 minutos a 4 °C. Los sobrenadantes se recolectaron y se ultracentrifugaron a 100,000 g por 30 minutos a 4 °C. El precipitado se recuperó y solubilizó en Tris-HCl 40 mM, pH 9.5, urea 8 M y Tritón X-100 4%. La concentración de proteína se determinó usando el ensayo de BCA.

Western blot

Las muestras se corrieron en un gel de acrilamida al 10% o 6% en el caso de mTOR, en condiciones desnaturalizantes (SDS-PAGE) posteriormente se electro-transfirieron a una membrana de nitrocelulosa. Para prevenir la unión inespecífica las membranas se bloquearon en TBS/Tween (Tris pH 7.6, NaCl y Tween 20 al 0.1%) con leche Blotto o albúmina de suero bovino (BSA) al 5% a 4 °C toda la noche con agitación. Las membranas se incubaron con el anticuerpo primario correspondiente, después de la incubación las membranas se lavaron 3 veces en TBS/Tween. A continuación, se incubó con el anticuerpo secundario correspondiente acoplado a la peroxidasa de rábano. Finalmente, la presencia de las proteínas se determinó por quimioluminiscencia incubando las membranas con el sistema de ECL y exponiendo una placa fotográfica. Para analizar las diferentes proteínas en la misma membrana después de cada quimioluminiscencia, las membranas se sometieron a un despegado de los anticuerpos con NaOH 0.2 mM para poder repetir el procedimiento anterior con cada uno de los anticuerpos de las proteínas de interés. Se utilizó el marcador de peso molecular biotinilado para identificar las bandas de las proteínas según su peso. Para la detección del marcador de peso molecular se agregó la anti-biotina junto con los anticuerpos secundarios. Los análisis densitométricos se realizaron utilizando el software ImageJ versión 1.50 g (Wayne Rasband, NIH, MD, EUA). Para la normalización de los datos obtenidos se utilizaron la β -tubulina o la β -actina.

Inmunofluorescencia

Los ratones se trataron con BSO y se sedaron con 70 mg/kg de pentobarbital sódico y se perfundieron con solución salina, seguido de paraformaldehído al 4% en PB, pH 7.4. Posteriormente los animales se decapitaron y el cerebro completo se removió cuidadosamente, se postfijó en solución crioprotectora de sacarosa al 20% y 30% por 24 h a 4 °C y posteriormente se congelaron con 4-metilbutano. Se cortaron secciones de 50 μ m

en criostato y se colectaron en placas de 24 pozos con PB. Los cortes se lavaron tres veces con PB + Triton X-100 0.3% (PBT), y se incubaron con los anticuerpos primarios: anti-NeuN (marcador neuronal; 1:600) y anti-TrkA (1:200) o anti-NGF (1:200) en PBT+ BSA 0.3% y suero de caballo 2%. Los cortes se lavaron tres veces con PBT y se incubaron con los anticuerpos secundarios anti-conejo Alexa Fluor 546 (1:600) anti-ratón Alexa Fluor 488 (1:400) durante 2 h. Finalmente, los núcleos se tiñeron con DAPI siguiendo las instrucciones del fabricante. Los cortes se montaron en medio de montaje de fluorescencia. Se adquirieron imágenes confocales con un confocal laser Nikon A1R⁺ acoplado a un microscopio invertido Eclipse Ti-E (Nikon Corporation, Tokio, Japón). Para analizar las imágenes se utilizó el programa ImageJ 1.50g.

Análisis estadístico

Los datos se analizaron con la prueba *t* de Student utilizando el software GraphPad Prism versión 6.00 (GraphPad Software, San Diego, CA, EUA). Los datos se graficaron con los promedios \pm error estándar (SE). Los valores de $p < 0.05$ se consideraron significativos.

Modelo *in vitro*

Cultivo primario de astrocitos corticales

Los astrocitos se aislaron de la corteza de ratas Wistar de 1-2 días de edad. Las cortezas se disectaron removiendo las meninges y los vasos sanguíneos. El tejido se desmenuzó en pequeños pedazos y se digirió con 0.25 mg/ml de tripsina a 37 °C por 15 minutos. Posteriormente se añadió solución de DNasa al 0.016% y se incubó en baño maría por 10 minutos, mezclando periódicamente. La digestión se detuvo con medio de cultivo DMEM/F-12 con suero bovino fetal (SBF) 10 %, penicillina (200 unidades/ml)- streptomicina (200 μ g/ml). A continuación, las cortezas se trituraron con pipetas Pasteur y se añadió más solución de DNasa con medio de cultivo, después se realizó una centrifugación a 1700 rpm por 5 minutos. Finalmente, las células se filtraron a través de un filtro de 70 μ m, se diluyeron

con medio, se contaron y se sembraron. Los astrocitos se mantuvieron en una incubadora a 37 °C con CO₂ 5% en una atmósfera húmeda hasta que alcanzaron una confluencia de 90-95%.

Los astrocitos se trataron con BSO 500 µM y con inhibidores de la vía de señalización de mTOR: mTORC1, mTORC1/2 y la proteína S6K, así como de los transportadores de aminoácidos y con inhibidores de la función mitocondrial, en los resultados se indican las diferentes estrategias de tratamiento utilizadas. Por otro lado, las células se transdujeron con vectores de expresión que expresan la proteína verde fluorescente redox sensible (roGFP), tanto en citosol (cito-roGFP) como en mitocondria (mito-roGFP), para determinar la presencia de estrés oxidante en la célula.

Determinación de la muerte celular (pérdida de la integridad de membrana y depleción de GSH) para determinar la viabilidad celular

La pérdida en la viabilidad celular se determinó por citometría de flujo en presencia de PI 1 µg/ml como un marcador de pérdida de la integridad de membrana. Además, se midieron los niveles intracelulares de GSH utilizando el marcador mBCI 5 µM. La fluorescencia del PI se detectó usando FL-3 (488 nm excitación, 695/40 nm emisión), y para mBCI, las células se excitaron con un laser ultravioleta (UV) (405 nm excitación, 440/40 nm emisión). Tanto el consumo de PI como la concentración de GSH se determinaron en todas las condiciones experimentales para asegurar que las dosis utilizadas en los tratamientos no resultaran citotóxicas.

Extracción de proteína y Western blot

Las muestras se homogenizaron con amortiguador de radioinmunoprecipitación (RIPA) (Tris HCl 50 mM pH 8, NaCl 150 mM, sodio deoxicolato 0.5%, SDS 0.1%, Tritón X-100 1%) con inhibidores de proteasas. Las células se sonicaron y se centrifugaron descartando el precipitado. La concentración de proteína se determinó usando el ensayo de BCA.

Las muestras se corrieron siguiendo el protocolo utilizado en el modelo *in vivo*, con la excepción de que los geles fueron de Bis-Tris acrilamida utilizando el amortiguador 3-N-morfolino y ácido propansulfónico (MOPS) + 5 mM de bisulfito de sodio y las membranas se revelaron en un fotodocumentador VersaDoc (Bio-Rad, Hercules, CA, EUA).

Determinación de la concentración celular de ATP

La concentración de ATP en las células se determinó con el ensayo cell titer-Glo luminiscent cell viability, los datos se normalizaron con el marcador de viabilidad celular calceína AM. Este ensayo cuantifica el ATP presente en las células, marcando las células metabólicamente activas; utiliza a la enzima luciferasa para mono-oxigenar a la luciferina en presencia de magnesio (Mg^{2+}), ATP y oxígeno molecular. La calceína AM es absorbida por las células vivas donde las enzimas esterases la transforman en calceína la cual es fluorescente. La concentración de ATP se muestra en función de los valores de calceína y los datos se normalizaron con el grupo control.

Análisis estadístico

Los datos se analizaron utilizando un análisis de varianza (ANOVA) de dos vías con la prueba posthoc adecuada utilizando el software GraphPad Prism. Los datos se graficaron con los promedios \pm SE. Los valores de $p < 0.05$ se consideraron significativos.

RESULTADOS

Modelo *in vivo*

Cambios en los niveles de GSH y GSSG en el hígado de ratones tratados con BSO

Para demostrar la eficacia del BSO bloqueando la síntesis *de novo* de GSH, se determinaron los niveles de GSH y GSSG en el hígado. No se observaron cambios en los niveles de GSH hasta 2 h después de la inyección con BSO (Fig. 4a). Pero, sí se encontró una disminución significativa en los niveles de GSSG a las 0.5 h (Fig. 4b). Sin embargo, tampoco se observaron cambios en el cociente GSH/GSSG (Fig. 4a, b), el cual es un indicador del estado redox celular (Schafer y Buettner, 2001), por lo que estos resultados sugieren que las células están exportando o metabolizando GSSG como un mecanismo de desintoxicación para prevenir la generación de estrés oxidante en el hígado (Franco y Cidlowski, 2012).

Niveles de GSH y GSSG en diferentes regiones del cerebro de ratones tratados con BSO

En estudios previos de nuestro grupo, se demostró que la inhibición sistémica de la síntesis de GSH con una inyección ip de BSO generó un incremento de los niveles de GSH en homogenado total de cerebro 1-3 h después del tratamiento, aunado a una activación de ERK2 y Nrf2 (Limón-Pacheco et al. 2007). En el presente trabajo se determinaron los niveles de GSH y GSSG en diferentes regiones del cerebro (corteza, hipocampo, estriado y cerebelo). No se encontraron cambios en los niveles de GSH y GSSG de la corteza, hipocampo y estriado (Fig. 5-7), sin embargo, en el cerebelo sí se observó una respuesta redox en respuesta al tratamiento sistémico con BSO (Fig. 8).

Hígado

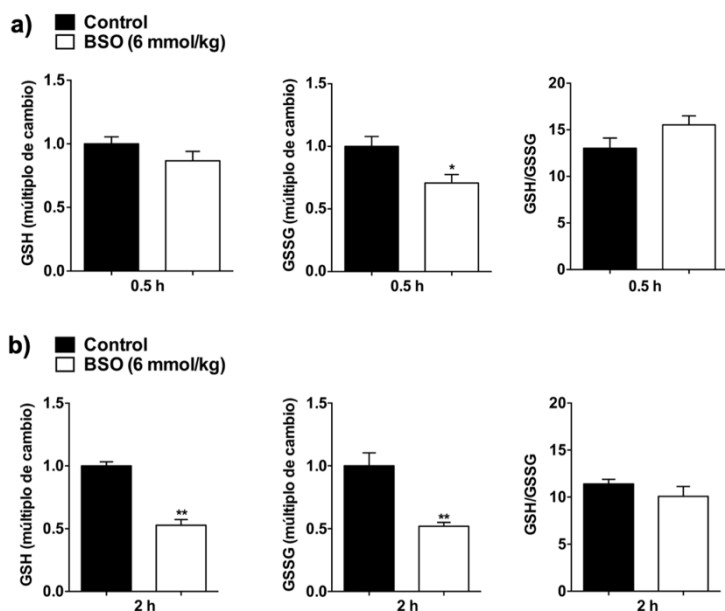


Figura 4. Efecto de BSO en los niveles de GSH y GSSG en el hígado de ratones tratados ip con BSO 6 mmol/kg. Niveles normalizados de GSH y GSSG, y cociente entre GSH/GSSG a la 0.5 h (a) y 2 h (b) después del tratamiento con BSO. Las gráficas representan promedios \pm SE n=6. Prueba de *t* de Student * p <0.05, ** p <0.01 vs Control se consideran significativos. Abreviaturas: BSO, L-butionina-S-R-sulfoximina; GSH, glutatión; GSSG, glutatión disulfuro; SE, error estándar.

Corteza

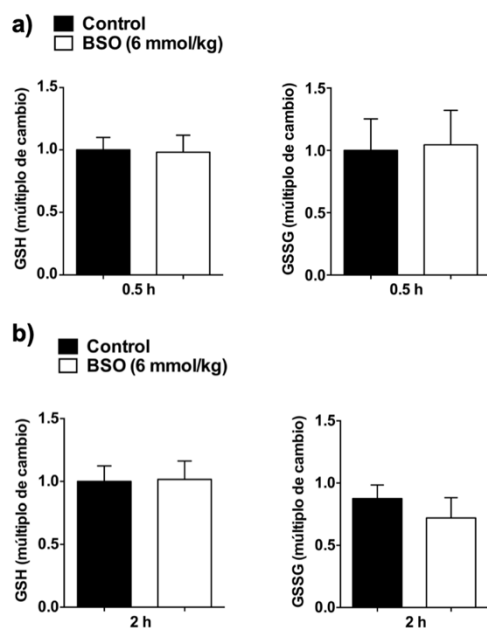


Figura 5. Efecto de BSO en los niveles de GSH y GSSG en corteza de ratones tratados ip con BSO 6 mmol/kg. Niveles normalizados de GSH y GSSG a la 0.5 h (a) y 2 h (b) después del tratamiento con BSO. Las gráficas representan promedios \pm SE n=6. Prueba de *t* de Student * p <0.05, ** p <0.01 vs Control se consideran significativos. Abreviaturas: BSO, L-butionina-S-R-sulfoximina; GSH, glutatión; GSSG, glutatión disulfuro; SE, error estándar.

El tratamiento con BSO induce un incremento en los niveles de GSH del cerebelo

En el cerebelo no se observaron cambios significativos en los niveles de GSH y GSSG después de 0.5 h de tratamiento con BSO (Fig. 8a), sin embargo, los pequeños cambios en las concentraciones dieron lugar a un incremento significativo del cociente GSH/GSSG (Fig. 8a). Además, 2 h después de la inyección con BSO se observó un incremento en la concentración de GSH (Fig. 8b). Estos resultados revelan un incremento en el ambiente reductor de la célula a la 0.5 h, así como un aumento en los niveles de GSH a las 2 h después de la administración de BSO. El cerebelo está respondiendo a los cambios en la homeostasis redox de la periferia, aunque el BSO no sea transportado hacia el cerebro (Limón-Pacheco y Gonsebatt, 2007; Steinherz et al., 1990).

Hipocampo

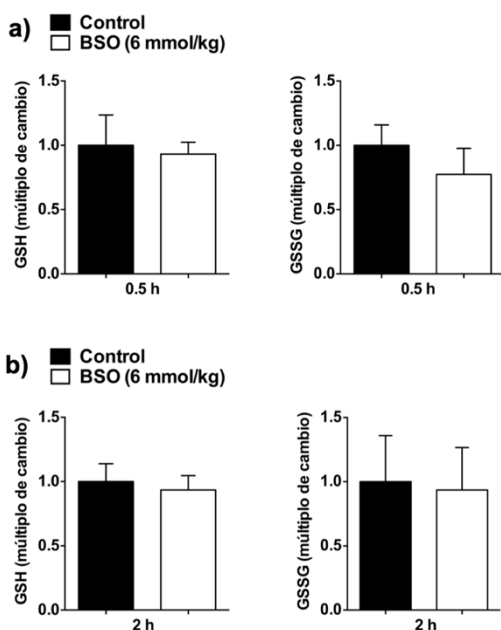


Figura 6. Efecto de BSO en los niveles de GSH y GSSG en hipocampo de ratones tratados ip con BSO 6 mmol/kg. Niveles normalizados de GSH y GSSG a la 0.5 h (a) y 2 h (b) después del tratamiento con BSO. Las gráficas representan promedios \pm SE n=6. Prueba de t de Student *p<0.05, **p<0.01 vs Control se consideran significativos. Abreviaturas: BSO, L-butionina-S-R-sulfoximina; GSH, glutatión; GSSG, glutatión disulfuro; SE, error estándar.

Estriado

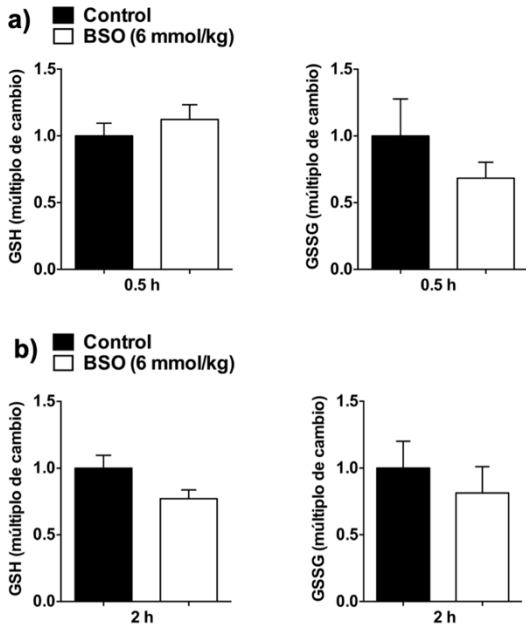


Figura 7. Efecto de BSO en los niveles de GSH y GSSG en estriado de ratones tratados ip con BSO 6 mmol/kg. Niveles normalizados de GSH y GSSG a la 0.5 h (a) y 2 h (b) después del tratamiento con BSO. Las gráficas representan promedios \pm SE n=6. Prueba de *t* de Student * p <0.05, ** p <0.01 vs Control se consideran significativos. Abreviaturas: BSO, L-butionina-S-R-sulfoximina; GSH, glutatión; GSSG, glutatión disulfuro; SE, error estándar.

Expresión de los transportadores involucrados en la síntesis de GSH (LAT1, xCT, EAAT3) en el cerebelo

La síntesis de GSH en el cerebro se ha asociado con un incremento en la expresión de los transportadores de cistina/cisteína (Limón-Pacheco et al., 2007; Nelson-Mora et al., 2018; Ramos-Chavez et al., 2015). Para determinar si el incremento en los niveles de GSH en el cerebelo estaba relacionada con los niveles de los transportadores involucrados en el transporte de cistina/cisteína, se utilizó la técnica de Western blot de fracciones membranales para determinar los niveles proteicos de los transportadores. No se observaron cambios en los niveles del transportador de aminoácidos neutros LAT1 ni de la subunidad xCT del sistema xc-, después del tratamiento con BSO (Fig. 9a-b, d-e).

Sin embargo, sí se observó un incremento en los niveles de proteína del transportador neuronal de glutamato EAAT3, que también está involucrado en el transporte de cisteína

principalmente en las neuronas, 2 h después de la inyección con BSO (Fig. 9f); pero no a la 0.5 h (Fig. 9c).

Cerebelo

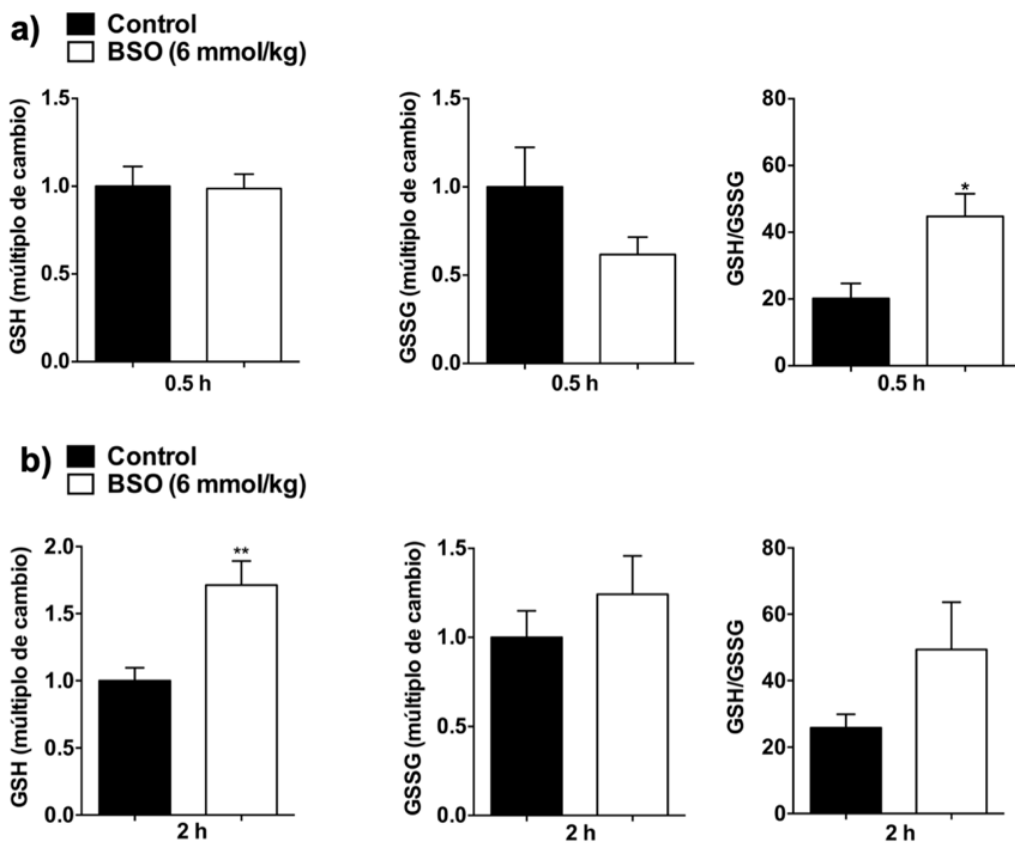


Figura 8. Efecto de BSO en los niveles de GSH y GSSG en el cerebelo de ratones tratados ip con BSO 6 mmol/kg. Niveles normalizados de GSH y GSSG, y cociente entre GSH/GSSG a la 0.5 h (**a**) y 2 h (**b**) después del tratamiento con BSO. Las gráficas representan promedios \pm SE n=6. Prueba de *t* de Student * p <0.05, ** p <0.01 vs Control se consideran significativos. Abreviaturas: BSO, L-butionina-S-R-sulfoximina; GSH, glutatión; GSSG, glutatión disulfuro; SE, error estándar.

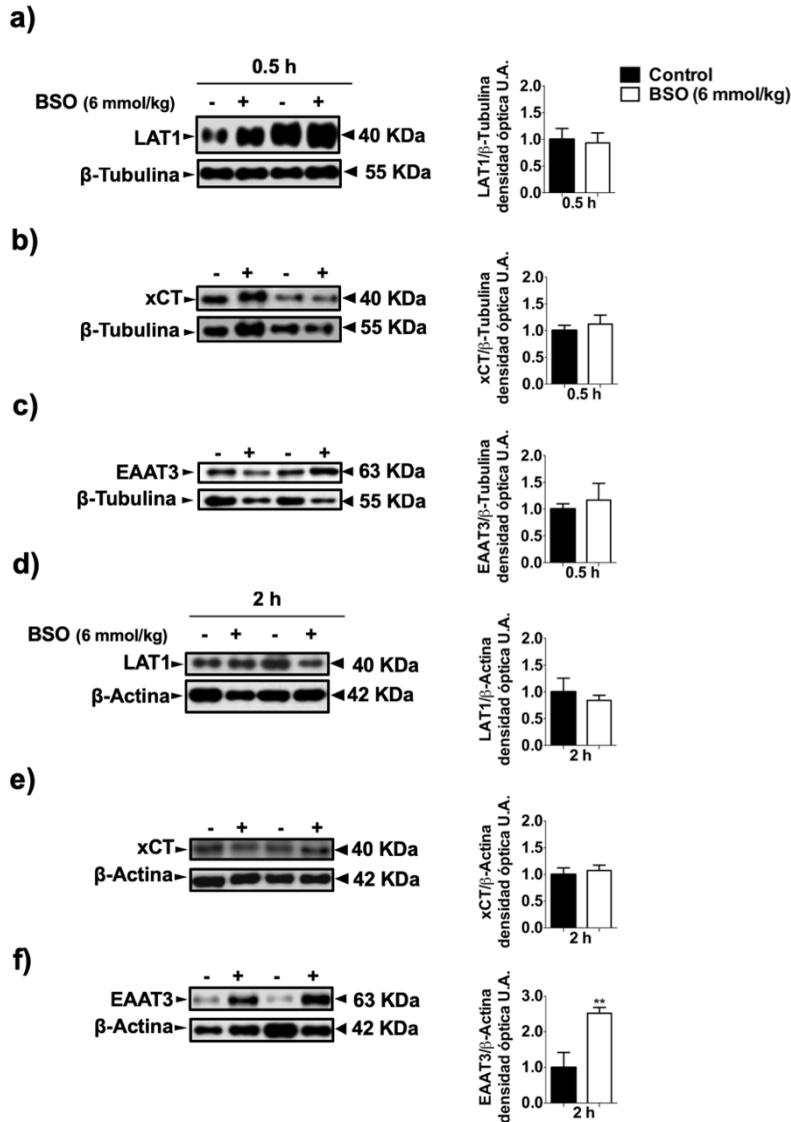


Figura 9. Efecto del BSO en los niveles de proteína de los transportadores de aminoácidos, LAT1, xCT y EAAT3, en el cerebelo de ratones tratados ip con BSO 6 mmol/kg. Se evaluaron los cambios en los niveles de proteína de la fracción de proteínas membranales con Western blot, a la 0.5 y 2 h después de la inyección con BSO. Las gráficas representan promedios \pm SE de los análisis densitométricos de las bandas normalizadas con β -tubulina (a-c) o β -actina (b-d) n=6. Prueba de *t* de Student *p<0.05, **p<0.01 vs Control se consideran significativos. Abreviaturas: BSO, L-butionina-S-R-sulfoximina; LAT1, transportador de aminoácidos tipo L; xCT, subunidad del sistema xc-; EAAT3, transportador de aminoácidos excitadores 3; U.A.; unidad arbitraria; SE, error estándar.

El inhibidor BSO activa las vías de señalización de mTOR y NGF en el cerebelo

Posteriormente, se decidió investigar si el tratamiento con BSO estaba activando la vía de señalización de mTOR en el cerebelo debido a la estrecha relación entre mTOR y los transportadores de aminoácidos (Goberdhan et al., 2016; Kim y Guan, 2011). No se encontró un incremento en la fosforilación ni en la expresión de mTOR (Fig. 10a, c). No

obstante, se encontró un aumento significativo en la fosforilación de, la cinasa blanco de mTORC1, S6K a la 0.5 h de tratamiento, lo que sugiere que la vía de mTORC1 está activada y puede estar participando en el aumento del transportador EAAT3.

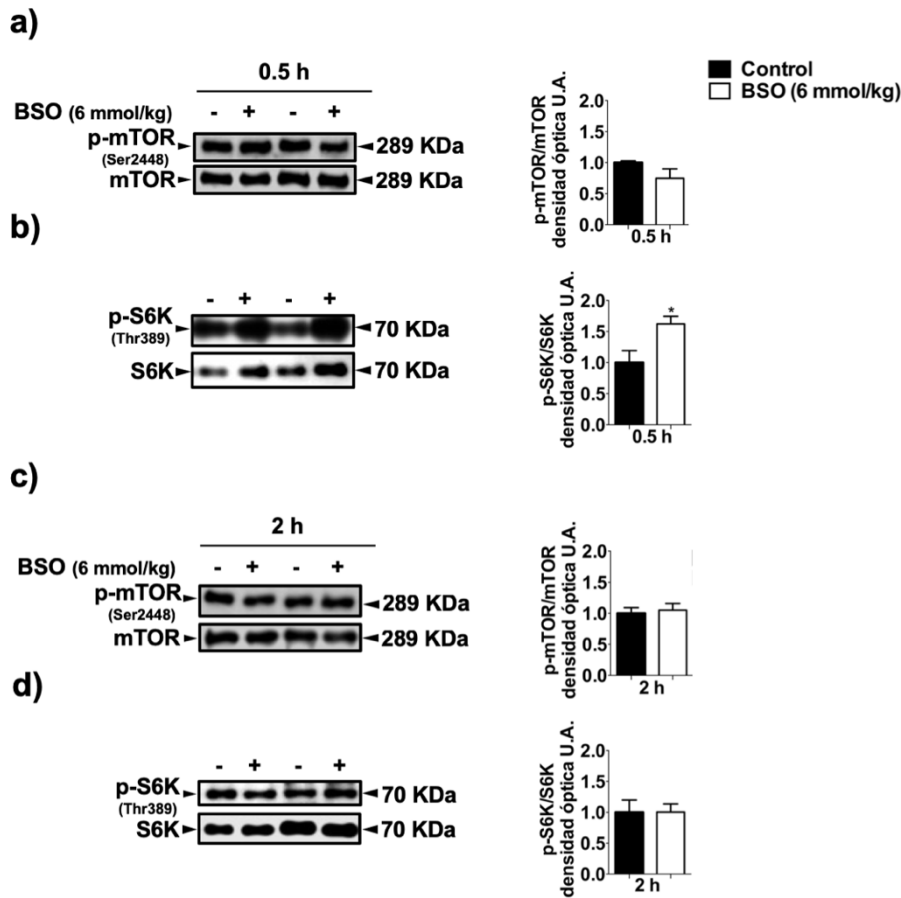


Figura 10. Efecto del BSO en los niveles de fosforilación de mTOR y S6K en el cerebelo de ratones tratados ip con BSO 6 mmol/kg. Se evaluaron los cambios en la fosforilación con Western blot, a la 0.5 y 2 h después de la inyección con BSO. p-mTOR (Ser 2448) (a, c) y p-S6K (Thr 389) (b,d) Las gráficas representan promedios±SE de los análisis densitométricos de las bandas normalizadas con mTOR o S6K respectivamente n=6. Prueba de *t* de Student **p*<0.05, ***p*<0.01 vs Control se consideran significativos. Abreviaturas: BSO, L-butionina-S-R-sulfoximina; mTOR; blanco funcional de la rapamicina; S6K, proteína ribosomal S6 cinasa beta-1; U.A.; unidad arbitraria; SE, error estándar.

Como se mencionó en la introducción, en estudios previos se demostró que la vía de NGF/TrkA/AKT/IKK/I κ B /NF κ B es activada en el hígado de ratón después del tratamiento con agentes que consumen GSH, induciendo una respuesta antioxidante (Valdovinos-Flores y Gonsebatt, 2013). En este estudio se determinaron los niveles de NGF y la activación de su receptor TrkA, para evaluar si la vía de señalización de NGF/TrkA estaba

activa en el cerebelo en respuesta al BSO. El análisis con Western blot demostró que el tratamiento con BSO indujo la expresión de NGF, así como la fosforilación de su receptor TrkA a la 0.5 h de tratamiento (Fig. 11a, b) pero no a las 2 h (Fig. 11a, b).

Las inmunofluorescencias confirmaron los datos obtenidos con Western blot, se observó un incremento de NGF y TrkA en las neuronas a la 0.5 h después de la inyección con BSO. Además, la expresión de TrkA se distinguió en el soma de las neuronas de la capa granular del cerebelo y en la capa molecular que contiene axones y dendritas (Fig. 12). No se observaron cambios de NGF ni de TrkA a las 2 h después del tratamiento (Fig. 13). Estos resultados sugieren que las vías de señalización de NGF y mTOR están involucradas en la regulación de la homeostasis de GSH, induciendo una respuesta antioxidante asociada a la depleción periférica de GSH. Esta activación podría estar relacionada con el incremento del transportador EAAT3 y de los niveles de GSH en el cerebelo.

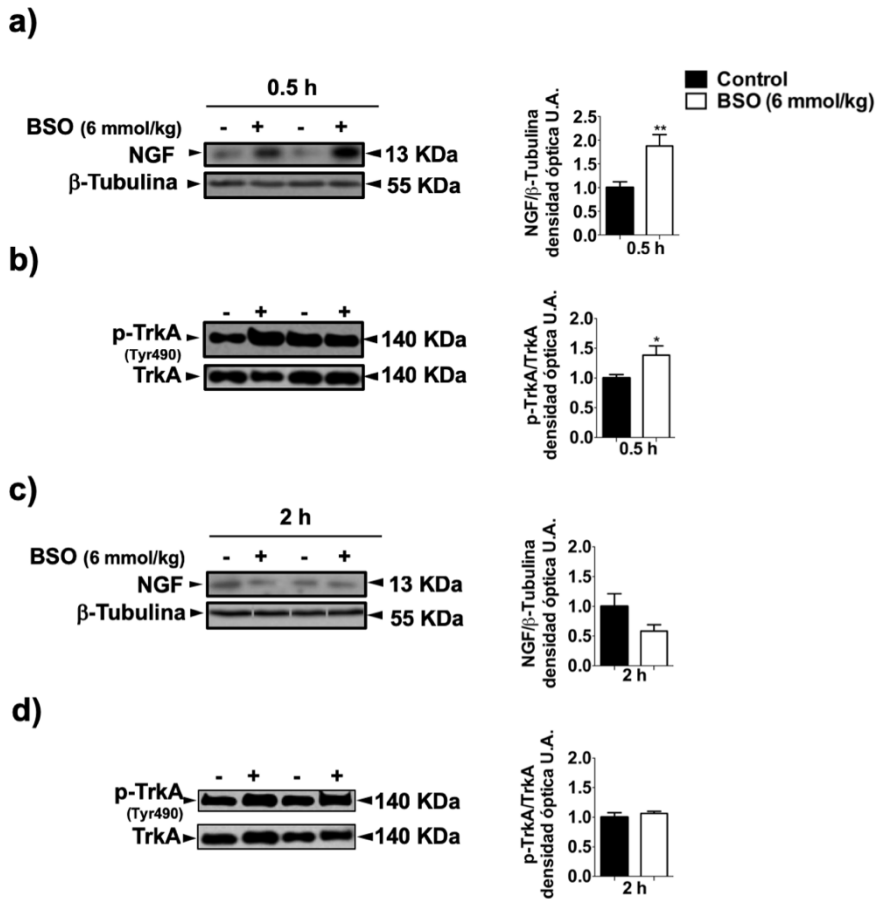


Figura 11. Efecto del BSO en los niveles de proteína de NGF y de fosforilación de TrkA en el cerebelo de ratones tratados ip con BSO 6 mmol/kg. Se evaluaron los cambios en los niveles proteicos y en la fosforilación con Western blot, a la 0.5 y 2 h después de la inyección con BSO. NGF (**a,c**) y p-TrkA (Tyr 490) (**b,d**). Las gráficas representan promedios±SE de los análisis densitométricos de las bandas normalizadas con β-tubulina o TrkA respectivamente n=5. Prueba de *t* de Student **p*< 0.05, ***p*<0.01 vs Control se consideran significativos. Abreviaturas: BSO, L-butionina-S-R-sulfoximina; NGF, factor de crecimiento neuronal; TrkA, receptor de tropomiosina tipo cinasa A; U.A.; unidad arbitraria; SE, error estándar.

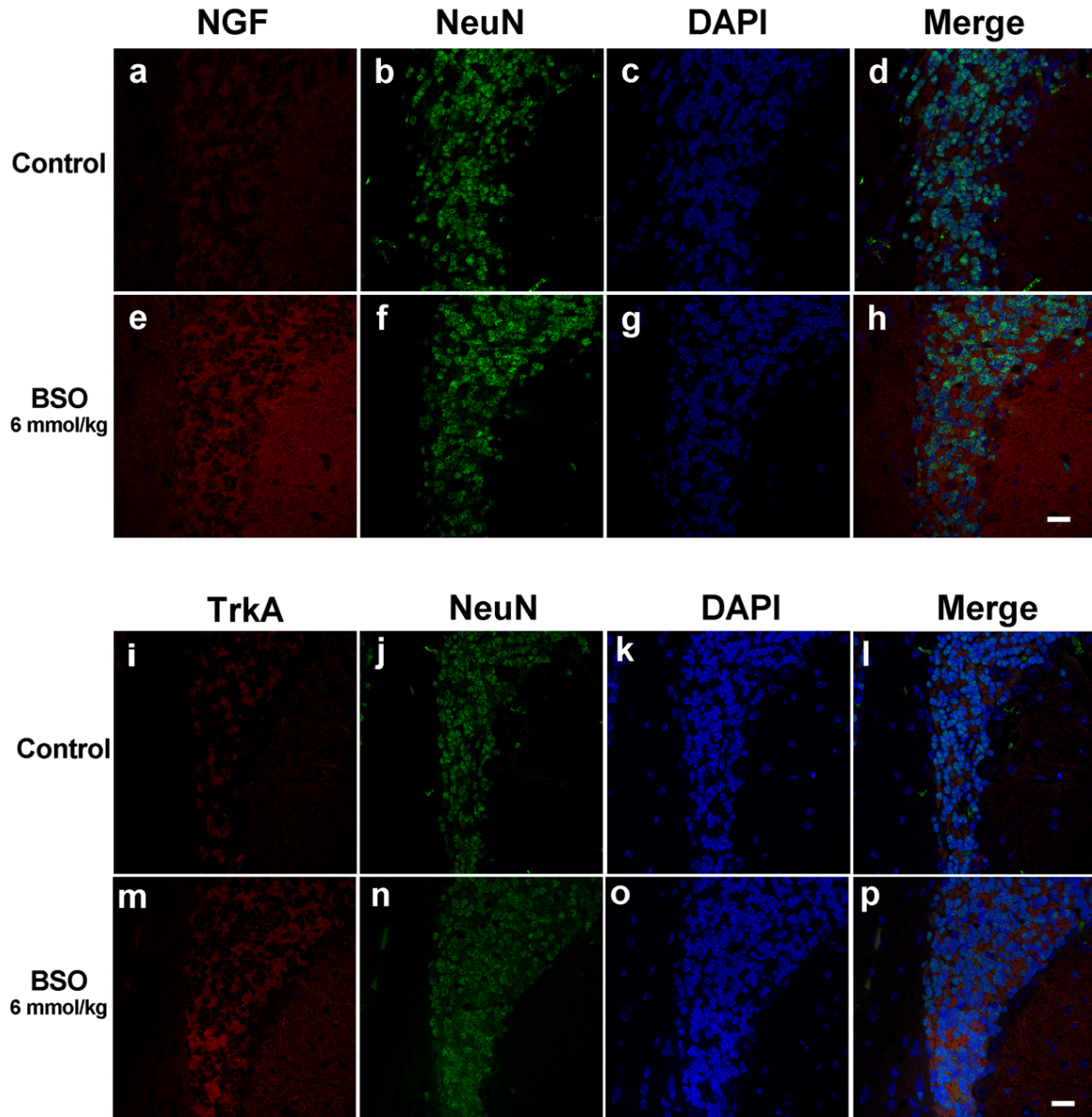


Figura 12. Efecto del BSO en los niveles de proteína de NGF y TrkA en el cerebelo de ratones tratados ip con BSO 6 mmol/kg. Se evaluaron los cambios en los niveles proteicos con inmunofluorescencias, a la 0.5 h después de la inyección con BSO. Imágenes confocales de ratones control y tratados. (a, e) muestra imágenes inmunofluorescentes de NGF (rojo), (b, f) marcador neuronal NeuN (verde), (c, g) marcador de núcleos DAPI (azul) y (d, h) merge. El segundo panel muestra imágenes inmunofluorescentes de (i, m) TrkA (rojo), (j, n) NeuN (verde), (k, o) DAPI (azul) y (l, p) merge. Escala: 20 micrómetros. Abreviaturas: BSO, L-butionina-S-R-sulfoximina; NGF, factor de crecimiento neuronal; TrkA, receptor de tropomiosina tipo cinasa A; NeuN, núcleos neuronales; DAPI, 4',6-diamino-2-fenilindol.

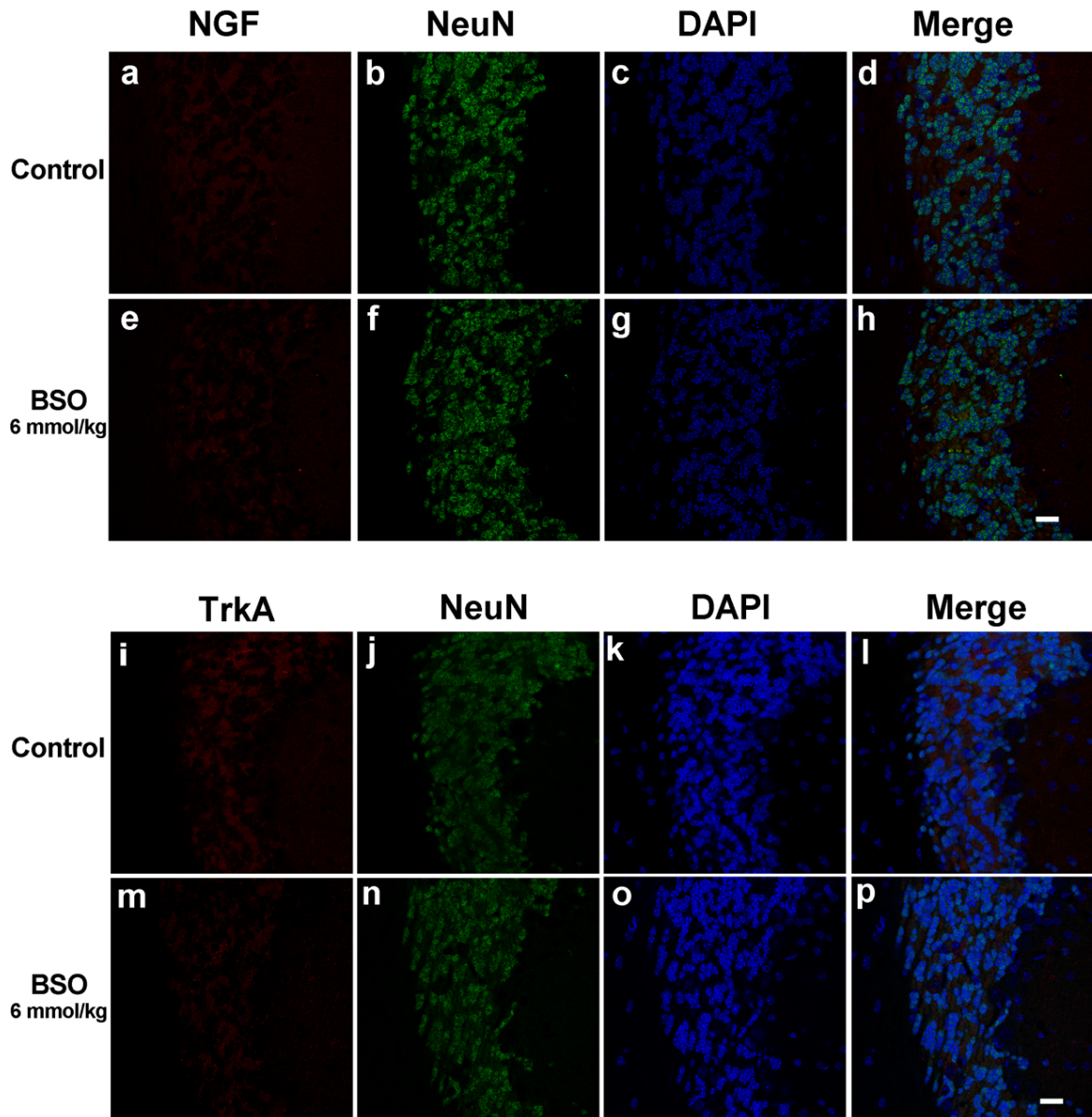


Figura 13. Efecto del BSO en los niveles de proteína de NGF y TrkA en el cerebelo de ratones tratados ip con BSO 6 mmol/kg. Se evaluaron los cambios en los niveles protéicos con inmunofluorescencias, a la 2 h después de la inyección con BSO. Imágenes confocales de ratones control y tratados. (a, e) muestra imágenes inmunofluorescentes de NGF (rojo), (b, f) marcador neuronal NeuN (verde), (c, g) marcador de núcleos DAPI (azul) y (d, h) merge. El segundo panel muestra imágenes inmunofluorescentes de (j, m) TrkA (rojo), (j, n) NeuN (verde), (k, o) DAPI (azul) y (l, p) merge. Escala: 20 micrómetros. Abreviaturas: BSO, L-butionina-S-R-sulfoximina; NGF, factor de crecimiento neuronal; TrkA, receptor de tropomiosina tipo cinasa A; NeuN, núcleos neuronales; DAPI, 4',6-diamino-2-fenilindol.

Modelo *in vitro*

Depleción y recuperación de los niveles de GSH en astrocitos

Para tratar de entender los mecanismos que utilizan los astrocitos para mantener la homeostasis de GSH se utilizó el inhibidor BSO. La inhibición de la síntesis *de novo* de GSH con BSO (500 μ M) induce la depleción de GSH de forma tiempo dependiente en astrocitos, alcanzando un 80% de disminución a las 12 h de tratamiento (Fig. 14a). Sin embargo, esta depleción no tuvo efecto en la viabilidad celular (Fig. 14b). Posteriormente, se demostró que la disminución en la concentración de GSH no está relacionada a la actividad de la MRP1, ya que el inhibidor de este transportador ácido 5-(3-(2-(7-cloroquinolina-2-il)etenil)fenil)-8-dimetilcarbamil-4,6-ditiaoctanoico (MK571) no previene la pérdida de GSH en las células (Fig. 14c), lo que indica que el GSH no está siendo exportado fuera de la célula a través de la MRP1 en respuesta al BSO. La depleción de GSH crónica (24 h) genera estrés oxidante, determinado por un aumento en la proteína roGFP oxidada en el citoplasma (Fig. 14d). Cuando se retiró el BSO después de 12 h de tratamiento se observó que su efecto es reversible, los resultados muestran que las células pueden reponer el GSH casi a niveles del control 12 h después de retirar el BSO (Fig. 14e).

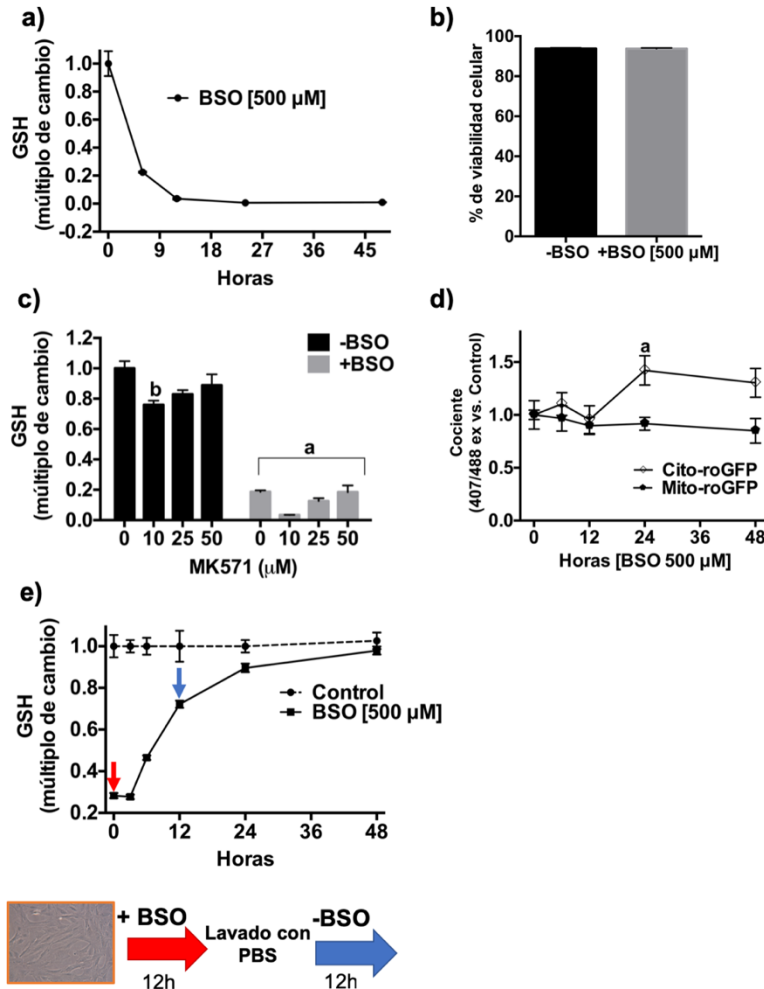


Figura 14. Efecto de BSO en los niveles de GSH. **(a)** Curso temporal de depleción de GSH inducida por BSO 500 μM , se evaluaron los niveles de GSH en los astrocitos con citometría de flujo utilizando mBCL. **(b)** Efecto del BSO en la viabilidad celular, la pérdida en la viabilidad celular se determinó usando citometría de flujo midiendo el consumo de PI y los niveles de GSH con mBCL. **(c)** Efecto del inhibidor de MRP1, MK571 en la depleción de GSH inducida por BSO. **(d)** Efecto de BSO en el estado redox citosólico y mitocondrial determinado a través de la oxidación de roGFP. **(e)** Depleción de GSH inducida por BSO y recuperación de GSH después de retirar el BSO. 12 h BSO (flecha roja), 12 h sin BSO (flecha azul). Las gráficas representan promedios \pm SE $n=3$. ANOVA de dos vías, prueba post hoc Holm-Sidak ^a $p<0.05$ vs Control; ^b $p<0.05$ -MK571 vs +MK571. Abreviaturas: BSO, L-butionina-S-R-sulfoximina; GSH, glutatión; PI, ioduro de propidio; mBCL, monoclorobimano; roGFP, proteína verde fluorescente redox sensible; MRP1, proteína 1 de resistencia a multidroga; MK571, ácido 5-(3-(2-(7-Cloroquinolina-2-il)etenil)fenil)-8-dimetilcarbamil-4,6-ditiaoctanoico; SE, error estándar.

Papel aditivo de los transportadores de aminoácidos en la homeostasis de GSH

Se utilizaron inhibidores de los transportadores de aminoácidos, sulfasalazina (SAS) para inhibir xCT, 2-aminobiciclo-(2,2,1)-heptano-2-ácido carboxílico (BCH) para inhibir LAT1 y pirrolidina-2,4-ácido dicarboxílico (PDC) para inhibir EAAT3. Por separado ninguno de los inhibidores tuvo efecto en la recuperación de los niveles intracelulares de GSH (Fig. 15a-

c). Sin embargo, cuando se utilizaron los 3 inhibidores de manera simultánea la recuperación de GSH se evitó significativamente (Fig. 15d), lo que indica que en los astrocitos los transportadores de cistina/cisteína tienen un papel complementario, si uno es inhibido los otros pueden compensar el efecto. Como en los astrocitos la mayoría del glutamato es transformado en glutamina para las neuronas, éste también puede ser un aminoácido limitante en la síntesis de GSH (Rose et al., 2017); se utilizó el inhibidor del transportador de glutamato EAAT1 2-Amino-5,6,7,8-tetrahidro-4-(4-metoxifenil)-7-(naftaleno-1-yl)-5-oxo-4H-cromeno-3-carbonitrilo (UCPH) pero tampoco tuvo efecto sobre la recuperación de GSH (Fig. 15e).

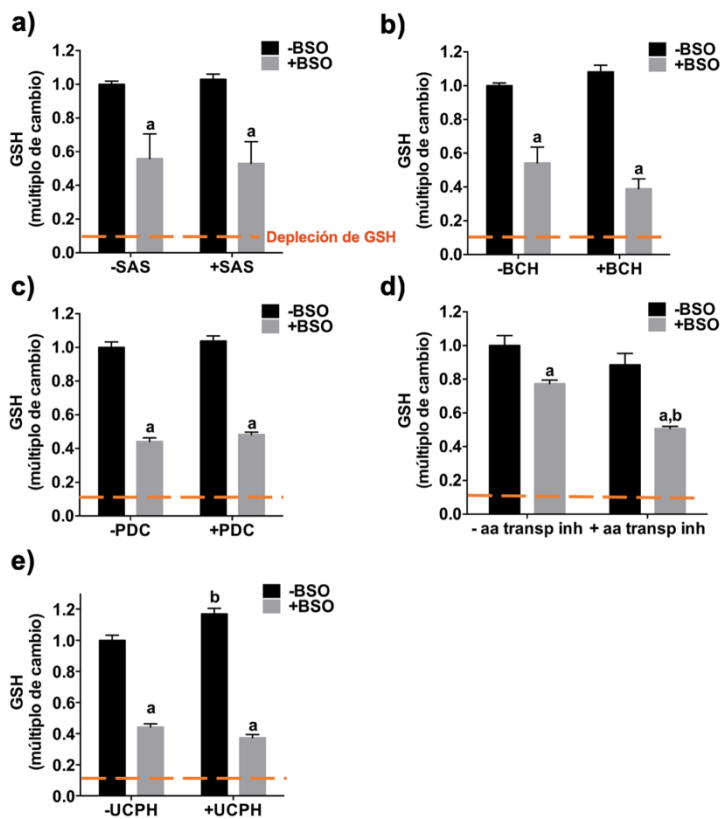


Figura 15. Efecto de la inhibición del transporte de aminoácidos en los niveles de GSH. Se evaluaron los niveles de GSH con citometría de flujo utilizando mBCL. (a) Los astrocitos se trataron con el inhibidor de xCT SAS 50 μ M (b) inhibidor de LAT1 BCH 5mM y (c) el inhibidor de EAAT3 PDC 100 μ M 12 h después del tratamiento con BSO 500 μ M. (d) Combinación de los tres inhibidores (SAS, BCH y PDC) 12 h después del tratamiento con BSO. (e) Los astrocitos también se trataron con el inhibidor de EAAT1 UCPH 20 μ M. La línea punteada indica los niveles de GSH después de 12 h BSO (Depleción de GSH). Las gráficas representan promedios \pm SE n =3. ANOVA de dos vías, prueba post hoc Holm-Sidak ^ap<0.05 vs Control (-BSO); ^bp<0.05 –inhibidores vs +inhibidores respectivamente. Abreviaturas: BSO, L-butionina-S-R-sulfoximina; GSH, glutatión; mBCL, monoclorobimano; SAS, sulfasalazina; BCH, 2-aminobiciclo-(2,2,1)-heptano-2-ácido carboxílico; PDC, pirrolidina-2,4-ácido dicarboxílico; UCPH, 2-Amino-5,6,7,8-tetrahidro-4-(4-metoxifenil)-7-(naftaleno-1-yl)-5-oxo-4H-cromeno-3-carbonitrilo; SE, error estándar.

El piruvato mitocondrial y el metabolismo de los ácidos grasos contribuyen a la homeostasis de GSH.

Los astrocitos son altamente glicolíticos, sin embargo se ha observado que durante condiciones de estrés o de falta de energía pueden activar el metabolismo mitocondrial (Rose et al., 2017). Para estudiar otros mecanismos que regulan la homeostasis de GSH además del transporte de aminoácidos, se decidió evaluar el papel de la actividad mitocondrial en la recuperación de GSH, mediante la inhibición del transportador de piruvato mitocondrial con 2-ciano-3-(1-fenil-1H-indol-3-il)-2-ácido propenónico (UK5099) (Fig. 16a) y la oxidación de ácidos grasos con etomoxir, inhibidor de la enzima mitocondrial carnitina palmitoiltransferasa 1 (CPT-1) que media el transporte de ácidos grasos de cadena larga a través de la membrana, uniéndolos a moléculas de carnitina (Fig. 16b). Estos dos inhibidores interesantemente redujeron la recuperación de GSH significativamente, lo que sugiere que el metabolismo mitocondrial también es importante en la regulación de la homeostasis del GSH en astrocitos.

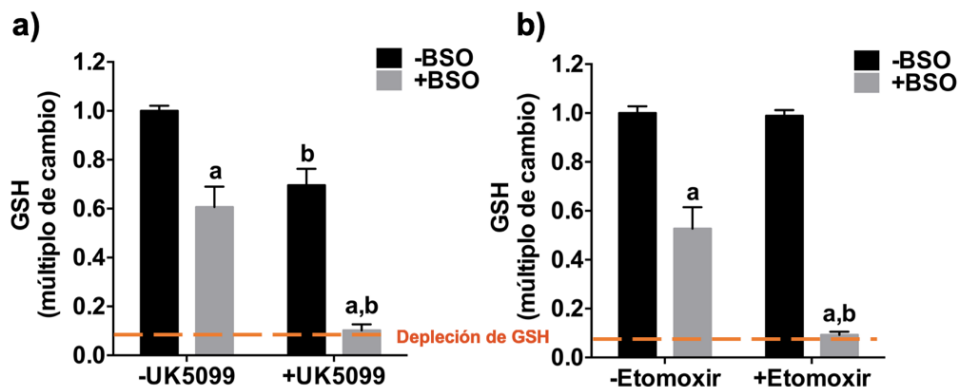


Figura 16. Efecto de la inhibición del transporte de piruvato y de la oxidación de ácidos grasos mitocondrial en la homeostasis de GSH. Se evaluaron los niveles de GSH con citometría de flujo utilizando mBCL. (a) Los astrocitos se trataron con el inhibidor del transporte de piruvato mitocondrial UK5099 5 μ M y con (b) el inhibidor de la oxidación de ácidos grasos Etomoxir 200 μ M 12 h después del tratamiento con BSO. La línea punteada indica los niveles de GSH después de 12 h BSO (Depleción de GSH). Las gráficas representan promedios \pm SE n=3. ANOVA de dos vías, prueba post hoc Holm-Sidak ^ap<0.05 vs Control (-BSO); ^bp<0.05 –inhibidores vs +inhibidores respectivamente. Abreviaturas: BSO, L-butionina-S-R-sulfoximina; GSH, glutatiión; mBCL, monoclorobimano; UK5099, 2-ciano-3-(1-fenil-1H-indol-3-il)-2-ácido propenónico; SE, error estándar.

La vía de señalización de mTOR regula la homeostasis de GSH en astrocitos

La vía de señalización de mTOR está involucrada tanto en el transporte de aminoácidos como en la actividad y biogénesis mitocondrial. Se utilizaron los inhibidores de la vía de señalización de mTOR, la rapamicina que sólo inhibe al mTORC1 y torin1 que inhibe a los dos complejos mTORC1/2. También se utilizó el inhibidor de la S6K, LY2584702 o tosilato (Fig. 17a-c). De manera interesante el único inhibidor que tuvo efecto en la recuperación de los niveles de GSH fue torin1, incluso se observa que por sí mismo disminuye los niveles de GSH (Fig. 17a). Existen estudios que sugieren que la rapamicina no inhibe todas las funciones de mTORC1 como la regulación de la traducción CAP-dependiente y la autofagia. Se realizaron Western blots para determinar los niveles de proteína de algunos blancos moleculares de mTORC1/2; se observó que la rapamicina sólo inhibe la fosforilación de la S6K y no la de 4EBP1 (Fig. 17d). Por otro lado, torin1 inhibió tanto los blancos moleculares de mTORC1 (S6K y 4EBP1), como la fosforilación de Akt (Ser 473) blanco de mTORC2 (Fig. 17d). El efecto de mTOR en la homeostasis de GSH en los astrocitos puede estar regulado por 4EBP1 en el caso de mTORC1 o por alguna de las vías donde participa mTORC2.

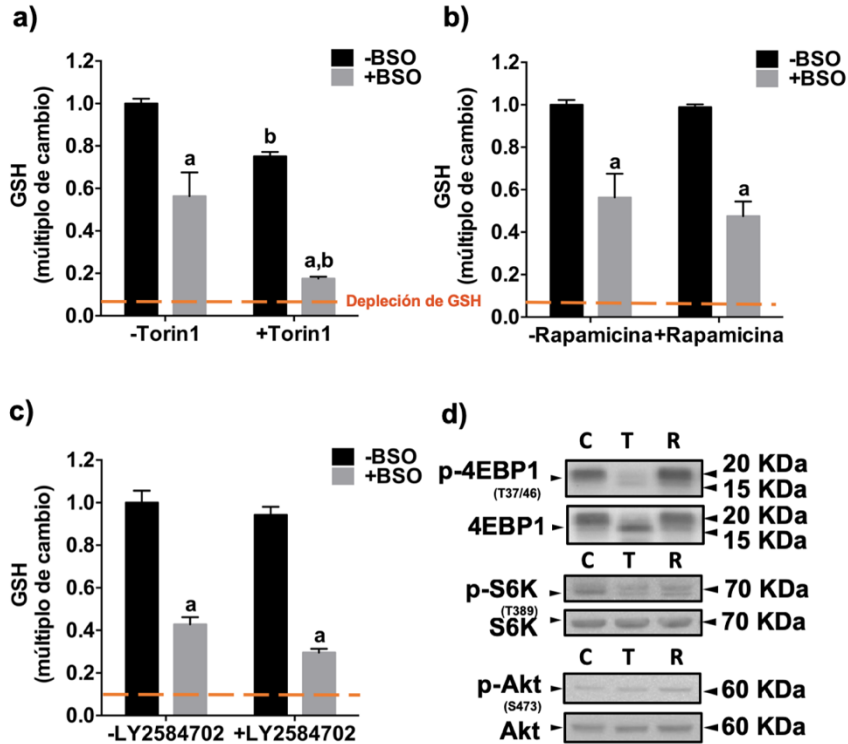


Figura 17. Efecto de la inhibición de la vía de señalización de mTOR en la homeostasis de GSH. Se evaluaron los niveles de GSH con citometría de flujo utilizando mBCL. (a) Los astrocitos se trataron con el inhibidor de mTORC1/2 torin1 250 nM, (b) el inhibidor del mTORC1 rapamicina 1 μ M o (c) el inhibidor de S6K LY2584702 5 μ M 12 h después del tratamiento con BSO. (d) Se determinaron los niveles de fosforilación de los blancos de mTORC1/2 (4EBP, S6K y Akt) por Western blot. Las gráficas representan promedios \pm SE n=3. ANOVA de dos vías, prueba post hoc Holm-Sidak ^ap<0.05 vs Control (-BSO); ^bp<0.05 -inhibidores vs +inhibidores respectivamente. Abreviaturas: BSO, L-butionina-S-R-sulfoximina; GSH, glutatión; mBCL, monoclorobimano; mTOR, blanco funcional de la rapamicina; S6K; proteína ribosomal S6 cinasa beta-1, 4EBP1, proteína de unión al factor de inicio de la traducción eucariota eIF-4E; SE, error estándar.

La inhibición de mTOR exagera el estrés oxidante en la célula

Se evaluó el estado redox de la célula con las proteínas roGFP citoplásmica y mitocondrial durante la recuperación después de la administración de BSO junto con el tratamiento de torin1 (Fig. 18a y b). El tratamiento con torin1 exacerbó la generación de estrés oxidante en los astrocitos, incrementando la oxidación de las proteínas roGFP en citoplasma y mitocondria.

Por otro lado, se determinaron los niveles de proteína de las subunidades moduladora y catalítica de la enzima GCL (GCLc y GCLm) sin embargo no hubo cambios ni en presencia sólo de BSO o con el co-tratamiento con torin1 (Fig. 18c). Esto indica por un lado que la inhibición por torin1 está induciendo un incremento en el estrés oxidante y que la

recuperación de los niveles intracelulares de GSH después del tratamiento con BSO no está incrementando los niveles de la enzima de síntesis. La inhibición de la recuperación de GSH que se observó con torin1 no se debe a un efecto en los niveles de GCL si no a un efecto en el estado redox celular.

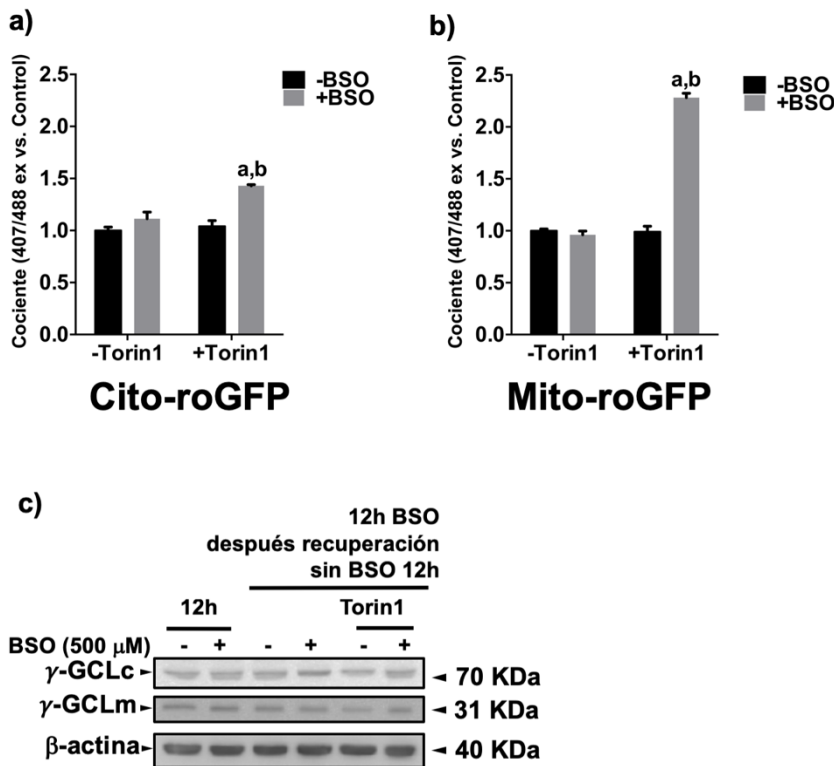


Figura 18. Efecto de la inhibición de mTOR en el estado redox de la célula y en los niveles de la enzima GCL. El estado redox (a) citosólico y (b) mitocondrial se determinaron a través de la oxidación de la proteína roGFP citosólica y mitocondrial en los astrocitos tratados con torin1 250 nM 12 h después del tratamiento con BSO. (c) Se determinaron los niveles proteicos de las subunidades GCLm y GCLc de la enzima GCL por Western blot normalizados con β -actina. Las gráficas representan promedios \pm SE n=3. ANOVA de dos vías, prueba post hoc Holm-Sidak ^ap<0.05 vs Control (-BSO); ^bp<0.05 -Torin1 vs +Torin1. Abreviaturas: BSO, L-butionina-S-R-sulfoximina; GSH, glutatión; roGFP, proteína verde fluorescente redox sensible; mTOR, blanco funcional de la rapamicina; GCL cisteína-glutamato ligasa; GCLc, subunidad catalítica; GCLm, subunidad moduladora; SE, error estándar.

La vía de señalización de mTOR no regula la biogénesis mitocondrial, pero regula la generación de ATP

Otra de las vías que podría estar afectando la recuperación de los niveles de GSH a través de la inhibición de mTOR con torin1 es la biogénesis mitocondrial. Se midió la cantidad de mitocondrias con Mitotracker red un colorante que marca mitocondrias, la expresión de

mRNA del gen de la citocromo c oxidasa subunidad 2 (COX2) específico de la mitocondria y los niveles de proteína del factor transcripcional mitocondrial (mtTFA) y no se encontraron cambios (Fig. 19). El mTOR no está regulando la homeostasis de GSH a través de la síntesis de nuevas mitocondrias.

Finalmente, se determinó la concentración de ATP en los astrocitos con el ensayo cell titer-Glo luminiscent cell viability normalizando con el colorante calceína AM (Fig. 19d). Se encontró que tanto el tratamiento con BSO, como la presencia de UK5099 y torin1 disminuyen considerablemente la concentración de ATP en las células vivas. Estos resultados sugieren que el mTOR y la mitocondria regulan la generación de energía en respuesta a la depleción de GSH inducida con BSO.

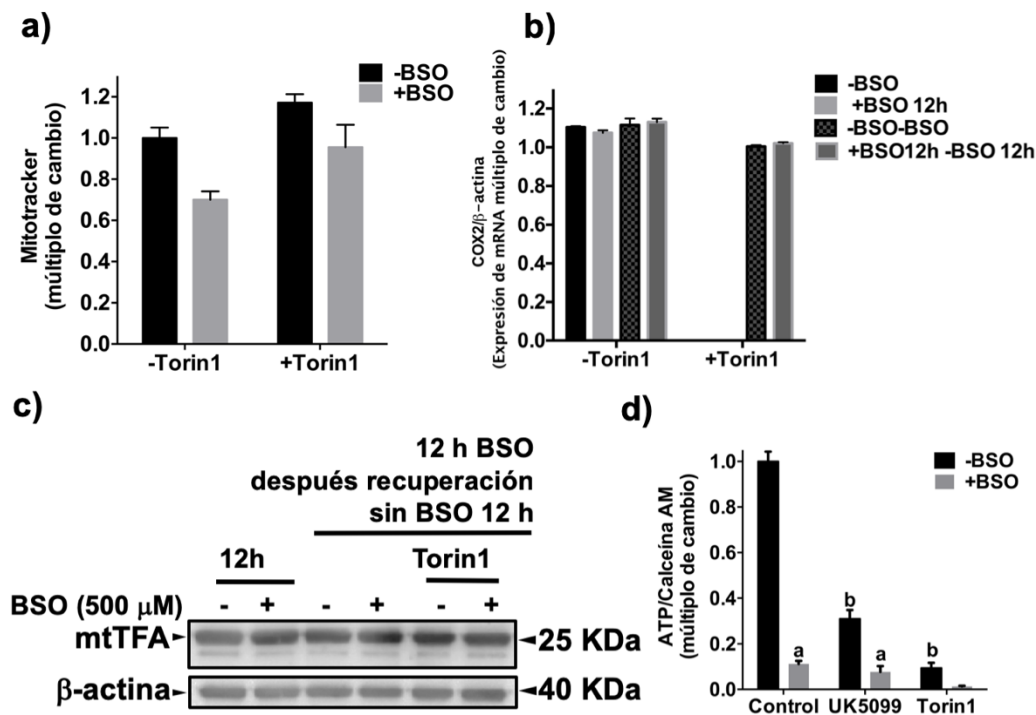


Figura 19. Efecto del BSO y la inhibición de mTOR en la biogénesis mitocondrial y la concentración de ATP (a) Acumulación mitocondrial en astrocitos tratados con torin1 250 nM 12 h después del tratamiento con BSO determinada por el colorante rojo mitotracker por citometría de flujo. (b) Expresión del gen mitocondrial COX2 determinado por qPCR y (c) Niveles de expresión de mtTFA determinados por Western blot. (d) Concentración de ATP en astrocitos tratados con UK5099 y torin1 12 h después del tratamiento con BSO, la concentración de ATP se determinó con el ensayo cell titer-Glo luminiscent cell viability, los datos fueron normalizados con el colorante calceína AM. Las gráficas representan promedios±SE n=3. ANOVA de dos vías, prueba post hoc Holm-Sidak ^ap<0.05 vs Control (-BSO); ^bp<0.05 -inhibidores vs +inhibidores respectivamente. Abreviaturas: BSO, L-butionina-S-R-sulfoximina; COX2, subunidad 2 de la citocromo c oxidasa; mtTFA; factor de transcripción mitocondrial; UK5099, 2-ciano-3-(1-fenil-1H-indol-3-il)-2-ácido propenónico; SE, error estándar.

DISCUSIÓN

Varios procesos celulares como la reparación del DNA o los antioxidantes tienen vías redundantes que compensan la ausencia o baja actividad de alguno de sus componentes. Sin embargo, el caso de la síntesis del GSH es interesante porque su ausencia no es compatible con la vida. Embriones que no presentan la enzima GCL no pueden realizar la gastrulación y mueren antes del día 8 (Dalton et al., 2000; Shi et al., 2000).

Desde que el BSO fue desarrollado en 1979 como el inhibidor más específico y efectivo de la síntesis de GSH (Griffith y Meister, 1979b) se han realizado diversos estudios donde es utilizado para estudiar los efectos de la depleción del antioxidante. En este estudio primero se decidió medir la concentración de GSH en el hígado para confirmar el efecto inhibitor del BSO (Fig. 4). Los mismos autores que sintetizaron el BSO descubrieron que los órganos responden diferencialmente a la depleción del GSH y demostraron que una sola dosis del inhibidor disminuye rápidamente los niveles de GSH en el hígado, sin embargo presenta una recuperación dentro de las siguientes 12 h, lo que sugiere que en el hígado hay un incremento de las enzimas involucradas en la síntesis de GSH o que tiene una alta capacidad de metabolizar el inhibidor (Griffith y Meister, 1979a). Los resultados de este trabajo coinciden con otros dos estudios que encontraron una baja en la concentración del GSH en el hígado, llegando a valores cercanos al 50% dentro de las primeras 2 h después de la inyección ip con BSO (Drew y Miners, 1984; Minchinton et al., 1984). También se encontró una disminución en la concentración de GSSG después del tratamiento con BSO (Fig. 4a y b), este resultado puede estar relacionado a un incremento en la actividad de la GR como una respuesta para compensar la inhibición de la síntesis de GSH con BSO, reduciendo el GSSG a GSH. La sobreexpresión de la GR eucarionte mejora la resistencia a estrés oxidante en *Escherichia coli* (Yoon et al., 2005). Además, en células de pulmón y fibroblastos el Nrf2 disminuye los niveles de GSSG incrementando la actividad de la GR,

aumentando la sobrevivencia celular en un estado de estrés oxidante (Harvey et al., 2009). Otra explicación de la disminución de los niveles de GSSG puede ser la liberación de éste en respuesta a los cambios redox; el GSSG puede ser exportado fuera de la célula como un mecanismo de desintoxicación y protección (Franco y Cidlowski, 2012).

En el mismo sentido, los estudios previos de nuestro grupo han demostrado que el BSO no sólo es capaz de disminuir los niveles de GSH en el hígado y riñones en donde activa vías de señalización específicas y, al mismo tiempo aumentar los niveles del tripéptido en homogenado de cerebro completo (Limón-Pacheco et al., 2007). El incremento observado en el cerebro se dio a partir de 1 h y duró 2 h después de la inyección con BSO, regresando a los valores control a las 3 h después del tratamiento. Se observó que el aumento en la síntesis de GSH en cerebro se acompaña de un incremento en la activación de ERK2 y de la transcripción de *nrf2*, *xCT* y *GCL*. Por lo que el objetivo de este trabajo fue investigar la respuesta de las diferentes regiones del cerebro a un tratamiento periférico con BSO, así como las vías de señalización involucradas en esta respuesta, utilizando un modelo experimental similar, que permitiera evaluar la activación de estas vías a la 0.5 h y la respuesta final a las 2 h después del tratamiento.

De las regiones evaluadas en este estudio sólo el cerebelo presentó una respuesta al tratamiento con BSO (Figs. 5-8). El cerebro es particularmente vulnerable al estrés oxidante y la concentración del GSH varía en las diferentes regiones, siendo la corteza y el cerebelo las regiones con mayor concentración (Hjelle et al., 1994; Kang et al., 1999; Kudo et al., 1990). Se ha observado que las distintas regiones del cerebro tienen diferente capacidad antioxidante, también se ha documentado que las diferentes poblaciones de neuronas responden de manera diferencial al estrés y daño durante el envejecimiento y el desarrollo de enfermedades neurodegenerativas (Hussain et al., 1995; Siqueira et al., 2005; Wang y Michaelis, 2010).

Interesantemente en el cerebelo se observó un aumento en la concentración de GSH a las 2 h de exposición con BSO (Fig. 8b). Esta respuesta fue precedida por la activación de las vías de señalización NGF/TrkA y mTOR (Fig. 10b, Fig. 11a-b y Fig. 12) seguido de un incremento en los niveles de proteína del transportador EAAT3 (Fig. 9f), lo que sugiere que el cerebelo responde a los cambios periféricos en los niveles de GSH.

Los resultados observados en el cerebelo sugieren que esta región puede tener una resistencia mayor al estrés oxidante comparado con otras regiones del cerebro. El mecanismo que explica una mayor resistencia del cerebelo al estrés oxidante todavía no se ha dilucidado. En estudios previos se ha demostrado que la sensibilidad del cerebelo a compuestos que inducen estrés oxidante es menor comparado con otras regiones (Son et al., 2016; Vandresen-Filho et al., 2015). Algo que podría ayudar a explicar esta mayor resistencia es la heterogeneidad de los microvasos sanguíneos. Austin y colaboradores demostraron que los microvasos del cerebelo tienen mayor capacidad antioxidante que los del hipocampo y la corteza (Austin et al., 2015).

La homeostasis redox y la regulación del GSH han sido ampliamente estudiadas en el cerebelo. Un balance entre los niveles de GSH y la producción de ROS es requerida para la sobrevivencia en el desarrollo de las neuronas granulares cerebelares (CGN) (Coyoy et al., 2013; Olguin-Albuerne y Moran, 2015). Por otro lado, la concentración del GSH es un factor importante en la vulnerabilidad a un daño excitotóxico inducido por ácido kaínico en CGNs (Ceccon et al., 2000). Además, el cerebelo es capaz de adaptarse enzimáticamente para resistir la depleción de GSH inducida por falla hepática aguda, al disminuir los niveles de la GPx pero manteniendo la actividad de la GR (Singh et al., 2014). El balance entre el GSH y la producción de ROS está altamente regulado en el cerebelo durante el desarrollo, la exposición a xenobióticos y el desarrollo de patologías.

Los transportadores xCT y LAT1 participan en el transporte de la cisteína hacia el cerebro y los astrocitos, sin embargo, no se encontraron cambios en los niveles proteicos después del tratamiento con BSO (Fig. 9a-b, d-e). Los ratones transgénicos con una delección del gen de xCT no presentan un aumento en el estrés oxidante (De Bundel et al., 2011; Massie et al., 2011), estos resultados sugieren que debe haber otros transportadores de cistina/cisteína compensando la falta de xCT. LAT1 media el transporte de varios aminoácidos y su actividad es importante en el transporte de cisteína de la BHE al cerebro; sin embargo, este transportador parece ser más importante durante el desarrollo mas que en la vida adulta (Boado et al., 2004). A diferencia de los ratones knock-out para xCT, los ratones con una expresión reducida o con una delección de EAAT3 exhiben alteraciones en la captación de cisteína neuronal, niveles neuronales reducidos de GSH y estrés oxidante crónico, que promueven la muerte celular neuronal y el deterioro cognitivo (Berman et al., 2011; Cao et al., 2012; Wang et al., 2015). La evidencia y nuestros resultados proponen que EAAT3 tiene un papel crucial en el transporte de cisteína a las neuronas y la BHE (Aoyama y Nakaki, 2013; Himi et al., 2003; O'Kane et al., 1999; Shanker y Aschner, 2001). Los resultados de este trabajo sugieren que EAAT3 participa en la respuesta del cerebelo frente a los cambios redox inducidos por el efecto periférico del BSO, a pesar de que el BSO no cruza la BHE, en estos tiempos de tratamiento (Limón-Pacheco y Gonsebatt, 2007; Steinherz et al., 1990). Adicionalmente, la disfunción del transportador EAAT3 se ha asociado a enfermedades como Alzheimer y Parkinson en pacientes y modelos murinos (Aoyama y Nakaki, 2013; Nafia et al., 2008). Los cambios en la expresión de EAAT3 también se han observado en otras condiciones patológicas, como ataques epilépticos y en condiciones de hipoxia/isquemia (Bianchi et al., 2014).

También se observó un aumento en la fosforilación de la S6K a la 0.5 h después del tratamiento con BSO (Fig. 10b), lo que sugiere una activación de la vía de señalización de

mTORC1 en respuesta a BSO. En este trabajo no se encontró un aumento en la fosforilación de mTOR, sin embargo, hay estudios que sugieren que la fosforilación en el residuo Ser 2448 no está relacionada a la activación de esta cinasa, incluso una mutación en este sitio no tiene efecto en su actividad (Mothe-Satney et al., 2004; Sekulic et al., 2000). No obstante, el papel de este sitio todavía no se ha descrito. Su correlación con la actividad de mTOR sigue en controversia pues dependiendo del modelo de estudio y el tipo de estimulación algunos estudios muestran que en respuesta por ejemplo a la insulina, a ácido palmítico o a suero, existe un aumento en la fosforilación de este residuo (Calvo-Ochoa et al., 2017; Rosner et al., 2010). Figueiredo et al. sugieren que un aumento en la fosforilación de este residuo podría reflejar un incremento generalizado de la vía, pero que es preferente utilizar otros blancos moleculares o proteínas efectoras para analizar la activación de mTOR (Figueiredo et al., 2017).

Se ha observado que las vías de señalización de mTOR y ERK modulan la traducción y expresión de EAAT3 después de la activación de receptores de glutamato metabotrópicos (mGluR) 1 y 5 (Ross et al., 2011). Además, se demostró en un modelo de ovocitos de *Xenopus* coexpresando mTOR y EAAT3, un incremento de EAAT3 en la superficie de la membrana, lo que prueba el papel de mTOR en la regulación positiva de este transportador de aminoácidos (Almilaji et al., 2012).

En el SNC se ha visto que el estrés oxidante activa respuestas antioxidantes mediadas por mTOR (Chong et al., 2012; Ichimura et al., 2013; Zhang et al., 2014; Zhou et al., 2016). La activación de la vía de señalización de PI3K/AKT/mTOR incrementó la expresión de la enzima GCL resultando en un aumento en la síntesis de GSH como una respuesta de protección frente a la generación de estrés oxidante (Kimura et al., 2009; Okouchi et al., 2006). Además, Limón-Pacheco et al. (2007) observaron la transcripción aumentada de GCL y la activación de ERK2 en cerebro.

Finalmente, se encontró un incremento en los niveles proteicos de NGF y la fosforilación de su receptor TrkA 0.5 h después de la inyección de BSO (Fig. 11a y b). Además, en las imágenes de las inmunofluorescencias no sólo se observó un aumento de NGF y TrkA, sino que TrkA se observó tanto en el soma como en las dendritas de las neuronas cerebelares (Fig. 12); estos resultados sugieren que la respuesta a BSO induce un incremento en la síntesis y el tráfico del receptor TrkA. Generalmente, los receptores TrkA recién sintetizados en los somas de la célula son transportados anterógradamente a través de los axones y dendritas donde se pueden unir a NGF e iniciar la señalización (Marlin y Li, 2015; Scott-Solomon y Kuruvilla, 2018).

Como se mencionó en la introducción, el NGF puede inducir respuestas antioxidantes en modelos *in vitro* e *in vivo* (Arsenijevic et al., 2007; Pan y Perez-Polo, 1993; Pan y Perez-Polo, 1996). También se ha observado que el NGF puede inducir la liberación de glutamato en CGNs, lo que sugiere su participación en la modulación de la neurotransmisión excitadora junto con la regulación del transporte de aminoácidos (Numakawa et al., 1999). La activación de la vía de señalización de PI3K/AKT vía NGF/TrkA está relacionada con una respuesta de supervivencia celular (Huang y Reichardt, 2003). En células epiteliales de pigmento retinal (RPE), el NGF protege contra la apoptosis generada por H₂O₂, estimulando la supervivencia celular a través de la activación de mTOR (Cao et al., 2011).

Los astrocitos participan en funciones complejas del SNC, incluyendo la transmisión sináptica, el procesamiento de información, así como el metabolismo y la homeostasis celular (Sofroniew y Vinters, 2010). Además, están involucrados en el desarrollo de patologías, pueden llegar a perder su función, pero también pueden montar una respuesta de defensa contra daño (Verkhatsky et al., 2015). Sus extensiones cubren la superficie de los capilares lo que los hace estar en contacto con la BHE (Fig. 1), esto genera que sean la primera línea de defensa contra la exposición a xenobióticos (Rose et al., 2017). El modelo

de astrocitos primarios ayuda a investigar las propiedades y funciones de estas células en el SNC (Lange et al., 2012). En la segunda parte de este trabajo se decidió evaluar el papel de los astrocitos en la regulación de la homeostasis de GSH. Se planteó un protocolo experimental *in vitro* para estudiar cómo responden después de una exposición aguda a BSO. Este diseño experimental buscó tener una aproximación a lo que se estudió *in vivo* ya que el BSO tiene una baja permeabilidad para cruzar la BHE (Limón-Pacheco y Gonsebatt, 2007; Steinherz et al., 1990), pero genera una respuesta en el cerebelo (Garza-Lombó et al., 2018a). Además, el tratamiento con BSO es una aproximación para estudiar la liberación de GSH de los astrocitos para las neuronas, así como el consumo de éste para el metabolismo de xenobióticos y ROS.

En primer lugar, se encontró que los astrocitos en presencia de BSO no están exportando GSH, ya que al inhibir la proteína MRP1 la depleción continúa (Fig. 14c). Una opción es que el GSH está siendo utilizado para contrarrestar el estrés generado por el BSO (Fig. 14d). Además, se ha observado que la liberación de GSH también puede generar alteraciones en el estado redox que pueden llevar a muerte celular (Franco y Cidlowski, 2012) por lo que los astrocitos pueden estar previniendo esto al reciclar el GSSG a través de la GR.

Una vez que se demostró que los niveles de GSH se recuperan después de la exposición a BSO (Fig. 14e), se decidió estudiar los mecanismos a través de los cuales los astrocitos estaban recuperando los niveles de GSH. En los astrocitos el transporte de cistina/cisteína parece ser complementario, ya que sólo se observó un efecto parcial en la recuperación del GSH cuando se inhibieron al mismo tiempo los tres transportadores, LAT1, xCT y EAAT3 (Fig. 15d).

Posteriormente se decidió evaluar el papel de la mitocondria en la regulación de la homeostasis de GSH. Como se mencionó, los astrocitos son principalmente glicolíticos,

durante condiciones de estrés o de falta de energía pueden activar el metabolismo mitocondrial (Rose et al., 2017). Por lo mismo, los astrocitos son menos susceptibles, que las neuronas, a compuestos que inducen disfunción mitocondrial (Bolanos et al., 1995); sin embargo, se ha observado que la depleción de GSH aumenta el complejo I de la cadena respiratoria (Vasquez et al., 2001), los mecanismos que regulan esta respuesta todavía no son entendidos. En este estudio, la inhibición del transporte de piruvato así como la inhibición del transporte de ácidos grasos a la mitocondria previno la recuperación de los niveles de GSH (Fig. 16). La mitocondria puede estar regulando diversos mecanismos en respuesta a la depleción de GSH. Por un lado, puede estar generando glutamato como precursor para la síntesis de GSH a través del ciclo de los ácidos tricarboxílicos (TCA) o ciclo de Krebs (Rose et al., 2017). En astrocitos, el glutamato también es un aminoácido limitante para la síntesis de GSH, debido a que es convertido a glutamina para su transporte a las neuronas. En la mitocondria este aminoácido puede ser sintetizado a partir de α -cetoglutarato, un intermediario del ciclo de los TCA (Schousboe et al., 2014). Otro mecanismo que puede estar regulando la mitocondria durante la recuperación de los niveles de GSH, es la síntesis de ATP a través de la fosforilación oxidativa. Los astrocitos pueden estar aumentando la actividad mitocondrial en respuesta a la depleción de GSH para completar los requerimientos energéticos para la recuperación en los niveles de GSH ya que las enzimas que lo sintetizan requieren energía. Los resultados revelan que tanto el BSO como la inhibición del transporte de piruvato a la mitocondria disminuyen significativamente la concentración de ATP en los astrocitos (Fig. 19d). Por último, la actividad mitocondrial puede estar regulando la homeostasis de GSH al regenerar NADPH como poder reductor para la reducción del GSSG (Blacker y Duchon, 2016). Todos estos mecanismos ayudan a explicar por qué la disfunción mitocondrial afecta la recuperación de los niveles de GSH en este modelo.

Por otra parte, las mitocondrias al igual que otros organelos contienen GSH, que es transportado desde el citoplasma hacia el interior de la mitocondria. Procesos relacionados a la síntesis, degradación, transporte, oxidación y reducción del GSH pueden tener influencia en la homeostasis de este antioxidante en la mitocondria (Calabrese et al., 2017). Se ha demostrado que la poza de GSH en el espacio intermembranal se encuentra en equilibrio con el GSH citoplasmático, sin embargo, el que se encuentra en la matriz mitocondrial parece tener mecanismos homeostáticos diferentes e independientes (Calabrese et al., 2017). Los cambios en los niveles citoplásmicos de GSH pueden también estar regulando la homeostasis de GSH mitocondrial.

Finalmente, los resultados de este trabajo revelan, de manera interesante, que la vía de señalización de mTOR también está involucrada en la recuperación de los niveles de GSH en los astrocitos (Fig. 17). Además, su inhibición con torin1 afecta el estado redox de la célula exacerbando la generación de estrés oxidante (Fig. 18). Como se mencionó en la introducción, el mTOR regula la biogénesis mitocondrial (Morita et al., 2013) pero contrario a lo que se esperaba mTOR no induce la generación de mitocondrias en respuesta al BSO (Fig. 19 a-c).

Los resultados de este trabajo sugieren que mTOR regula la recuperación de los niveles de GSH a través de la modulación de funciones bioenergéticas de la célula. La inhibición de mTOR con torin1 afecta los niveles de ATP (Fig. 19d), una de las opciones es que esté regulando la glicólisis, mecanismo a través del cual los astrocitos obtienen la energía para transportar lactato a las neuronas (Belanger et al., 2011; Bolanos, 2016). El mTOR puede estar regulando el aumento en la función glicolítica al activar a HIF1 α , un factor de transcripción que regula la expresión de enzimas y transportadores glicolíticos (Brix et al., 2012; Duvel et al., 2010; Semenza et al., 1994).

CONCLUSIONES

Los resultados de este trabajo ayudan a entender los mecanismos involucrados en la regulación de la homeostasis de GSH.

Modelo *in vivo*

La inhibición de la síntesis *de novo* de GSH periférica induce una depleción de los niveles de GSH en el hígado. La única región cerebral que respondió al tratamiento con BSO, fue el cerebelo. En el cerebelo la inhibición aguda de la síntesis de GSH, aumenta los niveles de GSH. Esta respuesta está asociada con la activación de las vías de señalización NGF/TrkA y PI3K/AKT/mTOR llevando a un aumento en los niveles del transportador de cisteína EAAT3.

Los resultados del modelo *in vivo* ayudan a explicar los mecanismos involucrados en la regulación de la homeostasis redox y el metabolismo del antioxidante GSH en el cerebelo. Esta inhibición podría presentarse por el tratamiento con fármacos o por la exposición a agentes tóxicos que no atraviesan la BHE pero tienen efectos en el SNC, así como el desarrollo de enfermedades neurodegenerativas.

Modelo *in vitro*

Los resultados del modelo *in vitro* muestran por primera vez que la vía de señalización de mTOR y el transporte mitocondrial de piruvato y de ácidos grasos tienen un papel significativo en la regulación de la homeostasis de GSH en los astrocitos.

La comprensión de los mecanismos a través de los cuales los astrocitos regulan la homeostasis redox y la defensa antioxidante ayudarán a entender el papel de los astrocitos en la protección del SNC frente a los retos que afecten el estado redox cerebral.

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ANEXOS

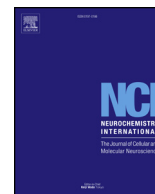
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Systemic L-buthionine-S-R-sulfoximine administration modulates glutathione homeostasis via NGF/TrkA and mTOR signaling in the cerebellum



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ABSTRACT

Glutathione (GSH) is an essential component of intracellular antioxidant systems that plays a primordial role in the protection of cells against oxidative stress, maintaining redox homeostasis and xenobiotic detoxification. GSH synthesis in the brain is limited by the availability of cysteine and glutamate. Cystine, the disulfide form of cysteine is transported into endothelial cells of the blood-brain barrier (BBB) and astrocytes via the system x_c^- , which is composed of xCT and the heavy chain of 4F2 cell surface antigen (4F2hc). Cystine is reduced inside the cells and the L-type amino acid transporter 1 (LAT1) transports cysteine from the endothelial cells into the brain, cysteine is transported into the neurons through the excitatory amino acid transporter 3 (EAAT3), also known as excitatory amino acid carrier 1 (EAAC1). The mechanistic/mammalian target of rapamycin (mTOR) and neurotrophins can activate signaling pathways that modulate amino acid transporters for GSH synthesis. The present study found that systemic L-buthionine-S-R-sulfoximine (BSO) administration selectively altered GSH homeostasis and EAAT3 levels in the mice cerebellum. Intraperitoneal treatment of mice with 6 mmol/kg of BSO depleted GSH and GSSG in the liver at 2 h of treatment. The cerebellum, but not other brain regions, exhibited a redox response. The mTOR and the neuronal growth factor (NGF)/tropomyosin receptor kinase A (TrkA) signaling pathways were activated and lead to an increase in the protein levels of the EAAT3 transporter, which was linked to an increase in the GSH/GSSG ratio and GSH concentration in the cerebellum at 0.5 and 2 h, respectively. Therefore, the cerebellum responds to peripheral GSH depletion via activation of the mTOR and NGF/TrkA pathways, which increase the transport of cysteine for GSH synthesis.

1. Introduction

Glutathione (γ -L-glutamyl-L-cysteinylglycine or GSH) is the predominant low-molecular-weight thiol in mammals. Its concentrations range from 1 to 10 mM in different tissues (Janssen-Heininger et al.,

2013). Diverse functions are attributed to GSH, including maintenance of redox homeostasis, detoxification of xenobiotics and/or metabolites via GSH S-transferases (GST), cysteine storage and the regulation of numerous cellular functions, such as proliferation and apoptosis (Aquilano et al., 2014; Lu, 2013). Exposure to metals, pesticides,

Abbreviations: 4F2hc, 4F2 cell surface antigen; BBB, blood-brain barrier; BSO, L-buthionine-S-R-sulfoximine; CNS, central nervous system; DAPI, 4',6-diamidino-2-phenylindole DTPA; diethylenetriamine penta-acetic acid, EAAC1; excitatory amino acid carrier 1, EAAT3; excitatory amino acid transporter 3, ERK; extracellular signal-regulated kinases, GCL; γ -glutamylcysteine ligase, GR; GSH reductase, GPx; GSH peroxidase, GS; GSH synthetase, GSH; glutathione, GSSG; disulfide-oxidized glutathione, GST; GSH S-transferase, H₂O₂; hydrogen peroxide, ip; intraperitoneal, LAT1; L-type amino acid transporter 1, mGluR; metabotropic glutamate receptors, mTOR; mechanistic or mammalian target of rapamycin, mTORC1; mTOR Complex 1, NAC; N-acetylcysteine, NeuN; neuronal nuclei NF κ B; nuclear factor kappa B, NGF; neuronal growth factor, OPA; o-phthalaldehyde, PI3K; phosphoinositide 3-kinase, PIKK; PI3K-related kinase, PKB/AKT, ROS; reactive oxygen species, S6K; S6 kinase beta-1, SE; standard error TrkA, Tropomyosin receptor kinase A; xCT, system x_c^- subunit

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ionizing radiation, UV light and some pharmaceutical drugs compromise GSH levels (Limon-Pacheco and Gonsebatt, 2009). Aging and degenerative and neuropsychiatric diseases, such as Parkinson's, Alzheimer's, autism, schizophrenia, pulmonary and cystic fibrosis, are also associated with disruption in cellular GSH and alterations of GSH-dependent enzymes (Gu et al., 2015; Johnson et al., 2012).

Cells synthesize GSH in two ATP-dependent enzymatic steps: γ -glutamylcysteine ligase (GCL) catalyzes the formation of γ -glutamylcysteine from glutamate and cysteine, and GSH synthetase (GS) synthesizes GSH from γ -glutamylcysteine and glycine. The availability of GSH precursors, primarily cysteine, limits GSH synthesis (Valdovinos-Flores and Gonsebatt, 2012). L-buthionine-S-R-sulfoximine (BSO) binds reversibly to GCL and blocks *de novo* GSH synthesis thus, decreasing intracellular GSH levels (Limon-Pacheco et al., 2007).

GSH and cysteine are unable to cross the blood-brain barrier (BBB), and cystine, the disulfide form of cysteine, is transported across the BBB via the Na^+ -independent cystine/glutamate exchanger system x_c^- , which is composed of xCT and the heavy chain of 4F2 cell surface antigen (4F2hc) subunits (Sato et al., 1999; Shih et al., 2006). Cystine is reduced inside the BBB, and the resulting cysteine is transported out of the endothelial cells into the brain via L-type amino acid transporter 1 (LAT1) (Killian and Chikhale, 2001; Wade and Brady, 1981). Cysteine may be reoxidized once inside the brain and transported through the system x_c^- system into the astrocytes (Shih et al., 2006). Astrocytes release GSH via the multidrug resistance protein 1 (MRP1) as the first step in supplying cysteine for GSH synthesis in neurons (Hirrlinger and Dringen, 2005; Wang and Cynader, 2000). Neurons take up cysteine via excitatory amino acid transporter 3 (EAAT3), which is a glutamate transporter that is part of the x_{AG}^- system in the postsynaptic neurons. It is also known as excitatory amino acid carrier 1 (EAAC1), which also transports cysteine (Himi et al., 2003; Valdovinos-Flores and Gonsebatt, 2012; Zerangue and Kavanaugh, 1996). EAAT3 dysfunction was associated with Alzheimer's and Parkinson's diseases in patients and murine models (Aoyama and Nakaki, 2013; Nafia et al., 2008). Changes in EAAT3 expression were also observed in other pathological conditions, such as epileptic seizures and hypoxia/ischemia conditions (Bianchi et al., 2014).

The mechanistic/mammalian target of rapamycin complex 1 (mTORC1) is a serine/threonine protein kinase of the PI3K-related kinase (PIKK) family that regulates cell growth and metabolism in response to different stimuli, such as variations in the amino acid content, changes in cellular bioenergetics, growth factors and oxidative stress (Saxton and Sabatini, 2017). Therefore, we investigated the role of the mTORC1 pathway in the expression of these amino acid transporters. mTORC1 is also a key downstream molecule of the signaling pathways activated by neurotransmitters and neurotrophin signals in the brain (Garza-Lombo and Gonsebatt, 2016; Garza-Lombo et al., 2018).

Neuronal growth factor (NGF) and its receptor, tropomyosin receptor kinase A (TrkA) are also involved in the regulation of the amino acid transport and GSH synthesis (Pan and Perez-Polo, 1993; Valdovinos-Flores and Gonsebatt, 2013). NGF binds to the TrkA receptor, which results in its dimerization and transphosphorylation (Huang and Reichardt, 2003). Activation of this pathway during the modulation of amino acid transport was also an aim of the present study.

We observed that the systemic inhibition of GSH synthesis and exposure to arsenic, upregulated the expression of amino acid transporters, such as xCT and EAAT3, in the brain in murine models (Limon-Pacheco et al., 2007; Ramos-Chavez et al., 2015) and modulated glutamate availability, which may lead to neurotoxicity (Nelson-Mora et al., 2018). Chen et al. demonstrated that cadmium-induced reactive oxygen species (ROS) activated mTOR, and the GSH analog N-acetyl cysteine (NAC), blocked mTOR activation in cultured neuronal cells (Chen et al., 2011).

To investigate if the peripheral inhibition of GSH synthesis is associated with an upregulation of cystine/cysteine transporters and the

activation of the mTORC1 pathway in the brain, we injected mice intraperitoneally (ip) with an inhibitor of the GCL, L-buthionine-S-R-sulfoximine (BSO), which is poorly transported into the brain in adult animals (Limon-Pacheco and Gonsebatt, 2007; Steinhilber et al., 1990). We observed a depletion of GSH and GSSG in the liver at 2 h after BSO treatment. At this time point, in the central nervous system (CNS), the cerebellum, but not other brain regions, revealed activation of mTOR and the NGF/TrkA pathways associated with an increase in EAAT3 protein levels (i.e., the cysteine transporter in neurons), the GSH/GSSG ratio and GSH concentration at 0.5 and 2 h respectively. These results suggest that the cerebellum exhibits a higher antioxidant capacity.

2. Material and methods

2.1. Reagents

Antibodies against phosphorylated (p)-p70 S6K (Thr 389, #9234), p-mTOR (Ser 2448, #5536), p-TrkA (Tyr 490, #9141), p70 S6K (#2708), mTOR (#2983), NGF (#2046), the secondary anti-rabbit (#7074) and the biotinylated protein ladder (#7727) were purchased from Cell Signaling Technology (MA, USA). Antibodies against EAAT3 (ab124802), TrkA (ab76291), xCT (ab37185), NeuN (ab177487) and NGF (ab52918, for immunofluorescence) were purchased from Abcam (MA, USA). LAT1 (sc-134994) was purchased from Santa Cruz Biotechnology (CA, USA). Antibodies against β -tubulin (T4026) and β -actin (GT5512) were purchased from Sigma-Aldrich and GeneTex, respectively. Anti-mouse (61–6520) secondary antibody was from Thermo Fisher Scientific (MA, USA). The secondary Alexa Fluor 546 anti-rabbit and Alexa Fluor 488 anti-mouse antibodies were purchased from Invitrogen (CA, USA).

2.2. Animals and treatment protocol

Four- to five-week-old BALB/c male mice were obtained from the Animal Care Facility of the Instituto de Investigaciones Biomédicas of the Universidad Nacional Autónoma de México. Mice were maintained at 23–25 °C at a relative humidity of 50–60% and under a 12 h light/dark cycle. The animals had access to food and water *ad libitum*. Mice received BSO dissolved in saline solution ip at a dose of 6 mmol/kg. Animals were sacrificed at 0.5 and 2 h after treatment, and the livers and cerebella were dissected and processed immediately or stored at –80 °C.

Experiments were performed following the guidelines stated in the “Principles of Laboratory Animal Care” (National Institutes of Health, NIH) and “Especificaciones técnicas para la producción, cuidado y uso de los animales de laboratorio (Clave NOM-062-ZOO-1999)” of the “Norma Oficial Mexicana de la Secretaría de Agricultura, Ganadería, Desarrollo Rural, Pesca y Alimentación (SAGARPA)” (2001).

2.3. Determination of GSH and GSSG levels

Tissue GSH and GSSG levels were measured by the fluorometric o-phthalaldehyde (OPA) method (Senft et al., 2000), adapted to opaque microplates (Ramos-Chavez et al., 2015). Briefly, tissues were weighed and homogenized in 10 vol of ice-cold homogenization buffer containing 154 mM KCl, 5 mM diethylenetriamine penta-acetic acid (DTPA), and 0.1 M potassium phosphate buffer, pH 6.8, followed by the addition of 10 vol of cold buffer containing 40 mM HCl, 10 mM DTPA, 20 mM ascorbic acid, and 10% trichloroacetic acid. Samples were centrifuged at 14,000 $\times g$, and the supernatant was filtered through a 0.45 μm filter. Samples were stable at –80 °C for at least 4 weeks. The OPA reagent was added, and fluorescence was determined at 365 nm excitation and 430 nm emission using a DTX 800/880 Multimode Detector (Beckman Coulter, CA, USA). The final values were calculated using standard curves after subtracting the background reaction (non-glutathione-dependent fluorescence) and normalized to the tissue

Liver

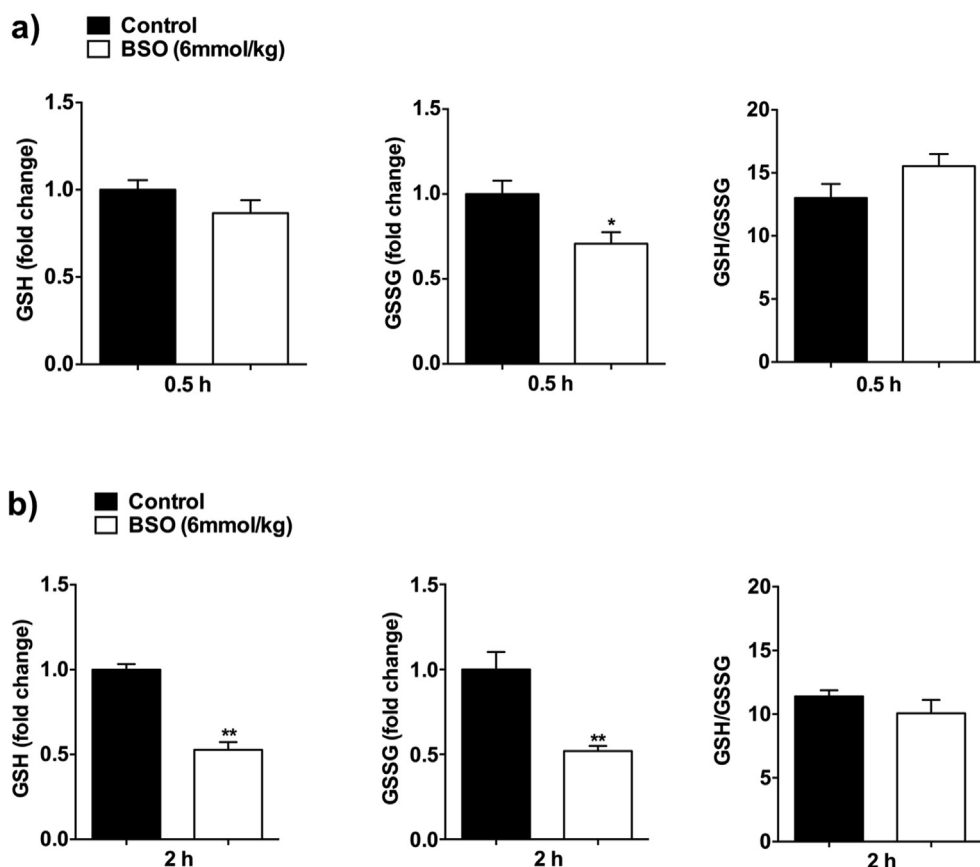


Fig. 1. BSO effect on GSH and GSSG levels in the liver of mice treated ip with 6 mmol/kg BSO. Normalized levels of GSH, GSSG, and GSH/GSSG ratio at 0.5 h (a) and 2 h (b) after BSO administration. Data in graphs represent means \pm SE; n = 6. Student's *t*-test. **p* < 0.05, ***p* < 0.01 vs Controls are considered significant. Abbreviations: BSO, L-buthionine-S-R-sulfoximine; GSH, glutathione; GSSG, disulfide-oxidized glutathione; SE, standard error.

weight.

2.4. Protein extraction and western immunoblot

Membrane-enriched fractions were obtained from tissue samples as described previously (Schindler et al., 2006) for Western blot determinations of EAAT3, TrkA, xCT, and LAT1. Tissues were homogenized in 10 vol of extraction buffer containing 10 mM HEPES, 10 mM NaCl, 1 mM KH_2PO_4 , 5 mM NaHCO_3 , 5 mM EDTA, 1 mM CaCl_2 , 0.5 mM MgCl_2 , 1 mM Na_3VO_4 , 1 mM PMSF, and a protease inhibitor cocktail (Roche, Switzerland). Homogenates were centrifuged at $6300 \times g$ for 10 min at 4 °C. Supernatants were recovered and centrifuged at $100,000 \times g$ for 30 min at 4 °C. Pellets were resuspended in 40 mM Tris-HCl, pH 9.5, 8 M urea and 4% (w/v) Triton X-100 supplemented with 1 mM Na_3VO_4 , 1 mM PMSF, and a protease inhibitor cocktail. Protein concentrations were determined using a Pierce BCA Protein Assay kit (Thermo Scientific, MA, USA).

Cytoplasmic fractions were extracted for S6K, mTOR and NGF determinations as previously described (Basaki et al., 2007). Tissues were lysed in Buffer A (10 mM HEPES, pH 7.9, 10 mM KCl, 10 mM EDTA, 1 mM DTT, 0.4% v/v IGEPAL, with 1 mM Na_3VO_4 , 1 mM PMSF, and a protease inhibitor cocktail), incubated for 10 min on ice, and then centrifuged for 15 min at $4000 \times g$. The supernatant fractions containing cytoplasmic soluble proteins were collected.

Samples (5–40 μg protein) were subjected to sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE) and transferred onto nitrocellulose membranes (Bio-Rad Laboratories, Germany). The

membranes were blocked with 1x Tris-buffered saline (TBS) and 0.1% Tween-20, containing 5% Blotto or bovine serum albumin (BSA) according to the antibody's specifications. Membranes were incubated with the primary antibodies. Mouse anti- β -tubulin or anti- β -actin were used as loading controls. Normalization for p-mTOR was performed against mTOR instead of β -tubulin or β -actin to reflect changes in mTOR phosphorylation, and not mTOR protein levels.

Protein bands were visualized using the appropriate HRP-linked secondary antibodies and the ECL Prime Western blotting detection reagent (GE Healthcare Bio-Sciences, PA, USA). Images were captured, and densitometry analysis was performed using ImageJ version 1.50 g software (Wayne Rasband, NIH, MD, USA).

2.5. Immunofluorescence

Mice were treated with BSO and perfused with a cold saline solution followed by ice-buffered paraformaldehyde (4%). The brains were removed, postfixed for 24 h at 4 °C, immersed in 20% and 30% sucrose cryoprotection solutions and frozen in 4-methylbutane. Sections (50 μm) were cut using a cryostat and collected in 24-well culture plates filled with 0.1 M phosphate buffer (PB). Sections were washed three times with PB + 0.3% Triton X-100 (PBT) and incubated overnight at 4 °C with the primary antibodies: mouse anti-NeuN (neuronal nuclei; 1:600) and rabbit anti-TrkA (1:200) or anti-NGF (1:200) in PBT containing 0.3% BSA and 2% normal horse serum (Vector Laboratories, CA, USA). Sections were washed three times with PBT and incubated with the anti-rabbit Alexa Fluor 546 (1:600) and anti-mouse Alexa Fluor 488

Cerebellum

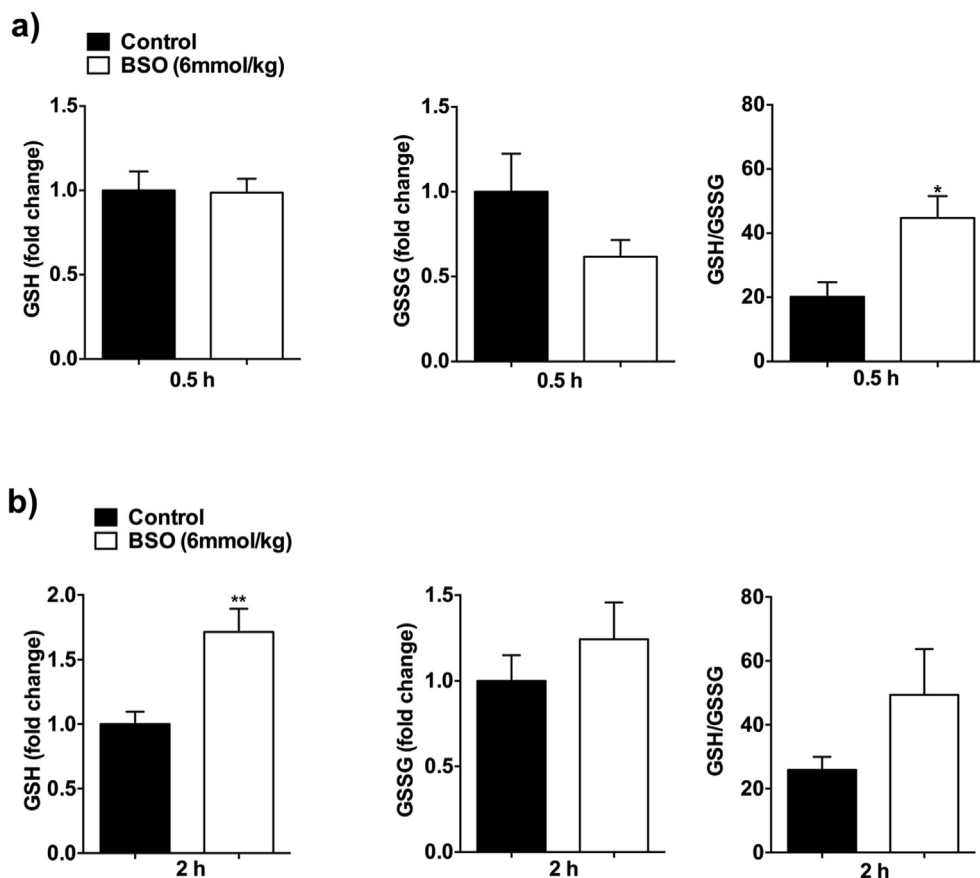


Fig. 2. BSO effect on GSH and GSSG levels in the cerebellum of mice treated ip with 6 mmol/kg BSO. Normalized levels of GSH, GSSG, and GSH/GSSG ratio at 0.5 h (a) and 2 h (b) after BSO administration. Data in graphs represent means \pm SE; $n = 6$. Student's *t*-test. * $p < 0.05$, ** $p < 0.01$ vs Controls are considered significant. Abbreviations: BSO, L-buthionine-S-R-sulfoximine; GSH, glutathione; GSSG, disulfide-oxidized glutathione; SE, standard error.

(1:400) secondary antibodies for 2 h. Then, the sections were washed in 0.1 M PB, and nuclei were counterstained with 4',6-diamidino-2-phenylindole (DAPI, Invitrogen), according to the manufacturer's protocol. Brain sections were mounted in Fluorescence Mounting Medium (DAKO, Denmark). Confocal images were sequentially acquired using a Nikon A1R⁺ laser scanning confocal head coupled to an Eclipse Ti-E inverted microscope (Nikon Corporation, Japan) equipped with a motorized stage (TI-S-E, Nikon). ImageJ version 1.50 g software (Wayne Rasband, NIH; MD, USA) was used to analyze the final images.

2.6. Statistical analysis

Collected data were analyzed using Student's *t*-test using GraphPad Prism version 6.00 (GraphPad Software, CA, USA). Data were plotted as the means \pm standard error (SE). *P* values < 0.05 were considered as statistically significant.

3. Results

3.1. Changes in GSH and GSSG levels in the liver following BSO treatment

GSH and GSSG levels were determined to demonstrate that ip BSO diminished the GSH concentration in mouse liver. No decrease in GSH levels was observed 0.5 h after BSO treatment (Fig. 1a). However, a significant decrease in GSSG levels was found (Fig. 1a). A significant decrease in GSH and GSSG levels was observed 2 h after BSO injection (Fig. 1b) which suggests that BSO decreased intracellular GSH and

GSSG content via blockade of *de novo* GSH synthesis. The GSH/GSSG ratio is an indicator of the redox environment status (Schafer and Buettner, 2001), and it was not altered at either time point (Fig. 1a and b). These results suggest that cells export or metabolize GSSG as a detoxifying mechanism to prevent oxidative stress (Franco and Cidlowski, 2012).

3.2. BSO induces an increase in GSH levels in the cerebellum

We previously observed that BSO treatment (6 mmol/kg) increased GSH levels in whole brain homogenates (Limon-Pacheco et al., 2007). The present study measured GSH levels in different brain regions (data not shown), however a clear redox response was observed only in the cerebellum. BSO administration produced no significant changes in GSH or GSSG levels at 0.5 h (Fig. 2a), but the slight changes in their concentrations significantly increased the GSH/GSSG ratio (Fig. 2a). A significant increase in GSH levels was observed at 2 h (Fig. 2b). These results demonstrate an increase in the reductive environment and GSH levels in the cerebellum after BSO administration. BSO is poorly transported into the brain (Limon-Pacheco and Gonsebatt, 2007; Steinhilber et al., 1990), but the cerebellum responded to the changes in the redox state of the periphery.

3.3. Expression of xCT, EAAT3 and LAT1 transporters in the cerebellum

GSH synthesis in the brain is associated with an increased expression of cystine/cysteine transporters (Limon-Pacheco et al., 2007;

Cerebellum

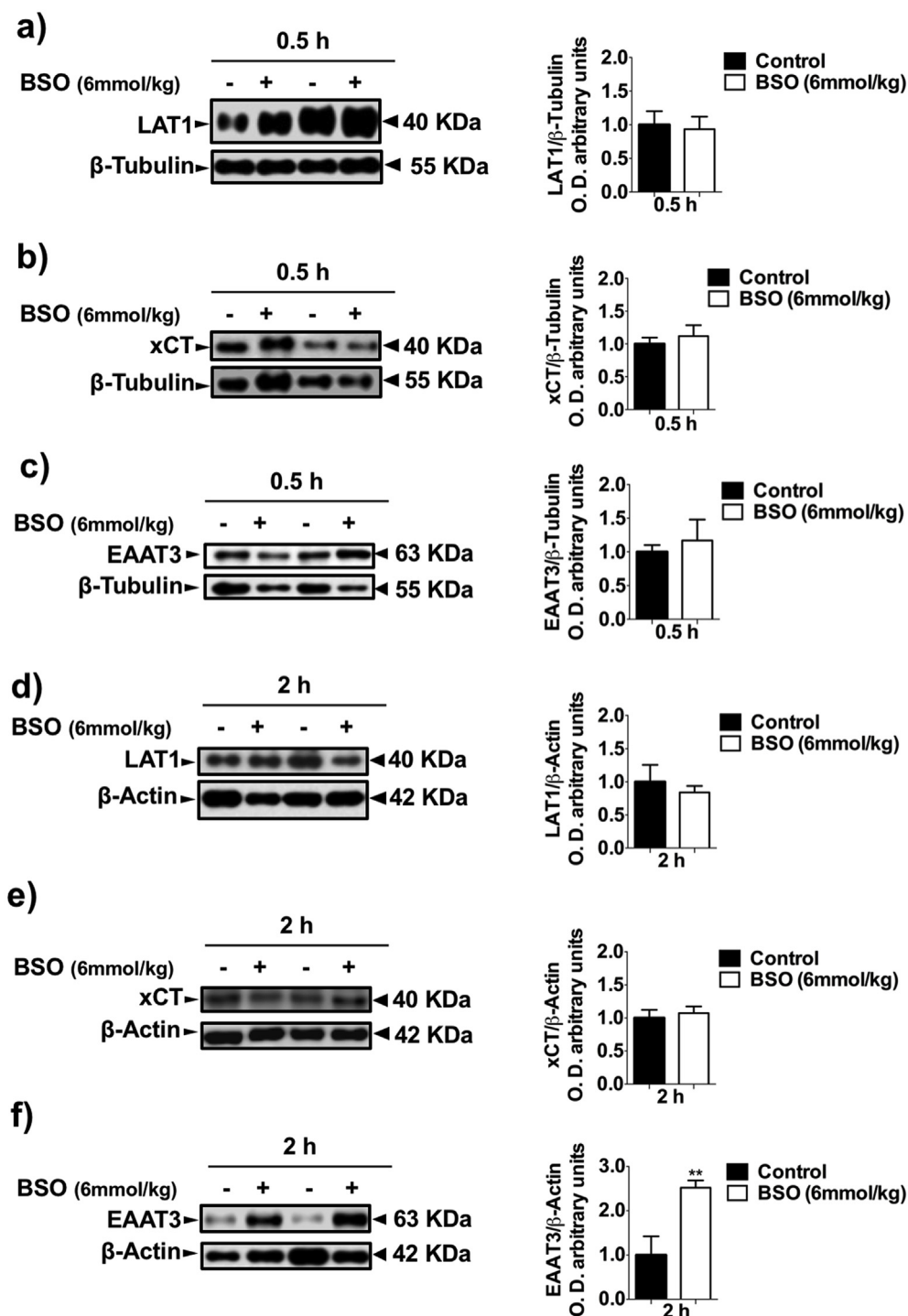


Fig. 3. BSO effect on the protein levels of the amino acid transporters, LAT1, xCT, and EAAT3, in the cerebellum of mice, treated ip with 6 mmol/kg BSO. Changes in the protein levels in enriched membrane fraction were evaluated by western blots, at 0.5 h and 2 h after BSO injection. Graphs show the densitometric analysis of the protein bands normalized to β -tubulin (a-c) or β -actin (b-d), means \pm SE; n = 6. Student's *t*-test. ***p* < 0.01 vs Controls are considered significant. Abbreviations: BSO, L-buthionine-S-R-sulfoximine; LAT1, L-type amino acid transporter; xCT, system xc-subunit; EAAT3, excitatory amino acid transporter 3; SE, standard error.

Nelson-Mora et al., 2018; Ramos-Chavez et al., 2015). Western blot analysis of membrane-enriched fractions was performed to determine the expression of the amino acid transporters involved in the import of cysteine for GSH synthesis. No changes in the expression of the xCT subunit of the x_c^- system, or the transporter of large neutral amino acids, LAT1 were observed after BSO treatment (Fig. 3 a-b, d-e). On the other hand, the expression of the neuronal glutamate transporter

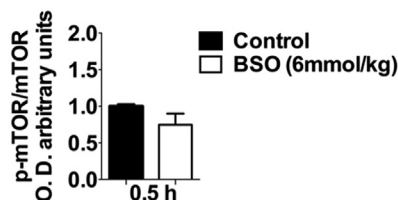
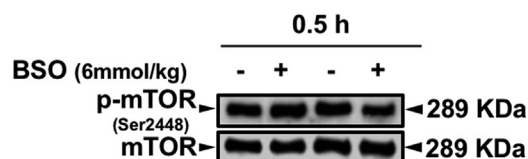
EAAT3, which is also involved in the uptake of cysteine primarily in neurons, was significantly upregulated 2 h after BSO treatment (Fig. 3 c and f).

3.4. BSO activates the mTOR and NGF pathways in the cerebellum

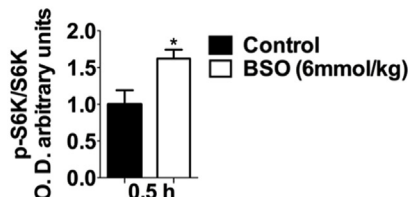
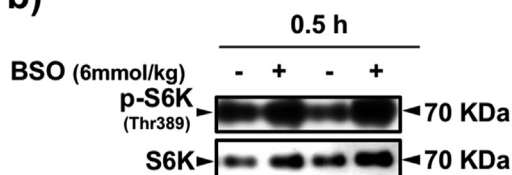
We investigated whether BSO treatment activated the mTOR

Cerebellum

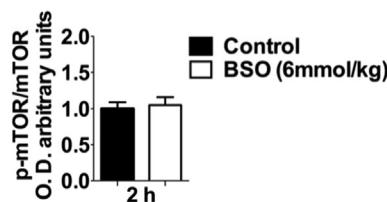
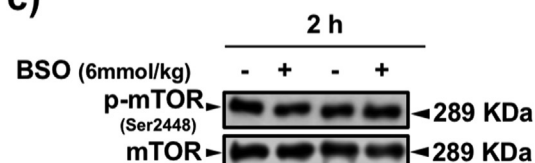
a)



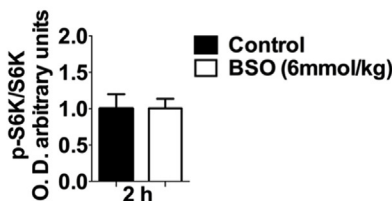
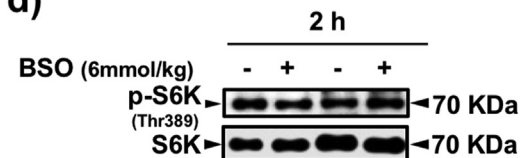
b)



c)



d)



signaling pathway in the cerebellum because of the close relationship between mTOR and the amino acid transporters (Goberdhan et al., 2016; Kim and Guan, 2011). Western blot analysis revealed no increase in the phosphorylation or the expression of mTOR (Fig. 4a, c). However, an increased phosphorylation of its downstream target ribosomal protein S6 kinase beta-1 (S6K) (Garza-Lombo et al., 2018) was found 0.5 h after treatment (Fig. 4b,d), which suggests that S6K could be participating in the activation of EAAT3.

We demonstrated that activation of the NGF/TrkA/phosphoinositide 3-kinase/protein kinase B/AKT/nuclear factor kappa B (PI3K/PKB/AKT/NFκB) pathway in mouse liver induced an antioxidant response after treatment with GSH-consuming agents (Valdovinos-Flores and Gonsbatt, 2013). It has also been shown that NGF is involved in the regulation of cellular GSH levels *in vitro* and *in vivo* (Arsenijevic et al., 2007; Pan and Perez-Polo, 1996). We measured NGF and TrkA expression using Western blot and immunofluorescence analysis to evaluate whether the NGF/TrkA pathway was activated in the cerebellum in response to BSO. Western blot analysis demonstrated that BSO treatment significantly induced NGF expression and TrkA phosphorylation at 0.5 h (Fig. 5a and b) but not at 2 h (Fig. 5c and d).

Fig. 4. BSO effect on the phosphorylation of mTOR and S6K in the cerebellum of mice treated ip with 6 mmol/kg BSO at 0.5 h and 2 h. Changes in the phosphorylation levels were evaluated by western blots, at 0.5 h and 2 h after BSO injection (a, c) p-mTOR (Ser 2448) and (b, d) p-S6K (Thr 389). Graphs show densitometric analysis of protein bands normalized with respect to total mTOR and S6K respectively and represent means \pm SE; n = 6. Student's t-test. *p < 0.05 vs Controls are considered significant. Abbreviations: BSO, L-buthionine-S-R-sulfoximine; mTOR mechanistic or mammalian target of rapamycin; S6K, S6 kinase beta-1; SE, standard error.

Immunofluorescence labeling revealed increased NGF and TrkA expression in neurons at 0.5 h. TrkA increase was found in the soma of the neurons of the granular cell layer and the molecular layer, which contains axonal and dendritic processes (Fig. 6, Supplementary movies). No change was observed at 2 h (Fig. 7). These results suggest that the NGF signaling pathway and mTOR are involved in GSH homeostasis and induce an antioxidant response that is associated with the depletion of peripheral GSH. We hypothesize that this activation drives the up-regulation of EAAT3 and increase in GSH levels.

Supplementary video related to this article can be found at <https://doi.org/10.1016/j.neuint.2018.10.007>.

4. Discussion

Our previous studies demonstrated that BSO diminished GSH levels in liver and kidneys but surprisingly increased the GSH levels in whole brain homogenates (Limon-Pacheco et al., 2007) despite the limited permeability of BSO across to the BBB (Limon-Pacheco and Gonsbatt, 2007; Steinherz et al., 1990). This increase began 1 h after BSO injection and lasted 2 h. The GSH content returned to the control value at

Cerebellum

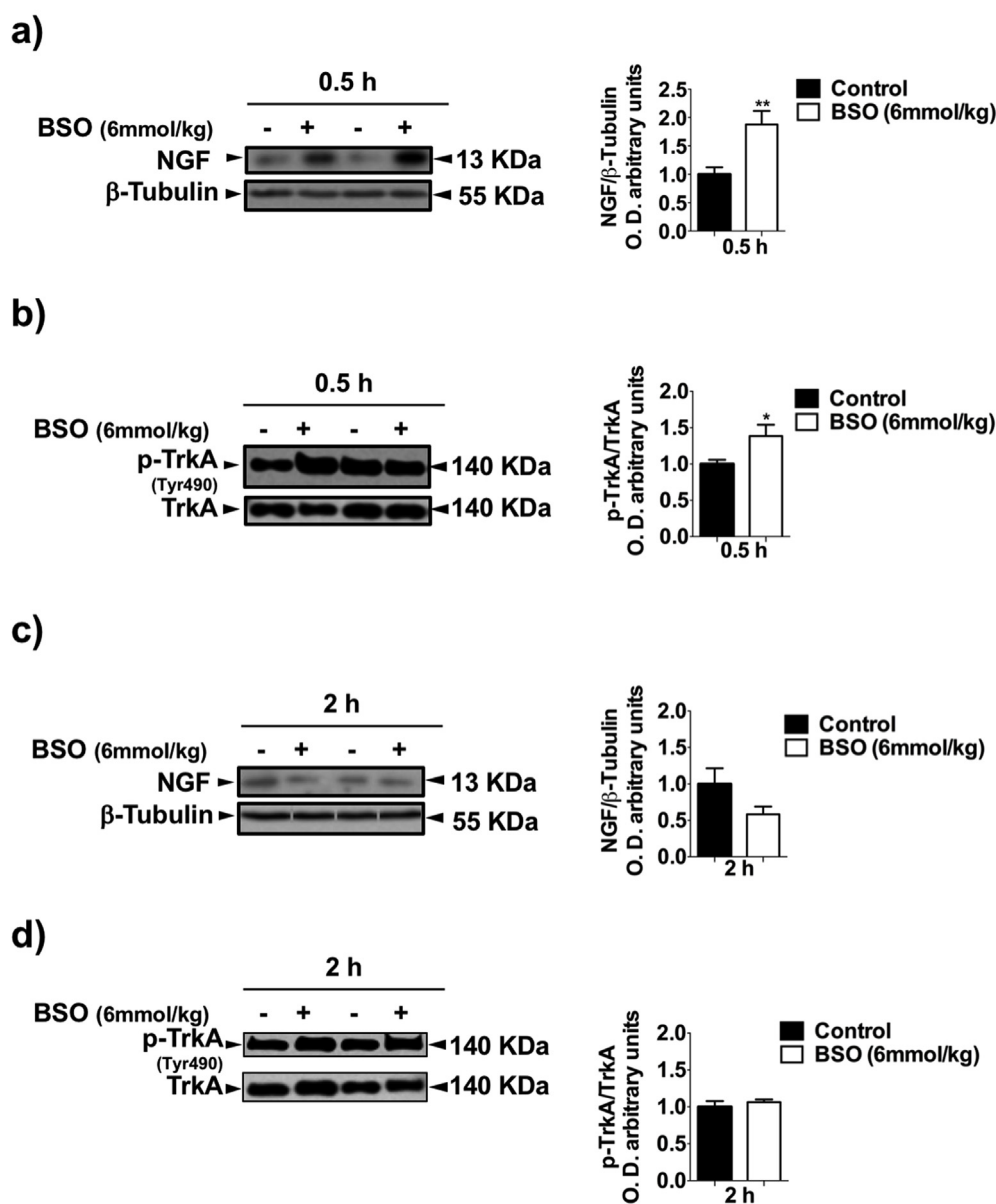


Fig. 5. BSO effect on NGF protein levels and the phosphorylation of TrkA in the cerebellum of mice treated ip with 6 mmol/kg BSO at 0.5 h and 2 h. Changes in the protein and phosphorylation levels were evaluated by western blots at 0.5 h and 2 h after BSO injection (a, c) NGF; p-TrkA (Tyr 490) (b, d). Graphs show densitometric analysis normalized with respect to total TrkA and represent means \pm SE; n = 5. Student's *t*-test. **p* < 0.05, ***p* < 0.01 vs Controls are considered significant. Abbreviations: BSO, L-buthionine-S-R-sulfoximine; NGF, neuronal growth factor; TrkA, Tropomyosin receptor kinase A. SE, standard error.

3 h. A single dose of BSO rapidly decreased GSH levels, but GSH content recovered within 12 h in the liver, which suggests an increase rate of enzyme synthesis or a great capacity to metabolize the inhibitor (Griffith and Meister, 1979). The present study investigated the responses of different brain regions to peripheral BSO and the potential signaling pathways involved in this response using an experimental protocol to observe signaling pathways activation at 0.5 h and the final response at 2 h.

We observed an increase in GSH concentration in the cerebellum after BSO exposure (Fig. 2a). This response was preceded by the activation of the NGF/TrkA and mTOR signaling pathways (Figs. 4b and 5a and b and Fig. 6) and increased protein levels of the EAAT3 transporter (Fig. 3f), which suggests that the cerebellum responds to peripheral changes in GSH.

The brain is especially vulnerable to oxidative stress, and different regions contain varying concentrations of GSH. The cortex and the cerebellum contain higher GSH levels (Kang et al., 1999). Our results suggest that the increase in GSH levels (Fig. 2b) and the GSH/GSSG ratio (Fig. 2a) observed in the cerebellum after peripheral BSO exposure might be related to a higher resistance of the cerebellum to oxidative stress compared to other brain regions.

The mechanism of the increased resistance of the cerebellum to oxidative stress is not clear. Previous reports demonstrated that the sensitivity of the cerebellum to compounds that induce oxidative stress was lower than other brain areas (Son et al., 2016; Vandresen-Filho et al., 2015). The cerebellum exhibited higher GSH content (~1.5 mmol/g tissue) compared to other brain regions (Hjelle et al., 1994; Kang et al., 1999; Kudo et al., 1990). Notably, the heterogeneity

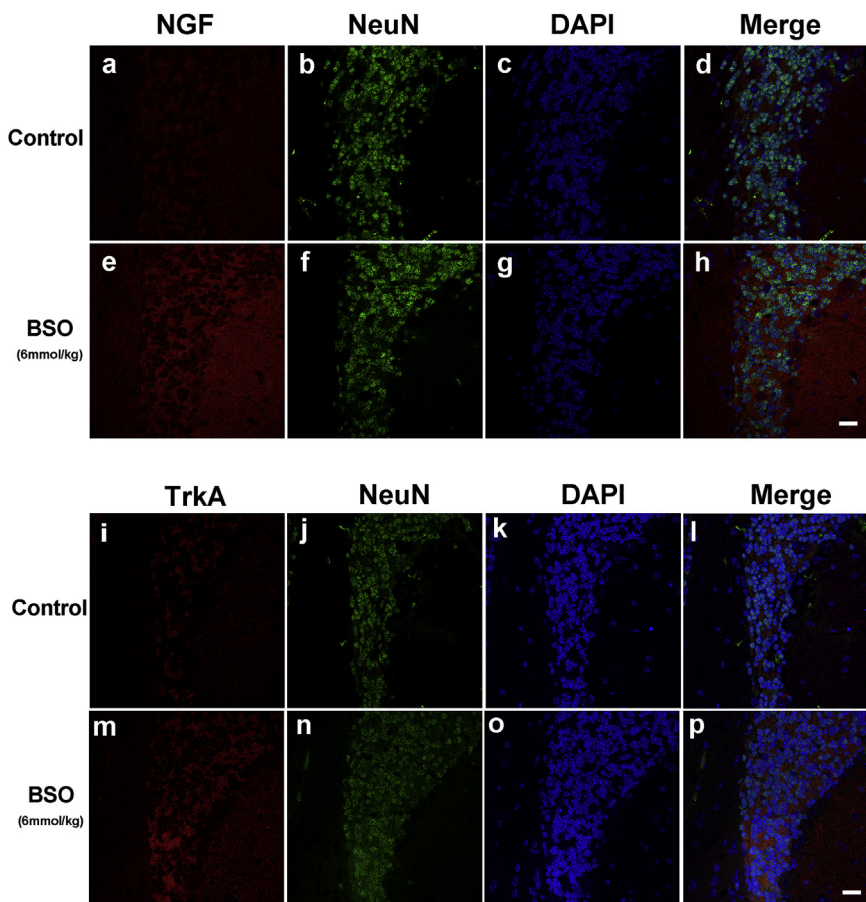


Fig. 6. BSO effect on NGF and TrkA protein levels in cerebellum of mice treated ip with 6 mmol/kg BSO at 0.5 h. Confocal images of immunostained sections from the cerebella of control and BSO treated mice. (a, e) shows immunofluorescence images of NGF (red), (b, f) neuron marker anti-NeuN (green), (c, g) nuclei marker DAPI (blue) and (d, h) merge, in control and treated mice. The second panel shows immunofluorescence images of (i, m) TrkA (red), (j, n) NeuN (green), (k, o) DAPI (blue) and (l, p) merge in control and treated mice. Please note the relative increase of intensity in both NGF and TrkA of BSO-treated animals. Scale bar: 20 μ m. Supplementary material shows a 3D reconstruction of the molecular layer of the cerebellum immunostained with TrkA (red), NeuN (green) and DAPI (blue); movie1 (control), movie 2 (6 mmol/kg BSO at 0.5 h). Abbreviations: BSO, L-buthionine-S-R-sulfoximine; NGF, neuronal growth factor; TrkA, Tropomyosin receptor kinase A; NeuN, neuronal nuclei DAPI, 4',6-diamidino-2-phenylindole.

of cerebral microvessels may help explain the different susceptibility. Austin and colleagues have demonstrated that the microvessels of the cerebellum exhibited greater antioxidant capacity than the hippocampus or cortex (Austin et al., 2015).

Additionally, redox and GSH regulation in the cerebellum has been widely studied. A balance between GSH levels and ROS production is required for cerebellar granule neurons (CGN) survival during early development (Coyoy et al., 2013; Olguin-Albuerna and Moran, 2015). GSH content is also a critical factor in the sensitivity to excitotoxic injury from kainic acid in the CGN (Ceccon et al., 2000). The cerebellum adapts enzymatically to resist GSH depletion induced by acute liver failure via decreasing GSH peroxidase (GPx) levels but not GSH reductase (GR) activity (Singh et al., 2014). The important balance between GSH and ROS production in the cerebellum during development, exposure to xenobiotics and the development of pathologies, is tightly regulated in this brain region.

The increased GSH levels in the cerebellum associated with the liver depletion of GSH was linked to the upregulation of EAAT3 but not xCT or LAT1 (Fig. 3). xCT and LAT1 are crucial for cysteine transport into the brain and astrocytes, but we did not find any significant upregulation in xCT or LAT1 protein levels (Fig. 3a–b, d–e). Transgenic mice with deletion of the xCT gene do not exhibit any signs of increased oxidative stress (De Bundel et al., 2011; Massie et al., 2011), which suggests the participation of additional cystine/cysteine transporters. LAT1 mediates the transport of several amino acids, and its activity is important to transport cysteine from the BBB to the brain. However, LAT1 seems to be more important during development than during adult life (Boado et al., 2004). In contrast to xCT knock-out mice, mice with reduced EAAT3 expression or lacking EAAT3 expression exhibit impaired neuronal cysteine uptake, reduced neuronal GSH levels and chronic oxidative stress, which promote neuronal cell death and cognitive impairment (Berman et al., 2011; Cao et al., 2012; Wang et al.,

2015). This evidence suggests that EAAT3 plays a crucial role in cysteine uptake in neurons and the BBB and the regulation of GSH homeostasis (Aoyama and Nakaki, 2013). Our results suggest that EAAT3 participates in the cerebellar response against redox changes induced by the peripheral effect of BSO although BSO is poorly transported through the BBB (Limon-Pacheco and Gonsebatt, 2007; Steinherz et al., 1990).

We also observed an increase in the phosphorylation of the mTORC1 target S6K at 0.5 h after BSO treatment (Fig. 4b), which suggests activation of the mTORC1 pathway in response to BSO. Although we did not find an increase in mTOR phosphorylation, there are diverse studies that suggest that mTOR phosphorylation on Ser 2448 is not directly involved in its activation additionally, its mutation has no effect on mTOR activity (Mothe-Satney et al., 2004; Sekulic et al., 2000).

The mTOR and extracellular signal-regulated kinases (ERK) pathways mediated EAAT3 translation and protein following activation of the metabotropic glutamate receptors (mGluR) 1 and 5 (Ross et al., 2011). Increased EAAT3 protein abundance on the membrane surface, was observed in *Xenopus* oocytes coexpressing mTOR and EAAT3, which demonstrates the role of mTOR in EAAT3 upregulation (Almilaji et al., 2012).

mTOR is protective in the CNS, and it induces antioxidant responses, against oxidative stress (Chong et al., 2012; Ichimura et al., 2013; Zhang et al., 2014; Zhou et al., 2016). In two studies, activation of the PKB/AKT/mTOR pathway clearly increased GCL expression and resulted in GSH synthesis and protection against oxidative stress (Kimura et al., 2009; Okouchi et al., 2006).

We also found an increase in NGF expression and phosphorylation of its receptor TrkA 0.5 h after BSO treatment (Fig. 5a and b). Similar results were observed using immunofluorescence labeling. TrkA upregulation was observed in the soma, axons and dendrites of cerebellar

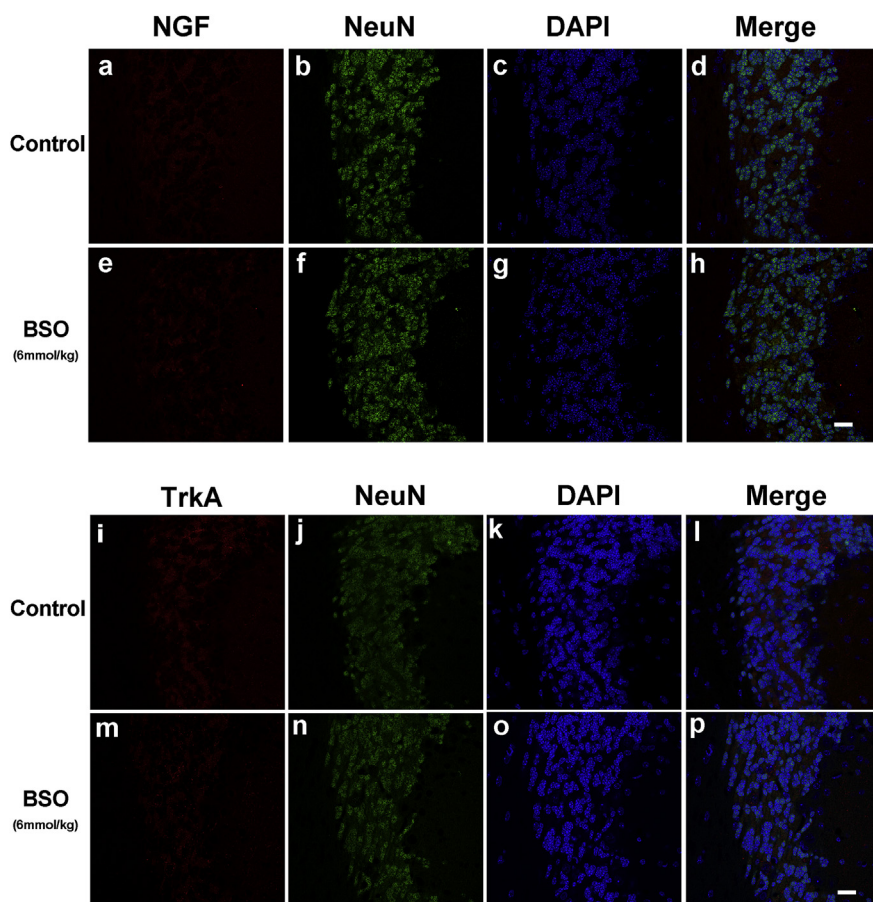


Fig. 7. BSO effect on NGF and TrkA protein levels in cerebellum of mice treated ip with 6 mmol/kg BSO at 2 h. Confocal images of immunostained sections from the cerebella of control and BSO treated mice. (a, e) shows immunofluorescence images of NGF (red), (b, f) neuron marker anti-NeuN (green), (c, g) nuclei marker DAPI (blue) and (d, h) merge, in control and treated mice. The second panel shows immunofluorescence images of (i,m) TrkA (red), (j,n) NeuN (green), (k, o) DAPI (blue) and (l, p) merge in control and treated mice. There are no differences between BSO-treated and control animals at this time point. Scale bar: 20 μ m. Abbreviations: BSO, L-buthionine-S-R-sulfoximine; NGF, neuronal growth factor; TrkA, Tropomyosin receptor kinase A; NeuN, neuronal nuclei DAPI, 4',6-diamidino-2-phenylindole.

neurons (Fig. 6, Supplementary movies), which suggests that BSO induced the synthesis and trafficking of the TrkA receptor. New TrkA receptors synthesized in cell bodies undergo anterograde transport through axons and dendrites, where they bind NGF and initiate signaling (Marlin and Li, 2015; Scott-Solomon and Kuruvilla, 2018).

NGF induced an antioxidant response in *in vitro* and *in vivo* models (Arsenijevic et al., 2007; Pan and Perez-Polo, 1993, 1996). NGF induced glutamate release from cerebellar granule cells, which suggests its involvement in the modulation of excitatory neurotransmission and amino acid transport regulation (Numakawa et al., 1999). Activation of the PI3K/PKB/AKT pathway via NGF/TrkA, is recognized as a pro-survival pathway (Huang and Reichardt, 2003). In human retinal pigment epithelial (RPE) cells, NGF protects against hydrogen peroxide (H_2O_2)-induced apoptosis and stimulates cell survival via the activation of the mTOR signaling pathway (Cao et al., 2011).

In summary, our results show a response activated in the cerebellum to remedy the redox changes induced by BSO. The ip administration of BSO induced GSH depletion in the liver and increased GSH levels in the cerebellum. These changes are likely associated with activation of the NGF/TrkA and mTOR signaling pathways and increased expression of the cysteine importer EAAT3. We hypothesize that the changes in the liver and other peripheral organs, such as kidneys (Limon-Pacheco et al., 2007), induce redox responses in the cerebellum. These observations are important because the liver controls the detoxification of most chemicals in the body, including drugs. Exposure to xenobiotic agents that consume antioxidants, including metals, ionizing radiation, pesticides or ozone (Limon-Pacheco and Gonshebbat, 2009), affects GSH pools. The current results help elucidate the mechanisms involved in the regulation of GSH metabolism and cellular redox changes that occur during oxidative stress. Chronic exposure to high levels of these xenobiotic agents may lead to the deregulation of GSH metabolism that is observed in neurodegenerative diseases.

Authors disclosure statement

The authors declare no conflict of interest.

The movies complement Fig. 6 showing an increase TrkA levels in the molecular layer of the cerebellum.

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Mammalian Target of Rapamycin: Its Role in Early Neural Development and in Adult and Aged Brain Function

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The kinase mammalian target of rapamycin (mTOR) integrates signals triggered by energy, stress, oxygen levels, and growth factors. It regulates ribosome biogenesis, mRNA translation, nutrient metabolism, and autophagy. mTOR participates in various functions of the brain, such as synaptic plasticity, adult neurogenesis, memory, and learning. mTOR is present during early neural development and participates in axon and dendrite development, neuron differentiation, and gliogenesis, among other processes. Furthermore, mTOR has been shown to modulate lifespan in multiple organisms. This protein is an important energy sensor that is present throughout our lifetime its role must be precisely described in order to develop therapeutic strategies and prevent diseases of the central nervous system. The aim of this review is to present our current understanding of the functions of mTOR in neural development, the adult brain and aging.

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INTRODUCTION

The mammalian target of rapamycin (mTOR) is a serine/threonine kinase that is involved in the control of cell growth and proliferation. This kinase integrates signals triggered by different stimuli such as variations in the amino acid supply, changes in the cellular energy state, and by receptors for various hormones and growth factors and in the brain by transduction of neurotransmitters and neurotrophin signals (Harris and Lawrence, 2003; Gal-Ben-Ari et al., 2012; Burket et al., 2015). Several studies have shown that mTOR participates in multiple functions of the brain. Its activation contributes to processes involved in synaptic plasticity and metabolic regulation (Garelick and Kennedy, 2011). Additionally, mTOR participates in key processes during neural development, particularly in axon and dendrite development, neuron differentiation, and gliogenesis. Furthermore, consistent with its role as a nutrient and growth factor sensor, decreased mTOR signaling reduces aging and thereby extends lifespan (Cornu et al., 2013). The aim of this

Abbreviations: 4E-BP1, eukaryotic initiation factor 4E-binding protein; DEPTOR, DEP domain-containing mTOR-interacting protein; eEF2, eukaryotic elongation factor 2; eEF2K, eukaryotic elongation factor 2 kinase; eIF4E, eukaryotic translation initiation factor 4E; FKBP12, FK506-binding protein; mLST8, mammalian lethal with SEC13 protein 8; mPFC, medial prefrontal cortex; mSIN1, stress-activated MAP kinase-interacting protein 1; mTOR, mammalian target of rapamycin; mTORC1, mammalian target of rapamycin complex 1; mTORC2, mammalian target of rapamycin complex 2; NSCs, neural stem cells; PRAS40, 40 kDa Pro-rich AKT1 substrate 1; PROTOR, Pro-rich protein 5; RAPTOR, regulatory associated protein of mTOR; Rheb, Ras homolog enriched in brain; RICTOR, rapamycin-insensitive companion of mammalian target of rapamycin; S6K1, S6 kinase; SVZ, subventricular zone; TSC1, tuberous sclerosis complex proteins, hamartin; TSC2, tuberous sclerosis complex proteins, tuberin.

review is to present our current understanding of the functions of mTOR in neural development, the adult brain and aging.

THE mTOR MULTI-PROTEIN COMPLEX AND SIGNALING PATHWAYS

Metazoans have a single *TOR* gene, whereas yeast has two genes, *TOR1* and *TOR2*. In mammals, the *mTOR* gene (also known as *FRAP*, *RAFT1*, or *SEPT*) encodes a protein of 2549 amino acids with 42 and 45% sequence identity to yeast *TOR1* and *TOR2*, respectively (Harris and Lawrence, 2003).

mTOR exists in two distinct multi-protein complexes; mTOR complex 1 (mTORC1) which is sensitive to rapamycin and consists of the proteins: regulatory associated protein of mTOR (RAPTOR), 40 kDa pro-rich AKT1 substrate 1 (PRAS40), mammalian lethal with SEC13 protein 8 (mLST8), and DEP domain-containing mTOR-interacting protein (DEPTOR). On the other hand, mTOR complex 2 (mTORC2) is relatively insensitive to rapamycin and consists of rapamycin-insensitive companion of mTOR (RICTOR), pro-rich protein 5 (PRR5, also known as PROTOR), DEPTOR, mLST8, and stress-activated MAP kinase-interacting protein 1 (mSIN1). However, prolonged treatment with rapamycin can also inhibit mTORC2, most likely due to the progressive sequestration of mTOR pools by rapamycin-FK506-binding protein (FKBP12; Sarbassov et al., 2005; Weber and Gutmann, 2012).

Rapamycin is an antifungal agent originally isolated from a strain of the soil bacterium *Streptomyces hygroscopicus*. It has potent immunosuppressive and antiproliferative properties and forms an inhibitory complex with its intracellular receptor, FKBP12, which binds to the C-terminus of TOR proteins, thereby inhibiting TOR activity (Weber and Gutmann, 2012). Because of the promising therapeutic potential of rapamycin, several rapamycin analogs have been synthesized to improve its pharmacokinetic properties (Tsang et al., 2007).

Nutrients, energy, stress, oxygen levels, and growth factors are among the major upstream signaling inputs for mTORC1. In this regard, the canonical mTORC1 pathway begins with the activation of tyrosine kinase receptors (Trk) through the induction of phosphoinositide-3-kinase (PI3K) and protein kinase B (PKB, also known as Akt) and includes the phosphorylation and inhibition of tuberous sclerosis complex proteins, hamartin (TSC1) and tuberin (TSC2). The TSC1/TSC2 complex acts as a GTPase-activating protein (GAP) for Ras homolog enriched in brain (Rheb). Subsequently, the increase in GTP-bound Rheb stimulates mTORC1 (Sarbassov et al., 2005; Weber and Gutmann, 2012).

Mitogens can also activate mTOR independently of Akt through phospholipase D (PLD) as well as through the extracellular signal-regulated kinase (ERK)-mitogen-activated protein kinases (MAPK) pathway (Jaworski and Sheng, 2006). The cellular energy levels (amino acid concentration) also require Rheb to activate mTORC1, however, instead of through the tuberous sclerosis complex (TSC), the signal is transduced via the Ras-related GTPase (Rag) complex, a heterodimer small GTPase-containing RagA or B with RagC or D. The increase

in the amino acids concentration, induces the movement of mTORC1 to the lysosomal membranes where the Rag complex resides. The complex “Ragulator” consisting of Rag GTPase-interacting proteins (p18, p14, and MP1) has been identified in the interaction with the Rag GTPases and its consequent localization to the lysosome (Sancak and Sabatini, 2009; Kim and Guan, 2011).

Under conditions of energy deprivation that increase the AMP/ATP ratio, AMP-activated protein kinase (AMPK) becomes active and phosphorylates TSC2 to stimulate its GAP activity, therefore inhibiting Rheb and presumably mTORC1. Oxygen sensing by the mTORC1 pathway also requires the TSC1/2 complex, but it functions through a distinct mechanism that involves the hypoxia-inducible factor-dependent expression of regulated in development and DNA damage responses 1 (REDD1) and REDD2, two growth regulators (Sarbassov et al., 2005).

It has long been known that translational machinery operates in neuronal dendrites and synapses, and that local protein synthesis and its regulation is important for diverse processes of the central nervous system (CNS), e.g., memory and synaptic plasticity (Taha et al., 2013). In neurons, neurotransmission modulates the translation machinery, however, all the components of this delicate processes have not been identified yet. mTORC1 is a key downstream molecule in a signaling cascade beginning with the transduction of neurotransmitters and neurotrophin signals. Among the receptors found to activate mTORC1 in neurons, we can mention the muscarinic acetylcholine receptors, AMPA receptors, the glutamate metabotropic receptors (mGlu1/5), the dopaminergic D1 and D3 receptors, the opioid receptor, the amino acid/glutamate T1R1–T1R3 receptors, the serotonin 5-HT6 receptor, the cannabinoid 1 receptor (CB1R), and the GABAB receptors (Gal-Ben-Ari et al., 2012; Bockaert and Marin, 2015). Burket et al. (2015) discusses different articles where *N*-methyl-D-aspartate receptor (NMDAR) activation is downregulating mTOR signaling activity.

The hallmark of mTORC1 activity is the stimulation of ribosome biogenesis, mRNA translation, nutrient metabolism, and autophagy inhibition. In this regard mTORC1 regulates protein synthesis through the phosphorylation and inactivation of a repressor of mRNA translation, eukaryotic initiation factor 4E-binding protein (4E-BP1), and through the phosphorylation and activation of the S6 kinase (S6K1). Thus, S6K1 or 4E-BP1 phosphorylation is often used as an *in vivo* readout of mTOR activity (Hay and Sonenberg, 2004; Sarbassov et al., 2005). Phosphorylation of 4E-BP1 by mTORC1 signals the onset of cap-dependent translation; it allows the binding of several important initiation factors, as well as the positioning of the 40S ribosomal subunit at the 5′ end of the mRNA to begin the process of translation (Harris and Lawrence, 2003).

Active S6K1 stimulates the translation of mRNAs containing unique 5′-terminal oligopyrimidine tracts (TOPs). TOP-containing mRNAs encode ribosomal proteins, elongation factors and other critical components of ribosome production. However, S6K1 activity is not obligatory for this important process: cells lacking S6K1 still actively translate TOP mRNAs in response to growth factor stimulation (Weber and Gutmann,

2012). Furthermore, S6K regulates both the initiation and elongation phases of translation. It phosphorylates and inactivates the eukaryotic elongation factor 2 kinase (eEF2K) resulting in the dephosphorylation of the eukaryotic elongation factor 2 (eEF2) which mediates the translocation step of elongation (Wang et al., 2001; Taha et al., 2013). eEF2K is also named as calcium/calmodulin (CaM)-dependent protein kinase III (CaMKIII) because it can be activated by elevated levels of calcium and binding of CaM. In dendrites, this process depends on glutamate signaling and NMDAR activation, which suggests a complex regulation of the elongation step, dependent on particular cellular conditions (Taha et al., 2013; Heise et al., 2014).

Besides, mTORC2 plays an important role in Akt activation. Akt itself possesses pleiotropic cellular effects, regulating events including metabolism, survival, and proliferation. In addition to Akt, mTORC2 also regulates the actin cytoskeleton through unknown mechanisms that involve protein kinase C alpha (PKC α) and Rho. Evidence also points to mTORC2 as a key player in mRNA translation processes that have been isolated in polysomes and associated with individual ribosomal proteins (Sarbasov et al., 2005; Weber and Gutmann, 2012). Inactivation of mTORC2, but not mTORC1, conditional knockout (CKO) mice disrupted motor coordination early in life. The Purkinje cells using of these mice showed developmental alterations in the processes of climbing fiber elimination and dendritic self-avoidance (Angliker et al., 2015). Little is known about the upstream activating signals for mTORC2. Moreover, most of the activity of this protein complex has been studied in nervous system cancer cells such as glioblastomas where mTORC2 plays a central role in the metabolic reprogramming of this cancer pathology (Masui et al., 2015). The activity of mTORC2 in transformed cells is not discussed in this review (Figure 1).

mTOR AND EARLY CNS DEVELOPMENT

Early CNS development is a complex, dynamic process that relies on a precisely orchestrated interplay of inductive signals and cellular migration. Building this complex and highly organized system involves the generation of a wide variety of specialized neural and non-neural cell types that must be placed at appropriate locations and with the right timing (Budday et al., 2015; Jiang and Nardelli, 2015).

Neurons, oligodendrocytes, astrocytes, and the ependymal lining of the central lumen are generated from a common source, the neuroepithelial cells that are part of the neural tube in early embryos (Kintner, 2002). Later, cell migration and extensive synapse formation are responsible for the initial establishment of the neural circuitry in the brain (Purves, 2012; Bury and Sabo, 2015). The first step in this process is to generate both axons and dendrites in the newly generated neurons. Axons must grow to reach the appropriate target cells and begin to make the synaptic connections that will form neural circuits (Barnes and Polleux, 2009; Purves, 2012).

Clinical evidence from developmental disorders that affect the CNS, including Lhermitte–Duclos disease (LDD), TSC, and

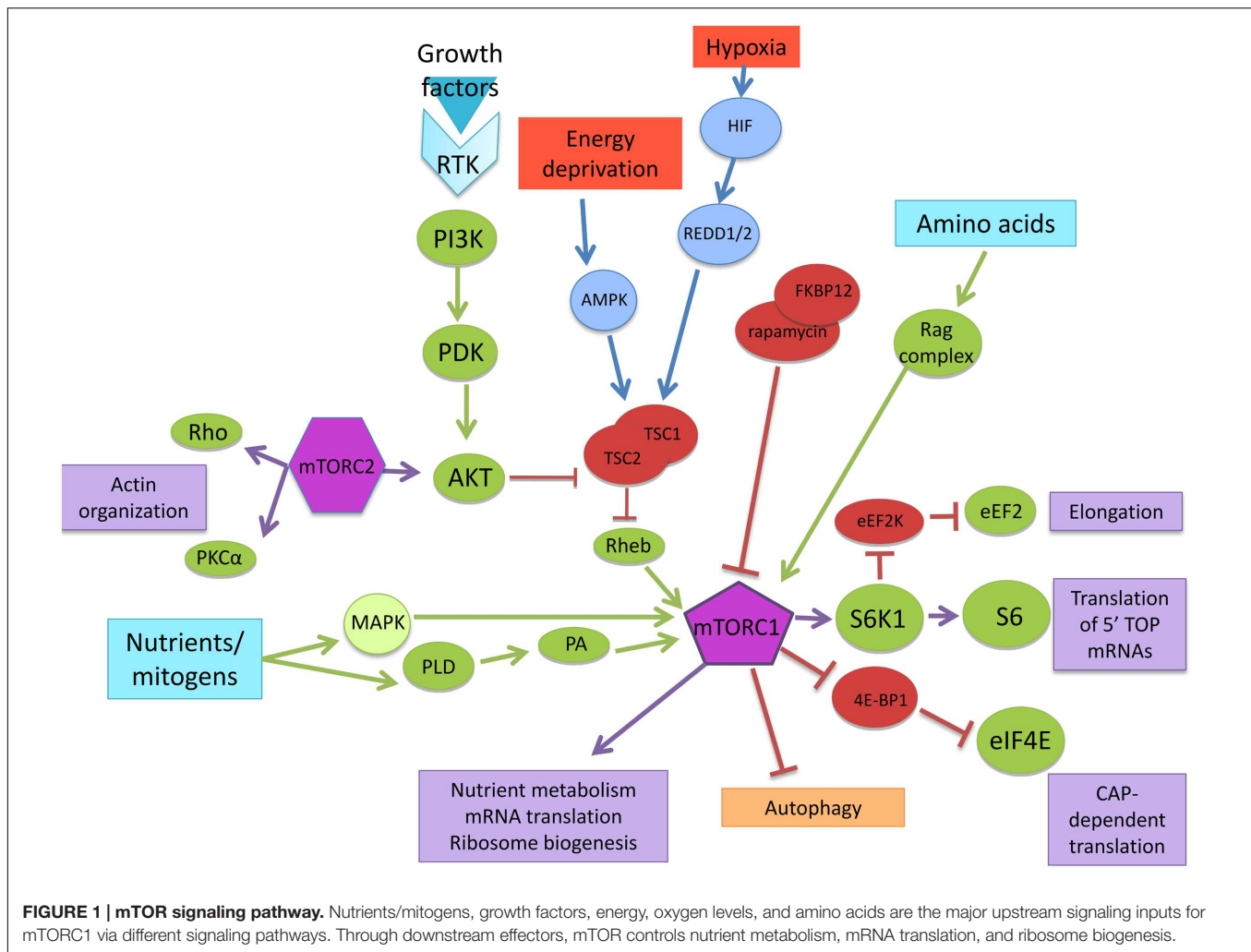
neurofibromatosis type 1 (NF1) suggest that mTOR plays a key role in cell differentiation and growth control (Sandsmark et al., 2007; Crino, 2011). These inherited neurodevelopmental disorders and cancer syndromes are caused by mutations in genes that encode negative regulators of the mTOR-signaling pathway. The continued expression of mTOR in TSC affected individuals leads to benign overgrowths in multiple organs including brain. Neurological alterations such as epilepsy, autism, and learning disabilities are frequent among them and the administration of mTOR inhibitors result beneficial (Tee et al., 2016). Also, patients with germinal mutations in phosphatase and tensin homolog (*PTEN*; a negative modulator of mTOR) have been observed in 11 out of 31 LDD patients and associated with granular cell hypertrophy (Abel et al., 2005). Cognitive impairment is the most common neurological impairment in NF1 children which is frequently associated with neuropathological abnormalities (Gipson and Johnston, 2012).

Neuron Differentiation

During embryonic development, the brain undergoes a dramatic transformation from a simple tubular structure to a highly convoluted shape. Neurulation is the process of forming the neural tube, which will become the brain and spinal cord. Soon after the neural tube forms, the forerunners of the major brain regions become apparent as a result of morphogenetic movements. Eventually, the anterior and posterior regions of the neural tube become the brain and spinal cord, respectively. Morphogenesis of the neural tube occurs in a specific spatiotemporal pattern along the length of the embryo (Sadler, 2005; Purves, 2012; Filas et al., 2013).

Neural stem cells (NSCs) in the early neural plate and tube and subsequently within each nascent brain region must follow instructions to differentiate into nerve cells specific to each region; balanced control of neural progenitor maintenance and neuron production is crucial for the establishment of functional neural circuits (Purves, 2012). *Mtor* null mice die before the differentiation of cortical neural progenitors into neurons (Ka et al., 2014). Thus, conditional mutant mTOR mice were developed to study functions and mechanisms of mTOR in developing brain. Conditional mutant mTOR mice had smaller brains with lower numbers of cells in the proliferating progenitors and cortical layer neurons. According to these authors an abnormal cell cycle progression disrupted the population of neural progenitors and thereby the progenitor self-renewal process (Ka et al., 2014).

Similar disruptive effects were observed in mice with a knock-in mutation in the PH domain of 3-phosphoinositide dependent protein kinase-1 (PDK1) and chick embryos treated with PI3K and TOR inhibitors exhibit deficient neuron production. Furthermore, rapamycin treatment repressed the expression of early neuronal differentiation genes, such as neurogenin 2 (*Ngn2*). Exposure to rapamycin can also disrupt coordination of cell cycle exit and progression of the neuronal differentiation program and interfere with the neuroepithelial organization (Fishwick et al., 2010). Rapamycin treatment in the early days of development resulted in a decrease in the number of progenitor stem cells available in the dentate gyrus of the hippocampus,



as well as an impairment in the development of this region (Raman et al., 2013). Thus, TOR signaling levels may function as a checkpoint for the progression of differentiation, and appears to be essential for the production of NSCs and a proper development of the dentate gyrus of the hippocampus.

Decreasing mTORC1 activity with Rheb and RAPTOR knockdowns in neonatal NSCs in the subventricular zone (SVZ) prevented their differentiation resulting in reduced lineage expansion and aborted neuron production (Hartman et al., 2013). Also, the constitutive activation of the translational repressor 4E-BP1 had similar effects: it prevented hyperactive mTORC1 from inducing NSC differentiation and promoted self-renewal. By contrast, mTORC1-activated S6K1/S6K2 regulated NSC size but not differentiation, indicating different functions of 4E-BPs and S6K1/S6K2 in NSCs. These data demonstrated a crucial role of mTORC1 and 4E-BP for switching cap-dependent translation on and off in NSCs (Hartman et al., 2013).

On the other hand, Fu et al. (2012) generated CKO mice with selective deletion of the *Tsc1* gene in GABAergic interneuron progenitor cells, which have impaired growth and decreased survival. In this case, the cortical and hippocampal GABAergic

interneurons of CKO mice were enlarged and showed increased mTORC1 signaling. Ectopic clusters of cells with increased mTORC1 signaling are also observed, suggesting impaired interneuron migration. Increased mTORC1 signaling may have negative effects on the CNS development, so regulatory proteins, such as TSC1, play important roles in keeping mTOR in check (Fu et al., 2012). In neuronal cultures from rat cortices, a triiodothyronine (T3)-dependent increase in the size of the soma in GABAergic neurons was mediated mainly by mTOR signaling. Both TrkB and mTOR signaling mediate the T3-dependent reduction of GABAergic axon extension, suggesting the existence of parallel regulatory pathways for T3-dependent changes (Westerholz et al., 2013).

When cortical cells from embryonic stages E13.5 and E16.5 were treated with transforming growth factor β (TGF β) and insulin growth factor 1 (IGF1), IGF1 induced PI3K, Akt and mTORC1/mTORC2 primarily in E13.5-derived cells, resulting in proliferation, survival, and neuronal differentiation. At E16.5, TGF β did not directly activate the Akt-mTOR pathway but required active PI3K-mTORC2-signaling to mediate the neuronal differentiation of cortical cells (Wahane et al., 2014).

The data presented in these studies suggest that mTOR plays an important role in the development of neuronal progenitors, controlling proliferation and differentiation in various regions of the CNS. It seems that mTOR may function as a checkpoint for the differentiation progression, while its hyperactivation does not inhibit but can affect interneuron migration and neuron differentiation.

Axon and Dendrite Development

Once nerve cells have been generated, neurons must become interconnected to form the neural circuits. The first step in this process is to establish axons and dendrites in the newly generated neurons. Differentiation of axons and dendrites is a critical step in neuronal development (Cheng and Poo, 2012; Purves, 2012). Neurons typically form a single axon and multiple dendrites, which underlie the directional flow of information transfer in the CNS. Axons grow to reach appropriate target cells and begin to make the synaptic connections that will form neural circuits. Dendrites integrate synaptic inputs, triggering the generation of action potentials, making presynaptic contacts onto target cells. There are multiple signaling pathways underlying the establishment of axon-dendrite development (Barnes and Polleux, 2009; Purves, 2012). As in neuron differentiation, there are several studies that show that mTOR plays a pivotal role in both dendritic and axonal growth.

The pharmacological stimulation of the serotonin receptor subtype 7 (5-HT₇R) using a highly selective agonist, LP-211, enhances neurite outgrowth in primary neuronal cultures derived from embryonic mouse brain, via ERK, cyclin-dependent kinase 5 (Cdk5), mTOR, and cell division control protein 42 homolog (Cdc42). However, the neurite elongation induced by the agonist stimulation of 5-HT₇R is dependent on mTOR, because the outgrowth is completely inhibited by both rapamycin and torin 1, a specific ATP-competitive mTOR inhibitor (Speranza et al., 2015).

Methylcobalamin (MeCbl), a vitamin B12 analog, increases mTOR activity via the activation of Akt and promotes neurite outgrowth in cerebellar granule neurons while rapamycin decreased the effect of MeCbl on neurite outgrowth (Okada et al., 2011).

In a shRNA-induced selective knockdown of RAPTOR and RICTOR, it was shown that both mTORCs are needed for the presence of proper dendritic morphology of neurons, whether grown under basal culture conditions and treated with insulin or transfected with constitutively active PI3K. Neurons with knockdown of either RAPTOR or RICTOR produced fewer new dendrites, whereas the number of retracted dendrites remained relatively stable (Urbanska et al., 2012).

However, different outcomes have been reported with respect to the positive role of mTOR in neurite elongation and growth. The overexpression of the mammalian nicotinamide-adenine dinucleotide-dependent deacetylase sirtuin 1 (Sirt1) promoted neurite outgrowth and improved cell viability under both normal and stress conditions, such as nutrient deprivation or neurotoxic insult, in primary culture systems. Enhanced Sirt1 expression in neurons downregulated the protein levels and phosphorylation of mTOR. Correspondingly, rapamycin markedly improved

neuronal cell survival in response to nutrient deprivation and significantly enhanced neurite outgrowth in wild-type mouse neurons. Sirt1 is activated in low energy availability promoting tissue repair processes, while mTOR is activated during high energy conditions (Garcia-Rodriguez et al., 2014). In this case, the above results suggest that mTOR could have negative effects on CNS development, so regulatory proteins such as Sirt1 play important roles in keeping mTOR in check (Guo et al., 2011).

Regarding axon and dendrite development, the studies presented here show that mTOR participates in the processes of neurite production, promoting outgrowth and elongation, as well as in maintaining proper dendritic morphology. On the other hand, Guo et al. (2011) showed that rapamycin also enhances neurite outgrowth. These apparently contradictory results could be interpreted in terms of spatiotemporal participation of mTOR in these processes, which is extremely tightly regulated. During embryonic development, the temporary silencing of some proteins has been reported as a switch between stages (Hirabayashi and Gotoh, 2010; Golbabapour et al., 2013). However, we must consider that most of these studies used *in vitro* models where cell type and culture conditions could greatly influence the results mainly in key regulators of cell metabolism such as Sirt1 and mTOR. Further *in vivo* studies are necessary to be able to confirm the role of mTOR in axon and dendrite development.

Gliogenesis

Glia constitute the majority of the brain cells, they perform key functions vital to CNS physiology, including blood–brain barrier formation and maintenance, synaptogenesis, neurotransmission, and metabolic regulation. Glial cell generation starts late in embryonic stage. Regulation of neuron to glia switch involves complex neuron–glial interactions as well as spatiotemporal interplay of both cell-intrinsic factors and extracellular signals (Jiang and Nardelli, 2015; Molofsky and Deneen, 2015).

mTORC1 signaling pathway has a crucial function in the process of astrocyte differentiation (Lee da, 2015). Evidence from different reports show that the axon inhibitor Nogo-66 promotes the NSCs differentiation into the glial lineage via mTOR and the signal transducer and activator of transcription 3 (STAT3; Rajan et al., 2003; Wang et al., 2008; Cloetta et al., 2013). Similar to mTORC1, in NF1 genetically engineered mice and derivative NSC neurosphere cultures, was shown that hyperactivation of RICTOR containing mTORC2 activation also increases gliogenesis in the brainstem (Lee da et al., 2010).

Oligodendrocytes are the glial cells that generate CNS myelin; myelin is a multilamellar differentiation of the oligodendrocyte plasma membrane that sheaths axons to facilitate electrical conduction. Progression through the oligodendrocyte lineage is tightly regulated by a multitude of intrinsic and extrinsic cues, which control myelination both spatially and temporally during development and after demyelination. These signals include growth factors, protein kinases, and extracellular matrix molecules, all of which influence epigenetic modifications, transcriptional and translational regulation, and the actin cytoskeleton in oligodendrocytes (Zuchero and Barres, 2013; Bercury and Macklin, 2015).

Both *in vivo* and *in vitro* studies have demonstrated that the mTOR pathway is an essential mediator during oligodendrocyte development and that it can be associated to several external growth factors or hormones with known roles in oligodendroglia differentiation and myelination (Wood et al., 2013). For example, conditionally ablation of either RAPTOR or RICTOR in the oligodendrocyte showed that RAPTOR is a positive regulator myelination whereas RICTOR ablation has a modest positive effect on oligodendrocyte differentiation, and very little effect on myelination (Bercury et al., 2014; Bercury and Macklin, 2015). Purified oligodendrocyte progenitor cells (OPCs) treated with CB receptor agonists and antagonists, as well as with PI3K-Akt and mTOR inhibitors. Maximal phosphorylation of mTOR was obtained after 10 min stimulation with the agonist HU210, and this level of phosphorylation was sustained for 60 min. In contrast, incubation with the other agonists ACEA or JWH133 provoked transient mTOR phosphorylation that peaked at 2 min and then fell below the basal level (Gómez et al., 2011).

The roles of *Rheb1* and mTORC1 in the mouse oligodendrocyte lineage were examined using separate *Cre* drivers to generate *Rheb1* or *mTOR* CKO animals for OPCs as well as for differentiated and mature oligodendrocytes. Deletion of *Rheb1* in OPCs impairs the differentiation to mature oligodendrocytes, which involves mTORC1. This was accompanied by a reduction in OPCs exiting the cell cycle, similarly as during neuron differentiation (Zou et al., 2014).

mTOR is downstream of known activators of PI3K-Akt signaling and upstream of a number of targets important for regulating many aspects of oligodendrocyte differentiation and myelination, including nuclear transcriptional regulators, mediators of cytoskeletal organization and enzymes necessary for lipogenesis (Wood et al., 2013). The finding that both *Rheb1* and mTORC1 are essential for early stage differentiation of OPCs to mature oligodendrocytes, which occurs during a narrow time window, reinforced its importance. Additionally, it seems that the endocannabinoids may be the extracellular signals that activate Akt and mTOR during oligodendrocyte differentiation; the activation of mTOR depended on the agonist used and the CB receptors activation.

mTOR IN THE ADULT CNS

As we mentioned in the previous section, during early postnatal life, the neural circuits process diverse types of information and build the main neural circuits. The sensory systems process information about the state of the organism and the environment, and the motor systems organize and generate actions, and associational systems link the sensory and motor components, providing the substrate for higher brain functions such as perception, attention, cognition, emotions, language, rational thinking, and consciousness (Purves, 2012).

Neurogenesis persists in adult mammals in specific brain areas known as neurogenic niches. Either physiological or pathological conditions can modulate the rate of proliferation of adult NSCs via the differentiation and fate determination of progenitor cells, as well as the survival, maturation, and integration of newborn

neurons. Adult neurogenic niches can be conceptualized as remnants of embryonic signaling centers: they are the source of instructive signals that determine the fate of neighboring stem cells. Furthermore, these cells may be required for some learning and memory processes (Zhao et al., 2008; Urban and Guillemot, 2014).

Learning, Memory, and Synaptic Plasticity

Learning-related changes include modulation of synaptic and non-synaptic ion channels and receptors, dendritic branching, spine density, and plasticity through genetic and epigenetic mechanisms (Sehgal et al., 2013; Stuchlik, 2014). Synaptic connectivity between neurons is a dynamic entity that is constantly changing in response to neural activity and other influences. At the shortest time scales, facilitation, augmentation, potentiation, and depression provide rapid but transient modifications in synaptic transmission (Klann and Dever, 2004; Purves, 2012; Bailey et al., 2015).

The biological processes mediating memory formation involve numerous tightly regulated molecular and cellular events. These include mRNA transcription, protein synthesis, mRNA and protein degradation, mRNA and protein trafficking, post-translational modifications such as phosphorylation and ubiquitination, and epigenetic modulation. Such processes can be brain hemisphere- and brain subregion-specific (Kandel, 2001; Middei et al., 2014; Rosenberg et al., 2014).

Long-lasting synaptic plasticity and memory rely on protein synthesis. Not surprisingly, TOR, one of the major controllers of translation, has been involved in important processes such as synaptic plasticity, memory and diverse types of behavior in various organisms, including mammals (Swiech et al., 2008).

As in early CNS development, mTOR also participates in processes such as synaptic plasticity, adult neurogenesis, learning, and memory. Its role depends on the regions of the CNS studied and the stimuli used. Here we describe the participation of mTOR in signaling pathways in the hippocampus, striatum, amygdala, medial prefrontal and auditory cortices.

Hippocampus

The hippocampus is essential for memory formation; in addition, its neuronal connections are highly ordered, and it is easy to identify specific populations of neurons and synapses. Here, we reviewed studies that suggest that mTOR participates in hippocampal neurogenesis, neurite growth and survival, and dendritic spine formation.

We have mentioned that Akt-mTOR participates in dendritic development. This signaling pathway was identified as an unexpected target of the gene disrupted-in-schizophrenia 1 (DISC1) regulating morphogenesis and dendritic development in new neurons in the adult mouse hippocampus (Kim et al., 2009). There is also evidence that insulin receptor (IR) regulates dendritic spine formation and excitatory synapse development in primary cultures of rat hippocampal neurons through the activation of the PI3K-Akt-mTOR signaling pathway, which in turn promotes Rac1-dependent actin cytoskeletal rearrangement and dendritic spine formation (Lee et al., 2011). Moreover,

Ezh2 (methyltransferase of histone H3K27, enhancer of zeste homolog 2) regulates adult neurogenesis and preserves cognitive functions via the Akt-mTOR pathway (Zhang et al., 2014). The methyltransferase suppresses PTEN expression, promoting the activation of Akt-mTOR. The deletion of *Ezh2* in progenitor cells leads to a decrease in neuron production *in vivo*; more importantly, *Ezh2*-null mice showed impairments in spatial learning and memory, contextual fear memory, and pattern separation.

Similarly, the administration of ABG001 (tetradecyl 2,3-dihydroxybenzoate), a neurotogenic substance, enhanced the survival and neurite growth of newborn cells in adult hippocampal via TrkA receptor-triggered ERK and PI3K-Akt-mTOR signaling pathways, that leads to an enhanced preferential spatial cognitive function. The treatment of amyloid beta_{25–35} (Aβ_{25–35})-mice with ABG001 protected the survival and neurite growth of newborn cells by increasing TrkA receptor-induced phosphorylation of Akt and mTOR, which was accompanied by improved spatial cognitive performance (Zhou et al., 2014).

In cultured hippocampal neurons, mTORC1 activity tags synapses, allowing the RNA-stabilizing protein HuD to capture the Ca²⁺ calmodulin-dependent protein kinase II α (CaMKII α) in a branch-specific manner, promoting site-specific and long-lasting forms of plasticity in the tagged branch. Thus, mTORC1 and HuD are good candidates to target the mRNAs coding for proteins required to strengthen neighboring synapses to facilitate late-stage plasticity (Sosanya et al., 2015).

Most importantly, Su et al. (2015) showed that the activation of mTOR pathway components was lower in the hippocampus of premature rats relative to full-term rats, and this was associated with poorer learning and memory performance. They showed that long-term consumption of a protein-rich diet can restore the impairment in learning and memory in pre-term rats via upregulation of mTOR-S6K1 signaling. In addition, mTOR activation and phosphorylation of S6K1 and 4E-BP1 in rat hippocampus was observed during a spatial learning paradigm. When mTORC1 was inhibited by chronic intracerebral ventricular infusion of rapamycin the phosphorylation of mTOR substrates were also inhibit as well as the learning-induced enhancement of protein synthesis and the acquisition of learning. These results show the activation of mTOR and its downstream targets during spatial learning in hippocampal pyramidal neurons (Qi et al., 2010).

There are several recent studies addressing the participation of mTOR and hormones in memory consolidation and learning. First, three different studies showed that the sex hormones estrogen and progesterone induced memory consolidation in the hippocampus. Estradiol induced the enhancement of object-recognition memory consolidation via PI3K-mTOR activation in the dorsal hippocampus (Fortress et al., 2013). Estradiol also modulated hippocampal synaptic plasticity by activating mTOR through a signaling pathway that involved TrkB activation, ERK phosphorylation, and calpain activation (Briz and Baudry, 2014). In young ovariectomized mice, bilateral dorsal hippocampal infusion of progesterone significantly increased the levels of ERK and S6K1. This activation was essential for the progesterone-induced facilitation of memory consolidation (Orr et al., 2012).

These studies showed that rapid protein synthesis is necessary for these hormones to modulate the consolidation of hippocampal LTP and memory.

Also, the neurotrophin brain-derived neurotrophic factor (BDNF) is an upstream activator of mTOR during and after training to regulate GluR1 translation in hippocampal synaptic plasma membranes during IA (inhibitory avoidance) training memory consolidation (Slipczuk et al., 2009).

The markers for initiation of translation, including eukaryotic translation initiation factor 4E (eIF4E), 4E-BP1, ribosomal protein S6, and eIF4F cap-complex formation, undergo diurnal oscillations in the mouse hippocampus. This diurnal oscillation in translation initiation has been associated with increased activity of ERK1/2 MAPK and mTOR, and it was lost in memory-deficient mice lacking calmodulin-stimulated adenylyl cyclases 1 and 8. Disruption of circadian rhythms leads to loss of diurnal translation oscillation and causes memory deficits; moreover, inhibition of protein synthesis during the midday for 4 days post-training impairs memory persistence (Saraf et al., 2014).

The stimulation of the cannabinoid receptor CB1R by endogenous and exogenous cannabinoids can trigger the activation of the mTOR pathway and protein synthesis in the hippocampus. Contrary to what has been observed in other cases, this activation causes long-term memory impairment and amnesic-like effects, probably due to the fact that CB1R is mainly expressed in GABAergic interneurons. These findings suggest that the activation of mTOR through CB1R would contribute to an imbalance between the excitatory and inhibitory inputs in the hippocampus (Puighermanal et al., 2009).

Moreover, disruption of DISC1 function in adult-born dentate granule neurons is sufficient to cause several profound behavioral phenotypes, including pronounced learning and memory deficits, as well as clear anxiety and depression-like phenotypes. The knockdown of *Disc1* leads to increases in mTOR, indicating that this signaling abnormality is responsible for the cognitive and affective deficits. Rapamycin reversed these behavioral deficits even when associated neuroanatomical abnormalities persisted; remarkably, the rapamycin treatment, which rescued memory deficits in shRNA-DISC1 mice, caused memory deficits in control mice (Zhou et al., 2013).

Most studies also showed that mTOR is involved in both memory and learning consolidation processes, as well in the responses of various behavior to hormones, BDNF, and circadian changes. Furthermore, long-term memory deficits can be associated with an overactivation of the mTOR signaling pathway and an imbalance in protein synthesis, suggesting that mTOR requires mechanisms for tight spatiotemporal control of its expression.

Striatum

For motor control and learning, the basal ganglia, the motor cortex, and the cerebellum cooperate to enable movement; the striatum, part of the basal ganglia, plays a significant role in the learning processes of motor skilled tasks. Bergeron et al. (2014) analyzed whether mTOR activity is influenced or engaged during the execution of motor movement and motor learning. They showed that mTOR activity of the dorsal striatum is an important

molecular step involved in learning consolidation during the acquisition of a complex motor skill in mice, but it is not related to motor abilities. These data are consistent with the studies in the hippocampus showing the role of mTOR in memory and learning consolidation.

Mice with disrupted mTORC2 signaling in the striatum exhibit altered striatal dopamine-dependent behaviors, such as increased basal locomotion, stereotypic counts, etc., by altering the D2R and ERK1/2 pathway (Dadalko et al., 2015).

Amygdala

The amygdala mediates neural processes that relate sensory experience with emotional significance, and it is also the site where learning about fearful stimuli occurs. It was found that rapamycin increases neuronal activity and anxiety-related behavior, impairs both consolidation and reconsolidation of an auditory fear memory, and produces impairment of IA memory. Given the importance of the amygdala in mood regulation, associative learning, and modulation of cognitive functions, it is important to consider the role of mTOR in this region; rapamycin can be used as a treatment for reducing the emotional strength of established traumatic memories analogous to those observed in acquired anxiety disorders, but it may also induce alterations in mood regulation.

In three different studies, Jobim et al. (2012a,b) and Pedroso et al. (2013) showed that infusion of rapamycin into the basolateral complex of the amygdala and hippocampus before and after a reactivation (retrieval) session produced IA memory impairment. These data showed that non-reinforced fear memory retrieval could lead to memory reconsolidation through a mechanism that requires protein synthesis and mTOR signaling in the amygdala and hippocampus.

The systemic administration of a single low dose of rapamycin led to enhanced neuronal activity in the amygdala and an increase in anxiety-related behaviors. The behavioral alterations correlated to enhanced amygdalar expression of KLK8 and FKBP51, proteins that have been implicated in the development of anxiety and depression (Hadamitzky et al., 2014). Moreover, systemic inhibition by rapamycin administration immediately or 12 h after either training or reactivation for auditory fear conditioning, blocks both consolidation and reconsolidation-like activities that contribute to the formation, retention, and maintenance of long-term memory. These data suggest that biphasic translational control through the mTOR pathway is normally required during the long-term formation and stabilization of memory through recurrent consolidation and reconsolidation-like events (Mac Callum et al., 2014).

Medial Prefrontal Cortex

The amygdala is connected with the medial prefrontal cortex (mPFC), a brain region that is involved in decision making, task switching, memory consolidation, and the retrieval of remote long-term memory. It was shown that the PI3K-Akt-mTOR signaling pathway is involved in the LTP and mPFC-dependent long-term trace fear memory (Sui et al., 2008). Another study in the mPFC demonstrated that overexpression of S6K1 produces antidepressant effects in the forced swim test without altering

locomotor activity. Conversely, expression of dominant-negative S6K in the mPFC resulted in prodepressive behavior in the forced swim test and was sufficient to cause anhedonia in the absence of chronic stress exposure. These data demonstrate a critical role for S6K1 activity in depressive behaviors and suggest that pathways downstream of mTORC1 may underlie the pathophysiology and treatment of major depressive disorder (Dwyer et al., 2015).

These results suggest that fear regulation is mediated by connections from the mPFC to the amygdala, and it seems that mTOR participates in this relationship; in the mPFC, the animals learn to predict aversive events via mTOR, and in the amygdala, the memory is retained. However, mTOR also participates in avoiding anxiety and depression.

Auditory Cortex

The auditory cortex of mammals mediates particular aspects of auditory stimulus processing, task-specific performance, and learning; one report (Schicknick et al., 2008) showed that the memory required for the discrimination of complex sensory stimuli is controlled by dopaminergic activity via mTOR.

In the same way, the dopaminergic inputs to the gerbil auditory cortex regulate mTOR-mediated, protein-synthesis-dependent mechanisms, thereby controlling the consolidation of memory required for the discrimination of complex auditory stimuli (Schicknick et al., 2008). In a more recent work of this group, Reichenbach et al. (2015) tested the impact of local pharmacological activation of different D1/D5 dopamine receptor signaling modes in the auditory cortex and found differentially regulation of several protein profiles related to rearrangement of cytomatrices, energy metabolism, and synaptic neurotransmission in cortical, hippocampal, and basal brain structures. These results may be mTOR-mediated, which, in turn, might enhance the ability to synthesize plasticity-related proteins locally on demand and facilitate the consolidation of discrimination memory (Reichenbach et al., 2015).

mTOR AND CNS AGING

During normal aging, the brain suffers both morphological and functional modifications that affect dendritic trees and synapses, neurotransmission, circulation, and metabolism; these changes promote neurodegeneration, impair neurogenesis, and can be considered a cause of cognitive impairment and sensory and motor deficits in the elderly (Mariani et al., 2005; Sarlak et al., 2013). Mounting evidence, however, appears to implicate increased susceptibility to the long-term effects of oxidative stress, mitochondrial dysfunction and inflammatory insults as major contributing factors (Mariani et al., 2005). Understanding the mechanisms and the detailed metabolic interactions involved in the processes of normal and pathological neuronal aging and thus improving health is critical to increasing the quality of life in the elderly population, especially given the dramatic increase in the aging population worldwide (Toescu, 2005; Yang et al., 2014).

In recent years, the manipulation of nutrient-sensing and stress-response pathways has extended the lifespans of organisms from yeast to mammals. Growth-promoting cell programs may

accelerate aging by generating metabolic by-products and by directly inhibiting the clearance of these by-products (Zoncu et al., 2011). mTOR is a prime target in the genetic control of aging, and evidence from genetic studies supports the view that mTOR may be a master determinant of lifespan and aging in yeast (Kaeberlein et al., 2005), worms (Vellai et al., 2003), flies (Bjedov et al., 2010), and mice (Harrison et al., 2009).

There is compelling evidence that cellular mechanisms and signaling pathways regulating brain aging and age-related neurodegenerative disorders are at least partially controlled by mTOR. The complex signaling networks underlying the age-related effects have not been fully elucidated. There are multiple reviews discussing the relationship between mTOR and CNS aging (Maiese et al., 2012; Sarlak et al., 2013; Jenwitheesuk et al., 2014; Perluigi et al., 2015); here, we describe recent studies on this topic.

One of the mechanisms that relate mTOR to aging is its participation in inhibiting autophagy. Autophagy is essential for removing damaged macromolecules and organelles from the cytoplasm and recycling amino acids (Mizushima et al., 2008). Studies suggest that autophagy declines with age and that this leads to an accumulation of damage, such as protein aggregates and degenerated mitochondria, that contribute to age-related cellular dysfunction (Cuervo, 2008).

A recent study using naked mole rats which live for up to 24 years, shows that they maintain high brain autophagy levels during the majority of their lifespan. Additionally, the p-mTOR/mTOR ratio showed a significant increase from the early to intermediate age group and a significant decrease from the intermediate age group to the old and oldest age groups (Triplett et al., 2015).

In mouse retinal pigment epithelium (RPE) explants and cultured human RPE cells, aged RPE cells contained more lysosome-associated mTOR and showed an increased response to amino acid stimulation. Increased mTORC1 activity caused a decreased rate of degradation of internalized photoreceptor outer segments. These data suggest that the Rag–Ragulator complex controls the lysosomal distribution of mTORC1 in RPE cells and may further exacerbate the lysosomal dysfunction of aged RPE (Yu et al., 2014).

The use of caloric restriction (CR) as a strategy to study mechanisms behind aging and age-associated diseases is based on evidence suggesting that CR can delay aging and protect the CNS from neurodegenerative disorders. Yang et al. (2014) used C57BL/6J mice with different diets and found that cognitive function declined with aging, especially after 12 months of age while CR ameliorated the age-dependent cognition deficit by deactivating mTOR and its upstream BDNF-Akt signaling in the hippocampus. Unexpectedly, they found a decline in mTOR signaling with aging, suggesting that other mediators play a more important role in regulating age-dependent autophagy than mTOR by itself in this model.

Dong and colleagues published two other studies using the CR strategy. C57BL/6 mice were randomly assigned to a NC group (standard diet), a CR group or a HC group (high-calorie diet) for 10 months. Activation of the mTOR/S6K1 and p62 signaling pathways was significantly upregulated in hippocampal

neurons of mice in the HC and NC groups and ameliorated by the CR treatment. They also found that the HC diet and CR have opposing effects on learning and memory related to age. Different caloric intake may be an important way to accelerate or slow the progression of age-related neurodegenerative disorders (Dong et al., 2015a,b).

Furthermore, when the epigenetic changes in old mice with dietary restriction (DR) were analyzed, the histone methylation levels of H3K27me3, H3R2me2, and H3K79me3 in 22-month-old mouse brain were lower than in 3-month-old animals. However, either DR or rapamycin treatment prevented the age-induced losses of H3K27me3, H3R2me2, and H3K79me3. Moreover, DR and rapamycin each enhanced the levels of H3K18ac and H3K4me2. The level of H3K4me declined with age and was further diminished by either DR or rapamycin. The results from this study suggest that either DR or rapamycin can restore, at least partially, the age-related alterations in histone methylation levels (Gong et al., 2015).

Mild mitochondrial uncoupling is similar to the physiological energetic challenges, including exercise and intermittent fasting, that seem to protect the CNS from the effects of aging. The induction of mild mitochondrial uncoupling using 2,4-dinitrophenol (DNP) triggers a complex integrated cellular response in the brain that includes suppression of mTOR and insulin signaling, enhanced autophagy, and upregulation of cAMP response element-binding (CREB), changes that are known to play important roles in synaptic plasticity. Moreover, DNP treatment improves the performance of mice in a learning and memory task (Liu et al., 2015).

In terms of cognitive function and memory in the elderly, genome-wide screening showed a novel association of a polymorphism in the pro-apoptotic gene *FASTKD2* (fast-activated serine/threonine kinase domains 2) with better memory performance in older adults. Complementary analyses at the gene and pathway levels identified additional genome-wide significant associations with episodic memory and the genes *LARS2* (leucyl-tRNA synthetase 2, mitochondrial) and *mTor*, which along with *FASTKD240*, encode proteins with critical roles in mitochondrial function. These new findings identify potential targets to help improve risk stratification and therapeutic development in normal cognitive aging and dementia (Ramanan et al., 2015).

Adult neurogenesis is another process that decreases with age. This is mainly because of the reduction in the proliferation of active NSCs. As mice age, the activity of the mTOR signaling pathway decreases in the NSCs. Short-term treatment with ketamine significantly restored the proliferation of NSCs in the aged mice via mTOR signaling activity. Stimulating mTOR signaling revitalized the NSCs, restored their proliferation, and enhanced neurogenesis in the hippocampus of the aged brain. These data show the potential of mTOR for restoring neurogenesis in elderly individuals, but it is important to be aware that overstimulation of mTOR may also lead to other unwanted effects, such as stem cell depletion, aging, and carcinogenesis (Romine et al., 2015).

Also Paliouras et al. (2012) showed that mTOR is pivotal in determining proliferation versus quiescence in the adult

forebrain niche. mTOR inhibition yielded a quiescence-like phenotype *in vitro*, while epidermal growth factor (EGF)-induced upregulation of mTOR activity enabled the reactivation of the quiescent SVZ niche within the aging brain. These findings

reveal that the mTOR signaling pathway is a key regulator of neurogenesis in the adult and aging brain.

Finally, the deficiency of the core clock protein BMAL1 increased mTORC1 activity. A significant increase in

TABLE 1 | mTOR role and signaling components in the different stages of the CNS.

Stage	Processes	Identified signaling pathway components	Reference	
Early CNS development				
	Check point for the progression of differentiation	<i>Ngn2, Pax6</i>	Fishwick et al., 2010	
	NSCs size and switching cap-dependent translation on and off	S6K1/2, 4E-BPs	Hartman et al., 2013	
	Neural progenitor development	GSK3, Sox2	Ka et al., 2014	
	Soma size increase and axon extension	T3, BDNF, TrkB	Westerholz et al., 2013	
	Impaired growth and interneuron migration and decreased survival	<i>Tsc1</i>	Fu et al., 2012	
	Proliferation, survival, and neuronal differentiation	IGF1, TGFβ	Wahane et al. (2014)	
	Neurite outgrowth	5HT7R, Erk, Cdk5, Cdc42 MeCbl Insulin, RAPTOR, RICTOR	Speranza et al., 2015 Okada et al., 2011 Urbanska et al., 2012	
	Impaired neurite outgrowth and cell viability	Sirt1	Guo et al., 2011	
	Oligodendrocyte development	Cannabinoid receptors Myelinating proteins: MBP, Tmem10, MOG, PLP	Gómez et al., 2011 Zou et al., 2014	
Adult CNS				
• Hippocampus	Neurogenesis	Ezh2	Zhang et al., 2014	
	Dendritic spine formation	IR, Rac <i>Disc1</i>	Lee et al., 2011 Kim et al., 2009	
	Late-stage plasticity	HuD, CaMKIIα	Sosanya et al., 2015	
	Enhanced spatial cognitive function	TrkA, ERK	Zhou et al., 2014	
	Learning and memory performance	S6K1, 4E-BP1	Qi et al., 2010; Su et al., 2015	
	Memory consolidation	Estrogen and progesterone, TrkB, ERK calpain BDNF, GluR1	Fortress et al., 2013; Briz and Baudry, 2014; Orr et al., 2012; Slipczuk et al., 2009	
	Long-term memory, protein synthesis	Circadian oscillations eIF4E, 4E-BP1, S6, ERK1/2 CB1R	Saraf et al., 2014 Puighermanal et al., 2009	
	Learning and memory deficits	DISC1	Zhou et al., 2013	
	• Striatum	Motor learning consolidation	S6K1, 4E-BP	Bergeron et al., 2014
	• Amygdala	Memory consolidation of fear memory	KLK8, FKBP51	Jobim et al., 2012a,b; Pedrosa et al., 2013 Hadamitzky et al., 2014 Mac Callum et al., 2014
• Medial prefrontal cortex	Trace fear memory Antidepressant effects	S6K1	Sui et al., 2008 Dwyer et al., 2015	
• Auditory cortex	Memory consolidation for the discrimination of auditory stimuli	Dopaminergic activity	Schicknick et al., 2008	
CNS aging				
	Increase lifespan	Decreased p-mTOR/mTOR	Triplett et al., 2015	
	Decreased rate of degradation	Rag-Ragulator complex	Yu et al., 2014	
	Decreased cognitive function	BDNF, Akt	Yang et al., 2014	
	Learning and memory dysfunction	p62, S6K1	Dong et al., 2015a,b	
	Alterations in histone methylation levels	H3K27me3, H3R2me2, H3K79me3 H3K4me2	Gong et al., 2015	
	Enhanced autophagy, synaptic plasticity	CREB, decreased mTOR	Liu et al., 2015	
	Better memory performance	<i>LARS2, FASTKD40</i>	Ramanan et al., 2015	
	Adult neurogenesis	S6, EGF	Romine et al., 2015 Paliouras et al., 2012	
	Circadian control of aging	BMAL1	Khahre et al., 2014	

phosphorylation of downstream targets of mTORC1 was observed at several time points in different tissues of *Bmal1*^{-/-} mice. Treatment with rapamycin increased the lifespan of *Bmal1*^{-/-} mice. The authors suggest that the circadian clock controls the activity of the mTOR pathway through BMAL1-dependent mechanisms and that this regulation is important for the control of aging and metabolism (Khapre et al., 2014).

The role of mTOR during aging seems to participate in more mechanisms than merely autophagy, and it will be challenging to untangle the role of mTOR in all these processes. The findings also depend on the model and the approach used. mTOR increases with age and inhibits autophagy, an important process in degradation of cellular debris, as well as impairing cognitive functions, and these effects can be ameliorated with a CR diet or with mTOR inhibitors such as rapamycin; in fact, rapamycin has been approved clinically for a variety of uses, including as an immunosuppressant and as an anticancer drug. Yang et al. (2014) report evidence of a decline in mTOR with aging, suggesting that there could be other longevity factors that can also regulate basal autophagy in the mouse hippocampus during normal brain aging.

mTOR is also regulated by the circadian rhythm and by mitochondrial uncoupling and is related to a polymorphism associated with better memory performance in humans. mTOR regulates processes such as epigenetic changes (histone methylation levels), neurogenesis and proliferation in various niches in the aging brain. Therefore, inhibiting mTOR to increase the lifespan should be undertaken with caution because this protein participates in pathways that are essential for health, and it is likely that alterations in mTOR activity could have negative effects throughout the entire system (Table 1).

CONCLUDING REMARKS

In early life mTOR participates in neurogenesis, in neurite outgrowth and elongation and finally in gliogenesis. All of these processes seem to be regulated by mTOR via translation, and it likely functions as a cell-cycle checkpoint. There is need of more *in vivo* studies that show the timing, region and cell specificity

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of mTOR activation/inhibition. It is also important to identify the signaling pathways and effectors that specifically participate in each of these processes.

In the adult brain, mTOR participates in key processes such as synaptic plasticity, adult neurogenesis, and learning and memory. Its role depends on many factors, and in some cases, it seems to have opposite actions. We also need to understand which mechanisms spatiotemporally modulate or balance mTOR expression and how their disruption is associated with neurodegenerative diseases. Addressing these gaps would help to generate therapeutic strategies.

Finally, during aging, mTOR seems to increase neurogenesis, decrease autophagy, and regulate epigenetic changes.

This kinase is an important energy sensor that is present throughout our lifespan. Several stimuli and transduction pathways tightly modulate its expression. Its role must be precisely described in order to develop therapeutic strategies and prevent CNS diseases.

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All authors listed, have made substantial, direct and intellectual contribution to the work, and approved it for publication.

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FORUM REVIEW ARTICLE

Neurotoxicity Linked to Dysfunctional Metal Ion Homeostasis and Xenobiotic Metal Exposure: Redox Signaling and Oxidative Stress

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Abstract

Significance: Essential metals such as copper, iron, manganese, and zinc play a role as cofactors in the activity of a wide range of processes involved in cellular homeostasis and survival, as well as during organ and tissue development. Throughout our life span, humans are also exposed to xenobiotic metals from natural and anthropogenic sources, including aluminum, arsenic, cadmium, lead, and mercury. It is well recognized that alterations in the homeostasis of essential metals and an increased environmental/occupational exposure to xenobiotic metals are linked to several neurological disorders, including neurodegeneration and neurodevelopmental alterations.

Recent Advances: The redox activity of essential metals is key for neuronal homeostasis and brain function. Alterations in redox homeostasis and signaling are central to the pathological consequences of dysfunctional metal ion homeostasis and increased exposure to xenobiotic metals. Both redox-active and redox-inactive metals trigger oxidative stress and damage in the central nervous system, and the exact mechanisms involved are starting to become delineated.

Critical Issues: In this review, we aim to appraise the role of essential metals in determining the redox balance in the brain and the mechanisms by which alterations in the homeostasis of essential metals and exposure to xenobiotic metals disturb the cellular redox balance and signaling. We focus on recent literature regarding their transport, metabolism, and mechanisms of toxicity in neural systems.

Future Directions: Delineating the specific mechanisms by which metals alter redox homeostasis is key to understand the pathological processes that convey chronic neuronal dysfunction in neurodegenerative and neurodevelopmental disorders. *Antioxid. Redox Signal.* 28, 1669–1703.

Keywords: neurodegeneration, redox, essential metals, heavy metals, neurotoxicity

Introduction

MOST ELEMENTS IN the periodic table are considered metals due to their propensity to lose electrons and react with molecular oxygen (O₂) to form oxides. Metals in biological systems may be broadly divided into four groups:

alkali and alkaline-earth metals, such as sodium (Na), potassium (K), magnesium (Mg), and calcium (Ca); essential transition metals, such as copper (Cu), manganese (Mn), iron (Fe), and zinc (Zn); and xenobiotic heavy metals such as mercury (Hg), lead (Pb), and cadmium (Cd). In addition, metalloids such as arsenic (As) are present in the

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environment and have chemical and physical properties of both metal and nonmetal elements. Some authors include aluminum (Al) and selenium (Se) as metalloids. For simplicity, herein we will refer to metalloids as metals. Importantly, while essential metals participate in normal biological functions, alterations in their handling or their increased accumulation are well reported to exert neurotoxicity (Supplementary Table S1; Supplementary Data are available online at www.liebertpub.com/ars).

Prospective epidemiological studies have associated cognitive, motor, and behavioral alterations to environmental exposure to metals and metalloids (153, 158, 250, 371), effects that are exacerbated when environmental exposures occur chronically and during development (153, 158, 250). Long-term effects of either environmental metal exposure or alterations in metal homeostasis in the central nervous system (CNS) and peripheral nervous system (PNS) have been proposed to play a role in neurodegenerative disorders (379). Importantly, alterations in the cellular redox environment of the cell are central to the toxic effects of metals.

Previous reviews address the general role of metals in neurodegeneration, or the mechanisms by which metals produce oxidative stress or neurotoxicity (85, 86, 89, 163, 355). In this work, we present an integrated review on recent advances in (a) the metabolism of both essential and xenobiotic metals; (b) the mechanisms by which distinct metals determine or modify the cellular redox homeostasis; (c) the link between metal redox activity and function in neural systems; and (d) how alterations in metal homeostasis or intracellular/extracellular levels participate in neurotoxicity and neurodegeneration.

Overview of Oxidative Stress and Redox Homeostasis

Reactive species is a term used to describe compounds that can receive or provide a couple of electrons or one electron participating in nucleophilic, electrophilic, or redox metabolic reactions, respectively. Reactive oxygen species (ROS) are molecules derived from O_2 , an obligate component of aerobic organisms. The reduction of O_2 is one of the primary reactions that sustain aerobic life, yet it is also the main source for ROS. ROS include free (\bullet) and nonfree radical species such as hydroxyl radicals ($\bullet OH$), superoxide anion radicals ($O_2^{\bullet -}$), and hydrogen peroxide (H_2O_2). Reactive nitrogen species (RNS) contain both nitrogen (N) and O (oxygen atom), and thus can be categorized as ROS. RNS include nitric oxide (NO^{\bullet}), nitrogen dioxide radical (NO_2), and peroxyntirite ($OOONO^{\bullet}$) (120, 252).

A major source of intracellular ROS production are the mitochondrial electron transport complexes, primarily the one-electron reduction of O_2 to $O_2^{\bullet -}$ by complex I (ubiquinone: NADH oxidoreductase), by the semiquinone of ubiquinone (coenzyme Q), and by complex III (cytochrome bc1 complex or CoQH2-cytochrome c reductase). $O_2^{\bullet -}$ undergoes rapid dismutation into H_2O_2 through the action of superoxide dismutases (SODs). Three types of SODs exist in mammalian cells that use an essential metal as cofactor. Cu/Zn-dependent SOD1 and 3 are localized in the cytosol (SOD1), the extracellular space (SOD3) and to a lesser extent, in the inner membrane space of the mitochondria (SOD1). MnSOD (SOD2) is solely localized in the mitochondrial matrix. The transition metal (Cu or Mn) in the

active site of SODs is required for the breakdown of $O_2^{\bullet -}$ by catalyzing both the one-electron oxidation and one-electron reduction of separate $O_2^{\bullet -}$ to give the overall disproportionation reaction that produces O_2 and H_2O_2 . Binding of Zn to SOD1 or 3 is not essential for $O_2^{\bullet -}$ dismutation reaction but confers higher thermal stability to the proteins (64).

One to 2% of the total mitochondrial O_2 consumed is leaked and contributes to the formation of ROS. Usually, this occurs at a slow rate and can be counteracted by mitochondrial antioxidant systems, but in damaged or aged mitochondria, increased ROS formation occurs. $O_2^{\bullet -}$ and H_2O_2 fuel $\bullet OH$ formation through Fenton/Haber-Weiss reactions, where H_2O_2 oxidizes a redox-active metal (Fe or Cu) leading to the formation of $\bullet OH$. Then, the oxidized metal is reduced back by $O_2^{\bullet -}$ or other cellular reductants promoting metal-catalyzed free radical chain reactions (100, 120, 252).

Other sources of ROS are the nicotinamide adenine dinucleotide phosphate (NADPH)-dependent oxidases (NOX), enzymes whose principal function is to generate $O_2^{\bullet -}$ or H_2O_2 . The formation of RNS begins with the synthesis of NO^{\bullet} , catalyzed by nitric oxide synthases (NOSs), which are Fe dependent. Zn is an important structural element of NOS enzymes and is also known to inhibit their activity. NO^{\bullet} reacts with $O_2^{\bullet -}$ to produce $OOONO^{\bullet}$, which is a strong oxidizing agent. Microsomes and peroxisomes are important sources of ROS due to the presence of NOX and NOS (302). In addition, ROS production can be mediated by the activity of enzymes such as xanthine oxidase (that contains an Fe-sulfur [S] cluster), the heme proteins cyclooxygenases, cytochrome P450 enzymes, lipoxygenases, and myeloperoxidases, as well as the protein folding machinery in the endoplasmic reticulum (ER) (96, 120, 252).

ROS/RNS act as signaling molecules affecting the stability, expression, function, and activity of a multiplicity of proteins controlling almost all cellular functions, including proliferation, cell survival, metabolism, and signaling. An adequate balance between the formation and elimination of ROS/RNS facilitates the signaling role of these reactive species. However, an imbalance between an increase in the steady-state levels of ROS/RNS and the ability of the cell to metabolize/detoxify them leads to a nonhomeostatic state referred to as oxidative stress. Oxidative stress results in the irreversible oxidative modification of biomolecules with the concomitant loss of function of proteins, damage to cellular organelles, and eventual cell death (96, 100, 252, 282). Polyunsaturated fatty acids are one of the preferred oxidation targets for ROS; particularly, free radicals that are potent initiators of lipid peroxidative chain reactions. Lipid peroxidation products, including malondialdehyde (MDA) and 4-hydroxy-2-nonenal (HNE), can react further with DNA bases and proteins (83). DNA bases are also susceptible to direct oxidation by free radicals that can cause mutations as well as deletions in both nuclear and mitochondrial DNA (328).

Protein oxidation can be a reversible or irreversible phenomenon depending on the type of modification, ROS involved, and the extent of oxidation. Tyrosine (Tyr) nitration, protein carbonylation, and protein crosslinkage generated by adduct formation between oxidized proteins, lipid peroxides, or glycative products are irreversible modifications that promote a loss of function, aggregation, and degradation of the targeted protein, and in some cases, the formation of toxic by-products (71). In contrast, reversible oxidative modifications

in the sulfur-containing amino acids methionine (Met) and cysteine (Cys) act as sensors and transducers of ROS/RNS-mediated signaling. Thiol-based oxidoreductases thioredoxins (Trxs), glutaredoxins (Grxs), and Met sulfoxide reductases reduce such modifications acting as the OFF-switch for redox signaling processes (101, 160). On the contrary, both Trxs and peroxiredoxins (Prxs) have been proposed to act as redox sensors, buffers, and relays for H_2O_2 - and NO^\bullet -mediated signal transduction (46, 195, 268, 323). Cys are also targeted by electrophiles generating irreversible modifications, which are thought to be a primary mechanism of toxicity by xenobiotics (193).

Cells are equipped with enzymatic and nonenzymatic antioxidant systems to counteract the toxic effects of ROS/RNS and maintain redox homeostasis (96, 100, 120, 252). The reducing power of glutathione (GSH) is essential for the detoxification of peroxides by GSH peroxidases (GPX) with the resultant conversion of GSH to GSH disulfide (GSSG). GSSG is reduced back by GSH reductase (GR) in an NADPH-dependent manner (105). Catalases also detoxify peroxides but their localization is primarily restricted to peroxisomes. Other endogenous nonenzymatic antioxidants include uric acid, lipoic acid, and ubiquinol (or reduced coenzyme Q), and those obtained from the diet, such as vitamins and flavonoids (96, 100, 120, 252).

The CNS is particularly sensitive to oxidative damage, from which neurons and oligodendrocytes seem to be more susceptible than astrocytes and microglia. The basis for this increased sensitivity is linked to the high levels of O_2 consumption (and electron leakage as a consequence), the low levels of antioxidant defenses when compared to other cells, and the abundance of lipids or fatty acids (262, 295).

Higher levels of endogenous antioxidants and antioxidant systems in astrocytes are explained by the activation of the nuclear factor erythroid-2-related factor 2 (Nrf2) transcription factor (314). Nrf2 recognizes antioxidant response elements to trigger the transcription of antioxidant systems. The ubiquitin ligase Kelch-like ECH-associated protein 1 (Keap1) negatively regulates Nrf2 signaling by inducing its ubiquitination and degradation. Upon modification of specific Cys residues within Keap1 by oxidants or electrophiles (including metals), Nrf2 is released from Keap1 and translocates to the nucleus to induce gene expression dependent on antioxidant response elements (ARE). Nrf2 signaling in neurons has been reported to be epigenetically silenced (27), and induction of the Nrf2 pathway does not seem to be able to promote antioxidant protection (148). Astrocytes also have higher levels of NADPH and glucose 6-phosphate dehydrogenase (G6PD) (109). In contrast, antioxidant genes in neurons seem to be transcriptionally regulated, independent from Nrf2 by synaptic activity, through the triggering of the activating transcription factor 4 (ATF4) and the activator protein 1 (AP-1) (23, 177). Furthermore, while both neurons and astrocytes can synthesize GSH, neurons depend on the supply of GSH precursors *via* GSH efflux (13, 26).

Neurotoxicity of Metals and Metalloids

Neurotoxicity is defined as a damaging effect on the nervous system caused by a biological or chemical agent. The neurotoxic effects of chemicals are the result of a series of

events that include the following: the entry and/or changes in the distribution of a chemical into the brain, interactions with specific cellular targets (neurons and glia), and the initiation of biochemical changes, resulting in structural and functional changes of the nervous system (270). Environmental neurotoxicants include organic and inorganic chemical compounds, such as heavy metals, organic solvents, and cytotoxic substances that can also contain heavy metal mixtures (*e.g.*, pesticides, cigarette smoke, diesel exhaust particles.). The neurotoxic effect of environmental agents is determined by their chemical composition, metabolic function, and pathological consequence, differing widely according to the brain region targeted and the mechanism(s) of action (270).

Essential Metals

Micronutrients are defined by their essentiality and very limited quantity in humans, where their deficiency results in the impairment of biological functions (103, 205). Some metals are essential for the maintenance of cellular homeostasis. Essential metals display important roles as signaling agents or cofactors and, in particular, as activators or redox system components (Supplementary Table S1) (103, 205). Traditionally, cellular osmotic balance and signaling (including synaptic communication and excitability) are associated with nontransition metal ions, such as Na^+ , K^+ , and Ca^{2+} , which form complexes with proteins using low-affinity binding sites, are found at high concentrations, and move quickly across cellular compartments. On the contrary, transition metal ions are known as catalytic cofactors or structural elements in enzymes. Transition metals are present in lower concentration (“trace elements”) and are usually coordinated to proteins at high-affinity binding sites. In the last decade, a role for Zn^{2+} ion as a second messenger has been recognized; however, the role of redox-active metals, such as Cu, Fe, and Mn, in cellular signaling is less explored.

Cu, Fe, and Mn are cofactors of many enzymes that catalyze redox reactions. Although the high reactivity of these metals is essential for life, they can also be involved in uncontrolled redox reactions associated with oxidative stress and cellular damage. Hence, a highly conserved network of proteins strictly regulates the homeostasis of redox-active metal ions, by controlling their uptake, intracellular distribution, storage, and export (205). In the following sections, we describe how brain homeostasis of redox reactive metal ions requires close communication between the blood-brain barrier (BBB), neurons, astrocytes, oligodendrocytes, and microglia. The cases where metal trafficking is tightly linked to the cellular redox environment are highlighted, while the potential role of metal redox cycling in redox signaling is also discussed. Finally, for each essential metal ion, we review how the disruption of its homeostasis may cause two major features associated with neurodegenerative diseases: dysfunction of metalloproteins and aberrant metal-protein interactions that can lead to protein aggregation and uncontrolled ROS production.

Copper

Cu is present in biological systems as Cu^+ (cuprous ion) and Cu^{2+} (cupric ion) (Supplementary Table S1). Cu is a redox-active metal and a cofactor of many enzymes involved in cellular respiration, radical detoxification, as well as

biosynthesis of neurotransmitters, neuropeptides, and hormones. For example, Cu is required as cofactor of several important enzymes in the brain, such as peptidylglycine monooxygenase (PHM), dopamine β -monooxygenase (DBM), tyrosinase (TYR), and cytochrome C oxidase (COX). Cu can activate O_2 for reduction and although its high reactivity with O_2 is essential for life, if uncontrolled it can promote oxidative stress and cellular damage. Cu^+ can react with H_2O_2 to produce highly reactive $\bullet OH$. Cu also induces microglial activation and mitochondrial ROS formation (137).

The control of Cu homeostasis in the brain requires a close interrelationship between the BBB, neurons, and astrocytes (300) (Fig. 1). Astrocytes regulate the properties of the BBB, which is the entry point for Cu into the brain from the blood stream, where Cu is bound to albumin or ceruloplasmin (Cp) (58) (Fig. 1a). At the same time, neurons require Cu as a cofactor and neuromodulator, while astrocytes are key players in synaptic transmission and Cu homeostasis (58). The Cu trafficking machineries of the BBB endothelial cells, neurons, and astrocytes resemble those of other extensively studied mammalian cells (Fig. 1a–c). Extracellular Cu is primarily transported into cells as Cu^+ via the Cu transporter 1 (CTR1) (58). Cu^{2+} reduction to Cu^+ , and Cu uptake from Cp via CTR1, has been proposed to involve a reduction step

but no Cu^{2+} reductase has been identified (281). CTR1-independent mechanisms have also been proposed. The divalent metal transporter 1 (DMT1) seems to play a compensatory role for Cu uptake under certain conditions such as in the absence of CTR1 or under low Fe conditions (147, 231). Interestingly, DMT1 loss promotes brain Cu accumulation and oxidative stress (122). Other potential candidates recently proposed to mediate Cu uptake are the Zrt (Zn-regulated transporter)- or Irt (Fe-regulated transporter)-like protein 4 (ZIP4) (11, 29).

Intracellular Cu distribution depends on the relative concentration and metal affinity of chaperones or chelators (18) (Fig. 1b, c). The antioxidant protein 1 (Atox1), the Cu chaperone for superoxide dismutase 1 (CCS1), and GSH have been proposed to take Cu^+ from CTR1 (197). Chaperones not only bind Cu but they also deliver it to specific targets. CCS1 transfers Cu to SOD1, where its reactivity with O_2 is required for SOD1 maturation via the formation of a disulfide bridge (17). Copper chaperones COX19 and COX17 deliver Cu to the COX assembly proteins (SCO1 and SCO2) and COX11. Finally, Atox1 transports Cu to the ATPase copper transporting alpha (ATP7A) and beta (ATP7B) in the secretory pathway, where cuproenzymes such as SOD3 are metalized (Fig. 1b, c). Upon an excess in cytosolic Cu levels, vesicles in

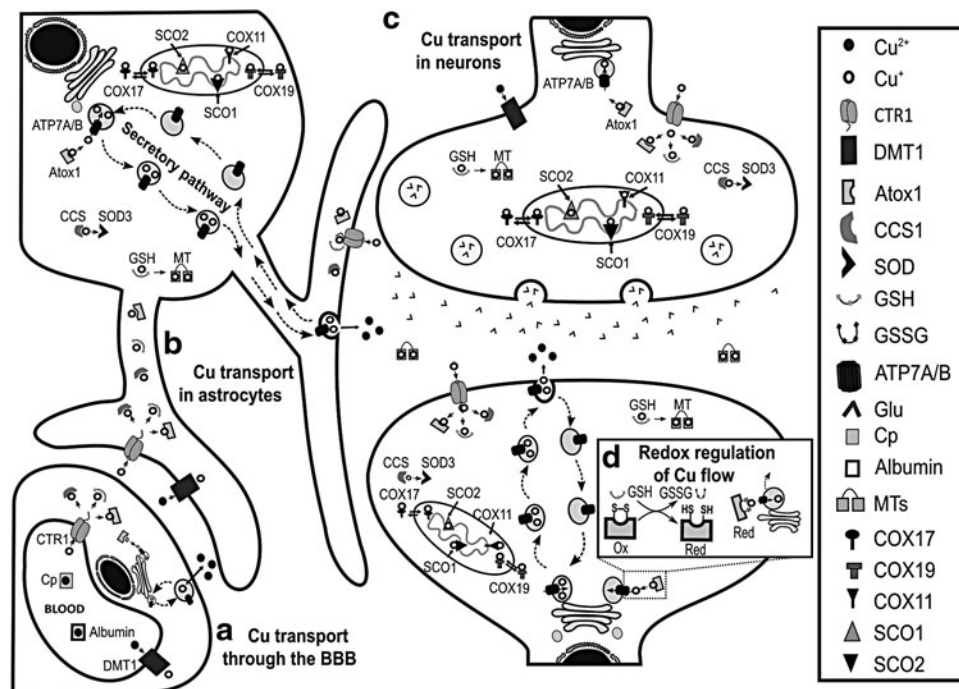


FIG. 1. Cu homeostasis in the brain and its redox control. Regulation of Cu homeostasis is a complex process requiring intercommunication between endothelial cells of the BBB, astrocytes, and neurons. These three types of cells have the same protein machinery as other mammalian cells: CTR1 and DMT1 for Cu uptake; Atox1, CCS1, and GSH for Cu delivery to ATP7(A/B), SOD3, and MT, respectively; COX17 and COX19 for Cu delivery to mitochondria, where SCO1, SCO2, and COX11 load Cu into COX; while ATP7 (A/B) participates in Cu export through the secretory pathway (a–c). (a) Cp- and albumin-bound Cu enters into the brain by crossing endothelial cells of BBB, which are in tight communication with astrocytes. (b) Astrocytes serve as an interface to deliver Cu to (c) neurons. (d) Recently, a redox control of Cu efflux was elucidated in neurons during differentiation: the redox state of Atox1 controls Cu delivery to the secretory pathway. ATP7A, ATPase copper transporting alpha; ATP7B, ATPase copper transporting beta; Atox1, antioxidant protein 1; BBB, blood-brain barrier; CCS1, copper chaperone for superoxide dismutase 1; COX, cytochrome C oxidase; Cp, ceruloplasmin; CTR1, copper transporter 1; Cu, copper; DMT1, divalent metal transporter 1; Glu, glutamate; GSSG, glutathione disulfide; GSH, glutathione; MT, metallothionein; SCO, cytochrome c oxidase assembly protein; SOD, superoxide dismutase.

the secretory pathway are loaded with Cu and trafficked to the plasma membrane, where Cu is released into the extracellular space (196, 197).

Strikingly, although GSH has a lower affinity for Cu, compared to Atox1 and CCS1, the rate of Cu entry into the cell *via* CTR1 is affected by GSH, but not by Atox1 or CCS1 depletion, likely due to the higher concentration of GSH (208). Thus, GSH is the most important cytosolic first acceptor of Cu from CTR1, providing a tight link between cellular Cu uptake and cellular redox homeostasis. GSH in turn is known to transfer Cu ions to metallothioneins (MTs), small Cys-rich proteins that play a major role as scavengers for metal ions (93) (Fig. 1b, c). Three distinct isoforms of MTs are expressed in the human brain. MT-I, MT-II, and MT-III are found in astrocytes, while MT-III is the main isoform expressed in neurons. MTs can be secreted, playing a crucial role in modulating Cu homeostasis and protecting the cell from oxidative damage (299).

Chaperones use Cys residues to coordinate Cu⁺ in their reduced state. Thus, Cys oxidation affects Cu dynamics. Atox1 coordinates Cu using a CysXXCys motif that can form a disulfide bond, which can be reduced directly by GSH or by Grx1 in a GSH-dependent manner (Fig. 1d) (41, 127). During neuronal differentiation, the GSH/GSSG ratio increases promoting a more reductive environment, which in turn reduces Cys residues at the Cu binding site of Atox1. These events enable Cu transport from Atox1 to ATP7A/B and enhance Cu availability to load the active sites of newly synthesized cuproenzymes (128) (Fig. 1d). After neuronal differentiation, both Cu and MT-III levels increase (249).

The recent development of fluorescent sensors has revealed new important roles of intracellular Cu in neuronal activity (78); for example, in the spine neck of hippocampal neurons, Cu is essential for the control of the dendritic actin cytoskeleton (269). Cu export by ATP7A has been reported to be triggered by the activation of glutamate (Glu)/N-methyl-D-aspartate receptors (NMDARs) (301) (Fig. 2a). At the synapse, Cu can modulate many neurotransmitter receptors (66). For example, Cu inhibits NMDAR activity by Cys nitrosylation, a neuroprotective mechanism associated with neuronal plasticity that requires the participation of the cellular prion protein (PrP^C) (110) (Fig. 2b). Accordingly, selective depletion of ATP7A in neurons and glia increases the susceptibility to NMDA seizures (132).

Cu trafficking at the synapse is complex and involves several Cu binding proteins, such as the membrane-bound PrP^C, the amyloid precursor protein (APP), and the amyloid beta (A β) peptide from neurons, or the neurokinin B (NKB) peptide from astrocytes (Fig. 2). PrP^C has several Cu binding sites and it might be involved in Cu sensing and transport into neurons (Fig. 3a). During synaptic transmission, the extracellular Cu concentration may reach $\sim 100 \mu\text{M}$. Cu binding to PrP^C induces its endocytosis, possibly contributing to Cu delivering into the cytosol (263). APP has been reported to regulate Cu efflux, as the APP knockout mice display higher levels of Cu in the brain and in neurons, while APP overexpression leads to decreased intracellular Cu concentrations (28, 330, 375). In contrast, A β peptides produced from the proteolytic cleavage of APP have been proposed to act as Cu scavengers (264), particularly those cleaved to yield 4–40 peptides that have higher affinity for Cu and make up to 50% of the A β in plaques (374). NKB has been suggested to

compete for Cu from PrP^C and transport it into astrocytes by endocytosis (Fig. 2c) (308). PrP^C and A β contain intrinsically disordered regions with Cu binding sites that have the capacity to adopt different Cu coordination modes, some of which have been proposed to activate O₂ and produce ROS (Fig. 3a) (184, 350).

A dysfunction in Cu homeostasis is reported to alter neuronal function and lead to disease progression, including neurodegeneration (Supplementary Table S1). Menkes disease and Wilson disease are caused by mutations or partial deletions in *ATP7A* and *ATP7B*, respectively. These Cu transporters have different patterns of expression in the CNS, explaining the distinct pathological features of each disease. *ATP7B* is found in the visual cortex, anterior cingulate cortex, caudate, putamen, substantia nigra (SN), and cerebellum. *ATP7A* is detected in astrocytes and neurons from the hippocampus and cerebellum, the BBB and choroid plexus, and during neural development (338). Wilson patients display parkinsonism, underscoring the importance of Cu homeostasis in the motor controlling systems. On the contrary, the ubiquitous expression of *ATP7A* has challenged mechanistic investigations in Menkes disease. However, a recent study shows that depleting *ATP7A* in neurons and glia does not lead to neurodegeneration, but to an increased susceptibility to NMDA seizures (132), underscoring its neuroprotective role as described above (Fig. 2a,b). Although neurodegeneration is clearly linked to alterations in Cu homeostasis in Menkes and Wilson diseases, the mechanisms are still unknown.

Neurodegenerative disorders such as amyotrophic lateral sclerosis (ALS), Huntington's disease (HD), Parkinson's disease (PD), and Alzheimer's disease (AD) have been associated with alterations in Cu homeostasis, but a link to specific genetic alterations in Cu transport or handling is missing (Supplementary Table S1). These neurodegenerative diseases are associated with the formation of amyloid aggregates composed of proteins that are either a Cu-dependent antioxidant enzyme, such as SOD1 in ALS, or Cu-binding proteins, such as A β and α -synuclein in AD and PD, respectively.

ALS is characterized by the degeneration of motor neurons, and mouse models show increased intracellular Cu levels and the formation of protein aggregates composed of SOD1 and Cu transport proteins such as Ctr1, CCS, Atox1, and Cox17 (344, 346). SOD1 aggregation has been associated with an alteration in protein stability, which is impacted by metallation and Cu-dependent dimerization. Although SOD1 plays an important role in clearing O₂^{•-}, studies have demonstrated that the mechanism is likely other than the alteration in the antioxidant capacity of SOD1 (312). Increased intracellular Cu levels have been reported in ALS models (346). Consistently, Cu chelators or MT-I overexpression extend the life span and slow disease progression of the *SOD1* (G93A) ALS mouse model (345).

HD is an autosomal dominant genetic disorder caused by polyglutamine (polyQ) repeat expansions near the N-terminus of the huntingtin (Htt) protein. HD is characterized by movement dysfunction, psychiatric and cognitive alterations linked to the degeneration of striatal spiny neurons. Cu accumulation in the striatum of HD transgenic mice has been reported (102). Mutant Htt forms toxic aggregates, but the mechanisms of toxicity are still unclear. A putative Cu binding site in Htt involving Met8 and His82 has

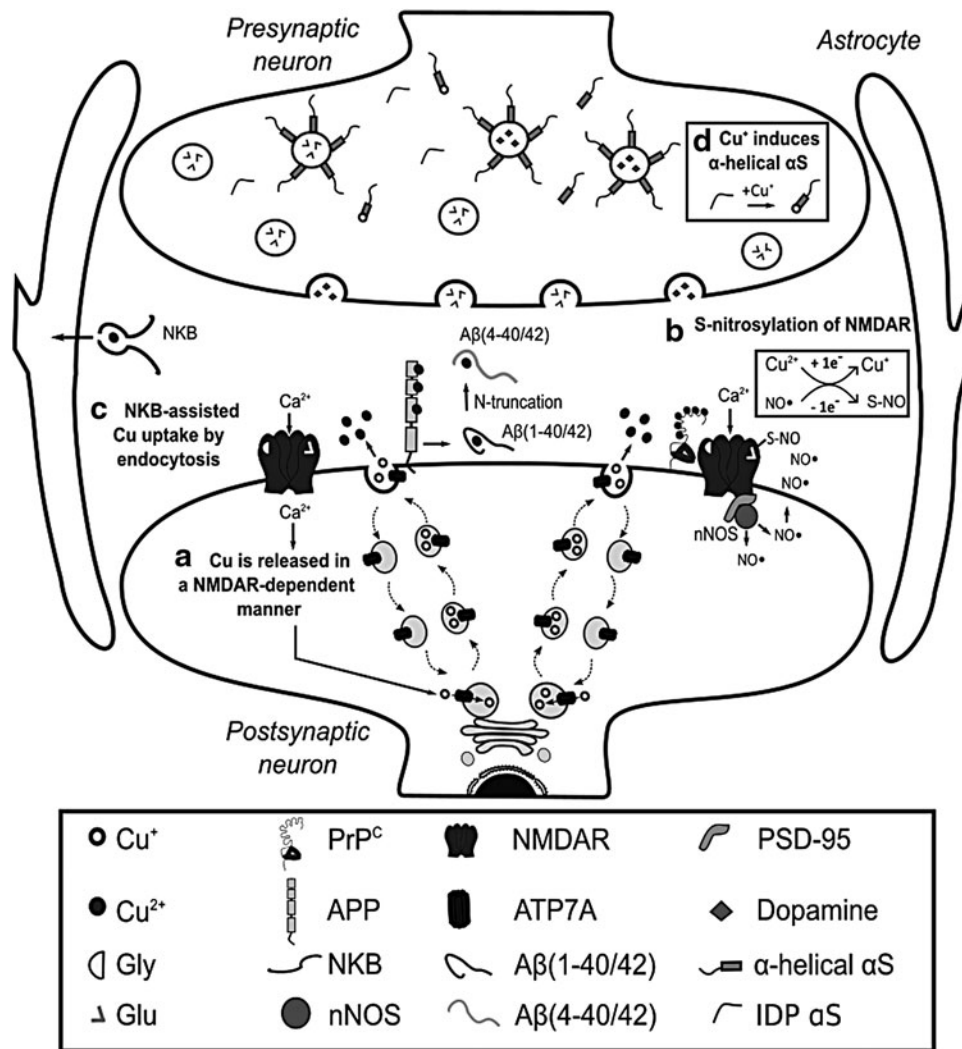


FIG. 2. Cu at synapse and redox signaling. (a) After activation of NMDAR, Cu is released at the synapse through the secretory pathway. Several Cu binding proteins are present in the synaptic cleft, including PrP^C, APP, Aβ peptides, and NKB. (b) The Cu-PrP^C interaction is particularly important for the modulation of NMDAR activity *via* S-nitrosylation. In turn, NO production is dependent on the activation of NMDAR and its interaction with nNOS through the PSD-95. (c) While NKB can assist Cu uptake into astrocytes, Cu distribution among Cu-binding proteins at the synapse likely depends on their relative concentration and affinities for Cu. (d) On the contrary, α-synuclein is an important presynaptic Cu-binding protein found in neurons; it is an IDP that can interact with membranes when it acquires α-helix structure at N-terminal region. Interestingly, Cu⁺ binding to the N-Terminal of α-synuclein enhances its α-helical conformation. Aβ, amyloid beta; APP, amyloid precursor protein; Cu⁺, cuprous ion; IDP, intrinsically disordered protein; NKB, neurokinin B; NMDAR, glutamate/N-methyl-D-aspartate receptor; nNOS, neural nitric oxide synthetase; PrP^C, cellular prion protein; PSD-95, postsynaptic density protein 95.

been identified, and this interaction promotes polyQ aggregate formation (102, 381), which is reduced by MT-III overexpression (123).

PD is characterized by the degeneration of dopaminergic neurons in the SN, which are rich in Cu. PD patients show decreased Cu content in the SN (70) without changes in Cu levels in serum, plasma, and cerebrospinal fluid (CSF) (203). Accordingly, decreased levels of CTR1 (70) have been reported in the SN, while MT-I and MT-II levels in active astrocytes are increased, reflecting a glial response to the loss of Cu homeostasis in PD (226). In contrast, occupational exposure to Cu has been linked to an increased risk to develop PD (115).

The accumulation of intracellular protein inclusions (Lewy bodies), where α-synuclein is the main protein component,

is another hallmark of PD (362). α-Synuclein is a small intrinsically disordered protein (IDP) enriched in presynaptic terminals and nucleus that can interact with cytoskeleton components and lipid membranes (170). IDPs are proteins that can adopt different conformations, and thus respond to changes in their biochemical environment. This property allows them to engage in interactions with multiple protein targets (23). Cu²⁺ and Cu⁺ ions are capable of binding to α-synuclein at three different sites (20, 33, 228, 361) (Fig. 3a). Interestingly, the H50Q *SNCA*/α-synuclein mutation linked to hereditary PD abolishes one Cu binding site altering Cu-induced α-synuclein aggregation (361). Moreover, Cu binding to the high-affinity Cu-binding site at the N-terminal region of α-synuclein accelerates its amyloid aggregation

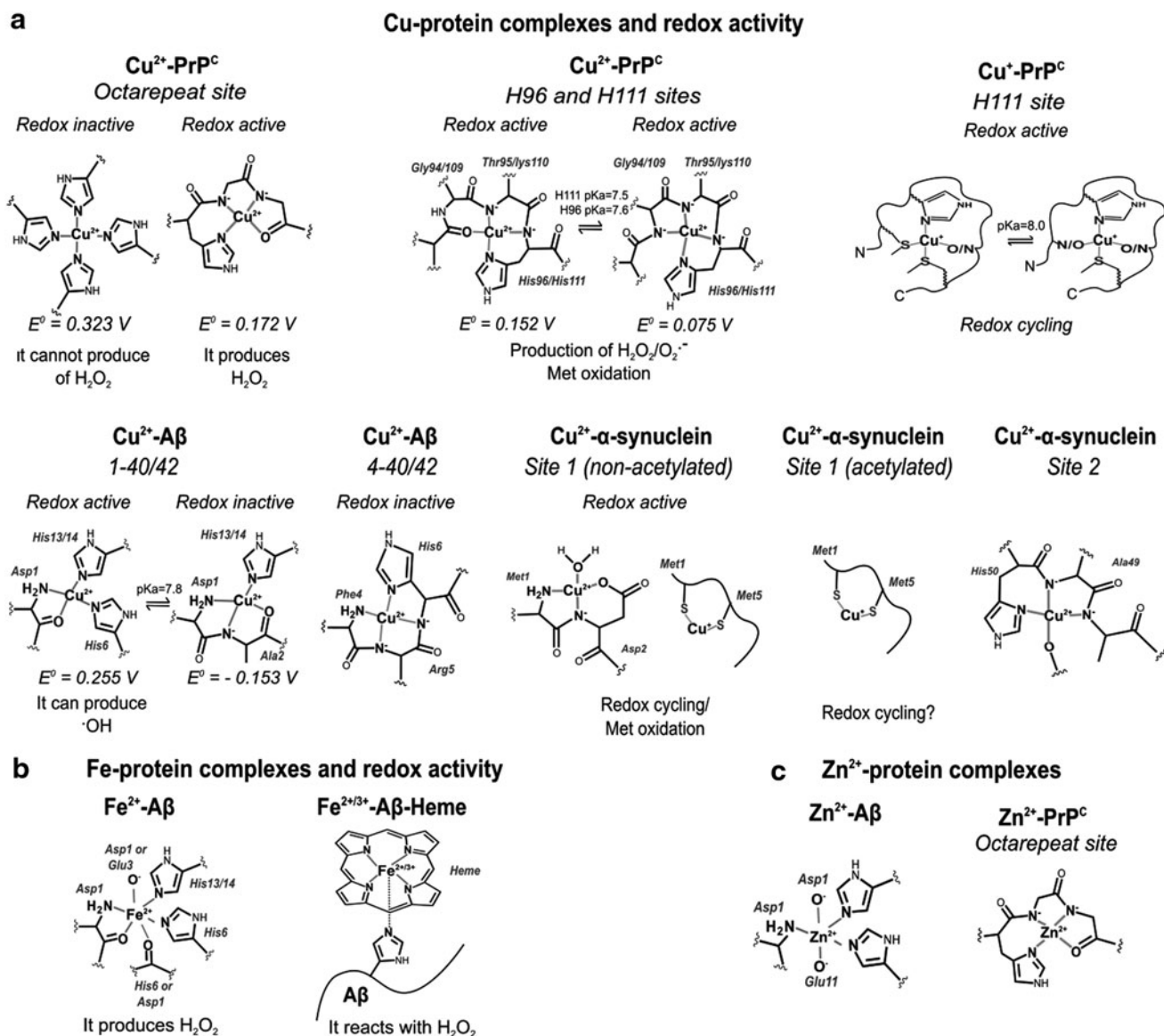


FIG. 3. Structural features and redox properties of relevant metal-protein complexes in neurodegenerative diseases. (a) Cu can interact with PrP^C, Aβ, and α-synuclein. PrP^C has three coordination sites: *histidine (His) His96*, His111, and an octarepeat. Cu²⁺ coordination to His96 and His111 yields very similar complexes different to those generated upon Cu⁺ binding to His111. The octarepeat region coordinates up to four Cu²⁺ ions depending on the Cu²⁺/PrP^C stoichiometric ratio. At low Cu:protein ratios, four His residues coordinate Cu²⁺, while at high ratios each His can bind one Cu²⁺ ion. The different coordination chemistry of these Cu-PrP^C complexes is reflected in their redox properties. Similarly, Cu²⁺ coordination to Aβ (1–40/42) yields two different coordination modes that display different redox properties. Recently, coordination to Aβ (4–40/42) has also been described; this site displays higher affinity for Cu²⁺ than Aβ (1–40/42), and it yields a redox silent complex. On the contrary, nonacetylated α-synuclein has two high-affinity binding sites for Cu²⁺: site one involving residues at the N-terminal, and site two at His50. Acetylation of α-synuclein, as described to occur *in vivo*, abolishes Cu²⁺ binding at site 1, although both forms of α-synuclein can bind Cu⁺. (b) Fe²⁺ can interact with Aβ, but the redox properties of Fe-Aβ complexes remain unclear. Interestingly, recent studies propose that heme can bind to Aβ, yielding a heme (Fe)-Aβ complex with peroxidase activity. (c) Finally, Zn²⁺ can bind to the octarepeat region of PrP^C and with Aβ. Cu²⁺, cupric ion; Fe, iron; Fe²⁺, ferrous; Zn, zinc.

in vitro (20, 33); although this effect is abolished in acetylated α-synuclein (234), which is found in Lewy bodies (10).

While several studies have suggested that Cu-induced aggregation of α-synuclein is directly linked to its neurotoxicity, recent studies suggest a lack of correlation between protein aggregation and cytotoxicity (361); in fact, it has been demonstrated that α-synuclein potentiates the toxicity of Cu in dopaminergic cells in the absence of enhanced ac-

cumulation of protein aggregates (8). Clearly, further investigations are needed to completely understand the structural impact of Cu-α-synuclein interactions and their role in PD. On the contrary, acetylation and Cu⁺ binding to α-synuclein are two synergistic events that turn the intrinsically disordered N-terminal region into an α-helix conformation (228) (Fig. 2d), which displays higher affinity for membranes (75). These observations suggest a potential link between Cu⁺-α-

synuclein interactions and the proposed function of α -synuclein in vesicle trafficking; a link that might be perturbed in PD.

Different redox modifications of α -synuclein are found in Lewy bodies, including Met oxidation, Tyr nitration (67), and formation of di-Tyr-linked α -synuclein dimers. Cu^+ - α -synuclein complexes have been implicated in these modifications, as they are capable of activating O_2 , leading to Met oxidation and di-Tyr bond formation (5, 227) (Fig. 3a). In contrast, a recent report suggests that Cu^+ complexes with oligomeric or fibrillar α -synuclein reduce metal-catalyzed ROS formation (264). Cu has also been shown to potentiate oxidative damage induced by the dopamine (DA) analog 6-hydroxydopamine (63). Cu also interacts with the early-onset PD recessive genes (protein) *PARK7* (DJ-1) and *PARK2* (Parkin). Cu binding to DJ-1 protects against metal toxicity, possibly acting as a chaperone for SOD1 (35, 114); while Parkin mutations have been reported to increase the cytotoxic effect of heavy metals, including Cu (1).

AD is a neurodegenerative disease associated with the degeneration of hippocampal and cortical neurons and eventual loss of memory and progressive dementia (326). Decreased levels of Cu are found in AD brains (42), while the total Cu content and labile nonprotein-bound Cu fraction are increased in the plasma of AD patients (325). Interestingly, polymorphisms in *ATP7B* have been linked to AD (326). AD is associated with the formation of extracellular amyloid plaques composed of Cu bound to $\text{A}\beta$ peptides 1–40 and 1–42 fragments produced by cleavage of the APP, as well as N-truncated forms 4–40 and 4–42, and to a lesser extent 11–40/42 (210, 273, 364). The Cu binding features of $\text{A}\beta$ 4–40/42 and 11–40/42 are different from those of 1–40/42, leading to the formation of Cu- $\text{A}\beta$ complexes with distinct redox properties (Fig. 3a) (229). Different aggregation properties have also been described, as illustrated by the faster fiber assembly rate of $\text{A}\beta$ 11–40/42 when compared with 1–40/42 (21). Substoichiometric Cu^{2+} concentrations trigger $\text{A}\beta$ aggregation through a different pathway that involves the formation of oligomers more neurotoxic than those generated by the peptide alone (25, 204). On the contrary, the redox activity of Cu- $\text{A}\beta$ complexes has also been proposed to lead to the generation of ROS (52, 214), but contradictory results exist as well (264). Interestingly, interaction of Cu with N-truncated 4–40 and 4–42 peptides yields redox-inactive Cu- $\text{A}\beta$ complexes (229, 350). A dysfunction in Cu homeostasis in AD is also evidenced by decreased levels of MT-III (390). MTs are capable of exchanging Cu^{2+} with $\text{A}\beta$ 1–40/42, reducing Cu and stabilizing it. This Cu exchange by MTs has been proposed as a redox-silencing mechanism that prevents ROS formation by Cu- $\text{A}\beta$ complexes (223).

The impact of dysfunctional Cu homeostasis in AD might go beyond the neurotoxicity of Cu- $\text{A}\beta$ complexes. APP, whose mutations are associated with AD, is a type 1 transmembrane protein that displays three Cu binding sites in its extracellular domain (22, 140). One Cu-binding site is located in the growth factor-like domain, and has been implicated in Cu-induced dimerization of APP, a process that would be important in cell adhesion and signaling (22). Cu was found to induce APP phosphorylation at Thr668 promoting its localization to the axonal membrane, suggesting an important link between Cu and APP functions at the synapse that might be perturbed in AD. $\text{A}\beta$ peptides can also interfere with Cu-PrP^C interactions implicated in the regu-

lation of NMDAR activity (Fig. 2b) (389). In addition, Cu has been reported to promote the degradation of the low-density lipoprotein receptor-related protein 1 (LRP1) *via* Tyr nitration and proteasomal degradation, which was linked to a decrease of $\text{A}\beta$ clearance and its resultant accumulation in brain vasculature (319). Clearly, Cu plays important roles in neuromodulation and signaling processes, which would be perturbed in AD.

Iron

Fe is found in biological systems primarily as ferrous (2+) and ferric (3+) ions (Supplementary Table S1). Fe is a redox-active metal involved in several redox reactions that catalyze the formation of ROS. Fe is tightly bound to Fe storage and transport proteins, while <5% is present as labile redox-active Fe bound to low-affinity molecules. Fe is required as cofactor of several important enzymes for respiration and synthesis of neurotransmitters, including tryptophan hydroxylase (serotonin) and Tyr hydroxylase (norepinephrine and DA), cholesterol, and fatty acids; the latter particularly important for nerve myelination (161, 342). Electron transfer in many Fe enzymes, including the mitochondrial respiratory complexes, is facilitated by heme and Fe/S clusters (291). Fe is also important as cofactor for peroxidases and catalases, which are important for cellular redox homeostasis (6).

Fe is heterogeneously distributed in the brain; it is highly concentrated in the SN, hippocampus, striatum, interpeduncular nuclei (125), and myelin (329) (Supplementary Table S1). Fe homeostasis is regulated by communication between the BBB and astrocytes. In the blood stream, Fe^{3+} is found coordinated to transferrin (Tf) or ferritin (Ft), and as heme. Fe uptake into the BBB can occur by two pathways: (a) by direct transport of Fe^{2+} into the cytosol *via* DMT1; or (b) by endocytosis of Tf-bound Fe^{3+} *via* the Tf receptor (TfR), where the low pH of the endosome causes the release of Fe^{3+} from Tf. In both cases, Fe^{3+} is reduced to Fe^{2+} by the duodenal cytochrome b (Dcytb) or by the six transmembrane epithelial antigen of the prostate 2 (Steap2) ferrireductases and then transported by DMT1 (Fig. 4a) (215, 218).

Fe efflux from endothelial cells to the interstitial space occurs *via* the coordinated activity of the Fe^{2+} transporter ferroportin (Fpn) and the Cu-dependent ferroxidases hephaestin (Hp) and soluble ceruloplasmin (sCp), which oxidize Fe^{2+} to Fe^{3+} . Astrocytes regulate the release of Fe from BBB by either secretion of sCp, which stimulates Fe release, or by production of hepcidin, a peptide that induces internalization and ubiquitination of Fpn and thus, decreased Fe efflux (216). Astrocytes also express a glycosylphosphatidylinositol (GPI)-anchored form of Cp, which interacts with Fpn and participates in Fe efflux (Fig. 4a) (144). In general, oligodendrocytes, astrocytes, microglia, and neurons have the same machinery for Fe efflux, involving the concerted action of Fpn with Cp or Hp (60).

The mechanisms of Fe uptake differ between brain cell types. Fe, Tf, and Ft are primarily found in oligodendrocytes (61). Most Tf in the brain is synthesized and secreted by oligodendrocytes as Fe-free Tf or apo-Tf and is required for Fe mobilization within the interstitial fluid brain (87). Although oligodendrocytes and astrocytes can accumulate high levels of Fe, they do not express TfR. Fe uptake into

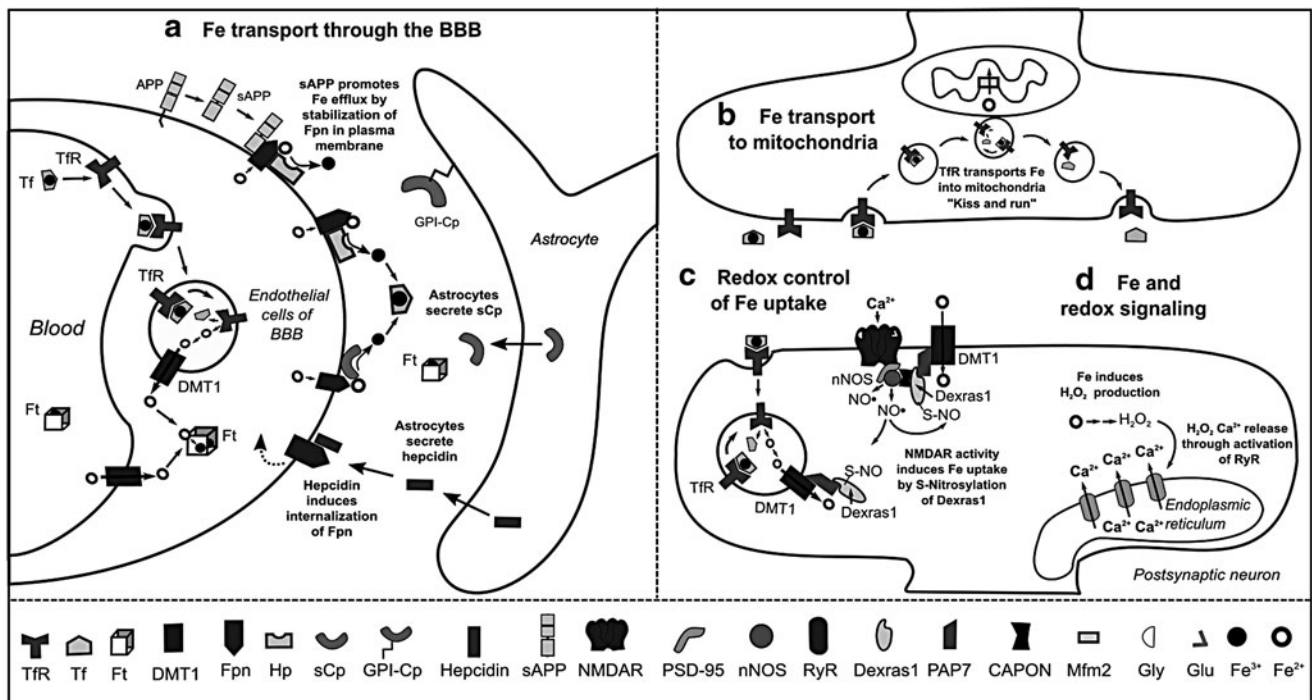


FIG. 4. Fe transport and redox signaling. (a) Fe transport across the BBB occurs *via* DMT1 or by endocytosis of Tf-bound Fe³⁺; followed by Fe release *via* the concerted action of Fpn with a ferroxidase, either Hp or sCp. Astrocytes modulate Fe transport through the production of sCp, sAPP, and hepcidin. sAPP stabilizes Fpn, while hepcidin induces its internalization. (b) Mitochondria are the organelles with highest demand of Fe. Although Fe transport into mitochondria is not fully understood, the recently demonstrated interaction between mitochondria and TfR-containing endosomes supports the “kiss and run” hypothesis. Inside the mitochondria, Fe crosses the inner membrane by Mfn2. (c) In hippocampal neurons, NMDAR activation induces Ca²⁺ entry and NO[•] production by nNOS, causing S-nitrosylation of Dexas1, which in turn induces Fe uptake through DMT1 and TfR. (d) Increased intracellular Fe also induces H₂O₂ production, inducing Ca²⁺ release from ER *via* RyR, which is important for neuronal plasticity. Dexas1, Ras-related dexamethasone induced 1; ER, endoplasmic reticulum; Fe³⁺, ferric; Fpn, ferroportin; Ft, ferritin; H₂O₂, hydrogen peroxide; Hp, hephaestin; Mfn2, mitoferrin-2; NO[•], nitric oxide; PAP7, peripheral benzodiazepine receptor-associated protein 7; RyR, ryanodine receptor; sAPP, soluble fragment of APP; sCp, soluble ceruloplasmin; Tf, transferrin; TfR: transferrin receptor.

oligodendrocytes has been recently proposed to involve the internalization of H-Ft by a mucin-domain containing protein (Tim-2) (343). In astrocytes, ascorbate-dependent Fe²⁺ uptake is mediated by DMT1 (167) and transient-receptor potential channels (265).

In neurons, the mechanisms involved in Fe uptake are still unclear. DMT1 is found in human neurons and its expression levels are negatively regulated by Fe exposure *via* ubiquitination and degradation (134). However, DMT1 seems to colocalize in cytoplasmic vesicles with TfR and to primarily contribute to Tf-bound Fe uptake (232, 266). The ZIP8 and ZIP14 members of the ZIP family of metal transporters have also been demonstrated to mediate Fe²⁺ uptake (188) and to be expressed in the brain (113). A recent report demonstrates that ZIP8 at the plasma membrane is the primary transporter involved in non-Tf-bound Fe into neurons (145).

In brain cells, the ferrireductases Dcytb and stromal cell-derived receptor, SDR2, are expressed in astrocytes (192, 351), while SDR2 and Steap2 are found in neurons (145). In all cases, it is important to note that Fe uptake and efflux always require redox cycling between Fe²⁺ and Fe³⁺ oxidation states.

Cytosolic Fe is stored by Ft, which is a protein complex formed by 24 subunits of heavy-ferritin (H-Ft) and light-ferritin (L-Ft) chains. Ft genes are regulated by Nrf2 (272).

While H-subunits have ferroxidase activity and participate in Fe uptake, L-subunits are involved in Fe mineralization and long-term storage. Ft can store ~4500 Fe ions in its core. However, the mechanism by which Fe is released from Ft remains unclear (47). Although Fe is mainly stored in the cytosol, mitochondria are the organelles with the highest Fe demand, as they require Fe-S clusters and heme groups for electron transfer during respiration. Similarly, mitochondria are also considered the main sources of ROS under physiological conditions. Therefore, mitochondrial Fe homeostasis must be tightly regulated to prevent uncontrolled ROS production.

The mechanism(s) involved in mitochondrial Fe uptake are still unclear. Fe is delivered by a direct “kiss and run” interaction between the endosomes containing Tf-bound Fe and mitochondria (69). Subsequently, the metal crosses the inner membrane *via* the Fe importer mitoferrin-2 (Mfn2) (Fig. 4b). In the mitochondrial matrix, Fe is either used for the biogenesis of prosthetic groups, Fe-S clusters, or heme, or it is stored by mitochondrial ferritin (FtMt), which is homologous to H-Ft, and it displays the same Fe uptake efficiency but lower ferroxidase activity. Fe distribution between mitochondria and cytosol depends on FtMt expression and the export of Fe prosthetic groups (106, 176).

Heme is a component of globins, a superfamily of heme-containing proteins involved in binding and/or transporting O₂, and a cofactor for cytochromes, catalase, NOX, NOS, and myeloperoxidase, which is also found in microglia (59, 151, 198). Hemoglobin (Hb) is involved in O₂, NO, and carbon dioxide (CO₂) transport in cells of erythroid lineage, but Hb α and β transcripts have been found in dopaminergic neurons, oligodendrocytes, and cortical or hippocampal astrocytes as well (32). Brain Hb levels are altered during neurodegeneration (94), but their functional consequences are unclear. Neuroglobin is another globin expressed in the CNS and PNS and found in both neurons and astrocytes. Neuroglobin has a higher affinity for O₂ than Hb and exerts a protective effect against oxidative and ischemic insults (7, 43, 81, 179, 331, 368). Oxidative stress has the potential to release heme from Hb, and labile heme can induce oxidative damage *via* Fenton reactions or NOX activation (165, 239). Heme oxygenases (HOs) catalyze heme degradation. HO-1 transcription is induced by oxidative stress, inflammation, hypoxia, and metal exposure, while HO-2 is constitutively expressed. HO activity has both antioxidant and pro-oxidant effects that relate to the ability of the cell to detoxify labile Fe released from heme (286, 369).

Cellular Fe trafficking is controlled by the iron regulatory proteins (IRP) IRP1 and IRP2 which regulate translation of proteins involved in Fe storage (H-Ft and L-Ft), Fe uptake (TfR), and Fe efflux (Fpn). Under conditions of Fe depletion, IRPs can bind to messenger RNAs (mRNAs), decreasing the levels of Ft and Fpn and promoting the translation of TfR *via* the stabilization of its mRNA. Conversely, Fe overload prevents mRNA binding to IRPs, promoting Ft and Fpn translation while reducing TfR levels. The ability of IRP1 and IRP2 to bind mRNAs exerts an important redox control *via* two distinct mechanisms. IRP1 has two conformations: (a) a closed one, triggered *via* an Fe-S cluster that prevents mRNA binding and has aconitase activity; and (b) an open conformation that is favored when NO[•], O₂, and H₂O₂ cause dissociation of the Fe-S cluster. In contrast, the ability of IRP2 to bind mRNAs is controlled by proteasomal degradation, involving the ubiquitin ligase F-box/LRR-repeat protein (FBXL5), which is also an Fe and O₂ sensing protein. FBXL5 has a binuclear nonheme Fe site, and it is stabilized on Fe and O₂ binding, promoting IRP2 degradation. Together, these two mechanisms illustrate the redox control of cellular Fe trafficking (164).

In neurons, Fe uptake is induced by a redox signaling cascade that starts with the activation of the NMDAR (Fig. 4c). Increased intracellular Ca²⁺ induces NO[•] production by the neuronal (n) NOS, leading to S-nitrosylation of the small GTPase Dexas1 (Ras-related dexamethasone induced 1), which in turn induces Fe uptake through DMT1 and TfR (51). In hippocampal neurons, NMDAR activation increases intracellular Fe and H₂O₂ production, which activates the redox-sensitive ryanodine receptor (RyR) and promotes Ca²⁺ release from the ER (237) (Fig. 4d). Thus, Fe uptake is clearly part of a redox signaling mechanism that might be important for neuronal plasticity.

Cell death induced by an increase in the labile Fe pool within cells has been defined as a specific entity named ferroptosis. Ferroptotic cell death is a necrotic-like cell death characterized by Fe-dependent lipid peroxidation due to either the formation of [•]OH and H₂O₂ *via* Fenton-like reactions

or the activation of lipoxygenases. As such, ferroptosis is counteracted by Fe-chelators and the GSH/GPX4 system. *GPX4* knockout in neurons induces motor neuron degeneration, paralysis (53), and cognitive impairment (121). During ferroptosis, Tf-dependent Fe uptake and release of Fe from lysosomal compartments have been shown to act as important sources for Fe. Interestingly, lysosomal permeabilization is a common phenomenon observed in a number of neurodegenerative disorders, including PD (40, 73). However, during pathological conditions such as neurodegeneration and hemorrhagic stroke, cell death is likely to involve a combination of different pathways and a complex balance between them, including apoptosis, necrosis, autophagic cell death, and ferroptosis as well (77, 143, 357, 398).

During aging, accumulation of Fe in the frontal lobes and striatum is associated with motor dysfunction, loss of myelin sheaths, and memory decline (2, 327). Inflammation, a common hallmark of many brain disorders, increases the expression of DMT1 and hepcidin (354).

Abnormal accumulation of Fe is a common feature of many neurodegenerative diseases, including a group of twelve diseases known as neurodegeneration with brain iron accumulation (NBIA) (225). The most common clinical features of NBIA are movement disorders, such as ataxia, parkinsonism, and dystonia. Although in NBIA Fe is usually accumulated in the globus pallidus, and in some cases in the SN and cerebellum, only two types of NBIA involve the dysfunction of a protein that participates in Fe trafficking: aceruloplasminemia (lack of Cp) and neuroferritinopathy (loss of function mutations in L-Ft) (65, 261, 290, 360). Another neurodegenerative disease associated with disturbed Fe homeostasis is Friederich ataxia, which is linked to mutations in frataxin, an Fe-chaperone involved in Fe-S cluster biogenesis (55).

Altered Fe homeostasis and mitochondrial dysfunction are also hallmarks of PD. While no significant differences in Fe levels have been found in the blood, serum, and CSF (203), Fe is increased in the SN of PD patients (365). Neuromelanin is an Fe-rich pigment found in the dopaminergic neurons targeted in PD (A9) and it has been suggested that its presence makes this neuronal population vulnerable to oxidative damage (91). Decreased levels of serum Cp or its oxidation has also been proposed to exacerbate Fe accumulation in PD (149, 251). DMT1 is found increased in the SN of PD brains (294). Interestingly, Parkin regulates DMT1 expression levels *via* ubiquitination and proteasomal degradation (289).

Fe accumulation in SN might be associated with a dysfunctional delivery of Fe to mitochondria through the “kiss and run” interaction mentioned above (Fig. 4b) (69). Indeed, a Tf/TfR2-dependent mechanism for Fe transport into the mitochondria of dopaminergic neurons has been described (211), while a role for *Tf* and *TfR2* genes in Fe accumulation and mitochondrial dysfunction in PD has been implicated as well (285).

Mitochondrial dysfunction in PD might lead to decreased synthesis of Fe-S clusters, which in turn would activate IRP1 binding to mRNAs, resulting in augmented Fe accumulation (142). Accordingly, knockdown of mitochondrial Grx2 impairs Fe-S cluster biogenesis in dopaminergic cells, decreases the activity of Complex I and aconitase, and increases the activation of IRP1 (171). Loss of PINK1/*PARK6*, another autosomal early-onset PD-related gene, has also been

reported to inactivate Fe-S clusters *via* $O_2^{\bullet-}$ formation. As such, overexpression of FtMt exerts a protective effect on mitochondrial dysfunction and oxidative stress induced by loss of PINK1 (88).

HO-1 protects against neuronal cell death induced by PD-related mitochondrial toxins and α -synuclein, suggesting a role of heme in dopaminergic cell loss. However, HO-1 becomes toxic at high levels, but this effect is counteracted by FtMt (391). Interestingly, the pathogenic PINK1 mutation G309D impairs the induction of HO-1 on oxidative stress (56).

Fe^{2+} can interact with the negatively charged C-terminal region of α -synuclein, accelerating its amyloid aggregation (34). Conversely, α -synuclein overexpression also enables Fe accumulation (254). In PD, oxidative stress has been linked to intracellular Fe levels due to the redox activity of Fe-DA and Fe-neuromelanin complexes (400). Furthermore, overexpression of FtMt protects against neuronal cell death induced by 6-hydroxydopamine (313). Interestingly, a recent report demonstrates that depletion of Fpn has no consequence on the survival of dopaminergic neurons. In contrast, loss of TfR causes Fe deficiency and a PD-like neurodegeneration in mice (212). Previous findings have also suggested a link between Fe deficiency and predisposition to PD, while Fe overload seems to be protective (157, 190, 271). Thus, the exact role of Fe homeostasis in PD is still far from being understood.

A role of Fe in AD has also been proposed based on observations showing that Fe levels are decreased in the serum of AD patients (324), and increased in AD-related brain areas such as the hippocampus, neocortex, and basal ganglia (168). Mitochondrial dysfunction is also observed in AD, which might be related to a disruption in Fe homeostasis. Accordingly, overexpression of FtMt protects against the toxicity of $A\beta$ (380). Fe is accumulated in amyloid plaques in the AD brain (38, 194), consistent with the observation that $A\beta$ is able to bind Fe^{2+} *in vitro* (Fig. 3b) (39). Fe bound to $A\beta$ plaques catalyzes H_2O_2 formation (321).

A novel mechanism for controlling Fe efflux from the BBB was recently discovered, involving the soluble fragment of APP (sAPP), which interacts with Fpn, stabilizing its membrane location (219) and counteracting the effects of hepcidin (216). APP expression is also negatively regulated by IRP1 (57), and production of sAPP and $A\beta$ is increased in AD. Thus, the proposed role of sAPP in Fe movement from BBB into the brain is consistent with the accumulation of Fe in AD brains and the observation of higher levels of $A\beta$ plaques surrounding the brain blood vessels. Indeed, BBB damage is a common feature in AD (217).

Heme metabolism also contributes to AD. APP binds and inhibits HO-1 activity and this effect is enhanced by pathogenic APP mutations (334). In addition, $A\beta$ can form a complex with heme that displays peroxidase activity (16, 112). Conversely, neuroglobin has been proposed to protect against the toxicity of 1–42 $A\beta$ peptides (180). Overall, disruption of Fe homeostasis in AD is likely linked to oxidative stress, and it may also impair NMDAR- and Fe- dependent redox signaling mechanisms (Fig. 4d) impacting neuronal plasticity and memory.

Manganese

Mn is an essential metal required for the activity of a plethora of enzymes, including hydrolases, isomerases, li-

gases, lyases, oxidoreductases, and transferases, involved in diverse metabolic functions such as amino acid (arginase and glutamine synthetase [GS]), lipid, protein, and carbohydrate metabolism (phosphoenolpyruvate decarboxylase), as well as protein glycosylation, energy production, and redox homeostasis (SOD2). The main source for Mn intake is food, but occupational/environmental exposures also occur associated with mining, smelting, welding, alloy, battery, pesticide, and electrical industries. Ingestion and inhalation are the primary routes of Mn exposure. Importantly, inhalation can transfer Mn directly to the brain. The brain is a major target for chronic Mn intoxication (manganism) where Mn is accumulated in nonheme Fe-rich regions. Manganism is defined as a parkinsonism that results in dystonia, hypokinesia, and rigidity as a consequence of impaired neurotransmitter function (133, 352).

Mn can be transported *via* TfR and DMT1 as it competes with Fe for its binding sites (333). Other proposed Mn transporters include the Zn carriers ZIP-8 and ZIP-14, voltage-regulated, store-operated, and ionotropic Glu receptor Ca^{2+} channels, and the Mn-citrate complex shuttle (Fig. 5a) (352). Mn is efficiently detoxified by Fpn at the plasma membrane. In addition, Mn is also detoxified by sequestration in the Golgi *via* the solute carrier family 30 member 10 or human Zn transporter 1 (*SLC30A10/hZnT1*) transporter whose mutations are directly associated with manganism (178). Alternatively, the Ca^{2+}/Mn^{2+} ATPases SPCA1 and SPCA2 also detoxify Mn *via* the secretory pathway (356). Finally, the autosomal recessive early-onset PD-related gene *ATP13A2/PARK9* mediates sequestration of Mn in lysosomes (Fig. 5b) (336). Recently, direct comparison of different detoxification proteins demonstrated that hZnT1 and SPCA1, but not ATP13A2, are involved in Mn detoxification and resistance (246).

Mn^{2+} is the predominant species found in cells that can be oxidized to the more reactive and toxic species Mn^{3+} . Neither Mn^{2+} nor Mn^{3+} can generate free radicals *via* Fenton-type reactions. However, it has been proposed that Mn enhances ROS generation *via* the Mn-catalyzed autooxidation of DA that involves the redox cycling of Mn^{2+} and Mn^{3+} and the generation of ROS and DA-o-quinone (Fig. 5c) (79, 89). Mn accumulates in the mitochondria *via* the mitochondrial Ca^{2+} uniporter (MCU) (111) and increases the accumulation of labile Fe. Both mitochondrial dysfunction and Fe lead to ROS formation and oxidative damage (Fig. 5d) (54, 206). Mn specifically generates H_2O_2 but not $O_2^{\bullet-}$ in the mitochondria *via* complex II (92, 186, 322). Furthermore, Mn impairs oxidative phosphorylation and ATP production.

Astrocytes seem to have a high capacity to accumulate Mn (14). Mn-induced neurotoxicity has been linked to a decrease in Glu uptake by astrocytes (156) leading to excitotoxicity in neurons, as well as the induction of inflammation and increased activity of NOS (Fig. 5e) (95, 185).

Zinc

Zn is a redox-inactive transition metal ion with an oxidation state of +2. The majority of intracellular Zn is bound to proteins and is distributed in the cytoplasm (~50%) and nucleus (~40%) (304) (Supplementary Table S1). The function of Zn as enzyme cofactor is limited to structural roles (*e.g.*, SOD1) (312), or as a Lewis acid that activates

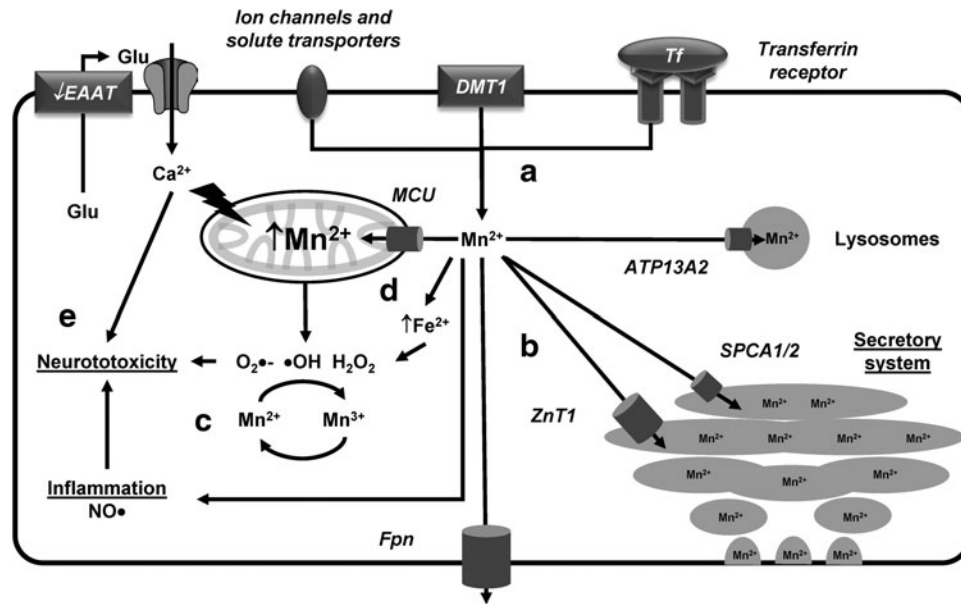


FIG. 5. Mn homeostasis and toxicity. (a) Mn can be transported *via* Tf and DMT1, as well as *via* Zn carriers, ion channels, and shuttle systems. (b) Mn is detoxified by Fpn at the plasma membrane or by its sequestration in the secretory system *via* the ZnT1 transporter or the $\text{Ca}^{2+}/\text{Mn}^{2+}$ ATPases SPCA1/2. ATP13A2 mediates sequestration of Mn in lysosomes. (c) Mn enhances ROS generation *via* Mn-catalyzed autoxidation of DA that involves the redox cycling of Mn^{2+} and Mn^{3+} and the generation of ROS and DA-o-quinones. (d) Mn accumulates in the mitochondria *via* the MCU and increases the accumulation of labile Fe. (e) Mn-induced neurotoxicity is linked to oxidative damage and mitochondrial dysfunction, and also to a decrease in Glu uptake by the EAATs in astrocytes (arrow in EAAT indicates reversal of Glu transport) leading to excitotoxicity in neurons, as well as the induction of inflammation. DA, dopamine; EAAT, excitatory amino acid transporter; Glu, glutamate; MCU, mitochondrial Ca^{2+} uniporter; Mn, manganese; ROS, reactive oxygen species; SPCA, secretory pathway Ca^{2+} ATPase; ZnT, zinc transporter.

substrates for nucleophilic attack (*e.g.*, carbonic anhydrase, where Zn^{2+} catalyzes the hydration of CO_2 to form bicarbonate [HCO_3^-]) (138). Enzymes with Zn-dependent catalytic activity control many cellular processes, including DNA synthesis and brain development. Zn also plays an important role in cell signaling associated with development and learning. In the brain, Zn is highly concentrated in the hippocampus and cortex (304).

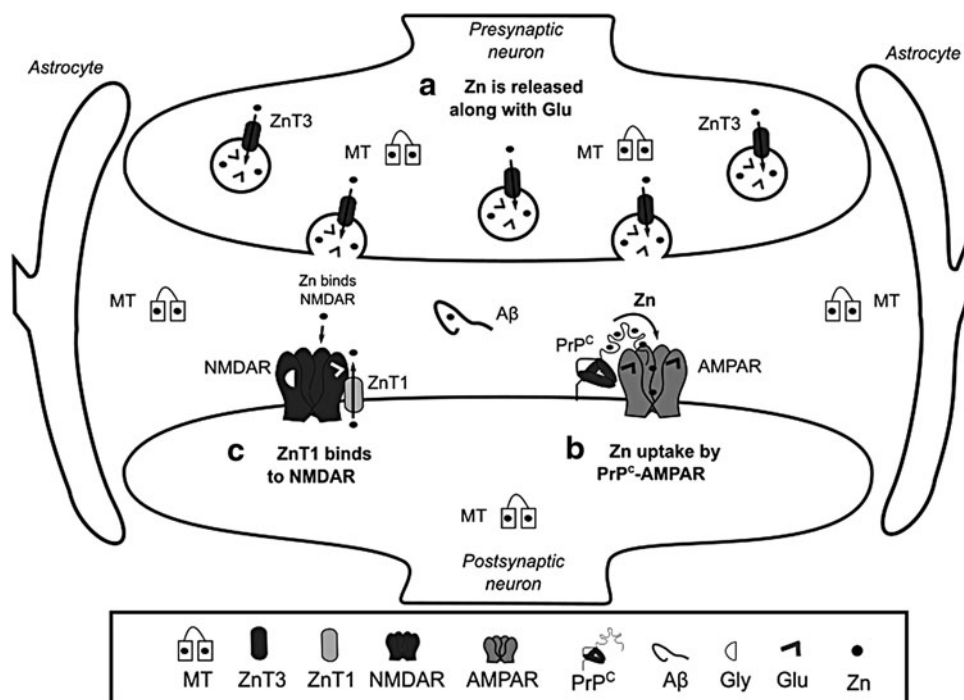
The key players in Zn homeostasis are the ZIP transporters that mediate Zn uptake into the cytosol, the zinc transporters (ZnT) that participate in Zn efflux, and MTs involved in Zn chelation. ZIP1 is expressed in astrocytes and microglia (303). In neurons Zn uptake is mediated by, voltage-gated Ca^{2+} channels, ZIP1 and 3 transporters, as well as Ca^{2+} and the Zn^{2+} permeable α -amino-3-hydroxy-5-methyl-4-isoxazolepropionate receptor (AMPA) (146, 278, 335). Interestingly, Zn has been reported to be transported into postsynaptic neurons through a complex formed by PrP^C, which is evolutionary linked to ZIP proteins, and the AMPAR (Fig. 6b) (373). ZnT1 is expressed in astrocytes, microglia, and oligodendrocytes, and its expression levels are directly modulated by Zn (247). Hypoxia decreases the levels of ZnT1 in astrocytes inducing the accumulation of cytosolic Zn (257). At the postsynaptic density, the ZnT1 transporter interacts with NMDAR and this complex is regulated during synaptic plasticity (Fig. 6c) (222, 373).

Cytosolic Zn is distributed to different organelles, including synaptic vesicles, Golgi, ER, and mitochondria. Similarly, Zn uptake by these organelles is performed by ZnTs, while ZIPs participate in Zn efflux into the cytosol (155). Zn

modulates cellular signaling pathways and acts as a neuro-modulator. ZnT3 participates in the transport and accumulation of Zn within synaptic vesicles of glutamatergic terminals (Fig. 6a) (125). During synaptic transmission, Zn is released with Glu, where it inhibits the activity of NMDAR and AMPAR (9, 154), modulating neuronal excitability and long-term synaptic plasticity (long-term potentiation [LTP] and long-term depression). In addition, Zn regulates the activation of the tropomyosin kinase receptor B (TrkB) (304). A metabotropic Zn-sensing receptor (mZnR) has also been reported (31). At the synapse, Zn can also bind to MTs, A β , and PrP^C (Figs. 3c and 6).

Although Zn^{2+} is a nonredox-active metal ion, it participates in redox signaling through several mechanisms. MTs bind about a fifth of the intracellular Zn with a stoichiometry of 1:7. MTs and proteins containing Zn-finger domains use Cys residues to bind to Zn^{2+} ions. Zn coordination stabilizes the reduced state of Cys thiol groups preventing their oxidation and subsequent formation of disulfide bonds. Transcription of MTs is induced by oxidative stress *via* Nrf2, and by heavy metal exposure *via* metal-response elements (MREs). MREs are recognized by the Zn-finger domain containing protein metal-responsive transcription factor-1 (MTF1, also known as MRE-binding transcription factor-1 or metal regulatory transcription factor-1). MTF1 senses Zn levels. Furthermore, *via* Zn displacement from MTs or Cys oxidation, MTF1 also senses heavy metal toxicity (Cd) and oxidative stress. In addition to MTs, MTF1 regulates the transcription of a number of genes involved in redox homeostasis and metal ion detoxification, including Zn transporters,

FIG. 6. Zn trafficking at the synapse. (a) Zn ions are loaded into neurotransmitter vesicles by ZnT3, and are coreleased with Glu during synaptic transmission. In the synaptic cleft, Zn can bind to MT, A β , PrP^C, and NMDAR. (b) Recently, two links between synaptic activity and Zn transport have been discovered: Zn uptake by the postsynaptic terminal occurs via a complex formed by PrP^C and AMPAR, (c) while ZnT1 interacts with NMDAR and modulates spine morphology. AMPAR, α -amino-3-hydroxy-5-methyl-4-isoxazolepropionate receptor.



Fr, Fpn, ATP7(A/B), Trx, selenoproteins, and γ -glutamylcysteine ligase (GCL), a rate-limiting enzyme in GSH synthesis (119). The role of MTF1 in brain function and redox homeostasis is unclear. MTF1 has been shown to regulate the expression of β -synuclein (220), which is thought to act as a negative regulator of its homologue α -synuclein (126). Interestingly, deletion of *MTF1* induces lethality in Parkin-deficient flies (*Drosophila melanogaster*) (293).

Altered Zn levels have been reported to promote neuronal injury. Upon Cys oxidation, Zn is released from MTs (255). Cellular acidification also releases intracellular Zn in neurons (159). In a recent report, AMPA-induced oligodendrocyte cell death was shown to be linked to Zn mobilization from mitochondria and protein-bound pools that were mediated by cytosolic acidification, independently from ROS (213). Exposure of mitochondria to Zn promotes increased ROS formation (305). While no specific mitochondrial Zn transporter(s) has been identified, potential candidates include the MCU, ZIP8, and Znt2 transporters (30, 199, 307). Zn also increases NOX-derived ROS formation and NOS activity (162). High extracellular Zn enhances microglia activation and ROS formation (130). Zn deficiency also induces oxidative stress via a reduction in the activity of SOD1 (378), and an impairment in the transcriptional regulation of GCL by Nrf2 (253).

Alterations in Zn homeostasis are associated to neurodegenerative diseases. Serum levels of Zn are decreased in AD patients (358), while Zn is enriched in A β plaques (364). Furthermore, a decrease in the levels of Znt3 and MT-III (390) is found in AD. Importantly, the predominant localization of A β plaques in Zn-containing glutamatergic synapses might explain why they are primarily found in the neocortex (304). Zn promotes a rapid, but reversible, aggregation of A β that is different to the aggregation of A β or A β -Cu complexes (25). Zn also reduces the toxicity of Cu-induced A β aggregates (214). *ZnT3* knockout increases

soluble A β in transgenic APP mice corroborating the role of extracellular Zn in plaque formation (172).

Elevated Zn levels have been found in the SN of PD brains (74), while reduced levels of Zn in serum and plasma have been linked to an increased risk for PD (80). Zn has been shown to potentiate the toxicity of DA as well (189). Furthermore, Zn chelation reduces the toxicity of mitochondrial PD-related toxins (310). Recently, ATP13A2 was identified as a Zn transporter localized to multivesicular bodies. Loss of function mutations of *ATP13A2* induces alterations in Zn homeostasis and mitochondrial dysfunction (259).

Xenobiotic Metals

Measurable concentrations of xenobiotic metals with no physiological functions are present in humans (Supplementary Table S1) (103). In addition, environmental or occupational exposures to xenobiotic metals may take place by inhalation, ingestion, or skin penetration and are often linked to the development of toxicity and pathological conditions (Supplementary Table S1). Metals can reach the CNS from the vascular lumen affecting neuronal and glial function. Metals hijack transport systems of essential metals to pass through the BBB and enter neuronal tissues (molecular mimicry). Metal toxicity is largely attributable to their physicochemical properties, which mediate their interference with cellular biochemical systems, including redox-related processes (205, 355).

Environmental or occupational exposure to xenobiotic metals has been reported to contribute to neuronal dysfunction (cognitive, motor, and behavioral) and in some cases, neurodegeneration. However, the mechanisms involved are largely unclear. We next review the sources and routes of exposure to xenobiotic metals; the metabolic pathways involved in their transport and activation, and the mechanisms by which they alter cellular redox balance to promote neurotoxicity.

Arsenic

As is naturally present in air, water, and soil and is the 20th most abundant element in the earth's crust and 12th in the human body. This metal is named inorganic As (iAs) when found combined with other elements such as O₂, chlorine (Cl), and sulfur (S). Combined with carbon (C) and hydrogen (H) is referred to as organic As. In the environment and within the human body, iAs predominantly exists in two oxidation states: arsenite +3 (or AsIII, found as arsenic trioxide [As₂O₃], sodium arsenite [NaAsO₂], and arsenic trichloride [AsCl₃]), and arsenate +5 (or AsV found as arsenic pentoxide [As₂O₅], arsenic acid [H₃AsO₄], and arsenates [PbHAsO₄, Ca₃(AsO₄)₂]).

iAs has been widely used as a therapeutic agent to treat leukemia. Currently, iAs compounds are predominantly used in pesticides, herbicides, cotton desiccants, wood preservatives, alloys for batteries, and in semiconductors and light-emitting diodes. Millions of individuals are currently exposed to iAs across the world due to natural groundwater contamination. Fish and crustaceans contain very high levels of organic arsenobetaine but no toxicity has been reported *in vivo* (382). The concentration of iAs in natural surface and groundwater is generally about 1 parts per billion (ppb) of water but it may exceed 1000 ppb in contaminated areas or where iAs soil levels are high (118, 200) (Supplementary Table S1).

While As is considered a carcinogen, in the brain, acute exposure to iAs can induce encephalopathy, with symptoms such as confusion, hallucinations, reduced memory, and emotional lability (exaggerated changes in mood or affect). Long-term exposure to lower levels of iAs can lead to the development of peripheral neuropathies.

There are reports of neurobehavioral alterations (cognitive function, verbal abilities, long-term memory, and motor skills) in children exposed to As concentrations ranging from 5 to 50 ppb in water, in Bangladesh (260), Mexico (45, 287), and in the United States (370). Although scientific understanding of the developmental neurotoxicity of As is still evolving, epidemiological and toxicological studies clearly show that As is a developmental neurotoxicant that affects intellectual function. Moreover, exposures even below current safety guidelines are associated with decrements in full-scale intelligence quotient (IQ) and memory (90, 347). Evidence in experimental models, including mice, rats, *Caenorhabditis elegans* (worm), and *Danio rerio* (zebrafish), has replicated many of the observations in humans supporting the notion that As can lead to cognitive, locomotor, and neurological impairment (85). Gestational exposure to NaAsO₂ leads to a significant iAs accumulation in the mice offspring's brain (280). As neurotoxicity has been linked to changes in neurotransmitter metabolism and synaptic transmission (85, 276, 280). However, the mechanisms involved remain unclear.

In the environment, oxygenated water contains iAsV species, while in reducing environments iAsIII species are prevalent. iAsV enters cells through phosphate transporters to be subsequently reduced to iAsIII, while iAsIII is transported *via* aqua(glycerol)porins (AQP), organic anion transporters, and glucose transporters (GLUT) (Fig. 7a) (44, 187, 348). Once in the cytoplasm, iAsIII is methylated by different mechanisms. Oxidative methylation (Fig. 7b) is

mediated by arsenite methyltransferase (AS3MT) that uses S-adenosylmethionine (AdoMet) as a cosubstrate. AS3MT methylates iAsIII to monomethylarsonic acid or arsonate (MMAV) that is reduced to monomethylarsonous acid (MMAIII) before being methylated again to dimethylarsinic acid (DMAV) by AS3MT (353, 372). Finally, DMAV is reduced generating dimethylarsonous acid (DMAIII). The reduction of pentavalent arsenicals (iAsV, MMAV, and DMAV) in this pathway is now well recognized to be mediated by the Trx/TR system, but GSH seems to increase the methylation rates by an unknown mechanism (76).

Developmental exposure to As alters the methylation patterns of genes involved in neuroplasticity likely due to changes in AdoMet, but its long-term implications are unclear (207). Recent *in vivo* studies demonstrated that the alterations in synaptic plasticity (LTP), memory, and learning induced by gestational exposure to iAs were associated with an increase in extracellular Glu levels and downregulation of AMPAR subunits (244).

As methylation *via* the GSH conjugation mechanism is based on the formation of GSH complexes with iAsIII resulting in arsenic triglutathione [As(SG)₃] (Fig. 7c). Conjugation of iAsIII with GSH has been proposed to occur nonenzymatically, but enzymatically as well by the activity of glutathione-S transferases (GST isoforms GSTO1, GSTM1, or GSTP1) (173, 372). As(GS)₃ is subsequently methylated by AS3MT to form monomethylarsinic diglutathione [MMA(GS)₂] and then again to generate dimethylarsinic GSH [DMA(GS)]. At low GSH levels, As(GS) conjugates are hydrolyzed and then oxidized to generate MMAV and DMAV (372). A third mechanism for iAsIII methylation has been recently proposed, where instead of As(GS) conjugate formation, iAsIII binds to protein-Cys (thiol) and is methylated while still being conjugated to proteins (Fig. 7d). This hypothesis is supported by the preferential binding of iAsIII to protein-Cys when compared to GSH (284).

Methylated (and maybe unmethylated) As metabolites are exported through the multidrug resistance proteins (MRP1, MRP2, or MRP4) (173, 317, 388) (Fig. 7e). AS3MT is ubiquitously expressed in all brain regions, and animal studies have shown that the iAs that crosses the BBB is methylated and accumulated across the brain, with the highest accumulation observed in the pituitary gland (297). Interestingly, knockout mouse for P-glycoprotein accumulates more As in the brain (183). Endothelial cells and astrocytes feet surrounding capillaries are the first barrier of detoxification of xenobiotics entering from the circulation. We (unpublished data) and others have observed that the resistance of astrocytes to iAsIII is mediated by MRPs (332).

iAs generates ROS and dimethylarsenic or peroxy radicals that in turn lead to lipid peroxidation and the accumulation of oxidized by-products (MDA and HNE) (Fig. 7f). Importantly, MMAIII and DMAIII are proposed to be more potent toxicants than iAsIII due to their increased ability to generate radicals (392). Oxidative stress has been reported in brain regions of different animal models and in neurons and glial cell cultures exposed to As compounds (48, 107, 108, 243, 394).

Mitochondria have been proposed to be a primary source for ROS formation by iAs (Fig. 7g) (97, 150). Chronic iAs exposure generates mitochondrial oxidative stress in the rat brain by impairment of mitochondrial complexes I, II, and IV

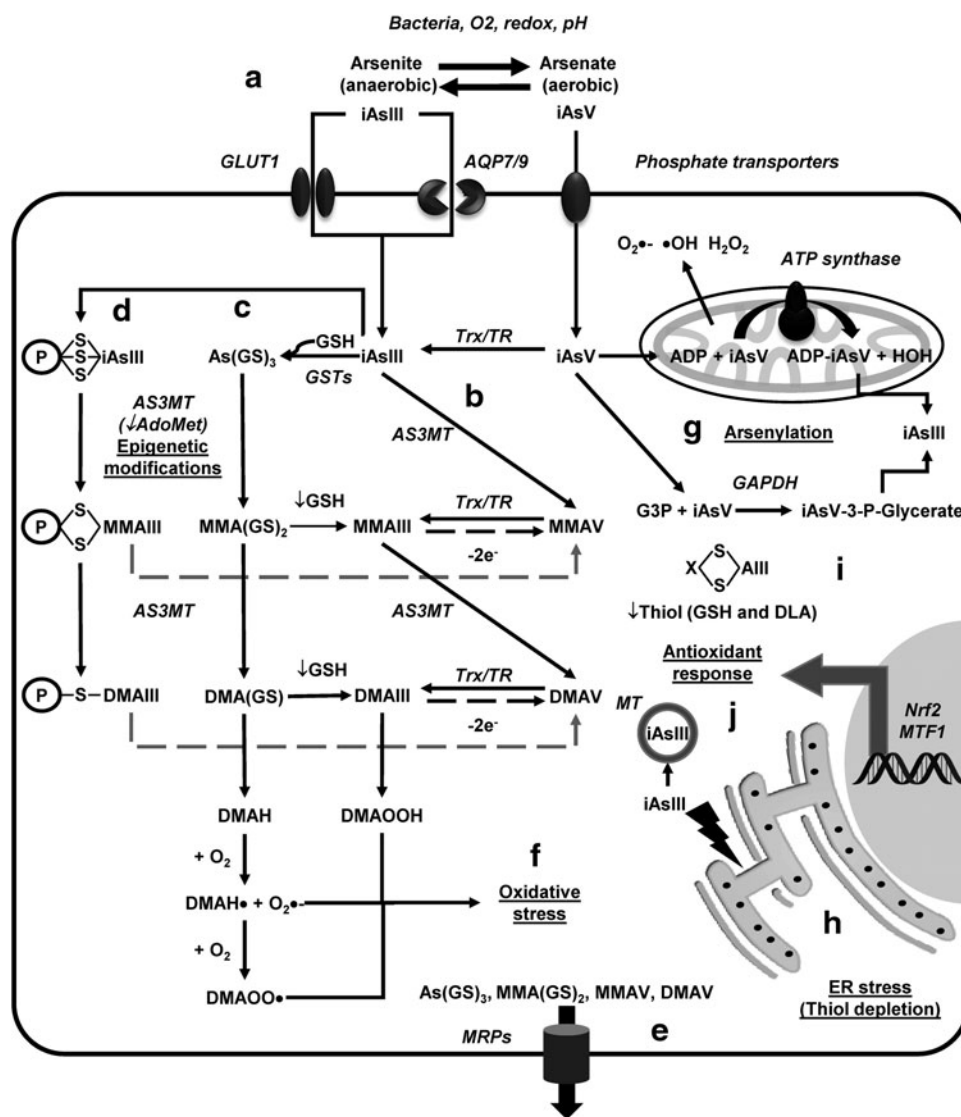


FIG. 7. iAs biochemistry, redox signaling, and neurotoxicity. (a) iAsIII species prevail in anaerobic conditions, while aerobic environments contain iAsV species. iAsIII enters cells through AQP9/7 and GLUT, while iAsV uses phosphate transporters. Three mechanisms for iAs methylation have been proposed. (b) Oxidative methylation refers to the progressive reduction of AsV to AsIII metabolites by the Trx/TR system and the oxidative methylation of AsIII species by AS3MT. (c) The GSH conjugation pathway is based on the formation of As(GS)₃ by the GSTs. As(GS)₃ is subsequently methylated by AS3MT. (d) The protein thiol conjugation mechanism suggests that instead of As(GS)₃, iAsIII binds to protein thiols and is methylated while still being conjugated to proteins. iAsIII methylation is likely to alter epigenetic signatures by alterations in AdoMet, a cosubstrate required for methyl group transfer. (e) Methylated metabolites and GSH/protein complexes are highly reactive and are exported through the MRPs. (f) DMA(GS) can form DMAH and react with O₂ to form DMAH• and DMAOO•. DMAIII also reacts with O₂ and forms DMAOOH. These reactive species lead to lipid peroxidation and protein carbonylation (oxidative stress). (g) AsV can replace phosphate in several metabolic pathways (arsenylation) where the end product is reduced AsIII. AsV binds ADP *via* ATP-synthase and uncouples oxidative phosphorylation and ATP formation in the mitochondria. AsV is also arsenylated by GAPDH to generate iAsV-3-P-glycerate from G3P. (h) iAsIII toxicity generates ER stress likely *via* thiol depletion and alterations in redox balance. (i) AsIII binds to thiol containing molecules (coenzyme A, DLA, GSH) and protein thiols inactivating enzymatic function. (j) iAsIII toxicity is counteracted by Nrf2 and MTF1 that mediate the transcriptional-dependent induction of antioxidant systems and MTs. AdoMet, S-adenosylmethionine; AQP, aqua(glycerol)porin; AS3MT, arsenite methyltransferase; AsIII, arsenite +3; As(SG)₃, arsenic triglutathione; AsV, arsenate +5; DLA, dihydroliipoamide; DMA(GS), dimethylarsinic GSH; DMAH, dimethylarsine; DMAH•, DMAH radical; DMAIII, dimethylarsinous acid; DMAOO•, dimethylarsine peroxy radical; DMAOOH, dimethylated arsenic peroxide; G3P, glyceraldehyde 3-phosphate; GAPDH, glyceraldehyde 3-phosphate dehydrogenase; GLUT, glucose transporters; GSTs, glutathione-S transferases; iAs, inorganic As; iAsV-3-P-glycerate, 1-arsenato-3-phospho-D-glycerate; MRPs, multidrug resistance proteins; MTF1, metal-responsive transcription factor-1; Nrf2, nuclear factor erythroid-2-related factor 2; O₂, molecular oxygen; Trx, thioredoxin.

activities followed by increased ROS generation, lipid peroxidation, and protein carbonylation (275). Mitochondrial pyruvate dehydrogenase is also directly inhibited by iAs (136). In addition, iAs reduces the levels of peroxisome proliferator-activated receptor gamma coactivator 1-alpha (PGC-1 α), downstream targets Nrf1 and Nrf2, and the mitochondrial transcription factor A (TFAM) decreasing mitochondrial biogenesis (274). ER stress has also been shown to contribute to iAs toxicity, but the mechanisms involved remain unclear (Fig. 7h) (182).

iAs toxicity has also been attributed to the ability of AsV to replace phosphate in several metabolic pathways (arsenylation) where the end product is the reduction of AsV to AsIII, because the arsenylated by-product is more readily reduced than AsV itself (Fig. 7g). AsV uncouples oxidative phosphorylation and ATP formation in the mitochondria by binding to ADP *via* ATP synthase. Replacement of phosphate in glycolysis also impairs carbon flux and ATP production. Reaction of AsV with glucose generates glucose 6-arsenate, an analog of glucose 6-phosphate that is suggested to act as an inhibitor of hexokinase. AsV is also arsenylated by glyceraldehyde 3-phosphate dehydrogenase (GAPDH) to produce the unstable product 1-arsenato-3-phospho-D-glycerate (iAsV-3-P-glycerate). Purine nucleoside phosphorylase, glycogen phosphorylase, and mitochondrial ornithine carbamoyl transferase (OCT) have also been shown to arsenylate AsV (139, 245, 340). Thus, energy failure, alterations in central carbon metabolism, and mitochondrial dysfunction are consequences of AsV toxicity.

AsIII binds to thiol containing molecules (coenzyme A, GSH, and dihydrolipoamide also known as dihydrolipoic acid [DLA]) and protein-Cys thiols inactivating enzyme function (Fig. 7d, i). AsIII has higher affinity for dithiols than monothiols as demonstrated by the transfer of AsIII from the GSH-adduct to 2,3-dimercaptosuccinic acid (DMSA) a sulfhydryl-containing metal chelator used to treat heavy metal toxicity. In addition, AsIII conjugated with GSH has the ability to bind protein thiols, which highlights the importance of detoxification of GSH-As adducts from the cell (230). Dithiol molecules such as the cofactor DLA and dithiol oxidoreductases Trxs, Trx reductase (TrxR), Prxs (except for monothiol Prx6), Grx, and GR, as well as proteins with adjacent Cys (MT), have been reported to avidly bind AsIII (Fig. 7d, j) (50, 279, 311, 393, 397). In addition to binding AsIII, Zn finger domains have been shown to be oxidized upon As binding (396). Binding of AsIII to DLA (Fig. 7i) is expected to interfere with the TCA cycle and energy production as DLA is a cofactor for the pyruvate dehydrogenase and 2-oxoglutarate dehydrogenase complexes that catalyze the synthesis of acetyl-CoA and succinyl-CoA, respectively. DLA reverses protein oxidation and loss of protein-SHs in the brains of rats exposed to high levels of iAs (82, 296, 315, 316).

As activates the cystine/Glu exchanger system (xCT) in microglia to increase extracellular Glu levels (320), while in astrocytes it decreases the expression levels and activity of GS and Glu transporters (GLAST/excitatory amino acid transporter (EAAT) 1 and GLT-1/EAAT2) (48, 395). Importantly, these effects were linked to an increase in GSH levels and Nrf2 activity (Fig. 7i), but not oxidative stress (48). Accordingly, activation of Nrf2 by As seems to involve a noncanonical pathway where inhibition of autop-

hagy leads to the accumulation of the ubiquitin-binding protein/adaptor p62 that sequesters Keap1 (169). iAsIII toxicity is also counteracted by the transcriptional regulation of MT *via* MTF1 (Fig. 7j) (129).

Lead

Inorganic Pb remains one of the most studied toxic elements due to several reasons. To begin with, human contact with Pb started very early in human civilization, and its toxic effects were also known since then. However, more importantly, Pb is neurotoxic leading to lower IQ even at lower doses than those recommended by the World Health Organization (10 ppb in drinking water). Human exposure to Pb not only occurs occupationally but also environmentally. The presence of Pb in the environment has multiple sources such as gasoline, industrial processes, paint, water pipes, and solder in canned food. It is present in air, household dust, soil, water, and food (Supplementary Table S1). Environmental Pb levels have fortunately decreased, especially in those countries where the Pb addition to gasoline and paints was banned. This prohibition was enforced after several studies associated the presence of high blood levels of Pb with impaired or diminished cognitive functions. Epidemiological studies have clearly shown that exposure to Pb in early stages of development is associated with significant deficits in neurobehavioral performance, including lower IQ, attention deficits, and aggressiveness later in life. Despite all the enforced restrictions, Pb contamination is still a major public health concern. For example, in November 2000 in Washington DC, there was a "lead drinking water crisis" triggered by a change in the disinfectant used to clean the water, this contamination affected hundreds of kids for 3 years. The health consequences of the recent crisis of Pb-contaminated water in Flint Michigan (United States, 2015) are still to be revealed in the future (68, 84, 124, 298).

Inhalation and ingestion of Pb and Pb-containing particles or products are the main routes of Pb entry into the body. Young children are especially vulnerable because they show higher gastrointestinal absorption than adults. Inhaled Pb particles are quickly absorbed in alveoli and distributed to other organs through the circulation. Thus, blood lead levels (BLL) are reliable biomarkers of exposure and risk. However, BLL do not reflect the total Pb body burden because Pb is absorbed in bones where it can be stored for several years (68). Currently, the acceptable BLL for children is lower than 10 $\mu\text{g}/\text{dl}$ (0.48 μM) (49, 376), but due to the devastating effects that might occur later in life, there is a consensus to recommend efficient surveillance methods for children protection to reduce BLL to the lowest possible level (141). Pb binds with high affinity to erythrocytes' δ -aminolevulinic acid dehydratase (ALAD) that catalyzes the second step in the porphyrin and heme biosynthetic pathway, causing the accumulation of aminolevulinic acid (ALA) in both plasma and urine, which is used as a biomarker of exposure (248).

Pb can cross the BBB and cell membrane because of its ability to mimic Ca^{2+} and Fe^{2+} ions (Fig. 8a) (205, 298). In children, due to a more permeable BBB and a lower bone storage capacity for Pb, the amount of Pb passing into the nervous system is higher than in adults. The highest accumulation of Pb has been reported in the hippocampus, amygdala (116), and choroids plexus (201). The PNS may

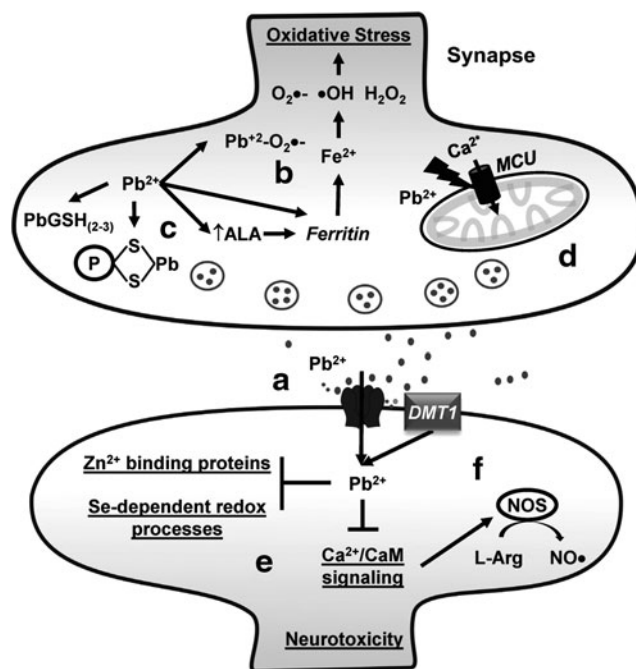


FIG. 8. Pb neurotoxicity and synaptic signaling. (a) Pb enters cells due to its ability to mimic Ca²⁺ and Fe²⁺ ions. (b) Inside the cell, Pb can trigger oxidative stress by different mechanisms, including the accumulation of ALA; the formation of Pb²⁺-O₂^{•-} complexes; and the release of labile Fe²⁺ from Ft. (c) Pb can also form complexes with GSH [Pb(GSH₂₋₃)] and bind to protein thiols. (d) Mitochondrial dysfunction and oxidative stress induced by Pb have also been linked to MCU. (e) Pb can displace Zn²⁺ and impair Zn²⁺ binding protein function. Furthermore, Pb interferes with the Se-dependent redox processes. (f) Finally, Pb can prevent CaM activation and thus reduce NOS activity. ALA, aminolevulinic acid; CaM, Ca²⁺/calmodulin; NOS, nitric oxide synthase; O₂^{•-}, superoxide anion radical; Pb, lead; Se, selenium.

accumulate considerably more Pb than the CNS. Animals chronically exposed to Pb had impaired dendritic spines and synapse formation (306). Developmental exposure to Pb impacts the prefrontal cerebral cortex, hippocampus, and cerebellum regions, which can lead to neurological disorders, mental retardation, behavioral problems, and nerve damage (242). Early life exposure to Pb has also been linked to neurodegenerative diseases such as AD and PD (62, 209).

The mechanisms of Pb toxicity include the ability of Pb to bind SH groups of proteins Cys and to mimic or compete with Ca²⁺, Fe²⁺, and Zn²⁺ (Fig. 8b, c, e, f) (99, 283). Zn deficiency increases the toxicity of Pb (4). The generation of oxidative damage by Pb *in vitro* and *in vivo* suggests that ROS also participate in Pb toxicity. For example, Pb acetate induces the opening of the mitochondrial permeability transition pore in human neuroblastoma SH-SY5Y cells *via* ROS (384). Pb can form a Pb²⁺-O₂^{•-} complex with higher oxidizing capacity than O₂^{•-} (3). In addition, accumulated δ -ALA by Pb-induced ALAD inhibition can be subsequently oxidized to generate O₂^{•-}, •OH, and H₂O₂. Pb *per se* has been reported to stimulate Fe²⁺-initiated lipid peroxidation (Fig. 8b) (337). Early postnatal exposure of rats to Pb leads to a higher accumulation of oxidative DNA damage in the cerebral cortical tissue when compared with aged controls or aged mice exposed acutely to Pb (36).

Perinatal exposure to Pb acetate inhibits the activity of brain acid and alkaline phosphatases, catalase, acetylcholinesterase, and ATPases (12). Similar observations have been made for the activities/levels of SOD1, GPX1, and GPX4 in the hippocampus, and for mitochondrial SOD2 and GSH,

both in the cortex and hippocampus (19). Antioxidant nutrients such as vitamin E, vitamin C, vitamin B6, β -carotene, and DLA, as well as metal chelators such as DMSA, or replenishment of displaced metals has been shown to be beneficial against Pb-induced oxidative stress in the brain (98, 236, 256, 258, 277, 367). Diet supplementation with Zn and Se, which participates in the regulation of the GSH and Trx antioxidant systems, can effectively outcompete Pb binding to Zn- and Se-binding sites (Fig. 8e) (135).

Pb interferes with and disrupts Ca²⁺ signaling and homeostasis leading to excitotoxicity. In addition, Glu potentiates Pb-induced cell death in PC12 cells (267). Recently, oxidative stress induced by Pb has been shown to be linked to changes in the levels of MCU (Fig. 8d) (383). Other important intracellular targets of Pb in the brain are both neural NOS and endothelial NOS due to an impairment in their Ca²⁺/calmodulin (CaM)-dependent activation (Fig. 8f) (241). Importantly, Pb amplifies Glu-induced oxidative stress in a Ca²⁺-independent manner, but neither Ca²⁺ nor ROS seem to be essential for the enhanced cytotoxicity of combined exposure to Glu and Pb (191, 238).

Mercury

Hg is a transition metal that exists as elemental, inorganic, and organic Hg (Fig. 9a). Hg is ubiquitously found in the environment as sulfide compounds generated from volcanic activity and erosion, or released by anthropogenic sources such as fuel combustion, waste disposal, and industrial activities (Supplementary Table S1). Elemental or metallic Hg

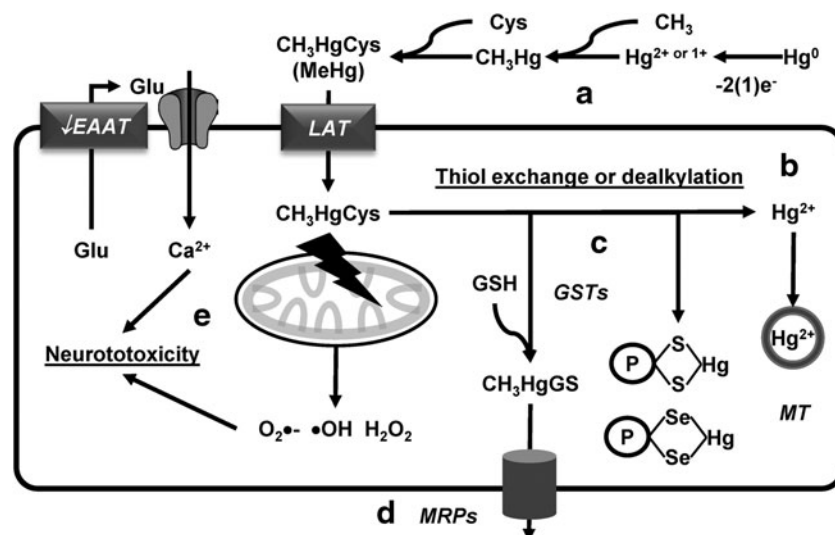


FIG. 9. Hg redox-related toxicity mechanisms in brain cells. (a) Hg species are highly transformed (oxidation or methylation) before they are absorbed into organisms. MeHg and EtHg form a complex with Cys (CH_3HgCys) and are transported across the membranes *via* LAT. (b) MeHg suffers dealkylation and thiol exchange to form Hg^{2+} . (c) Thiol exchange reactions of CH_3HgCys complexes with low-molecular-weight thiols (GSH) and protein thiols alter the cellular redox balance. MeHg also has a strong affinity for selenol groups. (d) GSH-MeHg adduct formation (CH_3HgGS) is catalyzed by the GSTs and adducts are detoxified by MRPs. (e) MeHg also induces mitochondrial ROS and energy failure. Furthermore, MeHg-induced neurotoxicity has been ascribed to a reduction in Glu uptake by astrocytes *via* EAAT triggering neuronal excitotoxicity (arrow in EAAT indicates reversal of Glu transport). Cys, cysteine; Hg, mercury; EtHg, ethylmercury; Hg^{1+} , inorganic mercurous ions; Hg^{2+} , inorganic mercuric ions; LAT, L-type neutral amino acid transporter; MeHg, methylmercury.

(Hg^0) used in thermometers and amalgams is primarily absorbed *via* inhalation, while inorganic mercury (Hg^{1+} or $2+$) used in medicine and everyday life products is partially absorbed through the gut. Organic Hg (ethylmercury [EtHg or C_2H_5Hg] and methylmercury [MeHg or CH_3Hg]) is originated from atmospheric sources that are deposited in water body surfaces to be biomethylated and magnified in the food chain (Fig. 9a). Around 95% of MeHg is absorbed by the gastrointestinal tract making it the most toxic Hg species. Neurotoxic signs of Hg intoxication are vast and include ataxia, dizziness, insomnia, speech impairment, arthralgia, cognitive and behavioral changes, seizures, fatigue, and sensory disruption. While there has been an association between Hg exposure and neurodegeneration or autism, the neurological effects of chronic exposure to Hg are largely unclear. However, research has clearly demonstrated that Hg impairs neuronal development, communication, and myelination (89).

Most of the studies regarding the mechanisms involved in Hg neurotoxicity have been done using MeHg. MeHg and EtHg are potent electrophiles that form a complex with Cys (CH_3HgCys or C_2H_5HgCys), and then transported across the BBB and into neuronal cells *via* L-type neutral amino acid transporters (LAT1 and 2) (Fig. 9a) (318, 385, 399).

A high percentage of Hg in individuals intoxicated with MeHg is found as Hg^{2+} , suggesting that dealkylation of MeHg is an important mechanism for the high persistence of Hg in the brain (Fig. 9b) (72). Thiol exchange from CH_3HgCys to low-molecular-weight thiols (GSH) and protein thiols has been proposed to be central mechanisms by which MeHg induces GSH depletion, inhibition of thiol-dependent antioxidant systems, and alters the activity or

function of proteins with redox-sensitive Cys (signaling proteins, metabolic enzymes, neurotransmitter receptors, and transporters) (Fig. 9c) (89). MeHg also has a stronger affinity for selenol groups (selenohydril groups in selenocysteines) compared with thiol groups. As such, selenoproteins are important targets for direct electrophilic attack of MeHg or transfer from thiol adducts (CH_3HgCys , CH_3HgGS , or CH_3HgPS [protein-Cys adduct]) (Fig. 9c) (104, 221). GSTs have been proposed to mediate the formation of CH_3HgGS adducts, which are detoxified by MRP1-mediated transport (Fig. 9d). GSH synthesis, GST, and MRP1 levels are regulated transcriptionally by the Nrf2 antioxidant system (152, 292, 349).

MeHg induces mitochondrial ROS and energy failure (175, 233). Neurotoxicity induced by MeHg has also been ascribed to its inhibitory effect on Glu uptake by astrocytes, triggering neuronal excitotoxicity (15, 235) (Fig. 9e).

Hg^0 absorbed through the respiratory tract is oxidized to inorganic mercurous (Hg^{1+}) and mercuric ions (Hg^{2+}) (Fig. 9a). While inorganic Hg ions have limited access to the CNS, they induce profound neurotoxic alterations that seem to be mediated as well by their binding to thiol groups (89). Accordingly, MTs exert protective effects against Hg^0 -induced neurotoxicity (387) (Fig. 9b).

Other xenobiotic metals

Aluminum. Al is one of the most abundant metals in the earth's crust (8.1%). Al has a plethora of uses in industry and manufacturing, as well as in food additives. As such, human exposure is primarily originated from food and drinking water. Importantly, pharmaceuticals have higher levels of Al

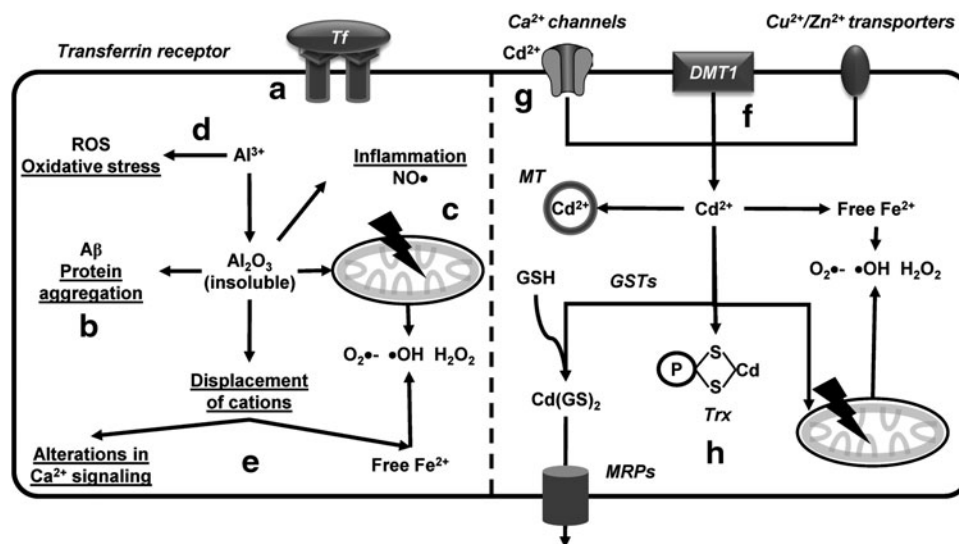


FIG. 10. Mechanisms of Al and Cd neurotoxicity. (a) Al is bound to Tf, which mediates its transport across the BBB *via* the Tf, but a Tf-independent Al transport also exists. (b) Al promotes A β aggregation and (c) mitochondrial dysfunction triggering neuroinflammation and NO \bullet formation. (d) Al³⁺ has been proposed to react with H₂O₂ to produce AlO₂^{•-} that can promote oxidative damage. (e) Al toxicity is also related to its ability to displace other metals (Ca or Fe). (f) Cd transport across membranes is through molecular mimicry *via* several transporters such as Cu/Zn transporters, DMT1, and Ca²⁺-channels. (g) High concentrations of Cd can block Ca²⁺ currents as well. (h) Cd toxicity is linked to its ability to bind thiol containing molecules such as GSH, and protein-Cys (Trx and MT), as well as the displacement of redox-active metals such as Fe. Cd detoxification of cells is facilitated by the activity of GST and the detoxification of GSH-Cd adducts *via* MRPs. Al, aluminum; AlO₂^{•-}, aluminum superoxide radicals; Ca, calcium; Cd, cadmium.

compared to food. Occupational exposures to Al are related to mining, processing, and welding (359) (Supplementary Table S1). While Al is poorly absorbed in the gut, inhalation mediates direct transfer to the brain *via* the olfactory system (341). Importantly, ~85% of Al in blood is bound to Tf, which is considered to mediate its transport across the BBB (Fig. 10a) (288), but Tf-independent Al transport also exists. Interestingly, monocarboxylate and xCT transporters have also been proposed to mediate the transport of Al-citrate complexes (240, 386). Acute Al toxicity occurs as a result of occupational exposure or chronic renal failure and is known to target the nervous system. Al is neurotoxic in animal models triggering the accumulation of neurofibrillary tangles and impairment of cognitive, behavioral, and motor functions. Al promotes A β aggregation, mitochondrial dysfunction, and triggers neuroinflammation (Fig. 10b, c) (24, 202, 309). However, conflicting results exist regarding the association of Al with any human disease, including AD (37, 359, 377).

Al exists primarily in a trivalent state (Al³⁺). While Al has no redox capacity, Al toxicity is linked to oxidative damage. Al³⁺ has been proposed to react with H₂O₂ to produce Al superoxide radicals (AlO₂^{•-}) that can deplete mitochondrial Fe and promote generation of ROS (Fig. 10d) (166). However, because of its high reactivity, Al is primarily found forming insoluble oxides whose toxicity seem to be related with the displacement of other biological cations (Ca²⁺, Fe²⁺, or Mg²⁺) (Fig. 10e) (377).

Cadmium. Cd is a transition metal whose use in industry has increased dramatically in the recent years. Cd is widely used in batteries, alloys, and pigments, and produced as a by-

product from the extraction of other metals from ores. Food is the major source for Cd exposure as both animals and plants accumulate high levels of Cd. Inhalation is the prevalent route of Cd exposure due to industrial emissions and occupational activities (tobacco) (Supplementary Table S1). Cd neurotoxicity seems to occur only during development, before complete BBB formation, or in association with BBB dysfunction. Cd transport across membranes is thought to be mediated by molecular mimicry *via* several transporters and receptors for essential metals such as Cu/Zn transporters, DMT1, and Ca²⁺-channels (Fig. 10f) (117, 131, 174, 224, 339). Importantly, at high concentrations, Cd also has the ability to block Ca²⁺ currents (Fig. 10g).

Cd toxicity is linked to its ability to bind thiol containing molecules such as GSH, and protein-Cys (Trxs and MT) and as a consequence, displacement of redox-active metals and mitochondrial and metabolic dysfunction (Fig. 10h) (363). Cd detoxification of cells is facilitated by the activity of GST and the detoxification of GSH-Cd adducts *via* MRPs (Fig. 10h) (181, 339). Accordingly, resistance to Cd-toxicity is directly associated with the Nrf2-mediated antioxidant response (366).

Conclusions and Perspectives

Metals are important for brain function and human health. Thus, alterations in their content and/or distribution are expected to exert neurotoxicity. Both alterations in the homeostasis of essential metals and environmental exposure to xenobiotic metals can have silent chronic effects leading to neurodegeneration and neurological dysfunction (behavioral and cognitive alterations). The neurotoxic mechanisms by

which metals impact neuronal or glial function are starting to become elucidated.

In this review, we have summarized how essential metals are trafficked in the brain. It is interesting to note that the mechanisms involved in metal transport and homeostasis are strongly linked to the chemical properties of each metal ion, while their coordination chemistry preferences also allow them to share some metal transport routes. For instance, Cu and Fe go through several redox cycles during their transport, while Mn and Zn remain in the same oxidation state. Metal trafficking in the cell is tightly regulated to control the high reactivity toward O₂ of some metal ions, such as Fe²⁺ and Cu⁺, or to keep in solution otherwise insoluble species such as Cu⁺ and Fe³⁺. Moreover, while similar O-based ligand coordination preferences of Mn²⁺, Fe²⁺, and Fe³⁺ allow them to share some transport systems, the affinity of Zn²⁺ and Cu⁺ for Cys ligands makes MTs important players in their homeostasis. In fact, a close relationship between cellular redox environment and metal transport has been recently demonstrated for Cu and Fe (Figs. 1D and 4C).

Since metal trafficking machineries in neurons and astrocytes resemble those of other extensively studied mammalian cells, our understanding of intracellular metal homeostasis has advanced significantly. In contrast, metal trafficking at the synapse and the role in neuromodulation have just begun to be revealed, and point to a close inter-relationship among Zn, Cu, and Fe. For example, the synaptic release of Zn and Glu ultimately leads to the activation of NMDAR and the activation of signaling pathways that lead to postsynaptic Cu release and Fe uptake. Clearly, the close interplay between these metals at the synapse must play an important role in neuromodulation, while disturbed metal trafficking in neurodegenerative diseases would impact these processes.

We have also illustrated the differential alteration of metal homeostasis that occurs in neurodegenerative disorders as well as the key metal-protein interactions that might be involved in protein aggregation and metal-mediated oxidative damage. Understanding these interactions at the molecular level will shed light into the role of essential metals in neurodegenerative diseases.

Metals are transported across the BBB and into brain cells by selective transport systems for essential metals, while xenobiotic metals hijack those transporters *via* molecular mimicry (Supplementary Fig. S1a). The ability of xenobiotic metals to be transported and/or react with cellular targets is strongly determined by their metabolism *via* reduction/oxidation reactions, methylation, or adduct formation (Mt0 → Mt1 → Mt2). Phase II enzyme systems, GSH/GST, and MTs are essential for the detoxification of metals (Supplementary Fig. S1b). Metals induce or enhance ROS and RNS formation leading to oxidative stress (Supplementary Fig. S1c). While oxidative damage is one of the causative mechanisms involved in cellular damage induced by metals, it is now clear that other redox processes participate as well. The intrinsic reactivity of xenobiotic metals with thiol and selenol groups (Supplementary Fig. S1d) and their capacity to displace essential metals (Supplementary Fig. S1e) are also central to their capacity to promote energy failure (mitochondrial dysfunction), protein damage/aggregation, and metabolic alterations that challenge neuro/glial function and survival and trigger excitotoxic and inflammatory processes (Supplementary Fig. S1f). Cells have the capacity to respond by

activating redox- or metal-dependent transcriptional regulation of antioxidant and anti-inflammatory responses (Supplementary Fig. S1g).

The aim of this review was to provide an integrated overview of the recent advances regarding how dysfunctional metal ion homeostasis of essential metals and exposure to xenobiotic metals alter cellular function to promote chronic neurodegeneration and neurotoxicity. Although the mechanisms involved in these processes are still being elucidated, the studies highlighted here are a starting point toward a better understanding of the pathological consequences of alterations in metal ion homeostasis, justifying the need of further studies regarding their metabolism and its impact on cellular homeostasis, function, and survival.

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Abbreviations Used

$A\beta$ = amyloid beta
 AD = Alzheimer's disease
 AdoMet = S-adenosylmethionine
 Al = aluminum
 ALA = aminolevulinic acid
 ALAD = δ -aminolevulinic acid dehydratase
 $AlO_2^{\bullet-}$ = aluminum superoxide radicals
 ALS = amyotrophic lateral sclerosis
 AMPAR = α -amino-3-hydroxy-5-methyl-4-isoxazolepropionate receptor
 APP = amyloid precursor protein
 AQP = aqua(glycerol)porin
 As = arsenic
 AS3MT = arsenite methyltransferase
 AsIII = arsenite +3
 As(SG)₃ = arsenic triglutathione
 AsV = arsenate +5
 Atox1 = antioxidant protein 1
 ATP7A = ATPase copper transporting alpha
 ATP7B = ATPase copper transporting beta
 BBB = blood-brain barrier
 BLL = blood lead levels
 Ca = calcium
 CaM = Ca^{2+} /calmodulin
 CCS1 = copper chaperone for superoxide dismutase 1
 Cd = cadmium
 CNS = central nervous system
 CO₂ = carbon dioxide
 COX = cytochrome C oxidase
 Cp = ceruloplasmin
 CSF = cerebrospinal fluid
 CTR1 = copper transporter 1
 Cu = copper
 Cu⁺ = cuprous ion
 Cu²⁺ = cupric ion
 Cys = cysteine
 DA = dopamine
 Dcytb = duodenal cytochrome b
 Dexas1 = Ras-related dexamethasone induced 1
 DLA = dihydroliipoamide or dihydroliipoic acid
 DMAIII = dimethylarsinous acid
 DMAV = dimethylarsinic acid
 DMSA = 2,3-dimercaptosuccinic acid
 DMT1 = divalent metal transporter 1
 EAAT = excitatory amino acid transporter
 ER = endoplasmic reticulum
 EtHg or C₂H₅Hg = ethylmercury
 FBXL5 = F-box/LRR-repeat protein
 Fe = iron
 Fe²⁺ = ferrous
 Fe³⁺ = ferric
 Fpn = ferroportin
 Ft = ferritin
 FtMt = mitochondrial ferritin
 GAPDH = glyceraldehyde 3-phosphate dehydrogenase
 GCL = γ -glutamate-cysteine ligase
 Glu = glutamate
 GLUT = glucose transporters

GPX = glutathione peroxidases
 GR = glutathione reductase
 Grxs = glutaredoxins
 GS = glutamine synthetase
 GSH = glutathione
 GSSG = glutathione disulfide
 GST = glutathione-S transferase
 H₂O₂ = hydrogen peroxide
 Hb = hemoglobin
 HD = Huntington's disease
 H-Ft = heavy-ferritin
 Hg = mercury
 Hg⁰ = elemental or metallic Hg
 Hg¹⁺ = inorganic mercurous ions
 Hg²⁺ = inorganic mercuric ions
 HNE = 4-hydroxy-2-nonenal
 HO = heme oxygenase
 Hp = hephaestin
 Htt = huntingtin
 iAs = inorganic As
 iAsV-3-P-glycerate = 1-arsenato-3-phospho-Dglycerate
 IDP = intrinsically disordered protein
 IQ = intelligence quotient
 IRP = iron regulatory proteins
 K = potassium
 Keap1 = kelch-like ECH-associated protein 1
 LAT = L-type neutral amino acid transporter
 L-Ft = light-ferritin
 LTP = long-term potentiation
 MCU = mitochondrial Ca^{2+} uniporter
 MDA = malondialdehyde
 MeHg or CH₃Hg = methylmercury
 Met = methionine
 Mfrn2 = mitoferrin-2
 Mg = magnesium
 MMAIII = monomethylarsonous acid
 MMAV = monomethylarsonic acid or arsonate
 Mn = manganese
 MRE = metal response element
 mRNA = messenger RNA
 MRPs = multidrug resistance proteins
 MT = metallothionein
 MTF1 = metal-responsive transcription factor-1
 Na = sodium
 NaAsO₂ = sodium arsenite
 NADPH = nicotinamide adenine dinucleotide phosphate
 NBIA = neurodegeneration with brain iron accumulation
 NKB = neurokinin B
 NMDAR = glutamate/N-methyl-D-aspartate receptor
 NO[•] = nitric oxide
 NOS = nitric oxide synthase
 NOX = NADPH oxidases
 Nrf1/2 = nuclear factor erythroid-2-related factor 1 or 2
 O₂ = molecular oxygen
 O₂^{•-} = superoxide anion radical
 •OH = hydroxyl radical
 OONO⁻ = peroxynitrite

Abbreviations Used (Cont.)

Pb = lead
 PD = Parkinson's disease
 PNS = peripheral nervous system
 polyQ = polyglutamine
 ppb = parts per billion
 PrP^C = cellular prion protein
 Prxs = peroxiredoxins
 RNS = reactive nitrogen species
 ROS = reactive oxygen species
 RyR = ryanodine receptor
 S = sulfur
 sAPP = soluble fragment of APP
 SCO = cytochrome c oxidase assembly
 protein
 sCp = soluble ceruloplasmin
 SDR2 = stromal cell-derived receptor
 Se = selenium

SLC30A10/hZnT1 = solute carrier family 30 member
 10 or human Zn transporter 1
 SN = substantia nigra
 SOD = superoxide dismutase
 SPCA = secretory pathway Ca²⁺ ATPase
 Steap2 = six transmembrane epithelial antigen
 of the prostate 2
 Tf = transferrin
 TfR = transferrin receptor
 Trxs = thioredoxins
 Tyr = tyrosine
 xCT = cystine/glutamate exchanger system
 ZIP = Zrt-(Zn-regulated transporter)-
 or Irt (Fe-regulated
 transporter)-like proteins
 Zn = zinc
 ZnT = zinc transporters



mTOR/AMPK signaling in the brain: Cell metabolism, proteostasis and survival

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Abstract

The mechanistic (or mammalian) target of rapamycin (mTOR) and the adenosine monophosphate-activated protein kinase (AMPK) regulate cell survival and metabolism in response to diverse stimuli such as variations in amino acid content, changes in cellular bioenergetics, oxygen levels, neurotrophic factors and xenobiotics. This Opinion paper aims to discuss the current state of knowledge regarding how mTOR and AMPK regulate the metabolism and survival of brain cells and the close interrelationship between both signaling cascades. It is now clear that both mTOR and AMPK pathways regulate cellular homeostasis at multiple levels. Studies so far demonstrate that dysregulation in these two pathways is associated with neuronal injury, degeneration and neurotoxicity, but the mechanisms involved remain unclear. Most of the work so far has been focused on their antagonistic regulation of autophagy, but recent findings highlight that changes in protein synthesis, metabolism and mitochondrial function are likely to play a role in the regulatory effects of both mTOR and AMPK on neuronal health. Understanding their role and relationship between these two master regulators of cell metabolism is crucial for future therapeutic approaches to counteract alterations in cell metabolism and survival in brain injury and disease.

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Mammalian target of rapamycin, Adenosine monophosphate-activated protein kinase, Autophagy, Mitochondria, Glycolysis, Cell death, Nutrient deprivation, Energy failure.

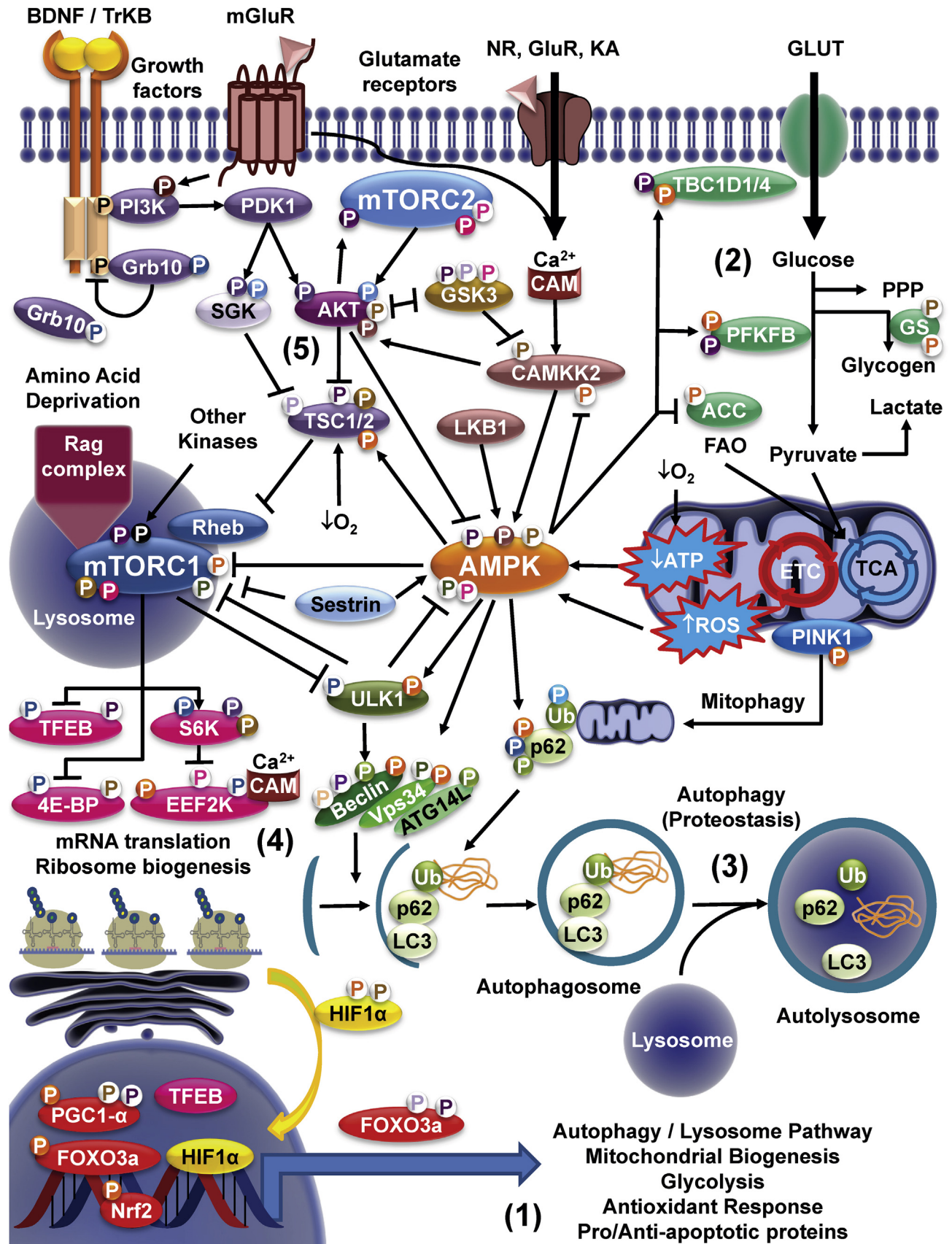
1. Introduction

The mechanistic (or mammalian) target of rapamycin (mTOR) and the adenosine monophosphate-activated protein kinase (AMPK) regulate cell growth and metabolism incorporating signals triggered by different stimuli such as variations in the amino acid content, changes in cellular bioenergetics, activation of hormone and growth factor signaling and stress such as oxidative stress, hypoxia or DNA damage. In the brain, AMPK and mTOR signaling are regulated by neurotransmitters and neurotrophin signals. mTOR and AMPK are considered master regulators of cell metabolism. Their activation is directly linked to the regulation of cellular metabolism (mitochondria homeostasis and central carbon metabolism), growth (protein synthesis) and survival (autophagy and cell death pathways). This Opinion paper aims to discuss the current state of knowledge regarding how mTOR and AMPK regulate brain metabolism and survival upon stress and more importantly, the close interrelationship between both signaling molecules (Figure 1 and Supplementary Table 1).

2. mTOR signaling in brief and its role in regulating cell metabolism

mTOR is a serine (Ser)/threonine (Thr) protein kinase in the PI3K-related kinase (PIKK) family that forms the catalytic subunit of two distinct protein complexes, known as mTOR Complex 1 (mTORC1) and 2 (mTORC2) (Figure 1). Together with mTOR, the mammalian lethal with sec13 protein 8 (mLST8 or GβL), and the inhibitory DEP domain containing mTOR-interacting protein (DEPTOR) are common to both mTORC1 and mTORC2. Phosphorylation of DEPTOR by mTOR and other kinases promotes its degradation and activation of mTORCs. mLST8 seems to stabilize the kinase activation loop of mTOR but is dispensable for its activity. mTORC1 also includes the regulator-associated protein of the mammalian target of rapamycin (Raptor or RPTOR) and the proline-rich protein kinase B (PKB or AKT) substrate of 40 kDa (PRAS40). Because the interaction between Raptor and mTOR is essential for the stability of the mTORC1 and the recruitment of substrates, post-translational modifications in Raptor (phosphorylation, cleavage or ubiquitination) regulate mTORC1 activity. PRAS40 inhibits the substrate recruitment sites of mTORC1 and its phosphorylation by AKT and mTOR promotes its dissociation from the complex. On the other hand, the mTORC2 includes the rapamycin-insensitive

Figure 1



companion of mTOR (Rictor), the mammalian stress-activated MAP kinase-interacting protein 1 (mSIN1), and the proteins observed with rictor 1 and 2 (PROTOR 1 and 2) [1].

The GTP binding protein Ras homolog enriched in brain (Rheb) is an obligate upstream activator of mTORC1 by growth factors and amino acids (Figure 1). Activation of the phosphoinositide-3 kinase (PI3K)/AKT pathway by growth factor receptors inactivates the tuberous sclerosis complex (TSC), a key negative regulator of mTORC1 (Figure 1). TSC is a heterotrimeric complex comprising TSC1, TSC2, and the Tre-2/BUB2/cdc 1 domain family member TBC1D7. TSC2 acts as a GTPase-activating protein (GAP) to inactivate Rheb (Rheb-GDP). mTORC1 activation requires its localization in the lysosomal surface which is regulated by amino acid and nutrient sensing via Rag GTPases (Figure 1). Induction of protein synthesis by mTORC1 involves the phosphorylation of the ribosomal protein S6 kinase beta-1 (S6K) and the eukaryotic translation initiation factor 4 (eIF4E)-binding protein (4E-BP) (Figure 1) [1]. Glucose metabolism has been reported to be regulated by translational regulation of the hypoxia-inducible factor 1-alpha (HIF1 α) via 4E-BP and mTORC1 [2]. Via 4E-BP, mTORC1 signaling regulates mitochondrial biogenesis as well [3]. mTORC1 also regulates lipid and nucleotide synthesis through the sterol responsive element binding protein (SREBP) transcription factors and the activation of the transcription factor 4 (ATF4), respectively [4,5].

mTORC2 primarily controls proliferation and survival via the activation of members of the AGC family of protein kinases such as PKC that regulate cytoskeletal remodeling and cell migration. AKT phosphorylation by mTORC2 is required for AKT-mediated phosphorylation of specific substrates such as Forkhead box O1/3a (FOXO1/3a). Reciprocally, AKT has been shown to phosphorylate mSIN1 enhancing mTORC2 kinase activity (Figure 1) [1]. mTORC2 has also been demonstrated to regulate glucose and amino acid metabolism [6–9]. Interestingly, a recent report also demonstrates that mTORC2 has the ability to act as a tyrosine kinase [10].

3. AMPK signaling in brief and its role in regulating cell metabolism

AMPK is a Ser/Thr kinase that exists as a heterotrimer composed of catalytic α and regulatory β and γ subunits.

In the absence of AMP, the autoinhibitory domain of AMPK α maintains the kinase in an inactive conformation. Upon ATP consumption, AMP/ADP directly bind to AMPK γ promoting the phosphorylation of AMPK α . The liver kinase B1 (LKB1) is the primary kinase that phosphorylates AMPK α at Thr172 (Figure 1). LKB1 is found constitutively active as a complex with Ste20-related adaptor (STRAD) and mouse protein 25 (MO25). A second binding event of AMP/ADP to AMPK γ induces a conformational change that protects AMPK α from dephosphorylation. AMPK α phosphorylation has also been reported to be mediated by the Ca²⁺/calmodulin (CaM)-dependent protein kinase kinase 2 or β (CAMKK2 or β), independent from changes in the AMP/ADP:ATP ratio (Figure 1), or by the transforming growth factor β -activated kinase 1 (TAK-1). AMP binding also upregulates allosterically the activation of AMPK [11]. A new study shows that AMPK can also be activated by sensing the absence of fructose-1,6-bisphosphate (FBP), via aldolase even if there are not changes in the AMP/ADP:ATP ratio [12].

AMPK activation inhibits anabolic processes, stimulates catabolism, and restores ATP levels. Several conditions that either interfere with ATP synthesis or promote ATP consumption can lead to AMPK activation. At least 60 targets have been identified as substrates of AMPK [11], but we will focus on those involved in the regulation of cell metabolism (Figure 1). AMPK inhibits the *de novo* synthesis of fatty acids and activates lipid catabolism via phosphorylation and inactivation of acetyl-CoA carboxylase (ACC). AMPK also stimulates glucose uptake via the phosphorylation of the TBC domain family members TBC1D1 and TBC1D4, and the thioredoxin-interacting protein (TXNIP) that results in an increased plasma membrane translocation of glucose transporters (GLUT) (Figure 1). Phosphorylation of the bifunctional 6-phosphofructo-2-kinase (PFKFB) by AMPK increases fructose-2,6-bisphosphate (F2,6P2), which activates glycolysis via phosphofructokinase 1 (PFK1) (Figure 1). In contrast, glycogen synthesis and hexosamine biosynthesis are inhibited by the phosphorylation and inhibition of glycogen synthase (GS) (Figure 1) and glutamine-fructose-6-phosphate aminotransferase-1 (GFPT1), respectively [13]. AMPK also promotes mitochondrial biogenesis by phosphorylation of the peroxisome proliferator-activated receptor gamma coactivator 1-alpha (PGC-1 α) increasing its transcriptional activity (Figure 1) [14,15], as well as mitochondrial fission and autophagy (mitophagy) [16].

mTOR/AMPK signaling crosstalk. Signaling by mTOR and AMPK integrates changes in the cellular environment linked to growth factors, nutrient, oxygen and energy availability, excitotoxicity (Ca²⁺) and stress (oxidative stress). Five major points of convergence include: 1) the transcriptional regulation of genes linked to cell survival/death, proteostasis, redox balance and bioenergetics; 2) metabolism (central carbon and bioenergetics); 3) autophagy; 4) mRNA translation and protein synthesis; and 5) cell survival and growth (AKT). Arrows indicate activation. Stop lines indicate inhibition. Phosphorylation events (P) are color coded according to the kinase involved in phosphorylating the corresponding targeted protein. White background/colored "P" highlights an inhibitory effect; Colored background/white P highlights an stimulatory (activation) effect. A detailed explanation of the phosphorylation events is included in the [Supplementary Table 1](#). Additional crosstalk might involve indirect pathways not highlighted in this figure.

Remarkably, it was recently shown that reactive oxygen species (ROS) activate AMPK triggering a PGC-1 α -dependent antioxidant response that limits mitochondrial ROS production [17]. Thus, AMPK is a central regulator of mitochondrial homeostasis.

4. mTOR-AMPK signaling crosstalk

While both mTOR and AMPK seem to regulate different pathways, there are key hubs of crosstalk where both converge to regulate homeostatic processes such as autophagy and cell metabolism (Figure 1 and Supplementary Table 1). AMPK utilizes different targets to effectively suppress mTORC1. AMPK inhibits mTORC1 both directly, through the phosphorylation of Raptor [18], as well as indirectly through the phosphorylation and activation of TSC2 [19]. Reciprocally, mTORC1 signaling has also been proposed to regulate AMPK as S6K has been found to phosphorylate and inhibit AMPK (Figure 1) [20].

Autophagy is a proteostatic quality control mechanism that requires the formation of double membraned autophagosomes that deliver cargo for degradation within the lysosome (Figure 1). The unc-51-like autophagy activating kinase 1 (ULK1 or autophagy related protein 1 [Atg 1]) drives autophagosome formation and mTORC1 suppresses autophagy by phosphorylating ULK1. In contrast, phosphorylation of ULK1 by AMPK promotes autophagy (Figure 1). Therefore, the relative activity of mTORC1 and AMPK in different cellular contexts largely determines the extent of autophagy induction [21].

Another point of convergence is that of protein synthesis. Within the polypeptide translation elongation cycle, translocation of the ribosome is mediated by the elongation factor eEF2. eEF2 is inhibited by phosphorylation catalyzed by the eEF2 kinase (EEF2K). EEF2K is phosphorylated and inactivated by S6K [22] and mTORC1 [23], while its phosphorylation by AMPK promotes its activation (Figure 1) [24].

FOXO3a is a transcription factor involved in cell survival whose phosphorylation by AKT is well known to inhibit its activity [25], suggesting a possible feedback loop via mTORC2 [26]. FOXO3a has been reported to inhibit mTORC1 activity via transcriptional control of TSC1 [27]. In contrast, phosphorylation by AMPK activates FOXO3a (Figure 1) [28].

5. mTOR/AMPK signaling in the brain

mTOR signaling is involved in a myriad of processes regulating neurodevelopment (proliferation and differentiation) and brain function (neuronal plasticity). Thus, a dysregulation of mTOR signaling has been linked to a number of brain disorders associated with neuronal dysfunction and cell death such as

neurodegeneration, epilepsy, autism and neuro-behavioral alterations. Previous reviews have focused on the role of mTOR in brain function and development [29,30]. In the brain, energy-sensing neurons in the hypothalamus are involved in the regulation of organismal energy balance via AMPK signaling. AMPK activation in the hypothalamus is modulated by energy-related signals associated with food intake (fasting and feeding), energy expenditure (ATP levels), and body weight (hormones and adipokines) [31]. We will next focus on the role of mTOR and AMPK on the survival and cell death of neuro-glial cells and their link with metabolic stress in brain disorders.

Brain metabolism is characterized by a complex interplay between different cell types. Glucose is the primary energy substrate of the brain and it has been proposed to be metabolized through two complementary metabolic pathways in neurons and astrocytes. Neurons seem to predominantly metabolize glucose through the pentose phosphate pathway (PPP) to produce the NADPH necessary for antioxidant defense. On the other hand, astrocytes primarily metabolize glucose through glycolysis to produce lactate, where lactate is shuttled as an energy substrate for oxidative phosphorylation in neurons [32–34]. While this astrocyte-neuron lactate shuttle seems to act at rest, recent studies demonstrate that during energy-demanding conditions neurons have the capacity to upregulate glycolysis [35].

Very little is known regarding the role of AMPK and mTOR signaling in normal brain metabolism. Deletion of Raptor (mTORC1) or Rictor (mTORC2) in the brain leads to neurodevelopmental alterations [36–39], but whether these effects are related to alterations in cell metabolism is unclear. AMPK α 2 has been reported to be the predominant catalytic subunit in neurons and astrocytes in the brain and spinal cord [40]. In contrast to mTOR, AMPK is not necessary for neuronal development or survival, but its hyperactivation impairs axon growth via inhibition of mTORC1 [41]. Indeed, AMPK antagonizes mTOR activation by neurotrophic factors in neurons [42]. We have observed that mTOR signaling is important for astrocytes' basal glycolytic rate (*unpublished results*). A recent report demonstrates that in astrocytes and neural stem cells, the G-protein-coupled receptor kinase-interacting protein 1 (GIT1) is a novel mTOR-binding protein within a unique mTOR complex regulated by AKT that lacks both Raptor and Rictor [43]. In glioblastoma cells, mTORC2 upregulates glycolysis via acetylation of FOXO1 and FOXO3a transcription factors that result in an increase in c-Myc levels [9].

6. mTOR/AMPK in neuronal cell death and survival

Because mTOR and AMPK are essential for the regulation of metabolism, their dysregulation can generate

negative effects leading to cell death and disease progression. There are different examples where the activation of these two kinases has been found to be protective against pathological processes, but it has also been shown that when dysregulated, their increased activity can be detrimental.

6.1. Brain ischemia and injury

In ischemic brain injury both mTOR and AMPK have been involved in cell death progression. While this topic has been studied extensively [44,45], there are still contradictory results depending on the experimental conditions used. mTOR protects against neuronal cell death induced by ischemic insults [46,47]. Similarly, mTOR signaling via S6K protects astrocytes from oxygen-glucose deprivation (OGD) and mice from middle artery occlusion (MCAO) [48]. Pharmacological inhibition of AMPK also protects against MCAO and OGD [49], but the opposite is found using a global cerebral ischemia model [50]. AMPK α 2, but not α 1 knockout in mice has been shown to protect against MCAO [51]. Interestingly, a dual role of AMPK in neuronal cell death in neonatal hypoxia has been reported, where inhibition of AMPK prior to OGD increases cell death, while its CAMKK2-dependent activation upon OGD mediates neuronal cell loss [52]. In traumatic brain injury (TBI), pharmacological stimulation of AMPK ameliorates cognitive dysfunction [53].

Accumulation of extracellular excitatory amino acids (glutamate) is a common event associated with neuronal cell death during ischemia and TBI. Neuronal cell death induced by glutamate excitotoxicity has been reported to involve AMPK activation and an increase in the levels of the pro-apoptotic Bim protein [54]. In contrast, AMPK-dependent translocation of GLUT3 and glucose availability have been reported to exert a protective effect against glutamate excitotoxicity [55]. mTOR signaling has also been proposed to contribute to the toxicity of glutamate receptor agonists (N-methyl-D-aspartate [NMDA]) [56]. Finally, mTOR is well known to mediate axon regeneration and myelination after injury [57–59].

6.2. Neurodegeneration

Both mTOR and AMPK signaling modulate the progression of different neurodegenerative disorders, but whether their activation is beneficial or detrimental remains unclear. One of the main mechanisms related to neurodegeneration where mTOR and AMPK converge is autophagy, which can exert protective effects via the degradation of misfolded, damaged or toxic proteins, as well as damaged organelles [60]. Parkinson's (PD) and Huntington's disease (HD) are characterized by the accumulation of intracellular misfolded protein aggregates. Because mTORC1 represses autophagy, its inhibition may represent a plausible therapeutic approach

[61]. Accordingly, rapamycin has been reported to protect neurons by promoting the clearance of protein aggregates of α -synuclein and mutant huntingtin which are found in PD and HD, respectively [62,63]. A decrease in mTOR activity also reduces Alzheimer's disease-like amyloid- β (A β) deposits *in vivo* via the induction of autophagy [64]. Interestingly, while mTOR activation is usually considered to inhibit autophagy, autophagy can be induced by mTOR stimulation as well. Accordingly, activation of mTORC1 signaling in the striatum stimulates autophagy, ameliorates mitochondrial dysfunction and protects against HD [65]. In contrast, hyperactivation of mTORC1 via striatum-specific deletion of TSC1 has been reported to accelerate motor dysfunction and mortality in HD mouse models [66].

Most of the studies regarding mTOR signaling and neurodegeneration have been focused on autophagy, but alterations in cell metabolism or proteostasis should also be considered. A recent report demonstrates that inhibition of mTOR with rapamycin preserves neuronal ATP levels upon inhibition of mitochondrial function, and this effect was associated with a decrease in energy consumption by protein synthesis [67]. Rapamycin-induced activation of 4E-BP reduces dopaminergic degeneration and mitochondrial dysfunction linked to mutations in the PD-related genes PTEN-induced putative kinase 1 (PINK1) and E3 ubiquitin-protein ligase Parkin [68]. Conversely, the PD-related protein leucine-rich repeat kinase 2 (LRRK2) has been shown to phosphorylate and inactivate 4E-BP [69]. Together these results suggest that alterations in protein translation via the mTORC1-4E-BP signaling pathway might be involved in PD.

Contradicting results have been reported regarding the role of AMPK in dopaminergic cell death associated with PD [70–75]. A protective role for AMPK against mitochondrial dysfunction and toxicity induced by Parkin-, LRRK2-mutations, α -synuclein and mitochondrial toxins has been previously reported [70–72]. In contrast, other reports have shown that AMPK mediates dopaminergic cell death induced by 6-hydroxydopamine (6-OHDA) and mitochondrial toxins as well [73,74]. We have demonstrated that AMPK exerts a protective effect against cell death induced by paraquat (PQ), a pesticide recognized as an important PD risk factor, in combination with the PD-related gene α -synuclein [76]. Importantly, while autophagy protects against PQ toxicity [77], the modulatory effects of AMPK seem to be primarily related to metabolic dysfunction [76].

The intracellular aggregation of abnormally and hyperphosphorylated tau proteins generates neurofibrillary tangles (NFTs), the pathological hallmark of neurodegenerative diseases commonly known as tauopathies. A β oligomers activate AMPK via CAMKK2, which mediates

tau phosphorylation and neurotoxicity [78,79]. In contrast, short-term exposure to A β oligomers transiently decrease AMPK activity and result in a reduction in glucose transport [80]. In HD, activation of AMPK mediates neuronal atrophy downstream of oxidative stress [81]. However, another study suggests that AMPK activation at early stages of HD pathology protects against neuronal cell death [82].

6.3. Environmental neurotoxicity

Exposure to environmental toxicants is a risk factor for neurodegenerative, cognitive and neurodevelopmental disorders. Arsenic, a natural occurring neurotoxicant, impairs neurite outgrowth by inhibition of AMPK signaling [83]. We have observed that AMPK signaling and autophagy promote apoptotic cell death in cortical astrocytes exposed to inorganic arsenic (*unpublished results*). Cadmium (Cd) neurotoxicity has been shown to be mediated via mTOR signaling [84]. Bisphenol-A (BPA), an endocrine disruptor released from the polycarbonate containers, activates AMPK while it down-regulates mTOR signaling, resulting in enhanced autophagy. AMPK signaling and autophagy were reported to exert a protective effect against BPA-induced neurotoxicity in hippocampal neurons [85]. In contrast, the neurotoxicity of tributyltin, a water organotin contaminant, has been linked to the activation of AMPK and excitotoxic glutamate release [84].

7. Conclusions and perspectives

It is now clear that both mTOR and AMPK pathways regulate cellular homeostasis at multiple levels. By continuously sensing the cellular energy and nutrient state mTOR and AMPK have the capacity to facilitate cellular adaptation to stress. In addition, Ca²⁺, growth factors and oxidative stress have the ability to activate mTOR and AMPK to regulate protein synthesis, autophagy and metabolism. We have aimed to discuss the current state of knowledge regarding how mTOR and AMPK regulate brain metabolism and survival upon stress and the close interrelationship between both signaling pathways. Studies so far have demonstrated that dysregulation in these two pathways is associated with neuronal cell death, but the mechanisms involved remain unclear. Most of the work has been focused on their convergence regulating proteostasis via autophagy, but recent findings highlight that changes in protein synthesis, metabolism and mitochondrial function are likely to play a role in the regulatory effects of mTOR and AMPK on neuronal health. While there is still controversy regarding whether AMPK and mTOR signaling can exert a neuroprotective or neurotoxic effect, some of these controversies might be addressed when considering: 1) the poor specificity of widely used pharmacological approaches to modulate their activity (rapamycin, torin 1, compound C, 5-Aminoimidazole-4-carboxamide ribonucleotide [AICAR] and others); and

2) the time and dose-dependent effect of modulating these signaling pathways. Understanding their roles and the relationship between these two master regulators of cell metabolism is crucial for future therapeutic approaches to counteract alterations in cell metabolism and survival during neuronal cell death and degeneration.

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Appendix A. Supplementary data

Supplementary data related to this article can be found at <https://doi.org/10.1016/j.cotox.2018.05.002>.

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mTOR/AMPK signaling in the brain: Cell metabolism, proteostasis and survival

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Supplementary Table 1. Effect of phosphorylation (depicted in Figure 1) on mTORC1-, mTORC2- and AMPK-dependent signaling pathways. Autophosphorylation sites are not included in this table

Target Protein (Alphabetical Order)	Kinase Involved and Phosphorylated Residues	Effect on the Target protein	References (Suppl)
ACC Acetyl-CoA carboxylase	<ul style="list-style-type: none"> • AMPK → Ser80, and Ser1201. Ser1216 does not play a regulatory role By PKA as well but effect is unclear 	Inhibition - Conformational changes leading to a decrease in the catalytic activity of ACC. ACC carboxylates acetyl-CoA to produce malonyl-CoA, a substrate of fatty acid biosynthesis.	[1,2]
AKT/PKB Protein kinase B	<ul style="list-style-type: none"> • PDK1 → Thr308 	Activation - Phosphorylation of the T-loop kinase domain in AKT.	[3]
	<ul style="list-style-type: none"> • CAMKK2/β → Thr308 		[4,5]
	<ul style="list-style-type: none"> • mTORC2 → Ser473 	Activation - Phosphorylation of the hydrophobic motif of AKT facilitates its interaction with PDK1. Might be dispensable for Akt activation under certain conditions.	[6-8]
	<ul style="list-style-type: none"> • mTORC2 → Thr450 	<i>Folding</i> - Thr450 is constitutively phosphorylated and is required for proper folding of AKT	[9,10]
	<ul style="list-style-type: none"> • GSK3 → Thr312 	Inhibition - Phosphorylation at the substrate binding site inhibits AKT activation	[11]
AMPK AMP-activated protein kinase Catalytic (α) and Regulatory (β or γ subunits)	<ul style="list-style-type: none"> • CDK2, TBK1, IKKε → Ser129, Ser137, Thr308, Ser 378, Ser473, Ser477, SerT479, Tyr? 	Activation - Different mechanisms, see references for details. <i>Not relevant for this review.</i>	[12]
	<ul style="list-style-type: none"> • LKB1 → αThr172 (Constitutive) 	Activation - Phosphorylation of the T-loop kinase domain in AMPK. AMPK activation switches on catabolic pathways that generate ATP while switching off biosynthetic pathways that consume it.	[13-16]
	<ul style="list-style-type: none"> • CaMKK2/β → αThr172 (Independent of nucleotide levels) 		[17-19]
	<ul style="list-style-type: none"> • ULK1 → β1Ser108 	Activation - Sensitizes AMPK to drugs/metabolites acting at the ADaM (allosteric drug and metabolism) site,	[20]

		independently of Thr172 phosphorylation.	
	• ULK1 → $\alpha\beta\gamma?$	Inhibition - Suppresses Thr172 phosphorylation and AMPK sensitivity to AMP via a negative feedback.	[21]
	• AKT → α 1Ser487	Inhibition - Inhibits subsequent phosphorylation of AMPK at Thr 172, and hence its activation.	[22,23]
	• GSK3 → α T479	Inhibition - Enhances the accessibility of the activation loop of the AMPK α subunit to phosphatases.	[24]
	• S6K → α Ser491	Inhibition - Reduces AMPK activity	[25]
ATG14L Autophagy-Related Protein 14-Like Protein	• ULK1 → Ser9	Activation - Regulates ATG14L-Vps34 lipid kinase	[26]
	• AMPK → Ser93 and Ser96	Activation - Promotes ATG14-dependent Beclin 1 activation.	[27]
	• AMPK → Thr 388	Activation - Autophagy induction via the regulation of Vps34-Beclin 1-ATG14 complex formation. Inhibition - Caspase 8-dependent cleavage.	[28] [29]
Beclin 1 Coiled-coil, moesin-like BCL2-interacting protein	• ULK1 → Ser14, Ser30 and Ser337	Activation - As a complex with VPS34, Beclin 1 increases VPS34 lipid kinase activity and promotes autophagy initiation.	[30,31]
	• AKT → Ser234 and Ser295	Inhibition - Sequesters Beclin 1 in a 14-3-3 / vimentin intermediate filament complex.	[32]
	• EGFR → Y229, Y233 and Y352	Inhibition - Decreased Beclin 1-associated VPS34 lipid kinase activity.	[33]
	• DAPK3, CAMKII and MAPKAPK2/3 (MK2/3) → Ser90	Activation - Different mechanisms, see references for details. <i>Not relevant for this review.</i>	[34-36]
CAMKK2/β Ca ²⁺ / CaM-dependent protein kinase kinase 2/β	• AMPK → Thr144		[37]
	• CDK5 → Ser137	Inhibition - Reduces autonomous, but not Ca ²⁺ / CaM-activated CaMKK2/β activity.	[38]
	• GSK3 → Ser129 and Ser133 (preceded by Ser137 phosphorylation by CDK5)		
	• mTORC1 → Thr37, Thr46, Ser65 and Thr70	Inhibition - Phosphorylation of Thr37 and Thr46 in 4E-BP serves as a priming event, which is followed by Thr 70 and Ser 65 phosphorylation. Phosphorylation of 4E-BP causes its release from eIF4E to allow cap-dependent protein translation.	[39,40] [41]
4E-BP Eukaryotic translation initiation factor binding protein	• GSK3 → Thr37 and Thr46		
	• p38, ERK, PIM2, ATM, CDK1 and LRRK2 → Thr37, Thr46, Ser65, Thr70 and Ser 112	Inhibition - See references for details. <i>Not relevant for this review.</i>	[42]

EEF2K Eukaryotic elongation factor 2 kinase	<ul style="list-style-type: none"> • AMPK → Ser398, Ser491 A similar mechanism might be involved in activation by PKA → Ser500 [43] 	Activation - Mechanism unknown but might be independent from changes in the sensitivity of EEF2K to Ca^{2+} / CaM. [44,45]
	<ul style="list-style-type: none"> • mTORC1 → Ser70, Ser78, Ser392 and Ser396 • GSK → Ser392 requires confirmation 	Inhibition - Phosphorylation of Ser 392 and Ser396 facilitates phosphorylation of Ser70 and Ser78 controlling the binding of Ca^{2+} / CaM to EEF2K. [46]
	<ul style="list-style-type: none"> • S6K and RSK1 → Ser366 	Inhibition - Decreases the sensitivity of EEF2K to activation by Ca^{2+} / CaM. Decreases eEF2 phosphorylation and inactivation by EEF2K. eEF2 mediates the translocation the mRNA-tRNA moiety on the ribosome at the elongation step. [47,48]
	<ul style="list-style-type: none"> • p38δ and ERK → Ser359 	Inhibition (p38 δ and ERK) and Activation (PKA) - See references for details. <i>Not relevant for this review.</i> [46,49]
FOXO3a The Forkhead Box O 3a	<ul style="list-style-type: none"> • AMPK → Thr179, Ser399, Ser413, Ser555, Ser588 and Ser626 	Activation - Increases FOXO3a DNA-binding and transcriptional activity. [50]
	<ul style="list-style-type: none"> • AKT and SGK → Thr 32, Ser253, Ser315 	Inhibition - Ser253 and Ser315 phosphorylation at the nuclear localization sequence (NLS) disrupt nuclear translocation and reveal the nuclear export signal (NES) of FOXO3a, respectively. [51,52]
	<ul style="list-style-type: none"> • ERK, p38, JNK, MST1, IKK, CK1, DYRK1A/B and LMTK3 → Ser7, Ser12, Ser209, Ser215, Ser231, Ser232, Ser284, Ser294, Ser318, Ser321, Ser325, Ser344, Ser425, Ser487, Ser574, Ser644 	Inhibition (ERK, p38, CK1 and IKK) and Activation (JNK, MST1 and LMTK3) - See references for details. <i>Not relevant for this review.</i> [53]
Grb10 Growth factor receptor-bound protein 10	<ul style="list-style-type: none"> • mTORC1 → Ser 501/503 	Activation - Promotes Grb10 stabilization leading to feedback inhibition of PI3K and ERK-MAPK pathways. [54,55]
		Inhibition - Promotes Grb10 dissociation from the receptor to interact with raptor, and thus suppresses mTORC1 signaling. [56]
GS Glycogen synthase	<ul style="list-style-type: none"> • GSK3 → Ser641, Ser645, Ser649 and Ser653 	Inhibition - Decrease in glycogenesis [57]
	<ul style="list-style-type: none"> • AMPK → Ser7 	[58,59]
	<ul style="list-style-type: none"> • PKA, PhK, CaMKII, CK2, DYRK, PASK, p38 → Ser10, Ser641, Ser645, Ser653, Thr713, Thr718 and Ser724 	See references for details. <i>Not relevant for this review.</i> [60]
GSK3 Glycogen Synthase Kinase 3 α or β	<ul style="list-style-type: none"> • AKT, S6K, SGK → αSer21 and βSer9 PKC and PKA as well 	Inhibition - Phosphorylation of the N-terminal tail of GSK3 makes it to act as an inhibitory pseudosubstrate. [61-64]
	<ul style="list-style-type: none"> • PKCζ, ERK and Dyrk1A → Thr23, Ser147 and Thr356 	Activation (PKC ζ) and Inhibition (ERK and Dyrk1A) - See references for details. <i>Not relevant for this review.</i> [65-67]

HIF1α Hypoxia-inducible transcription factor 1 α		<ul style="list-style-type: none"> • GSK3 → Ser551, Thr555 and Ser589; or Thr498, Ser502, Ser505, Thr506, and Ser510 	Inhibition - Promotes HIF-1 α degradation via the SCF complex	[68,69]	
		<ul style="list-style-type: none"> • AMPK → Ser419 	Inhibition - Decreases HIF-1 α levels	[70]	
		<ul style="list-style-type: none"> • S6K → Ser125 of PHD2 	Inhibition - Phosphorylation of PHD2 at Ser125 by S6K increases its ability to degrade HIF1 α	[71]	
		<ul style="list-style-type: none"> • CDK1, Plk3, ERK and ATM → Ser576, Ser641, Ser643, Ser657, Ser668, Ser696 	Activation (CDK1, ERK, and ATM) or Inhibition (Plk3) - See references for details. <i>Not relevant for this review.</i>	[72]	
mTORC Mechanistic (mammalian) target of rapamycin complex	mTOR	<ul style="list-style-type: none"> • S6K → Ser2448 	<i>Unknown</i>	[73,74]	
		<ul style="list-style-type: none"> • ? → Ser1261, Ser2159 and Thr2164 	Activation - Promote mTOR S2481 autophosphorylation and phosphorylation of downstream substrates	[75,76]	
	Deptor	<ul style="list-style-type: none"> • mTOR → Ser293, Thr295, and/or Ser299 mTOR primes Deptor for phosphorylation at Ser286 and Ser287 by CK1. 	Activation - Promotes the ubiquitination and degradation of DEPTOR, an inhibitor of mTORC, by phosphorylation of its degnon.	[77]	
		<ul style="list-style-type: none"> • S6K and RSK1 → Ser286, Ser287 and Ser291. S6K primes the phosphorylation by RSK1 		[78]	
		<ul style="list-style-type: none"> • p38γ and p38δ → Ser293 or Thr321 		[79]	
	PRAS40	<ul style="list-style-type: none"> • AKT → Thr246 of PRAS 	Activation - PRAS40 phosphorylation relieves its inhibitory action on mTORC1. However, knockout of PRAS40 can also exert a similar effect.	[80-84]	
		<ul style="list-style-type: none"> • mTOR → Ser183 and Ser221. Primed by Thr246 phosphorylation by AKT 		[85-87]	
		<ul style="list-style-type: none"> • PKM2, DYRK3 and PIM1 → Ser202, Ser203 and Thr246 			
		<ul style="list-style-type: none"> • mTOR → Ser283 		Activation - An important step for Rheb-dependent activation of mTORC1	[88,89]
		<ul style="list-style-type: none"> • GSK3 → Ser859 		Activation - Promotes mTOR and raptor interaction	[90]
Raptor	<ul style="list-style-type: none"> • AMPK → Ser722 and Ser792 	Inhibition - Raptor phosphorylation inhibits mTORC1	[91]		
	<ul style="list-style-type: none"> • ULK1 → Ser855 and Ser859 	Inhibition - Phosphorylation of Raptor by ULK1 inhibits its ability to recognize substrates	[92]		
	<ul style="list-style-type: none"> • p38β, CDK1 and NLK → Ser283, Ser696, Thr706, Ser771 and Ser863 	Activation (p38 β) and Inhibition (NLK) - See references for details. <i>Not relevant for this review.</i>	[93-95]		
mSIN1	<ul style="list-style-type: none"> • AKT or S6K → Thr86 and Thr398 	Activation - A positive feedback loop that enhances mTORC2 kinase activity, which leads to phosphorylation of Akt Ser473.	[96,97]		
	<ul style="list-style-type: none"> • mTOR → ? 	Inhibition - Suppresses mTOR kinase activity by dissociating Sin1 from mTORC2	[98]		
		<ul style="list-style-type: none"> • mTOR → ? 	Activation - Regulates stability of mSIN1 and mTORC2	[99]	

	<ul style="list-style-type: none"> • S6K → Thr1135 	Inhibition - A negative-feedback mechanism affecting Akt phosphorylation by mTORC2. It might also be involved in complex interactions and in the TORC2-independent role of Rictor	[100-103]
	<p>Rictor</p> <ul style="list-style-type: none"> • PIK1 → Ser1162 	<i>Unknown</i> - See references for details. <i>Not relevant for this review.</i>	[104]
Nrf2 Nuclear factor erythroid 2 - related factor 2	<ul style="list-style-type: none"> • AMPK → Ser558 • PKC and Fyn → Ser40 and Tyr568 	Activation - Phosphorylation occurs at the canonical export signal promoting nuclear accumulation of Nrf2.	[105]
		Activation (PKC) or Inhibition (Fyn) - See references for details. <i>Not relevant for this review.</i>	[106]
p62/SQSTM1 Sequestosome-1	<ul style="list-style-type: none"> • AMPK → Ser294 	Activation - p62 translocates to mitochondria and induces mitophagy.	[107]
	<ul style="list-style-type: none"> • ULK1 → Ser407 	Activation - Enhances the affinity of p62 to ubiquitin.	[108]
	<ul style="list-style-type: none"> • mTORC1 → Ser349 	Activation - Disrupts Keap1-mediated Nrf2 ubiquitination	[109]
	<ul style="list-style-type: none"> • PKA, LRRK2, CDK1, p38δ, PKCδ, CK2, and TBK1 → Ser24, Thr138, Thr269, Ser272, Ser349, S403 	Activation - See references for details. <i>Not relevant for this review.</i>	[110-116]
PFKFB (PFK-2/FBPase-2) 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase	<ul style="list-style-type: none"> • Akt → Ser466 and Ser483 of PFKFB2 • AMPK → Ser466 of PFKFB2 and Ser461 of PFKFB3 • PKA, PKC and MAPKAPK2 (MK2) → Ser32 of PFKFB1; Ser84, Ser466, Thr475 and Ser483 PFKFB2; and Ser461 of PFKFB3 	Activation - Increases glycolysis, by controlling the levels of fructose 2,6-bisphosphate, an allosteric activator of phosphofructokinase 1 (PFK-1)	[117] [118]
		Inactivation (Ser32 of PFKFB1) and Activation (Ser461 of PFKFB3) - See references for details. <i>Not relevant for this review.</i>	[119,120]
PGC-1α Peroxisome-proliferator-activated receptor γ coactivator 1 α	<ul style="list-style-type: none"> • AMPK → Thr177 and Ser538 • AKT → Ser570 • GSK3 → Thr295 (to be confirmed) • Clk2, PKA and p38 → Ser194, Ser241, Ser256, Thr262, Ser265 and Thr298 	Activation - Enhances the co-transcriptional activity of PGC-1 α	[121]
		Inhibition - Inhibition of the recruitment of PGC-1 α to cognate promoters	[122]
		Inhibition - Enhances the proteasomal degradation of PGC-1 α in the nucleus	[123,124]
		Inhibition (Clk2) and Activation (PKA and p38) - See references for details. <i>Not relevant for this review.</i>	[124]
PI3K Class I Phosphoinositide 3-kinase (p85 regulatory subunit)	<ul style="list-style-type: none"> • Src family kinases → Tyr688 • PKA → Ser83 • Growth factor/cytokines → Tyr508 • p110 (catalytic) → Ser608 • PKC (PKD/PKCμ) and IKK → Ser361, 	Activation - Relieves p85's inhibitory activity on p110	[125]
		Activation - Enhances Ras binding to p110	[126]
		<i>Unknown</i>	[127]
		Inhibition - Decreases p85-p110 activity	[128]
		Inhibition - Inhibits binding of p85 to phospho-Tyr. See	[129,130]

	Ser652 and Ser690	references for details. <i>Not relevant for this review.</i>	
PINK1 PTEN-induced putative kinase 1	• AMPK → Ser495	Activation - Promotes the recruitment of Parkin to depolarized mitochondria to trigger mitophagy	[131]
Rheb Ras homolog enriched in brain	• PRAK → Ser130	Inhibition - Phosphorylation of Rheb by PRAK impairs inhibits Rheb-mediated mTORC1 activation. See references for details. <i>Not relevant for this review.</i>	[132]
(p70)S6K Ribosomal protein S6 kinase	• mTORC1 → Thr389	Activation - Thr389 phosphorylation promotes docking of PDK1, which phosphorylates S6K at Thr229.	[133]
	• PDK1 → Thr229	Activation - Phosphorylation by PDK1 a critical component of the activation of S6K.	[134]
	• GSK3 → Ser371	Activation - Cooperates in the phosphorylation of Thr389 by mTORC1	[135]
	• JNK1, ERK, p38, CDK1, CDK5 → Ser411, Thr421 and Ser424	Activation (CDK5, JNK1) and Inhibition (CDK1) - See references for details. <i>Not relevant for this review.</i>	[136-139]
SGK Serum and glucocorticoid-regulated kinase	• mTORC2 → Ser 422	Activation - Phosphorylation of the hydrophobic motif of SGK facilitates its interaction with PDK1.	[140]
	• PDK1 → Thr256	Activation - Phosphorylation of the T-loop kinase domain of SGK	[141,142]
TBC1D1/4 Rab GTPase-activating protein TBC (Tre-2/BUB2/cdc) 1 domain. Family members 1 and 4 (AS160)	• Akt → Thr596 TBC1D1 and Thr642 TBC1D4		[143-145]
	• AMPK → Ser237 TBC1D1; Ser588 and Ser711 TBC1D4	Activation - Promotes traffic of glucose transporters to the plasma membrane.	[144-147]
TFEB Transcription factor EB	• mTORC1 → Ser211		[148]
	• AKT → Ser467	Inhibition - Prevents TFEB nuclear translocation.	[149]
	• MAP4K3 → Ser3		[150]
TSC1/2 Tuberous sclerosis complex TSC1-TSC2	• AMPK → Ser 1227 and Thr1345 on TSC2	Activation - Through its GAP (GTPase-activating protein) activity towards the small G-protein Rheb negatively regulates mTORC1 signaling.	[151,152]
	• GSK3 → Ser1371, Ser1375, Ser1379, and Ser1383 on TSC2		[153]
	• AKT → Ser939, Ser981, Ser1130, Ser1132 and Thr1462 on TSC2	Inhibition – Inhibition of TSC2's GAP action on Rheb (activity, localization, complex formation or degradation)	[154-156]
	• SGK → Ser 939, Ser981, Ser1130, Ser1132, Thr1462, and Ser1798 on TSC2	Inhibition - Activation of mTORC1.	[152,157]
	• ERK, RSK, MAPKAP2 (MK2), IKK and CDK1 → Ser540, Ser664, Ser939,	Inhibition (ERK, RSK, IKK and CDK1) - See references for details. <i>Not relevant for this review.</i>	[152]

	Ser1462, Ser1254 and Ser1798 on TSC2; Thr417, Ser487, Ser511, Ser584 and Thr1047 on TSC1		
Ub Ubiquitin	• PINK1 → Ser65	Activation - Accelerates the discharge of the thioester conjugate from the E2 conjugating enzyme and unlocks the autoinhibition of the catalytic cysteine in Parkin. Regulates Ub structure, chain assembly and hydrolysis	[158-161]
ULK1 Unc-51 like autophagy activating kinase	• AMPK → Ser317 and Ser777	Activation - Activates ULK1 and promotes autophagy	[162]
	• AMPK → Ser467 and Ser555		[163,164]
	• AMPK → Ser555	Activation - Regulates mitophagy via ULK1 translocation to the mitochondria	[165,166]
	• mTORC1 → Ser757	Inhibition - Disrupts the interaction with AMPK.	[162,163]
Vps34/PI3KC3 Class III PI3K	• AKT → Ser774	<i>Unknown</i>	[166]
	• AMPK → Thr163 and Ser 165	Inhibition - Vps34 phosphorylation suppresses PI(3)P production.	[27]
	• ULK1 → Ser249	<i>Unknown</i>	[31]
	• CDK1 → Thr159	Inhibition - See references for details. <i>Not relevant for this review.</i>	[167]

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