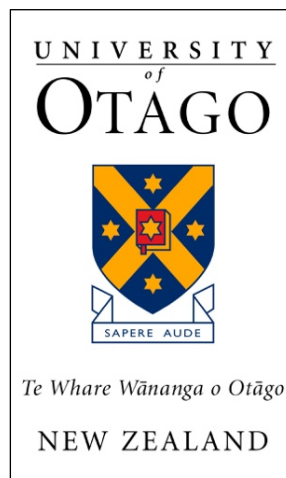


The Role of Calcium-Permeable AMPA Receptors and Arc in Secreted Amyloid Precursor Protein Alpha- Mediated Plasticity

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Abstract

The orchestrated regulation of the α -amino-3-hydroxy-5-methyl-4-isoxazolepropionic acid (AMPA)-subtype of glutamate receptors by neuronal activity and neuromodulators is critical to the expression of both long-term potentiation (LTP) and memory. In particular, GluA1-containing, Ca^{2+} -permeable AMPAR (CP-AMPA) comprise a unique role in these processes due to their transient, activity-regulated expression at the synapse. Importantly, many of the mechanisms which govern these processes are negatively affected in neurodegenerative disorders such as Alzheimer's disease, suggesting that understanding the mode of action of neuromodulatory molecules may reveal much needed novel therapeutic interventions. Secreted amyloid precursor protein-alpha (sAPP α), a metabolite of the parent amyloid precursor protein (APP) has been previously shown to enhance hippocampal LTP and facilitate memory formation. Accordingly, we hypothesised that sAPP α may act via modulation of AMPAR synthesis and cell surface expression.

Using primary hippocampal neurons grown in culture, we found that sAPP α (1 nM) differentially regulates the expression of cell surface GluA1-, GluA2-, and GluA3-containing AMPAR. Interestingly, using fluorescent non-canonical amino acid tagging with proximity ligation assay (FUNCAT-PLA), we found that short-term sAPP α treatments (1 nM, 30 min) rapidly enhanced the cell surface expression of newly synthesised extrasynaptic GluA1-, but not GluA2-containing AMPAR, while long-term treatments of sAPP α (1 nM, 120 min) increased levels of pre-existing GluA1/2-containing heteromers at the cell surface, indicating a dynamic regulation of distinct AMPARs following treatment. Moreover, using electrophysiology in area CA1 of acute hippocampal slices, we provide evidence that the expression of CP-AMPA is important in the induction of sAPP α -enhanced LTP. Using immunocytochemistry and siRNA knockdown, we provide evidence that internalization of CP-AMPA may be governed, at least in part by sAPP α -driven expression of the activity-regulated cytoskeletal-associated protein (Arc). Further, we show that Arc expression is not induced by the related APP metabolite sAPP β , but is dependent on synergistic activation of N-Methyl-D-Aspartate and α 7-nicotinic acetylcholine receptors, as well as downstream activation of CaMKII, MAPK, and PKG.

Together, these findings suggest that application of sAPP α to hippocampal neurons engages a cascade of mechanisms which enhance the synthesis and expression of AMPAR and Arc protein, in the regulation of synaptic strength and the expression of hippocampal LTP. These experiments expand upon our current knowledge underlying mechanisms of synaptic plasticity in hippocampal neurons.

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Table of Contents

Abstract	i
Acknowledgements	ii
Table of Contents.....	vii
Table of Figures	vii
Table of Tables.....	x
Abbreviations.....	xi
Chapter 1: Controlling Plasticity with Molecules and What This Means for Memory and Disease: Mediators, Messengers, Modulators and More	1
1.1. Learning and Memory	1
1.1.1. The Hippocampus	2
1.2. Mechanisms of Cellular Memory.....	7
1.2.1. Long Term Potentiation.....	7
1.2.2. Long-Term Depression	11
1.2.3. Homeostatic plasticity.....	13
1.2.4. Metaplasticity.....	15
1.3. Mechanisms Governing the Expression of Cellular Memory.....	16
1.4. Mediators of Plasticity	17
1.4.1. NMDA Receptors	17
1.4.2. AMPA receptors.....	19
1.4.2.1. GluA1.....	21
1.4.2.2. Calcium-Permeable AMPA Receptors.....	24
1.4.2.3. GluA2, GluA3, and GluA4.....	28
1.4.3. The Role of Calcium	31
1.4.4. Calcium/Calmodulin-dependent Kinase II.....	32
1.5. Messengers of Plasticity	34
1.5.1. The A-ζ of Protein Kinases.....	34
1.5.1.1. Protein Kinase A.....	34
1.5.1.2. Protein Kinase C.....	36
1.5.1.3. Protein Kinase G	37
1.5.2. Scaffold and Auxiliary Proteins	40
1.5.3. Cytoskeletal Proteins	41
1.5.4. Immediate Early Genes.....	42
1.5.4.1. Activity-Regulated Cytoskeletal-Associated Protein, Arc.....	43
1.6. Modulators of Plasticity.....	52
1.6.1. Brain-Derived Neurotrophic Factor	54
1.6.2. APP: A Multifaceted Control of Plasticity.....	56
1.6.3. Amyloid Beta.....	58
1.6.4. sAPPα.....	61
1.6.4.1. sAPPα as a Biomarker	62
1.6.4.2. sAPPα as Neuroprotective	64
1.6.4.3. sAPPα as a Putative Treatment	65
1.6.4.4. sAPPα as a Promoter of Plasticity.....	66

Chapter 2: Materials and Methods	70
2.1. Primary Neuronal Culture Preparation.....	70
2.1.1. Dissection.....	70
2.1.2. Dissociation and Plating of Primary Neurons.....	71
2.1.3. Production of Conditioned Media for Cell Culture Maintenance	73
2.2. Adult Primary Neuronal Culture Preparation	75
2.2.1. Dissection.....	75
2.2.2. Dissociation and Plating of Primary Neurons.....	75
2.3. Experimental Procedures	76
2.3.1. Immunocytochemistry.....	76
2.3.1.1. Treatment of Primary Cultures.....	76
2.3.2. Primary Antibody Probe.....	77
2.3.3. Secondary antibody probe.....	78
2.3.4. Fluorescent Non-Canonical Amino Acid Tagging– Proximity Ligase Assay (FUNCAT-PLA)	80
2.3.4.1. Treatment and Incorporation of AHA.....	80
2.3.4.2. Click Reaction	80
2.3.4.3. Detection of Newly Synthesized Proteins.....	81
2.3.4.4. Proximity Ligation Assay (PLA)	81
2.3.5. Detection of Cell Surface Proteins Using BioPLAy.....	83
2.3.5.1. Treatment.....	83
2.3.5.2. Biotinylation	83
2.3.5.3. Proximity Ligation Assay (PLA)	84
2.3.6. Detection of Cell Surface Receptor Subunit Dimers (PLA)	85
2.3.7. Treatment.....	85
2.3.8. Addition of Antibodies	85
2.3.9. Proximity Ligation Assay	86
2.3.10. Treatment of Cultures With siRNA.....	87
2.4. Reverse Transcriptase Quantitative Polymerase Chain Reaction (RT-qPCR)	88
2.4.1. RNA Isolation and Purification	88
2.4.1.1. RNA Quality and Quantification.....	88
2.4.1.2. Primer Design	89
2.4.1.3. cDNA Synthesis.....	89
2.4.1.4. SYBR Green mRNA Assays	90
2.4.2. Reverse-Transcriptase Quantitative Polymerase Chain Reaction (RT-qPCR)	91
2.4.3. Western Blot.....	91
2.4.3.1. Protein Extraction and Sample Preparation	92
2.4.3.2. Gel Electrophoresis and Transfer	92
2.5. Preparation of Acute Hippocampal Slices for Electrophysiology and Biochemical Experiments.....	93
2.5.1. Acute Hippocampal Slice Preparation.....	93
2.5.2. Immunohistochemistry.....	94
2.5.3. Field Potential Electrophysiology.....	95
2.6. Microscopy and data analysis.....	96
2.6.1. Sample Choice and Blinding.....	96

2.6.2.	Light Microscopy.....	97
2.6.3.	Image Analysis	97
2.6.4.	Statistical Analysis.....	98
Chapter 3: Results		100
3.1.	Characterization of Primary Hippocampal Cultures	100
3.1.1.	Growth and Development	100
3.1.2.	Immunofluorescent Detection of Primary Neuron Development	102
3.1.3.	Cellular Populations Within Primary Hippocampal Cell Cultures	104
3.1.4.	Identification of Pre- and Post-Synaptic Markers of Mature Synapses in Neuronal Cultures.....	107
3.2.	Observations from the Culturing of Adult Cortical Mouse Neurons	109
3.2.1.	Growth and Development of Adult Neuronal Cultures	109
3.2.2.	Cellular Populations in Adult Primary Cortical Cultures.....	111
3.2.3.	Cultured Wild-Type and APP/PS1 Adult Mouse Neurons Express GluA1.....	113
Chapter 4.....		115
4.1.	Examining Arc Expression in Response to sAPP α	115
4.1.1.	sAPP α Facilitates an Increase in Arc and Zif268 mRNA Expression.....	115
4.1.2.	sAPP α Facilitates an Increase in Arc Protein Expression.....	118
4.1.3.	sAPP α Promotes an Increase in Arc Protein Throughout Primary and Secondary Dendrites	120
4.1.4.	Arc Protein Expression is Transcription- and Translation-Dependent	122
4.1.5.	Arc Protein Expression is Dependent on CaMKII/MAPK/PKG Signalling	124
4.1.6.	Dendritic Arc Protein Expression is Dependent on Activation of NMDA- and α 7nACh Receptors	126
4.2.	sAPP α Increases CREB Phosphorylation and Arc Protein in Acute Hippocampal Slices...128	
4.2.1.	Trend in CREB Phosphorylation and Arc Protein Expression in the Dentate Gyrus of Acute Hippocampal Slices.....	130
4.2.2.	Increases in Arc Protein is Specific to Area CA1 and Does Not Occur in Area CA3..132	
4.3.	Summary	134
Chapter 5.....		135
5.1.	The Role of Calcium-Permeable AMPAR (CP-AMPA) in sAPP α -Mediated Enhancement of LTP.....	135
5.1.1.	CP-AMPA Contribute a Small Fraction of Basal Synaptic Transmission	136
5.1.2.	CP-AMPA Do Not Contribute to LTP Following a Mild Theta-Burst Stimulation Protocol	138
5.1.3.	CP-AMPA Contribute to the Initial Enhancement of sAPP α -LTP.....	139
5.2.	Summary	141
Chapter 6		142
6.1.	sAPP α Regulates the Dynamic Control of AMPA Receptors at the Cell Surface	142
6.1.1.	sAPP α Promotes the Rapid and Persistent Expression of Cell Surface GluA1 in the Soma and Dendrites of Primary Hippocampal Neurons	142
6.1.2.	sAPP α Promotes the Rapid and Transient Trafficking of <i>de novo</i> GluA1- Containing AMPAR to the Somatic and Dendritic Cell Surface	144

6.1.2.1.	sAPP α Enhances the Extrasynaptic, but not the Synaptic Population of <i>de novo</i> Cell Surface GluA1.....	146
6.1.3.	Rapid Decrease in Dendritic <i>de novo</i> Cell Surface GluA2 Following sAPP α Treatment.....	148
6.1.4.	Accell™ Arc siRNA Inhibits Somatic and Dendritic sAPP α -Dependent, but not Basal, Arc Expression	150
6.1.5.	Internalization of <i>de novo</i> GluA1 is Dependent on Arc Expression.....	153
6.1.6.	Non-Targeting siRNA has no Significant Effect on <i>de novo</i> Cell Surface GluA1	155
6.1.7.	sAPP α Promotes the Delayed Expression of Cell Surface GluA1/2-Containing AMPAR.....	157
6.1.8.	sAPP α Promotes the Rapid and Sustained Internalization of GluA2/3-Containing AMPAR.....	159
6.2.	Summary	161
Chapter 7: Discussion.....		162
7.1.	Aims and Objectives	162
7.2.	sAPP α Mediates LTP Through the Expression of Ca ²⁺ -Permeable AMPA Receptors	163
7.3.	sAPP α regulates the Trafficking of Existing and Newly-Synthesized AMPAR Receptors	170
7.3.1.	GluA1-containing AMPA Receptors	170
7.3.1.1.	Regulation of <i>de novo</i> GluA2-containing AMPA Receptors	172
7.3.2.	GluA1/2-containing AMPA Receptors.....	173
7.3.3.	GluA3-containing AMPA Receptors	174
7.4.	A Role for Arc Expression and Function.....	176
7.4.1.	Arc regulates <i>de novo</i> GluA1 expression.....	183
7.5.	Mechanism of Action.....	185
7.6.	A Possible Role for Silent Synapses.....	191
7.7.	A Promising Role for sAPP α in Synaptic Disorders.....	197
7.8.	Future Directions.....	198
7.9.	Concluding Remarks	200
References		202
Appendix.....		290
1.	Image analysis.....	290
1.1.	Quantifying Arc Protein Expression in Primary Hippocampal Neurons	290
1.2.	Quantifying pCREB Protein in Primary Hippocampal Slices	292
1.2.1.	Quantifying Arc Protein Signal in Hippocampal Slices	293
1.3.	Quantifying PLA Signal in Primary Hippocampal Neurons	294
1.4.	Quantifying Colocalization of PLA Signal Within Synapses	297
2.	Cell Health	299
3.	Accell™ siRNA Specificity	300
4.	Antibody Specificity	302

Table of Figures

Figure 1-1 Homologous regions of the hippocampus in the human and rat brains.	3
Figure 1-2 Schematic diagram of the Hippocampal formation.	4
Figure 1-3 Principal cells of the hippocampus.	5
Figure 1-4 The discovery of LTP.	7
Figure 1-5 Schematic illustration of separate phases of synaptic long-term potentiation.	10
Figure 1-6 The discovery of LTD.	12
Figure 1-7 Conceptual illustration of synaptic scaling.	14
Figure 1-8 Schematic diagram of NMDAR Structure.	18
Figure 1-9 Schematic diagram of AMPAR Structure.	20
Figure 1-10 Regulated AMPAR synthesis and trafficking methods.	22
Figure 1-11 Model of local AMPAR trafficking at the synapse.	23
Figure 1-12 Schematic diagram of Arc protein properties.	43
Figure 1-13 Regulation of GluA1 and GluA2 endocytosis by Arc.	48
Figure 1-14 Arc aids in growth of the cytoskeleton during plasticity events.	50
Figure 1-15 Production and release of BDNF.	54
Figure 1-16 Structure and domains of the Amyloid Precursor Protein.	57
Figure 1-17 Stylized diagram of APP processing.	60
Figure 1-18 Hormetic relationship between APP metabolites and the expression of key neurotrophic mechanisms.	61
Figure 2-1 Hippocampal and cortical dissection.	72
Figure 2-2 Growth of neurons and proliferation of glia.	74
Figure 2-3 Copper-catalysed azide-alkyne cycloaddition (CuAAC).	81
Figure 2-4 Schematic diagram of FUNCAT-PLA experimental design.	82
Figure 2-5 Schematic diagram of BioPLAy experimental design.	90
Figure 2-6 Schematic diagram of A) GluA1/2 and B) GluA2/3 PLA experimental design.	91
Figure 2-7 Melt curve plots.	84
Figure 2-8 Experimental setup of RT-qPCR amplification and quantification cycles.	90
Figure 2-9 Acute transverse hippocampal slice dissection.	91
Figure 2-10 Hippocampal slice diagram.	96
Figure 3-1 Temporal development of hippocampal cells in primary culture.	101

Figure 3-2 Temporal development of MAP2- and Tau-positive neurites.....	103
Figure 3-3 Primary Hippocampal cultures contain Glial and Neuronal populations.	106
Figure 3-4 Development of synapses in vitro	108
Figure 3-5 Adult mouse culture growth and development.....	110
Figure 3-6 Cellular populations in adult cortical cultures.	112
Figure 3-7 GluA1-positive cells.	114
Figure 4-1 sAPP α promotes the transcription of <i>Arc</i> and <i>Zif268</i> mRNA	117
Figure 4-2 sAPP α promotes Arc protein expression in a concentration-dependent manner	119
Figure 4-3 Arc protein expression increases throughout primary and secondary dendrites.....	121
Figure 4-4 Arc protein expression is prevented by inhibitors of transcription and translation	123
Figure 4-5 Arc protein expression in response to sAPP α is affected by kinase inhibitors.....	125
Figure 4-6 Arc protein expression is dependent on NMDA and α 7nAch receptors.....	127
Figure 4-7 sAPP α increases CREB phosphorylation and Arc protein in acute hippocampal slices.....	129
Figure 4-8 sAPP α does not significantly increase pCREB or Arc protein in the Hilus of the dentate gyrus in acute hippocampal slices.....	131
Figure 4-9 sAPP α does not increase Arc protein in area CA3.	133
Figure 5-1 Reduction in basal synaptic transmission following CP-AMPA blockade.....	137
Figure 5-2 Early phase sAPP α -enhanced LTP is dependent on activation of CP-AMPA.....	140
Figure 6-1 sAPP α enhances cell surface expression of GluA1.....	143
Figure 6-2 Rapid increase in cell surface <i>de novo</i> GluA1 following treatment.....	145
Figure 6-3 sAPP α enhances <i>de novo</i> GluA1 at the extrasynaptic membrane.	147
Figure 6-4 Rapid decrease in <i>de novo</i> cell surface GluA2 following treatment.	149
Figure 6-5 sAPP α -promoted, but not basal, Arc expression is affected by Accell™ Arc siRNA.	152
Figure 6-6 sAPP α -induced <i>de novo</i> GluA1 persist at the cell surface following siRNA-mediated knockdown of Arc protein.....	154
Figure 6-7 Non-targeting siRNA does not affect <i>de novo</i> cell surface GluA1.....	156
Figure 6-8 sAPP α enhances cell surface GluA1/2-containing AMPAR following prolonged treatment.	158
Figure 6-9 sAPP α decreases cell surface GluA2/3-containing AMPAR expression.....	160
Figure 7-1 Regulation of cell surface AMPAR – Extrasynaptic Exocytosis model.....	188
Figure 7-2 Regulation of cell surface AMPAR – Extrasynaptic Endocytosis model.	190
Figure 7-3 Regulation of cell surface AMPAR at silent synapses.....	196
Figure A-1 Setting of MAP2 mask	290

Figure A-2 Measuring integrated density	291
Figure A-3 Accounting for background fluorescence.....	291
Figure A-4 Setting the ROI of the cell body layer	292
Figure A-5 Measuring integrated density of the cell body layer.....	292
Figure A-6 Measuring the fluorescence of the CA1 ROI	293
Figure A-7 Running the PLA quantification macro.....	294
Figure A-8 Defining the MAP2 threshold and mask.....	295
Figure A-9 Isolation of the cell of interest from surrounding cells.....	295
Figure A-10 Isolated target neuron.....	296
Figure A-11 Detection and quantification of PLA signal.....	296
Figure A-12 Running JACoP.....	297
Figure A-13 Setting of the threshold values.....	297
Figure A-14 Measuring distance to synapse centre.....	298
Figure A-15 Representative image of an unhealthy hippocampal neuron.	299
Figure A-16 Specificity of Accell™ siRNA expression.....	301
Figure A-17 Specificity of primary Antibodies.....	303

Table of Tables

Table 1-1 Identification of neurotrophic peptides involved in neuronal plasticity	53
Table 2-1 Catalogue of inhibitors and antagonists used throughout immunocytochemical and immunohistochemical experiments.	77
Table 2-2 Catalogue of primary and secondary antibodies used in immunocytochemistry (IC), immunohistochemistry (IH), western blot (WB), FUNCAT-PLA (F-PLA), BioPLAy (B), and PLA (PLA).....	79
Table 2-3 Summary table of siRNA and their targets used in FUNCAT-PLA experiments.	87
Table 2-4 Summary table of primer sequence pairs used in RT-qPCR experiments.	89
Table 7-1 Summary of literature examining CP-AMPA in LTP and behavioural paradigms	167

Abbreviations

5-HT	5-Hydroxytryptamine	cKO	Conditional Knockout
aCSF	Artificial Cerebrospinal Fluid	CNIH2/3	Cornichon Family AMPA Receptor Auxiliary Proteins 2/3
Act-D	Actinomycin-D	CNS	Central Nervous System
AD	Alzheimer's Disease	CP-AMPA	Ca ²⁺ -Permeable AMPAR
ADF	Actin Depolymerizing Factor	CPG2	Candidate Plasticity Gene 2
AHA	L-Azidohomoalanine	CPG55845	CPG 55845 Hydrochloride
AICD	APP Intracellular Domain	CREB	cAMP-response element binding protein
AKAP79/150	A-kinase Anchoring Protein 79	CSF	Cerebrospinal Fluid
AMPA	α -amino-3-hydroxy-5-methyl-4-isoxazolepropionic acid Receptor	CTD	Carboxy-terminal Domain
Aniso	Anisomycin	CV	Coefficient of Variation
APLP1/2	Amyloid Precursor-Like Proteins 1/2	DA	Dopamine
APOE	Apolipoprotein E	DAG	Diacylglycerol
APP	Amyloid Precursor Protein	DAPI	4',6-diamidino-2-phenylindole
APPL2	APP-like protein 2	DG	Dentate Gyrus
APV	D(-)-2-Amino-5-Phosphonopentanoic Acid	DIV	Days in Vitro
Ara-C	Cytosine arabinoside	DLGAP1	Discs Large Homologue-Associated Protein 1
Arc	Activity-Regulated Cytoskeletal-Associated Protein	DM	Dissection Media
ATD	Amino Terminal Domain	DNA	Deoxyribonucleic acid
A β	Amyloid-Beta	Dnm2	Dynamamin-2
BACE1	β -site Amyloid Precursor Protein-Cleaving Enzyme 1	DS	Down's Syndrome
BBB	Blood-Brain Barrier	DTT	Dithiothreitol
BCM	Bienenstock, Cooper and Munro	ECS	electroconvulsive stimulation
BD	Bipolar Disorder	eEF2K	eukaryotic elongation factor 2 kinase
BDNF	Brain Derived Neurotrophic Factor	Endo2/3	Endophilin-2/3
bFGF	Basic Fibroblast Growth Factor	EPSC	Excitatory Postsynaptic Current
Bic	Bicuculline	EPSP	Excitatory Postsynaptic Potential
CA	Cornu Ammonis	ER	Endoplasmic Reticulum
CAMKI	Ca ²⁺ /calmodulin-dependent protein kinase I	ERG-1	Early Growth Response Protein
CaMKII	Ca ²⁺ /calmodulin-dependent protein kinase II	EV	Extracellular Vesicles
cAMP	Cyclic Adenosine Monophosphate	fAD	Familial Alzheimer's Disease
CC	Chelerythrine Chloride	FUNCAT	Fluorescent Non-Canonical Amino Acid Labelling
cDNA	Complementary DNA	FV	Fibre Volley
cGK	cGMP-dependent Protein Kinase	GABA	Gamma Aminobutyric Acid
CI-AMPA	Ca ²⁺ -Impermeable AMPAR	GFAP	Glial fibrillary acidic protein
		GFBD	Growth Factor Binding Domain

GKAP	Guanylate Kinase-Associated Proteins	NSF	N-ethylmaleimide sensitive fusion protein
GI	Glycosylation	NTD	N-Terminal Domain
GRIP1/2	Glutamate Receptor-Interacting Protein 1/2	ODN	Oligodeoxynucleotide
H89	H-89 Dihydrochloride	PAK3	P21-Activated Kinase 3
HBD	Heparin-Binding Domain	PBS-MCS	Phosphate Buffered Saline- MgCl ₂ CaCl ₂ & Sucrose
HEK	Human Embryonic Kidney cells	PC1	Protein Convertase 1
HFS	High-Frequency Stimulation	PCL	Pyramidal Cell Layer
IEG	Immediate Early Gene	pCREB	Phosphorylated cAMP-response element binding protein
IEM-1460	N,N,N-trimethyl-5-[(tricyclo[3.3.1.1.3,7]dec-1-ylmethyl)amino]-1-pentanaminium bromide hydrobromide	PD	Postnatal Day
IntDen	Integrated Density	PDE5	Phosphodiesterase 5
IPSC	Induced Pluripotent Stem Cell	PDL	Poly-D-Lysine
IS	Interneuron Specific	PDZ	PSD-95/Drosophilla discs large/zona occludens-1
IS	Interneuron-specific	PI3K	Phosphoinositide 3-Kinase
JMR	Juxtamembrane Region	PICK1	Protein Interacting With PRKCA 1
KO	Knockout	PKA	Protein Kinase A
LBD	Ligand Binding Domain	PKB	Protein Kinase B
LFS	Low-Frequency Stimulation	PKC	Protein Kinase C
LTD	Long-Term Depression	PKD	Protein Kinase D
LTP	Long-Term Potentiation	PKG	Protein Kinase G
mAChR	Muscarinic Acetylcholine Receptor	PKM	Protein Kinase M
MAGUK	Membrane Associate Guanylate Kinases	PKMζ	Protein Kinase M-Zeta
MAP2	Microtubule Associated Protein 2	PKN	Protein Kinase N
MAPK	Mitogen activated protein kinase	PLA	Proximity Ligase Assay
MCPG	± A-Methyl-4-Carboxyphenylglycine	PLC- γ	Phospholipase C-Gamma
MEM	Minimal Essential Media	PML	Promocytic Leukaemia
mGluR	Metabotropic Glutamate Receptor	PMSF	Phenylmethylsulfonyl Fluoride
MQ	Milli-Q	PP1	Protein Phosphatase 1
mRNA	Messenger Ribonucleic Acid	Prox1	Prospero-Related Homeobox 1
mTOR	Mammalian Target of Rapamycin	PRP	Plasticity Related Proteins
MW	Molecular Weight	pS	Phosphoserine
NaF	Sodium Fluoride	PS1	Presenilin-1
NES	Nuclear Export Signal	PSD	Post-Synaptic Density
NFκB	Nuclear Factor-Kappa B	pT	Phosphothreonine
NGM	Normal Growth Media	PTM	Post-Translational Modification
Ni	Nitrosylation	PTM	Posttranslational Modifications
NLS	Nuclear Localization Signal	pY	Phosphotyrosine
NMDAR	N-Methyl- d-aspartate	RI	Rectification Index
NO	Nitric Oxide	RNA	Ribonucleic acid
NOS	Nitric Oxide Synthase	RT	Room-temperature
NRD	Nuclear Retention Domain	RT-qPCR	Reverse Transcription Quantitative Polymerase Chain Reaction
		sAD	Sporadic Alzheimer's Disease
		SAP97	Synapse-associated protein 97

SAPAP1	SAP90, PSD-95-associated protein 1
sAPP α	Secreted Amyloid Precursor Protein Alpha
sAPP β	Secreted Amyloid Precursor Protein Beta
sAPP η	Secreted Amyloid Precursor Protein Eta
SC	Schaffer Collateral
SEM	Standard Error of the Mean
sGC	Soluble Guanylyl Cyclase
siRNA	Small interfering RNA
STD	Short-Term Depression
STP	Short-Term Plasticity
SUMO	SUMOylated
TARP	Transmembrane AMPA Receptor Regulatory Proteins
TBI	Traumatic Brain Injury
TBS	Theta Burst Stimulation
TBTA	Tris (1-benzyl-1H-1,2,3-triazol-4- yl)methyl) amine
TCEP	Tris(2-carboxyethyl)phosphine hydro-chloride
THC	$\Delta(9)$ -tetrahydrocannabinol
TLE	Temporal Lobe Epilepsy
TMD	Transmembrane Domain
TNF- α	Tumour Necrosis Factor-Alpha
TrkB	tropomyosin receptor kinase B
TTX	Tetrodotoxin
Ub	Ubiquitination
WT	Wild-Type
$\alpha 7$ nAChR	$\alpha 7$ nicotinic acetylcholine receptors
α BGT	α -Bungarotoxin

Chapter 1: Controlling Plasticity with Molecules and What This Means for Memory and Disease: Mediators, Messengers, Modulators and More

1.1. Learning and Memory

Learning and memory are fundamental phenomena which describe the ability of both animals and humans to acquire, retain, and retrieve information (Seyfarth and Cheney, 2003). Many of these processes consist of mechanisms necessary to permit the recognition of the familiar, prediction of future events, and assessment of behaviour, allowing humans and animals to make sense of the environment around them (Sherry and Schacter, 1987; Camina and Güell, 2017). The formation, storage, and retrieval of both short- and long-term memories is understood to occur through cellular changes within the central nervous system (CNS), contributing to specific modifications in the strength and efficacy of neuronal cells to respond to stimulation (Okano, 2000). This idea was first proposed by American psychologist William James, who linked the properties of plasticity with those of behavioural habits (James, 2007). Here, William James proposes;

“When two elementary brain-processes have been active together or in immediate succession, one of them, on reoccurring, tends to propagate its excitement into the other.” (James, 1890)

The idea that the nervous system has intrinsic plastic properties capable of reshaping the relationships between neurons was later supported by descriptions, both philosophical and anatomical, of the synapse. The synapse was first described by Italian neuropsychiatrist Eugenio Tanzi (Tanzi, 1893) as *“minimal interruptions between adjacent and functionally related neurons”* through which activity *“increases the nutritional processes... accompanied by hypertrophy”* and effectively decreases the *“distance between adjoining and contiguous neurons”*. This proposition was further expanded upon by Tanzi’s disciple Ernesto Lugaro, who further suggested that repetition or habitual processes *“establish reciprocal connections”* and *“facilitates the transmission of functional activity from one to the other”* (Lugaro, 1898). These ideas were further supported by anatomical observations made by Italian biologist Camillo Golgi and Spanish pathologist Santiago Cajal (Golgi, 1885; Cajal, 1893; Cajal, 1909), who provided detailed descriptions of nerve cells as well the appearance of *“thorns or short spines”* (Cajal, 1888; Cajal, 1896), now considered the first observations of synapses (Berlucchi and Buchtel, 2009; Yuste, 2015).

The early concepts describing the plastic abilities of the nervous system, together with direct observations of neurons and the connections between them, was later refined into a concrete model of synaptic plasticity by Canadian psychologist Donald Hebb (Hebb, 1949). Simply put, Hebb describes synaptic plasticity as a mechanism through which repeated and persistent firing of a presynaptic cell, which leads to the firing of a consecutive postsynaptic cell, will increase the strength, stability, and efficacy of the connection, through a form of growth or metabolic change within the cell. This model has become to be known as Hebbian plasticity and remains one of the leading theories on how neural tissue adapts to change, and may contribute, in part, to the underlying processes of learning and the formation of long-term memories (Abbott and Nelson, 2000).

1.1.1. *The Hippocampus*

Observations of the mechanisms and functions of learning and memory have been made since as early as the late 19th century (Ribot, 1882; Freud and Breuer, 1895; Kennedy, 1898; Bregman, 1899; Barr and Bieliauskas, 2016). Around this time, Ebbinghaus, (1885) first introduced the division of short-term and long-term memory, while Ribot, (1882) began to describe the necessary conditions for memory (“*the conservation of certain conditions, their reproduction, and their localization in the past*”), beginning to distinguish between ‘temporary amnesia,’ ‘periodical amnesia,’ and ‘progressive amnesia’. However, many of these observations did so in the absence of references to the nervous system. The early 20th century bought with it observations of the mechanisms which may permit formation or maintenance of memories; including the pairing of stimuli in classical conditioning (Semon, 1911; Pavlov and Gantt, 1928), the importance of emotion in memory strength (Gregor, 1907), and the acquisition of mnemonic memories (Ranschburg, 1911). Importantly, these observations aided in cytoarchitectural (Brodmann, 1909) and physiological mapping of the cerebral cortex (Silverstein, 2012), and identification of a region-specific, functional representation of the entire body (Penfield and Boldrey, 1937). These observations were further characterised by limb amputations and attributable changes to cortical and peripheral sensitivity (Katz, 1920; Haber, 1955; 1958), which began to both localise brain function to anatomy as well as indicate that experience-dependent changes may correlate to changes in anatomy and physiology.

Following these findings, observations began to arise providing evidence towards the localization of memory formation specifically. Zingerle, (1912) first described marked memory disturbances and reduced intelligence in a 40-year-old patient in which the right temporal lobe was absent. Following this, Gamper (1928) and Grünthal (1947) described clear diencephalic damage and impaired memory related to alcohol-related brain damage and hypoglycaemia, respectively.

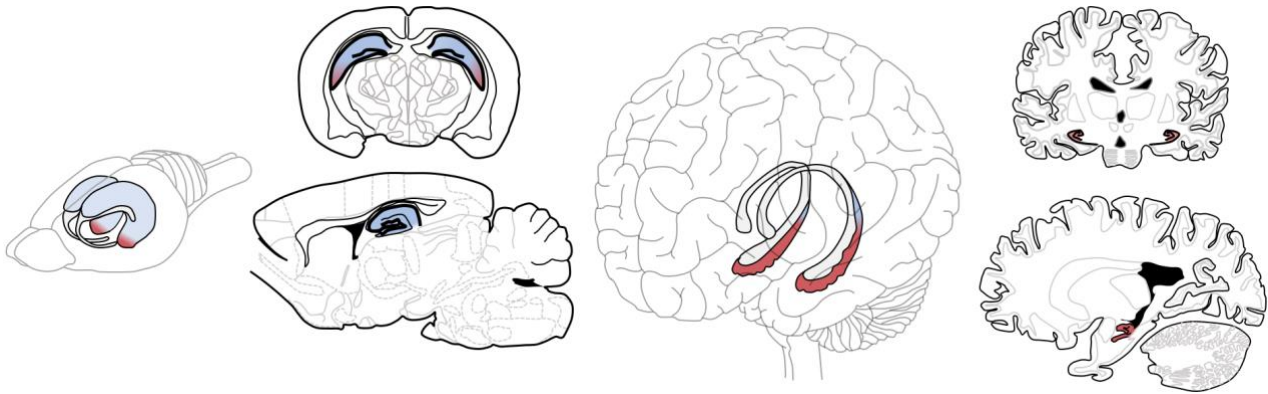


Figure 1-1 | Homologous regions of the hippocampus in the human and rat brains. Representative images show rat brain (left) and dorsal (■) and ventral (■) hippocampus, with coronal (top left) and sagittal (bottom left) sections. Right images show stylized human brain (right), and dorsal (■) and ventral (■) hippocampus, with coronal (top right) and sagittal (bottom right) sections.

Most recently, a well-known case of this involves patient Henry Molaison (H.M.) who suffered from major seizures following an accident in his childhood. In an effort to resolve this, H.M. underwent surgery for a bilateral medial temporal lobectomy, removing the hippocampus, amygdala, and the adjacent parahippocampal gyri (Squire, 2009). Following surgery, patient H.M. experienced profound impairments in his ability to form long-term declarative memories,

“so severe so as to prevent [H.M.] from remembering the location of the rooms in which he lives, the names of his close associates, or even the way to the toilet”

(Scoville, 1954)

leading neurosurgeon William Scoville to conclude:

“...that the anterior hippocampus and hippocampal gyrus, either separately or together, are critically concerned in the retention of current experience”

(Scoville and Milner, 1957)

Over the next decade, neuroanatomical studies began to evaluate the intricate structure and function of the medial temporal lobe memory system and its relationship to the central nervous system (Squire and Zola-Morgan, 1991).

Encompassing the hippocampus, in addition to associated entorhinal, perirhinal, and parahippocampal cortices, the medial temporal lobe memory system has come to be understood to

be responsible for the formation and consolidation of long-term memories, but ultimately is not an absolute storage structure as Scoville may have implied (Penfield and Milner, 1958; Marslen-Wilson and Teuber, 1975; Steinvorth et al., 2005; Kirwan et al., 2008).

Because of its elegant structure and very ordered cellular connections, the hippocampus has become a popular practice to examine underlying mechanisms of memory through electrophysiological, cellular, and molecular neurobiology practices. Early and ongoing experimental practices have utilized non-human

animals as a means of investigating the underlying mechanisms and behaviours which may drive many neurodegenerative, cognitive and affective disorders in human beings. Primarily, rodent models (especially *Mus musculus* and *Rattus norvegicus*) have been the most widely used models in biomedical research for many years, encompassing approximately 20% in the 1970s and 1980s to around 50% of neuroscience-related research in recent years (Ellenbroek and Youn, 2016). Arguably, the use of rodents has formed a strong basis for preclinical research regarding drug therapies, genome-editing technologies, and a means to investigate physiological, anatomical, biochemical and pharmacological underpinnings of neurodegenerative disorders. The anatomy of the rat cortex and hippocampus has been thoroughly characterised in order for comparisons to human be made. These comparisons allow the identification of possible anatomical, functional, and behavioural linkages. As shown by Figure 1-1., the gross anatomy of the hippocampus differs substantially. While the curved, elongated structure is constant throughout all mammals (Strange et al., 2014), the location and extent of the hippocampal boundaries differ with respect to the dorsoventral axis. The primate hippocampus is primarily contained within the temporal lobe, while much of the rodent hippocampus rests dorsally beneath the corpus callosum (Insausti, 1993; Royer et al., 2010; Lisman et al., 2017). Importantly, the overall pattern of connectivity shows a high degree of conservation across mammals, such that while the gross anatomy may differ, the fields of the hippocampal formation are linked by similar and largely unidirectional connections.

The hippocampus itself is subdivided into the Cornu Ammonis (CA), also referred to as CA1–4, and the dentate gyrus (DG; Figure 1-2). Parahippocampal and entorhinal cortices project afferents into the dentate gyrus via the perforant path (Burwell and Amaral, 1998; Wible, 2013). Here, afferent

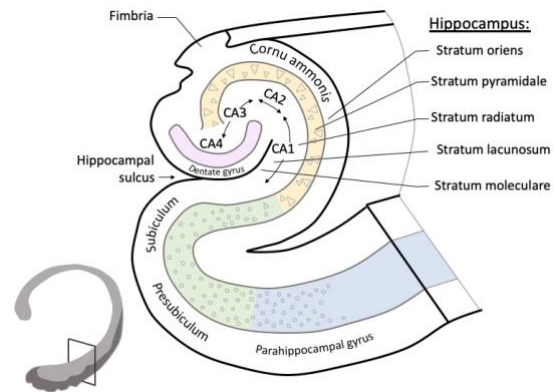


Figure 1-2 | Schematic diagram of the Hippocampal formation. Coronal cross-section (as indicated bottom left) of the hippocampus shows subfields, including the dentate gyrus (■), cornu ammonis (■), entorhinal cortex (■), and parahippocampal gyrus (■).

axons terminate on the granule cells of the dentate gyrus which in turn project mossy fiber tracts to the CA3 field of the hippocampus. Here, pyramidal cells of area CA3 send collateralized axons of the Schaffer collaterals, the major input to CA1. CA1 provides the major output of the hippocampus, sending efferent projections to the subiculum which in turn projects to many cortical and subcortical targets (Witter and Groenewegen, 1990; O'Mara et al., 2001). This conserved hierarchy of connectivity has led to the proposal that the hippocampus may serve as a central node of rapid synaptic change, such that information is processed through a limited number of synaptic changes to be gradually interleaved into existing networks of knowledge within the cortex (McClelland et al., 1995).

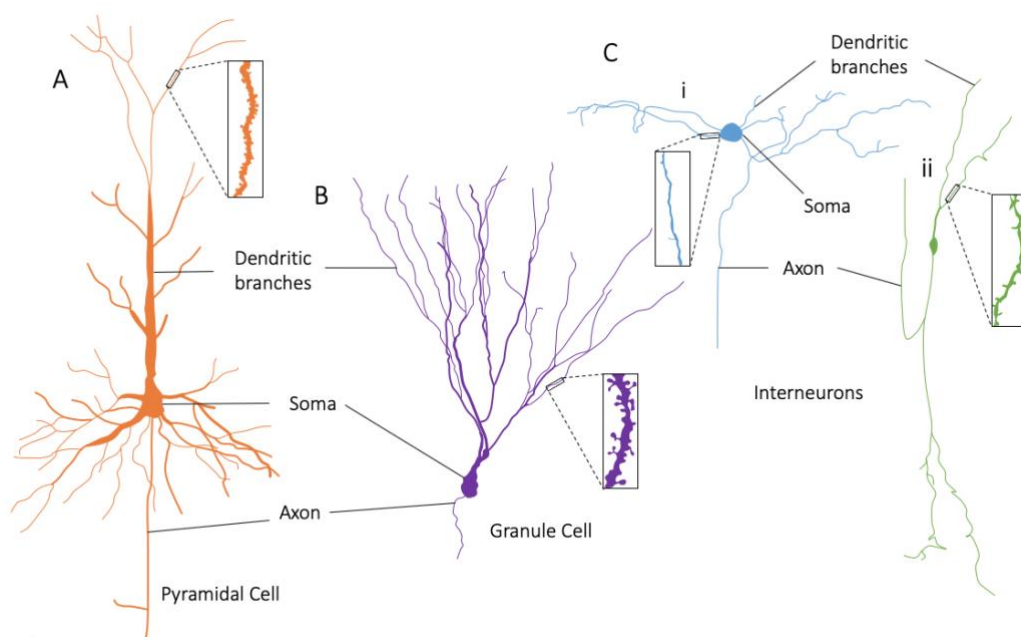


Figure 1-3 | Principal cells of the hippocampus. Morphological characteristics of A) CA1-3 pyramidal neurons (■), B) dentate gyrus granule cells (■), and C) i. basket (■), and ii. interneuron-specific (IS, ■) interneurons. Inset image shows representative magnification of pyramidal, granule, basket cell and bipolar spines. Scale bar = 50 μ M.

As mentioned above, primary cells of the hippocampus include glutamatergic granule and pyramidal cells of the DG and CA1–4 areas, respectively. As shown by Figure 1-3., pyramidal cells can be defined by their large pyramidal-shaped soma (approximately 20 μ m; Figure 1-3A) and distinct apical and basal dendritic arborization. Alternatively, granule cells of the DG are defined by their small soma (approximately 10 μ m; Figure 1-3B) and unique apical, cone-shaped arborization (Amaral et al., 2007), receiving information from the perforant path, and projecting mossy fiber axons towards CA3. The dendrites of both pyramidal and granule cells are the sites of small (< 1 μ m) protrusions called

spines, and are the site of the postsynaptic response (Nimchinsky et al., 2002; Bekkers, 2011). In addition to the excitatory principal cells, the hippocampus also contains subpopulations of interneurons, primarily expressing the inhibitory transmitter γ -aminobutyric acid (GABA; Figure 1-3C). The term interneuron conveys the unifying principle that these inhibitory cells regulate local circuit excitation, and display diverse morphological and chemical properties. Specific types of interneurons are classified based on their clear axonal or dendritic processes, such as basket cells (Figure 1-3 Ci.), which form dense connections on the soma of pyramidal cells (Fasano et al., 2017). In addition, various populations of interneurons were found to contain different peptides (e.g. parvalbumin, cholecystokinin, somatostatin, calbindin and calretinin), resulting in additional classifications based on neurochemical composition (Freund, and Buzsáki, 1996). While the expression of parvalbumin, calbindin and calretinin appears to identify specific groups of morphologically distinct and input-specific interneurons, some neurochemical markers overlap and have been found to co-exist within distinct population-specific, morphologically distinct populations (Kosaka et al., 1987; Losonczy et al., 2002), as well as neurochemically distinct populations of morphologically identical interneurons (e.g. parvalbumin- and cholecystokinin-positive basket cells; Fasano et al., 2017). Finally, populations have been identified based on their functional characteristics, such as interneuron-specific (IS) cells (Figure 1-3 Cii), which provide inhibitory feedback of other interneurons (Chamberland and Topolnik, 2012), and oriens-lacunosum moleculare (OLM) interneurons, which preferentially innervate CA1 pyramidal neuron dendrites (Müller and Remy, 2014; Maccaferri and Lacaille, 2003).

1.2. Mechanisms of Cellular Memory

1.2.1. Long Term Potentiation

Following decades of research, a canonical model has emerged, which permits observation and quantification of Hebbian plasticity following electrical or chemical stimulation. This model was initially described by Tim Bliss and Terje Lømo with work done in the dentate gyrus of the hippocampus of anaesthetized (Bliss and Lomo, 1973) and unanaesthetized (Bliss and Gardner-Medwin, 1973) rabbits. As shown by Figure 1-4., tetanisation of the perforant path by high frequency stimulation (HFS) produced a persistent increase in the efficacy of the excitatory postsynaptic potential (EPSP) to subsequent stimulations, specific to the tetanized pathway. This increase was found to last the length of the experiment in anaesthetized rabbits, but was found to slowly decay to baseline across 3 days in unanaesthetized rabbits (with one exception, still potentiated following 16 weeks). This long-lasting enhancement in the synaptic response was later termed long-term potentiation (LTP) and has become a principal experimental method and theoretical model for examining the processes and underlying mechanisms of Hebbian plasticity in neural tissue (Lomo, 2003). For Hebbian plasticity to serve as a mechanism through which cellular correlates of memory occur, four properties have been described which may permit this. Firstly, as described by Tim Bliss and Terje Lømo's early experiments, LTP exhibits *input specificity*, such that potentiation induced at individual synapses only affects those which contribute directly to LTP and does not spread to non-potentiated synapses. This has been proposed to occur through Frey and Morris' mode of 'synaptic tag and capture' (Dynes and Steward, 2007), wherein currently unidentified proteins or processes act to target plasticity related proteins (PRP) exclusively to activated or potentiated synapses. Secondly, LTP displays rules of *associativity*, such that weakly activated synapses can be strengthened by a strong stimulus at spatially distinct synapses (Shors and Matzel, 1997). Thirdly, and similar to associativity is *cooperativity*: LTP can be induced by either a strong stimulation or in the case of cooperative potentiation,

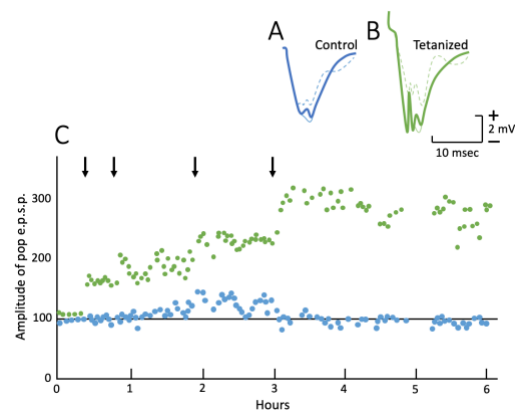


Figure 1-4 | The discovery of LTP. Long term potentiation was first reported in the perforant path in anaesthetized rabbits. Responses from both control and tetanized pathways A) before and B) after conditioning. C) Graph showing the amplitude of the population EPSP for control (●) and tetanized (●) pathways. Conditioning trains (arrows) were given at a rate of 15/sec for 10 sec.

many individual weak stimulations converging spatially and temporally at one pathway, neuron, or synapse may act to collectively depolarize the postsynaptic membrane enough to produce LTP (Kitajima and Hara, 1991). Lastly, and perhaps the most distinct characteristic of LTP is its *persistence*, that is the ability of LTP to last from several minutes to many months (Abraham, 2003), and it is this that distinguishes LTP from other forms of plasticity expressed on much shorter timescales (milliseconds to minutes), such as paired-pulse facilitation, and post-tetanic potentiation (Citri and Malenka, 2008).

Since 1973, the field has expanded, covering many of the plausible aspects that might contribute to the expression and persistence of Hebbian plasticity using LTP as a model, examining electrophysiology, molecular biology, biochemistry, genetics and epigenetics (Lynch et al., 1979; Teyler, 1999; Matynia et al., 2002). Early observations began to describe underlying mechanisms governing LTP. Of these, it was shown that learning paradigms were correlated with an increase in protein synthesis and preventing this process impaired the persistence and consolidation of memories (Flexner et al., 1962; Flexner et al., 1963; Agranoff and Klinger, 1964; Agranoff et al., 1965; Flexner et al., 1965; Flexner et al., 1966; Agranoff, 1967; Shashoua, 1976). Following this, the cellular correlate of protein synthesis-dependent memory consolidation was sought. In 1984, Manfred Krug showed that the maintenance of hippocampal dentate gyrus LTP beyond 3 hours *in vivo* could be blocked by application of the protein synthesis inhibitor anisomycin (Krug et al., 1984). Various researchers later replicated these findings, observing similar results throughout the hippocampus using a variety of stimulation methods (Frey et al., 1988; Frey et al., 1989; Otani and Abraham, 1989; Fazeli et al., 1993; Osten et al., 1996; Nayak et al., 1998). Through these observations, it was theorized that LTP displays distinct phases, depending on the necessity of protein synthesis. Short-term plasticity (STP) is defined as a form of plasticity which decays rapidly, lasting approximately 20–40 minutes, and is thought to be dependent on primarily presynaptic mechanisms (Hennig, 2013), including; residual presynaptic calcium (Katz and Miledi, 1968; Kamiya and Zucker, 1994; Wu and Saggau, 1994), saturation or dislocation of presynaptic calcium buffers (Caillard et al., 2000; Blatow et al., 2003; Timofeeva and Volynski, 2015), enhancement of presynaptic calcium currents (Borst and Sakmann, 1998; Leal and Klein, 2009), and changes in the sensitivity of calcium sensors such as synaptotagmins, controlling delayed versus fast presynaptic neurotransmitter vesicle release (Burgoyne and Weiss, 2001; Stevens and Sullivan, 2003; Burgoyne, 2004; Yoshihara and Montana, 2004; Jackman et al., 2016; Figure 1-5).

Early phase (E-LTP or LTP1) and late-phase (L-LTP or LTP2) LTP are further distinguished by their dependency on protein synthesis. LTP1 is thought to last anywhere from one to many hours and is independent of protein synthesis (Krug et al., 1984), emerging through post-translational

modifications of pre-existing proteins by calcium-dependent enzymes, as well as expansion of the spine cytoskeleton and glutamate receptor trafficking (Blundon and Zakharenko, 2008; Bosch et al., 2014; Park, 2018b; Figure 1-5). LTP2 on the other hand, is invariably long-lasting, persisting for up to many hours post-stimulation (Malenka, 1991a; Schulz and Fitzgibbons, 1997; Frey et al., 2001; Figure 1-5). Evidence suggests that LTP2 is dependent on the dendritic synthesis of PRPs, for its persistence. This 'local protein synthesis' comes from studies utilizing dendrites isolated from the soma, and thus preventing distal trafficking of new proteins. In these preparations, L-LTP could still be produced and was blocked by the application of protein synthesis inhibitors (Manahan-Vaughan et al., 2000; Cracco et al., 2005; Huang and Kandel, 2005; Vickers and Wyllie, 2007). These observations likely indicate a role in the local translation of pre-existing mRNA present at or near the activated synapses (Steward and Schuman, 2001), likely in order to engage mechanisms which consolidate the changes initiated during LTP1 (Hardt et al., 2013). There is increasing evidence that the consolidation of the synaptic changes during LTP2 occur, in part, through the synthesis and function of neuromodulators, such as dopamine (Frey et al., 1991a; Frey et al., 1991b; Huang and Kandel, 1995; Granado et al., 2008), BDNF (Ying et al., 2002; Lu et al., 2008; Panja and Bramham, 2014), and serotonin (Mlinar et al., 2015). Furthermore, evidence exists of an additional phase of LTP (LTP3) which requires the transcription of new mRNA (Nguyen et al., 1994; Frey et al., 1996; Vickers et al., 2005; Ryan et al., 2011), and has been described to underlie the persistence of long-term memories, lasting anywhere from hours (Nguyen et al., 1994; Frey et al., 1996) to months (Abraham et al., 2002). These gene transcripts may underlie mechanisms which expand the pool of newly synthesised proteins, replenish proteins and mRNA directly involved in early enhancements of LTP (Abraham and Williams, 2003), as well as orchestrate chromatin and epigenetic modifications (Alberini and Kandel, 2014).

As the expression characteristics of LTP were slowly being elucidated, a second debate arose within the field — that which was concerned with the mechanistic locus of LTP. For many years the debate sat split down the centre of the synaptic cleft. On one side, those believing presynaptic changes underlie the increased synaptic response, and on the other; those who believe postsynaptic changes dictate changes in potentiation. Early studies found evidence for the presynaptic component of LTP through increases in neurotransmitter release probability (Bekkers and Stevens, 1990; Malinow and Tsien, 1990), the number of active release sites (Bolshakov et al., 1997), or the quantal size of neurotransmitter vesicles (Kullmann and Nicoll, 1992; Stricker et al., 1996). Countering this, the postsynaptic argument posited that changes in the synaptic expression of N-Methyl-d-aspartate (NMDA) and α -amino-3-hydroxy-5-methyl-4-isoxazolepropionic acid (AMPA) receptors are responsible for the observed increase in the EPSP, as evidenced from increases in the AMPA:NMDA

current ratio (Watt et al., 2004; Sjöström et al., 2007), the number of AMPAR (Hayashi et al., 2000) and NMDAR (Berretta et al., 1991; Xie et al., 1992), the dependence on AMPAR expression (Zamanillo et al., 1999; Granger et al., 2013), as well as changes in structural plasticity (Matsuzaki et al., 2004).

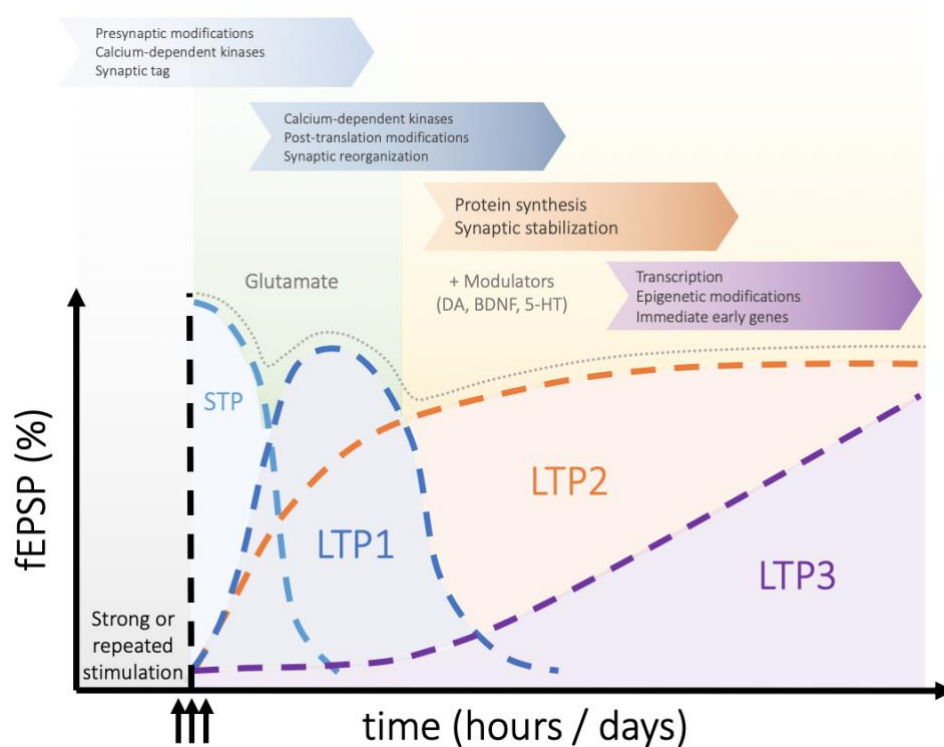


Figure 1-5 | Schematic illustration of separate phases of synaptic long-term potentiation. STP (■) is defined by a short-lasting potentiation of the EPSP induced by weak tetanisation. LTP1 (E-LTP, ■) is defined primarily by a sensitivity to kinase inhibitors, as well as increases in presynaptic quanta and requires strong tetanisation, decaying within an hour. LTP2 (L-LTP, ■) is a long-lasting potentiation which is sensitive to protein-synthesis inhibitors and additive to LTP1, lasting > 3 hours. LTP3 (■) is dependent on new gene transcription and is sensitive to inhibitors of this. LTP2 and LTP3 can be achieved through strong or repeated tetanization or addition of modulators including neurotrophins or growth factors including dopamine (DA), brain-derived neurotrophic factor (BDNF), and serotonin (5-HT). Originally defined by Reyman & Frey, (2007).

Importantly, throughout this debate, a proportion of researchers began to shift their focus to phenomena of ‘silent synapses’. These synapses are termed as such due to the absence of functional AMPAR during baseline responses, able to be ‘awoken’ or ‘unsilenced’ upon LTP stimulation through an NMDAR-dependent mechanism. Similar to the debate surrounding the locus of LTP expression, silent synapses sparked a parallel debate regarding the mechanism of synapse unsilencing. Many of those on the presynaptic side of the debate carry their beliefs to the unsilencing of silent synapses, such that these synapses can be explained primarily through low release probability of glutamate (Gasparini et al., 2000; Montgomery et al., 2001). Likewise, with LTP, postsynaptic mechanisms may also explain a mechanism to unsilence silent synapses. Initial studies posited that unsilencing occurs

throughout development, with many synapses initially containing NMDAR but little to no AMPAR, finding that miniature EPSCs (mEPSC) frequency increases throughout development – concluding that AMPAR insertion underlies synapse awakening (Petralia et al., 1999; Vincent-Lamarre et al., 2018; Wright et al., 2020; Xu et al., 2020). Further, evidence suggests that LTP underlies one mechanism through which silent synapses are awoken (Liao et al., 1995; Durand et al., 1996; Liao et al., 1999).

1.2.2. *Long-Term Depression*

Early studies investigating mechanisms that serve to increase the strength between neural connections (such as LTP) theorized that a system such as this must have a way to actively *decrease* synaptic strength in contrast. The reversible nature of LTP, such that LTP undergoes passive decay following extended potentiation over a period of days to weeks, could theoretically be sufficient to employ a mechanism of information storage. Yet, a system serving to only actively increase the strength of a synapse would inevitably reach a point of saturation of maximal information storage. Thus, the ability to actively decrease and reset individual synaptic weights adds a distinct computational advantage. Therefore, long-term depression (LTD) became the focus of many studies in the 80s and 90s as a mechanism which may act to 1) prevent the saturation of LTP (Byrne, 2010), 2) act as an active resetting of previously potentiated synapses (Barr et al., 1995; Muller et al., 1995; Villarreal et al., 2002), 3) amplify the signal-to-noise ratio of neighbouring potentiated synapses (Dayan and Willshaw, 1991; Kemp and Manahan-Vaughan, 2007), or 4) mediate mechanisms underlying forgetting (Tsumoto, 1993; Nabavi et al., 2014).

The earliest publications describing what we now understand to be LTD, described the effect of low frequency stimulation (LFS) on the postsynaptic response (Barrionuevo et al., 1980; Levy and Steward, 1983; Lynch et al., 1976; Lynch et al., 1977). Of note is Barrionuevo & Lynch (1980) who elicited LFS on both control (non-potentiated) and previously potentiated Schaffer collateral–Commissural projections in the rat hippocampus. Interestingly, they describe a persistent depression of both experimental groups, lasting 15–30 minutes following LFS, concluding LTD to be a mechanism by which the hippocampus employs to both offset enhancement by LTP and decrease the baseline strength of synapses (Figure 1-6). While it is argued that the depression of the previously potentiated pathway may in fact be depotentiation, a mechanism distinct from LTD (Huang and Hsu, 2001; Sanderson, 2012), the effect of LFS on control synapses was evident.

Following these findings, efforts were made to understand the mechanisms behind LTD. Dudek and Bear, (1992) first examined LTD under the principals previously applied to LTP, finding that LTD in the hippocampus shows *input specificity, cooperativity, associativity, and persistence*. These findings, and many more describe a similar mechanism to LTP. It has been found that the induction of LTD

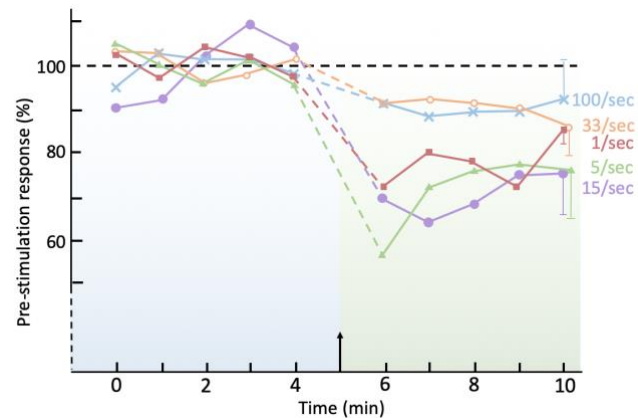


Figure 1-6 | The discovery of LTD. The effect of low frequency stimulation (arrow) on the population spike amplitude. 1/sec (■), 5/sec (▲), 15/sec (●), 33/sec (○), 100/sec (×). Data from Barrionuevo et al., (1980) | The discovery of LTD.

consistently yielded a depression of the EPSP, while 10Hz produced no change in EPSP and 50Hz caused potentiation (Dudek and Bear, 1992; Figure 1-6), 2) is blocked by an NMDA receptor antagonist (Mulkey and Malenka, 1992), 3) does not prevent later LTP by HFS, 4) reaches saturation, or maximal depression (Levy and Steward, 1983; Christie and Abraham, 1992), and 5) can be reversed by LTP (Abraham and Goddard, 1983). These discoveries generated a new outlook on the modification of synaptic information processing through controlled bidirectional changes in synaptic strength, defining a mechanism separate from LTP, produced through opposing stimulation patterns, yet converging through the necessity of the NMDA receptor.

As observed with LTP, the induction and persistence of LTD may be separated into distinct, overlapping mechanisms. Short-term depression (STD) is a transient form of synaptic depression shown to occur following trains of frequent stimulation. This STD is thought to occur through, 1) a depletion of the readily releasable pool (RRP) of neurotransmitter vesicles at the presynaptic terminal (Zucker and Regehr, 2002; Rizzoli and Betz, 2005; Regehr, 2012), 2) inactivation or saturation of vesicle fusion sites (Neher and Sakaba, 2008; Hosoi et al., 2009), 3) reduction in presynaptic calcium currents (Forsythe et al., 1998; Xu and Wu, 2005; Catterall and Few, 2008; Neher and Sakaba, 2008; Hosoi et al., 2009), and 4) desensitization of postsynaptic glutamate receptors (Antzoulatos et al., 2003; Koike-Tani et al., 2008). Similar to LTP, initial short-lasting changes such as STD, have the capacity to evolve into stronger, more persistent forms. As first shown by Barrionuevo et al., (1980) and later by Dudek and Bear, (1992b), decreasing the rate at which synapses are stimulated, greatly enhanced the level of synaptic depression observed, such that 5-10 Hz stimulation results in a short lasting LTD, “decaying” back to baseline (E-LTD), while lower 1-3 Hz stimulation results in long-lasting depression of synaptic depression (L-LTD; Dudek and Bear, 1992b; Kauderer and Kandel, 2000).

Importantly, as with early-phase LTP, both STD and E-LTD have been shown to be protein synthesis-independent, with the expression of E-LTD likely involving the activity of protein phosphatases (Lisman, 1989; Mulkey et al., 1993). Conversely, long-lasting L-LTD has been shown to involve an additional protein synthesis-dependent component, necessary for its maintenance (Huber et al., 2000; Kauderer and Kandel, 2000; Sajikumar and Frey, 2004), for at least 4-5 hours following induction *in vivo*. Interestingly, the persistence of L-LTP may depend on pre-existing mRNA for local translation of required proteins (Huber et al., 2000; Sajikumar and Frey, 2003). Beyond this, some evidence also exists for an additional requirement of transcription *ex vitro* (Lindecke et al., 2006) and a much later (> 24 hours) role *in vivo* (Kemp et al., 2013).

Importantly, while LTP involves the formation, growth, and maturation of dendritic spines and synapses, LTD may govern an opposing mechanism of synapse shrinkage and elimination. Application of NMDA to cultured neurons showed a protein phosphatase-, protein synthesis- and transcription-dependent reduction in the number of functional synapses and spines (Ramiro-Cortés and Israely, 2013; Henson et al., 2017), while LTD-inducing stimulation was found to shrink spines (Nägerl et al., 2004), in a manner which could be rescued by LTP-inducing stimulation (Zhou et al., 2004). These results have been further corroborated by *in vivo* studies, in which induction of LTD eliminated both depressed synapses, as well as weakly-integrated neighbouring synapses (Wiegert and Oertner, 2013). These results indicate that LTP- and LTD-like mechanisms promote bidirectional changes in both physiological as well as morphology to regulate the expression of plasticity.

1.2.3. *Homeostatic plasticity*

As mentioned above, Hebbian plasticity in the central nervous system acts to encode information through changes in the strength of synaptic connections. However, a caveat of this means stronger synapses are more likely to depolarize the postsynaptic neuron, increasing the probability that they will undergo further potentiation. A system such as this, without forces that prevent uncontrolled excitability, would lead to unconstrained synaptic strengthening, wherein the specificity of information breaks down and can no longer be effectively stored through differences in synaptic strength (Whitt et al., 2014). In theory, without a mechanism to maintain relative differences between competing inputs, a mechanism such as LTP, which aims to increase the excitability of cells or synapses, would only serve to further potentiate other inputs, increasing the probability of pre- and postsynaptic associations. Therefore, homeostatic plasticity allows for the adjustment of neuronal or synaptic weights, in order to avoid hyperexcitability, maintain the ability of inputs to remain plastic, and prevent the loss of valuable information following both strong synaptic activity or

sustained periods of inactivity. Here, relative strengths are maintained within a physiological range for Hebbian plasticity to occur (Figure 1-7A.)

There are several ways in which neurons may compensate for periods of increased or decreased activity. These include altering their intrinsic excitability (Camp, 2012), modifying the relative strength of inhibitory or excitatory inputs (Turrigiano and Nelson, 2004), as well as adapting the thresholds for the expression of

plasticity (Bienenstock et al., 1982; Bear et al., 1987; Bear, 1995; Figure 1-7B-C). The latter of these describes a mechanism wherein neighbouring synaptic weights are 'counterbalanced' following single input potentiation, such that when a single synapse increases in strength, neighbouring synapses decrease in compensation (Rabinowitch and Segev, 2006; 2008; Lee et al., 2013). Similarly, a global process that scales all synaptic weights up or down proportionally, regardless of previous potentiation, allows neurons to stabilize excitability and

firing without changing the relative strength of synaptic inputs (Turrigiano, 2008; Turrigiano, 2012). These models allow for the stabilization of overall cell excitability by maintaining stable excitability within a dendritic compartment, branch, or whole cell.

In the past decade, much effort has been made investigating mechanisms of homeostatic plasticity, first described by (Turrigiano et al., 1998). One method of homeostatic plasticity, synaptic scaling, has been investigated by measuring spontaneous miniature EPSPs (mEPSP) of neurons following treatment with GABA antagonists, such as bicuculline. This effect increases firing rates due to the prolonged decrease in network inhibition and the increase in spontaneous activity (Turrigiano et al., 1998). This group found that following treatment across a 48-hour period, mEPSPs returned to baseline values. Similarly, suppressing network excitability by overexpressing inward-rectifying potassium channels or application of the sodium channel blocker tetrodotoxin (TTX) was found to increase synaptic mEPSPs (Burrone et al., 2002; Gainey et al., 2009). Together these results indicate a

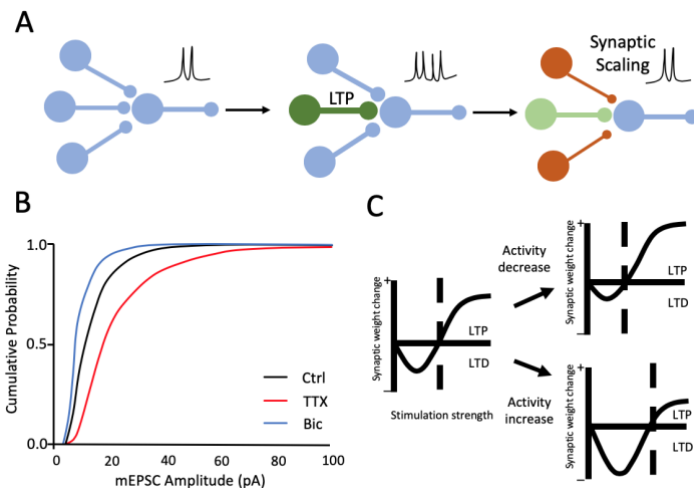


Figure 1-7 | Conceptual illustration of synaptic scaling.

A) Schematic depiction of individual synapses (●). LTP of one input increases postsynaptic firing (●), homeostatic scaling will reduce the strength of both potentiated (●) and non-potentiated (●) synapses, to restore firing rate to baseline levels. B) Global increases (TTX) or decreases (Bic) shift the excitation of cultured neurons. C) sliding threshold for LTP and LTD induction. Increases or decreases in activity shift the threshold to promote LTD or LTP, respectively.

mechanism for compensatory, bi-directional control over cell excitability (Figure 1-7B). However, if Hebbian plasticity acts to increase or decrease the strength of individual inputs, and homeostatic plasticity acts to move a neuron back towards its original state, how does homeostatic plasticity avoid erasing the encoded Hebbian information? Early insights theorised that changes in neuronal excitability may shift the threshold for the induction of plasticity. From this, the Bienenstock, Cooper and Munro (BCM) learning rule was developed and describes a model in which decreases in activity result in a reduced threshold for LTP — promoting synapse strengthening and making LTD harder to achieve (Bienenstock et al., 1982). Conversely, increases in activity are proposed to shift the threshold to favour LTD and promote LTP (Figure 1-7C), and vice versa. The BCM rule has been shown to be applicable *in vivo*, such that light deprivation shifts the threshold for promoting LTP in the visual cortex as a means to promote changes in synaptic efficacy with minimal stimulation (Kirkwood et al., 1996). Many mechanisms have been thought to carry out homeostatic plasticity such as changes in the size of releasable presynaptic neurotransmitter vesicles (Murthy et al., 2001), release of neuromodulators from glial cells (Stellwagen and Malenka, 2006), as well as changes in the accumulation of glutamate receptors at the synapse (Turrigiano, 2008; Gainey et al., 2009; Pozo and Goda, 2010; Hou et al., 2011).

1.2.4. *Metaplasticity*

As has been made clear, synaptic plasticity is not a unitary event. Alterations in synaptic efficacy, including but not limited to LTP, LTD, and homeostatic plasticity, are made not only at the synaptic level, but at the level of the dendrite (Williams et al., 2007b), the cell (Debanne, 2009), the memory trace or engram (Bocchio et al., 2017), and network (Kajiwara et al., 2019). Importantly, these mechanisms do not occur in isolation, and mounting evidence suggests that previous synaptic and cellular activity alters the expression of subsequent plasticity at each of these levels. This plasticity of synaptic plasticity has been termed Metaplasticity, and is described as prior cellular or synaptic activity or inactivity which elicits a persistent change in the state of the synapse, altering the outcome of subsequent potentiation, depression, or expression of memory (Abraham, 2008). While metaplasticity appears most obvious when it occurs in the absence of altered synaptic efficacy, metaplastic modifications may also be induced by long-lasting changes, such as those occurring during LTP and LTD (Abraham and Bear, 1996). Early work showed that synaptic activity which, by itself, does not produce long-lasting changes, significantly influenced the degree of subsequent plasticity (Huang et al., 1992) such that the degree of LTP was significantly reduced. Further, both homeostatic plasticity (Kirkwood et al., 1996; Guo et al., 2012), and behavioural learning have been

shown to alter the induction of LTP (Tsvetkov et al., 2002; Whitlock et al., 2006), indicating that both non-hebbian and Hebbian-like mechanisms contribute to aspects of metaplasticity. Many of the mechanisms which have been found to influence metaplasticity involve the activation of NMDAR (Rebola et al., 2011), metabotropic glutamate receptors (mGluR; Gisabella et al., 2003), Ca^{2+} (Mahajan and Nadkarni, 2019), and protein phosphatases (Kato et al., 1999) and kinases (Gisabella et al., 2003; Young et al., 2006; Zorumski and Izumi, 2012). Importantly, metaplasticity has also been observed following application of neuromodulators, including dopamine (Otani et al., 2003; Sheynikhovich et al., 2013; Otani et al., 2015), nicotine (Huang et al., 2013), serotonin (Inoue et al., 2014), noradrenaline (Inoue et al., 2013; Keralapurath et al., 2014), BDNF (Rivera-Olvera et al., 2016), and tumour necrosis factor- α (TNF- α ; Singh et al., 2019). In many cases these molecules act to prime synapses in order to enhance or suppress the induction of LTP, by shifting the threshold such that induction of LTP or LTD is more or less likely to occur.

1.3. Mechanisms Governing the Expression of Cellular Memory

So far, this review has aimed to summarise the characteristics which govern the expression of learning and memory at the cellular level. Early observations postulated that repetitive synaptic activity governs the metabolic change at the synaptic and cellular level. Research henceforth further characterised the role of high- or low-frequency stimulation in governing the synaptic potentiation and depression observed. Metabolic growth, initially postulated by (Hebb, 1949) has been further defined through the necessity of protein synthesis in regulating the persistence of memories, and gene expression in consolidating these changes. It is well understood that the genes and proteins expressed following the induction of LTP or LTD are strictly regulated, and govern discrete functions, each acting to directly or indirectly alter the postsynaptic potential. Henceforth, this review aims to address key questions which remain unanswered, firstly, what events occur during the initiation of LTP or LTD? Secondly, in what way are synapses altered following LTP or LTD, and how do these changes manifest into a persistent, stable memory? Thirdly, what is the role of growth factors in the induction and persistence of LTP? And lastly, how are these mechanisms altered in neurological diseases?

To answer these questions, I aim to characterise the relative contribution of proteins or molecules I believe to be innately linked to the expression of memory. Here, mediators, messengers, modifiers, and modulators form the foundations of a hierarchy, each contributing a specific set of functions in the expression of plasticity.

1.4. Mediators of Plasticity

Following the observations of the electrophysiological properties of LTP, LTD and homeostatic plasticity, research began to define the underlying molecular mechanisms which permit these changes. Much overlap exists between the proteins or processes responsible for many of the mechanisms which affect synaptic strength, however for the purpose of this literature review much emphasis will be placed on those which govern LTP. Consequently, I have defined four distinct categories of processes or molecule classes, which I believe to contribute to the expression of late LTP (LTP3) and plasticity in distinct ways. Mediators in this sense are defined as proteins or molecules, which are necessary for, and are directly involved in the mechanisms that lead to a change in synaptic strength. Genetic or chemical elimination of these mediators results in complete, or near complete obstruction of LTP, severely impairing plasticity, and ultimately affecting the expression of learning and memory.

1.4.1. *NMDA Receptors*

NMDA receptors (NMDAR) are ionotropic glutamate receptors with unique and extensive roles in mediating many of the changes during synaptic plasticity. NMDAR are heterotetrameric, formed from seven differentially expressed subunits: GluN1, which undergoes extensive splicing to produce eight variants (GluN1-1A–GluN1-4A & GluN1-1B–GluN1-4B), four GluN2 (GluN2A–GluN2D), and two GluN3 (GluN3A–GluN3B; Iacobucci and Popescu, 2017), produced from separate genes (*GRIN1-3*). Structurally, NMDAR are formed from the association of an obligatory GluN1 subunit with various GluN2 subunits to yield four major subtypes: GluN1/GluN2A, GluN1/GluN2B, GluN1/GluN2C, GluN1/GluN2D, characterised by distinct but overlapping regional and developmental expression patterns (VanDongen, 2008; Figure 1-8). Minor populations have also shown the association of GluN1 with GluN2A and GluN2B or GluN2C, as well as GluN1 with GluN2B and GluN2D, within the same receptor (Stephenson, 2001; Rauner and Köhr, 2011; Bhattacharya et al., 2018). Variations in GluN1 and GluN2A/2B compositions at the synapse regulate both the development of neural circuits, as well as the expression of plasticity (Sheng et al., 1994). The role of GluN3-containing subunits is not as clear; however, they appear to form functional receptors with GluN1, but not GluN2 subunits, primarily expressed during a short window of development (Pachernegg et al., 2012; Pérez-Otaño et al., 2016).

Following the characterization of NMDAR structure, many sought to determine the contribution of NMDAR to synaptic activity. It was Collingridge et al., (1983) who first described the sensitivity of hippocampal tissue to excitatory amino acids such as L-glutamate, and further described the dependence of NMDAR during LTP, finding that the NMDAR antagonist APV blocked LTP at Schaffer-collateral synapses. Around the same time, Lynch et al., (1983) described the importance of intracellular calcium (Ca^{2+}), by injection of the calcium chelator EGTA into the postsynaptic cell. This was found to significantly impair the induction of Schaffer collateral-CA1 LTP, indicating Ca^{2+} influx as a crucial mediator of downstream processes governing the expression of LTP in these cells. Importantly, later contributions found that NMDAR are highly permeable to both sodium (Na^+) and Ca^{2+} ions (Müller and Connor, 1991; Jahr and Stevens, 1993; Schneggenburger et al., 1993; McBain and Mayer, 1994; Garaschuk et al., 1996; Yu and Salter, 1998), and therefore may contribute significantly to processes of plasticity.

From this evidence, it seemed reasonable to propose an NMDAR-dependent influx of postsynaptic Ca^{2+} as a mechanism through which synaptic changes could occur. Therefore, following these results, a series of papers were published which further delineated the details of this. In 1984, Nowak et al., showed the importance of a Mg^{2+} -dependent NMDA receptor blockade, such that in conditions in which extracellular Mg^{2+} was reduced, the NMDA receptor response was largely facilitated (Nowak et al., 1984). In 1985, Wigström and Gustafsson showed that blockade of postsynaptic inhibition by use of GABA inhibitors strongly facilitated LTP (Wigstrom and Gustafsson, 1985a), while Malinow and Miller showed that hyperpolarization of the postsynaptic membrane reversibly blocked LTP (Malinow and Miller, 1986). These properties suggest a 'membrane voltage-dependent' role of postsynaptic depolarization in regulating LTP. In this sense, NMDAR is thought to act as a coincident detector for activity sufficient to promote LTP and compute the Hebbian conditions necessary for associative memory. It has been proposed that ionic non-NMDAR channels (passing Na^+ and K^+), or changes in the level of postsynaptic inhibition, is sufficient to provide postsynaptic depolarization and Mg^{2+} expulsion from the NMDAR channel, while consecutive presynaptic neurotransmitter release provides activation of NMDAR itself, promoting Ca^{2+} influx (Wigstrom and Gustafsson, 1985b). Later influential work by Morris et al., (1986) further tied NMDA

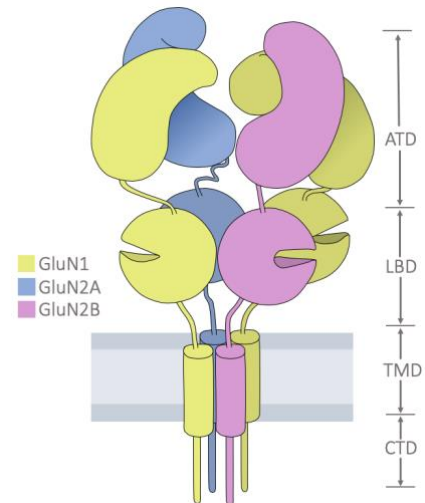


Figure 1-8| Schematic diagram of NMDAR Structure. Stylized diagram of GluN1 (■) and GluN2A (■) and GluN2B (■)-containing NMDAR showing amino terminal domains (ATD), ligand binding domains (LBD), transmembrane domains (TMD), and C-terminal domains (CTD).

receptor activation directly to memory formation during a spatial learning task. Chronic intraventricular infusion of APV was found to selectively impair both the memory formation and the expression of LTP. More conclusive evidence from genetic ablation of CA1-specific NMDAR found a distinct absence of LTP at these synapses and an impairment in spatial memory (Tsien et al., 1996), suggesting NMDA receptors as an enticing mechanism of action in permitting the changes observed during long-term potentiation and memory.

1.4.2. *AMPA receptors*

In addition to NMDAR, many glutamatergic synapses house an abundant population of AMPA receptors. AMPA receptors comprise the primary excitatory receptor in the CNS, belonging to a class of ionotropic glutamate receptors further divided based on the individual subunit compositions, these include AMPA (GluA1–GluA4), kainate (GluK1–GluK5), delta (δ) receptors (GluD1 and GluD2), as well as NMDAR (Traynelis et al., 2010). AMPAR are composed of four subunits by a dimer of two identical homo- or heterodimers that together form a tetramer. Each subunit contains one ligand-binding site, and upon binding the subunit undergoes a conformational change allowing the channel to open and ions to flow through the pore (Mayer, 2005). The structure of each subunit can be divided into a large extracellular amino-terminal domain (ATD), ligand-binding domain (LBD), transmembrane domain (TMD) forming the pore, as well as a cytoplasmic carboxy-terminal domain (CTD, Figure 1-9). GluA1 and GluA4 (and a splice variant of GluA2, GluA2L) contain long carboxy-terminal domains, while these are short in GluA2 and GluA3 subunits (Diering and Huganir, 2018). These carboxy-terminal domains allow the subunits to interact with specific cytoplasmic and transmembrane proteins, due to the presence of phosphorylation, palmitoylation, ubiquitination, and nitrosylation sites along its length (Figure 1-9A).

The synthesis of AMPAR subunits and the subsequent assembly into functional receptors is a highly regulated process and occurs through two possible routes. The primary method occurs through the canonical synthesis and trafficking pathway (Hangen et al., 2018; Figure 1-10). This process begins in the soma, where AMPAR subunits are synthesised and assembled in the endoplasmic reticulum (ER), first forming dimers, followed by the formation of tetramers (Herguedas et al., 2013). Before release from the ER, AMPAR undergo a form of quality control through their associations to AMPAR-interacting proteins (Rubio and Wenthold, 1999; Hebert and Molinari, 2007), dependence on external signals such as Ca^{2+} (Lu et al., 2014; Pick et al., 2017; Hangen et al., 2018), and detection of conformational state (Penn et al., 2008), and edited RNA motifs (Greger et al., 2002). In the neuronal soma, AMPAR traffic from the ER to Golgi apparatus. Here, AMPAR may undergo extensive

posttranslational modifications (PTM), such as glycosylation, palmitoylation, and phosphorylation (Jiang et al., 2006). These PTMs are dynamic, reversible, and sensitive to alterations in synaptic activity (Jiang et al., 2006). From here, AMPAR may undergo transport from the soma towards target sites throughout the dendrites (Passafaro et al., 2001), or delivered directly to the somatic cell surface to undergo lateral diffusion (Borgdorff and Choquet, 2002; Adesnik et al., 2005). Transport throughout the dendrites occurs under the guidance of chaperone proteins such as kinesin and myosin motor proteins (Wang et al., 2008; Hoerndli et al., 2013), and the Ca²⁺/calmodulin-dependent kinase (CaMKII; Hoerndli et al., 2015; Hangen et al., 2018), along microtubules into dendrites and

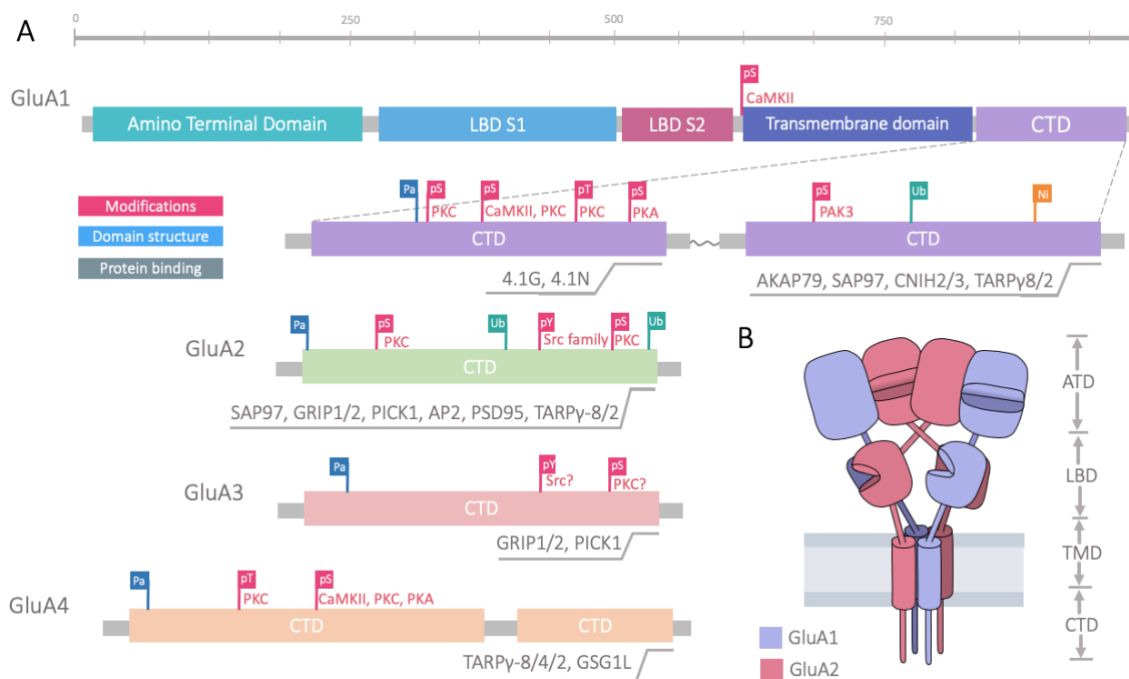


Figure 1-9 | Schematic diagram of AMPAR Structure. A) shows sites present in GluA1-4 subunits, including the amino terminal domain (ATD, ■), ligand binding domains S1 (■) and S2 (LBD, ■), transmembrane domain (TMD, ■), and the C-terminal domain (CTD) of GluA1 (■), GluA2 (■), GluA3 (■) and GluA4 (■). Post-translational modifications include: phosphoserine (pS), phosphothreonine (pT), phosphotyrosine (pY), ubiquitinated lysine (Ub), nitrosylation (Ni). Scale bar: amino acids. B) Shows a stylized example diagram of the GluA1- (■) and GluA2 (■)-containing heterodimers forming the tetrameric AMPAR structure.

spines.

Alternatively, AMPAR may also undergo synthesis at local sites within the dendrites (Torre and Steward, 1992; Kacharmina et al., 2000; Grooms et al., 2006; Sutton and Schuman, 2006). This method still involves the translation of mRNA by polyribosomes and ER located at the base of synapses (Steward and Levy, 1982; McCarthy and Milner, 2003; Ainsley et al., 2014), as well as specialized spine ER, called the spine apparatus (Frotscher and Deller, 2005; Jedlicka et al., 2008). However, as dendrites mostly lack the Golgi apparatus (Krijnse-Locker et al., 1995; Torre and Steward,

1996), AMPAR instead pass through a modified Golgi-related compartment, called the Golgi outpost (Horton and Ehlers, 2003; Horton et al., 2005). Conversely, recent evidence suggests AMPAR may undergo Golgi-independent trafficking, instead directly incorporating into the recycling endosome, following exit from the ER (Bowen et al., 2017; Figure 1-10). These mechanisms likely underlie distinct functional roles mediating the persistence of LTP (Vickers and Wyllie, 2007; Hangen et al., 2018).

1.4.2.1. *GluA1*

GluA1 (also referred to as GluR1 and GluRA) is undoubtedly the most studied AMPAR subunit in the context of synaptic plasticity and learning and memory. Considering its expression throughout many structures of the CNS, including the cortex, amygdala, cerebellum, thalamus, brainstem and the highest levels in the CA1–CA3 and DG regions of the hippocampus, it is clear to see why (Breese et al., 1996). GluA1 mRNA has been found extensively within both excitatory principal cells as well and inhibitory interneurons (Geiger et al., 1995), however expression has also been observed in GFAP-positive glial cells (Patneau et al., 1994; Matthias et al., 2003), as well as oligodendrocytes (Zonouzi et al., 2011; Evonuk et al., 2020). GluA1 has been shown to undergo both canonical *de novo* synthesis as well as activity-dependent local translation (Ju et al., 2004; Grooms et al., 2006; Cajigas et al., 2012), before highly regulated trafficking to the cell surface and synapse. GluA1 primarily forms heterodimers with GluA2 to form GluA1/2 AMPAR comprising approximately 80% of the total AMPAR population (Lu et al., 2009). However, it has also been shown to form GluA1 homomeric AMPAR (Lu et al., 2009) comprising 8% of the AMPAR population (Wenthold et al., 1996), yet the presence and contribution of these AMPAR is highly debated in the literature.

The differences in AMPAR subunit make-up impacts its trafficking and retention dynamics from the rough ER. While each subunit exhibits similar core structures, differences in the C-terminal domain (CTD) determine their trafficking dynamics in response to activity. Primarily, the long CTD present in the GluA1 subunit permits phosphorylation by activity-driven proteins such as Ca²⁺/calmodulin kinase (CaMKII), and protein kinase A (PKA), PKC and PKG to regulate the trafficking and stabilization of GluA1-containing AMPAR (Hayashi et al., 2000), by facilitating associations with crucial chaperone and scaffold proteins such as PSD-95/Drosophilla discs large/zona occludens-1 (PDZ) domain proteins (Shi et al., 2001; Anggono and Haganir, 2012), including Synapse-associated protein 97 (SAP97; Leonard et al., 1998) A-kinase anchoring protein 79 (AKAP79; Colledge et al., 2000), and Cornichon Family AMPA Receptor Auxiliary Proteins 2/3 (CNIH2/3; Herring et al., 2013), transmembrane AMPA receptor regulatory proteins (TARPs) γ 8 and γ 2 (Diering and Haganir, 2018), and protein 4.1N (Shen et al., 2000).

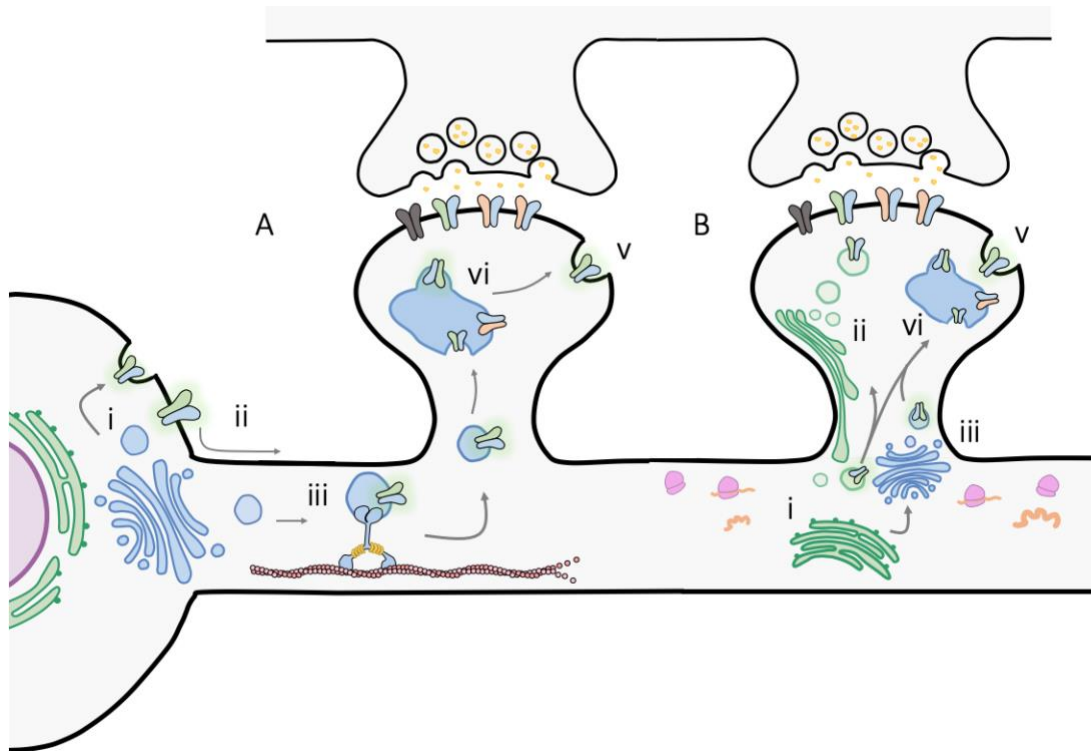


Figure 1-10 | Regulated AMPAR synthesis and trafficking methods. Schematic diagram shows both A) canonical and B) local mechanism governing AMPAR synthesis and trafficking. A) Following i) synthesis a within the soma AMPAR subunits exit the ER and pass through the Golgi apparatus, here AMPAR can be ii) exocytosed at the somatic cell surface and undergo lateral diffusion or iii) are trafficked within dendrites towards the synapse, where AMPAR are incorporated into vi) recycling endosomes before v) trafficking to the cell surface. Alternatively, B) AMPAR subunits may be synthesised locally at i) polyribosomes and ER or ii) spine apparatus present within the dendrites and spine. AMPAR may iii) pass through the Golgi apparatus or vi) incorporate directly into the recycling endosome before v) trafficking to the cell surface.

These associations permit GluA1 to contribute prominently to LTP through its activity-dependent regulation and delivery to potentiated synapses (Hayashi et al., 2000; Kakegawa et al., 2004; Williams et al., 2007a; Zhang et al., 2015; Yamasaki et al., 2016; Coombs et al., 2017; Bissen et al., 2019; Figure 1-9A). Conversely, inclusion of the shorter CTD present in GluA2 and GluA3 subunits results in longer retention within the ER, compared to AMPAR containing GluA1 subunits (Greger et al., 2003). Here, trafficking primarily occurs in a constitutive manner, thought to replace GluA1-containing AMPAR at the synapse (Araki et al., 2010; Casimiro et al., 2013). This trafficking is permitted through associations with PDZ protein such as N-ethylmaleimide sensitive factor (NSF; Nishimune et al., 1998), protein interacting with C-kinase 1 (PICK1; Lin and Huganir, 2007), and glutamate receptor-interacting protein 1 (GRIP1; Dong et al., 1997; Figure 1-9A). Within the CTD of GluA1 are six known phosphorylation sites: serine818 (Ser-818; Boehm et al., 2006) and threonine840 (t840; Lee et al., 2007) by protein kinase C (PKC), serine831 (Ser-831) by PKC and CaMKII (Barria et al., 1997a), serine567 (s567) by CaMKII, serine845 (s485) by PKA (Roche et al., 1996), and serine863

(s863) by P21-Activated Kinase 3 (PAK3; Park, 2018a; Figure 1-9A). Phosphorylation at these sites modifies the properties of the subunit by increasing channel conductance, increasing mean open probability, or permitting the trafficking of GluA1 to the cell surface or synapse (Hayashi et al., 2000; Lee et al., 2000). It has been generally accepted that phosphorylation of Ser-845 controls trafficking and retention of GluA1-containing AMPAR, as well as enhancing channel open-probability to facilitate either LTP or homeostatic up-scaling (Banke et al., 2000; Esteban et al., 2003; Oh et al., 2006; Lee et al., 2010a), while dephosphorylation of Ser-845 has been shown to facilitate receptor endocytosis and LTD (Lee et al., 2010a). Conversely, phosphorylation of GluA1 at Ser-831 has been previously thought to enhance LTP through changes in single channel conductance (Derkach et al., 1999), which may now be understood as the trafficking of higher conductance Ca²⁺-permeable AMPAR (Kim and Ziff, 2014; Yang et al., 2018; Park et al., 2019; Summers et al., 2019).

Following synthesis, trafficking of GluA1 to the cell membrane has been shown to be necessary for memory formation underlying fear conditioning (Rumpel et al., 2005), spatial memory (Sanderson et al., 2010), experience-dependent synaptic activity (Takahashi et al., 2003; Harms et al., 2005), and in both *in vitro* and *in vivo* LTP (Shi et al., 1999; Williams et al., 2007a; Zhang et al., 2015). While it is generally accepted that GluA1-containing AMPAR are delivered to the cell surface in an activity-dependent manner, the locus of exocytosis is greatly contested. Several studies have suggested that GluA1-containing AMPAR are initially inserted into the extrasynaptic dendritic membrane before laterally diffusing into the spine and PSD (Choquet and Triller, 2003; Adesnik et al., 2005; Ashby et al., 2006; Yang et al., 2008; Makino and Malinow, 2009; Figure 1-11) . However, it has also been suggested that AMPAR are inserted directly into both spines and perisynaptic sites lateral to the PSD (Yang et al., 2008; Kennedy et al., 2010). The dependence on these mechanisms has been deeply explored in a recent publication examining the role of AMPAR trafficking in LTP and memory formation (Penn et al., 2017). By cross-linking, and immobilizing cell surface GluA1/2-containing AMPAR, this group found that immobilization of surface pools of AMPAR

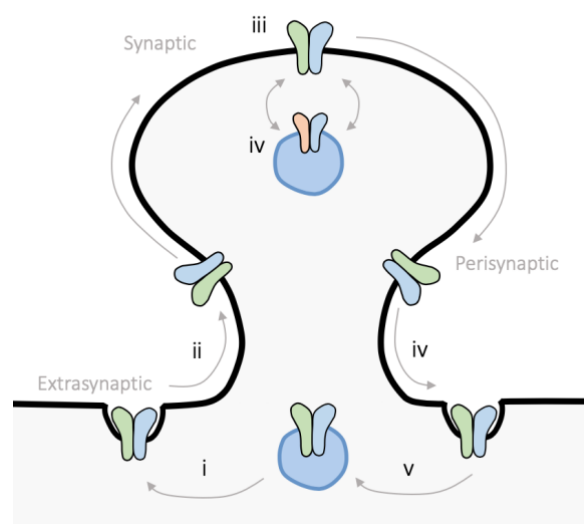


Figure 1-11 | Model of local AMPAR trafficking at the synapse. AMPARs enter the synapse by i) exocytosis at extrasynaptic sites, and ii) diffuse towards the perisynaptic domain and enter the PSD (iii). Here AMPAR may be exchanged directly by constitutive cycling (Gerges et al., 2006), or iv) diffuse out of the synapse to extrasynaptic sites to exit by endocytosis (v).

prevents both the induction and maintenance of LTP, as well as impairing the acquisition of contextual learning *in vivo*. Interestingly, permitting the mobility of surface receptors but restricting the diffusion of solely exocytosed AMPAR permits typical early induction of LTP, but impaired late phase consolidation. These results indicate that there may exist multiple steps in the regulation of synaptic AMPAR during LTP, governing distinct phases of potentiation.

Furthermore, a recent single-molecule trafficking study has sought to describe an alternate mechanism for AMPAR trafficking. (Morise et al., 2019) posit that AMPAR are unlikely to be formed as whole, functional tetrameric units within the ER, instead as individual monomeric AMPAR subunits which are trafficked to the cell surface, where they exist as monomers and dimers, rapidly (100-200 ms) exchanging in and out of tetrameric AMPAR assemblies, and able to diffuse rapidly in and out of the synapse, more readily than tetramers. Interestingly, GluA1/2 heterodimers and heterotetramers were found to be more stable than GluA1 homodimer and homotetramers. The formation of these complexes was found to be dependent on the interactions of N-terminus amino terminal domain (ATD) and C-terminal association with TARPy2. Importantly, GluA1 homotetramers were capable of forming functional receptors, present at synapses and highly permeable to Ca^{2+} (Morise et al., 2019).

1.4.2.2. *Calcium-Permeable AMPA Receptors*

Calcium-permeable AMPA receptors (CP-AMPA) are recognized as a rather elusive phenomenon within the memory and synaptic literature due to difficulties in detection (Shepherd, 2012), and their possibly transient nature, both developmentally (Gray et al., 2007; Ho et al., 2007; Lu et al., 2007; Sanderson et al., 2016), and following activity (Shi et al., 2001; Plant et al., 2006; Park et al., 2016; Morise et al., 2019). Regardless, CP-AMPA have been detected throughout the CNS, including the hippocampus (Katsumaru et al., 1988; Koh et al., 1995), motor and auditory cortices (Otis et al., 1995; Angulo et al., 1999), amygdala (Mahanty and Sah, 1998), dorsal horn (Albuquerque et al., 1999), cochlear (Gardner et al., 1999; 2001), basal ganglia (Götz et al., 1997), and retina (Mørkve et al., 2002).

CP-AMPA are formed through two possible mechanisms; firstly GluA1/2-containing AMPAR have been found to be permeable to Ca^{2+} under certain conditions. GluA2 subunit mRNA is subject to RNA editing by the ADAR2 enzyme (Horsch et al., 2011). ADAR2 converts the codon for glutamine (Gln607; Q) to arginine (Arg607; R). This editing restricts the flow of Ca^{2+} when in complexes with GluA1 and GluA3 subunits (Wright and Vissel, 2012), while unedited subunits permit Ca^{2+} influx. Interestingly, the presence of unedited GluA2 appears to accelerate GluA2 trafficking to the cell surface, while edited GluA2 AMPAR appear to show slower cycling rate, forming a more stable

recycling pool for later AMPAR formation (Greger et al., 2002). As GluA2 editing occurs in greater than 95–99% of all GluA2 mRNA (Isaac et al., 2007; Pachernegg et al., 2015), the contribution of unedited GluA2 in plasticity is unknown. Of note, a mouse line with genetically reduced Q/R editing showed a loss of hippocampal CA1 neurons, altered dendritic morphology and reductions in CA1 pyramidal cell spine density, as well as learning and memory impairments (Konen et al., 2020), indicating that chronic expression of GluA2-containing CP-AMPAR appears detrimental to neuronal health and plasticity. Alternatively, CP-AMPAR can be formed through the association of solely GluA1 subunits, forming homomeric GluA1 receptors (Rozov et al., 2012). The complete lack of GluA2 in this composition renders the receptor Ca^{2+} -permeable and inwardly rectifying, such that the outward ion flow is minimal, and at depolarised holding potentials (+40mV), CP-AMPAR exhibit a voltage-dependent block by endogenous polyamines. The rectification index (RI) is measured as the ratio of the AMPAR current observed between -60mV to that at +40mV, such that greater rectification displays a decrease in the RI. The presence of GluA2 is the determinant for this characteristic, if GluA2 is present, rectification of the AMPAR current does not occur at positive potentials, as Q/R editing renders the pore insensitive to polyamine blockade (Hayashi et al., 2000; Liu and Cull-Candy, 2000; Henley and Wilkinson, 2016). In addition to Ca^{2+} -permeability, CP-AMPAR are unique for displaying extremely fast kinetics and high conductance (Verdoorn et al., 1991; Geiger et al., 1995; Grosskreutz et al., 2003),

While GluA1 homomers are highly expressed during early periods of development (Pickard et al., 2000), in the adult CNS they appear absent from synapses, instead restricted to extrasynaptic or intracellular stores during basal conditions in adult animals (Lu et al., 2009; Yang et al., 2010; Jaafari et al., 2012). Yet, they have been found to contribute a significant proportion of AMPAR transmission following synaptic activity (Rozov et al., 1998) or the induction of LTP (Park et al., 2016; Plant et al., 2006; Guire et al., 2008; Lu et al., 2007; Yang et al., 2010; Yamanaka et al., 2017; Cepeda-Prado et al., 2019). However, these results have been contested by few groups, finding little to no contribution of GluA1 homomers to LTP (Adesnik et al., 2007; Gray et al., 2007). Regardless, genetic ablation of GluA1 in the hippocampus results in complete disruption of LTP at CA1 synapses (Zamanillo et al., 1999; Mack et al., 2001; Jensen et al., 2003; Selcher et al., 2012; Terashima et al., 2017), with animals experiencing disruptions in some (Reisel et al., 2002; Schmitt et al., 2004; Sanderson et al., 2007), but not all (Zamanillo et al., 1999) learning and memory processes.

Emerging bodies of evidence suggest CP-AMPAR play an important role in synaptic plasticity and memory formation (Man, 2011). Genetic knockout of GluA2 subunits in the mouse hippocampus has been found to enhance measures of both LTP and hippocampus-dependent learning tasks, due to

the increased likelihood that GluA1 subunits will associate to form homomers in the absence of GluA2 (Asrar et al., 2009; Wiltgen et al., 2010). A recent publication reported that spaced but not compressed theta burst stimulation (TBS) LTP protocols lead to the insertion of CP-AMPA in a protein kinase A (PKA)-dependent manner (Park et al., 2016), while many others report similar findings in response to various LTP stimulation paradigms (Guire, et al., 2008; Lu et al., 2007; Yamanaka et al., 2017; Plant et al., 2006; Purkey et al., 2018), as well as experience-dependent plasticity *in vivo* (Clem and Barth, 2006; Williams et al., 2007a; Clem et al., 2008; Conrad et al., 2008; Clem and Huganir, 2010; Wen and Barth, 2012; Hong et al., 2013; Zhang et al., 2016; Ouyang et al., 2017; Suyama et al., 2017; Takemoto et al., 2017; Whitehead et al., 2017; Torquatto et al., 2019). However, some groups have provided evidence to suggest that CP-AMPA do not govern all forms of LTP (Gray et al., 2007; Guire, et al., 2008; Adesnik et al., 2007; Purkey et al., 2018), and may be highly regulated by animal species and developmental age (Lu et al., 2007).

The trafficking and retention of CP-AMPA at the synapse is under strict influence of activity-dependent phosphorylation. Phosphorylation of the Ser-831 site by CaMKII (Derkach et al., 1999) and PKC (Roche et al., 1996; Boehm et al., 2006) as well as Ser-818, also by PKC (Lin et al., 2009; Jenkins et al., 2014), regulates the trafficking of CP-AMPA to the cell surface, while phosphorylation at Ser-845, a target of PKA phosphorylation, has been shown to be crucial for stabilization of CP-AMPA at perisynaptic sites (He et al., 2009). Alternatively, dephosphorylation of Ser-845 during LTD removes perisynaptic AMPAR from the cell surface, underlying synaptic depression (He et al., 2009; Sanderson et al., 2012), yet insertion of CP-AMPA may also underlie the induction of LTD, through low-frequency Ca^{2+} influx (Sanderson et al., 2016). Additionally, expression of the catalytic domain of the kinase CaMKI by viral vector in hippocampal neurons has been shown to promote the surface expression of CP-AMPA (Guire et al., 2008), while the scaffold protein TARPy2 has been shown to increase CP-AMPA pore permeability and channel conductance through attenuation of the polyamine block (Panchenko et al., 1999; Soto et al., 2014).

Following accumulation at the PSD, CP-AMPA are rapidly internalized and have been found to be quickly replaced by GluA2-containing AMPAR in an activity-dependent manner (Plant et al., 2006; Yang et al., 2010; Mattison et al., 2014). Preventing the interaction between GluA2 and trafficking proteins, or an absence of synaptic activity post-LTP induction prevents this switch, resulting in subsequent LTP mediated by CP-AMPA. Further, knockout of GluA1 and GluA2 protein compromised initiation or completion of this synaptic exchange, respectively (McCormack et al., 2006), which may indicate distinct phasic roles for these subunits.

Importantly, the expression of CP-AMPA at the synapse has been shown to promote a 'labile' synaptic state (Hong et al., 2013; Wright et al., 2020), such that activity governed through CP-AMPA may underlie expansion and stabilization of the spine cytoskeleton during potentiation (Kopeck et al., 2007; Fortin et al., 2010), while the synapse remains sensitive to depotentiation (Yang et al., 2008) until replaced by GluA2-containing Ca²⁺-impermeable (CI-AMPA; Wright et al., 2020). Through this, it is thought that CP-AMPA mediate the induction of LTP by initially trafficking to perisynaptic regions and further localizing to the PSD. To account for the rapid delivery of GluA1-containing AMPA to the PSD, it is thought that the accumulation of these AMPA initially occurs through lateral diffusion from extrasynaptic and dendritic membrane (Makino and Malinow, 2009; Petrini et al., 2009) and that later exocytosis of AMPA acts to replenish these surface pools (Williams et al., 2007a). However, this finding has been contested as increases in GluA1 (but not GluA2) have been found at the synapse following *in vitro* LTP induction, followed by an increase in GluA2-containing AMPA (Tanaka and Hirano, 2012), possibly supporting the notion for rapid GluA1 insertion and replacement of CP-AMPA with GluA2-containing AMPA.

While CP-AMPA have been shown to be directly involved in the induction of many forms of LTP, CP-AMPA may also contribute to supplementary mechanisms which underlie the formation of new synapses, through the unsilencing of silent synapses. Morita et al., (2013) have previously shown that immediately following the induction of LTP, previously AMPA-silent synapses show complete or very strong inward rectification, indicating the incorporation of solely CP-AMPA. A further 15 minutes of baseline stimulation results in a gradual decrease in rectification but the appearance of AMPA receptor-mediated EPSCs, indicating the insertion or replacement of CP-AMPA with GluA2-containing AMPA. Whether this indicates an 'and/or' mechanism of CP-AMPA during LTP is unknown. However, the presence of CP-AMPA has been further linked to the development of immature stubby, and thin spines following cocaine withdrawal-induced synapse unsilencing (Wright et al., 2020). This may indicate a strong role for CP-AMPA in synapse formation, yet CP-AMPA also appear to have a role in the growth and maturation of existing spines (Fortin et al., 2010).

Further, in addition to Hebbian plasticity, CP-AMPA may also regulate many of the mechanisms regulating non-Hebbian homeostatic plasticity (Lissin et al., 1998; Thiagarajan et al., 2005; Goel et al., 2006; Aoto et al., 2008; Hou et al., 2008; Lee, 2012; Soares et al., 2013; Werner et al., 2017), an effect which has been observed by increases in solely surface GluA1 protein, or AMPA rectification. However, there is some evidence that GluA2 is also involved in certain conditions (Wierenga et al., 2005; Anggono et al., 2011). Beyond neurons, homomeric CP-AMPA play a pivotal role in regulating Ca²⁺ transients in glial cells including hippocampal astrocytes and Bergmann glial cells in the cerebellum (Enkvist et al., 1989; Muller et al., 1992; Jabs et al., 1994; Porter and McCarthy,

1995; Bezzi et al., 1998; Verkhratsky and Kirchhoff, 2007). Interestingly, CP-AMPA have been shown to regulate neuron-glia LTP-like mechanisms (Ge et al., 2006), indicating a functional response to neurotransmitters released by neurons, mediated through CP-AMPA. Together this research shows that the expression and regulation of CP-AMPA in both a cell-type and activity-dependent manner may govern the expression of plasticity through a multitude of diverging mechanisms.

1.4.2.3. *GluA2, GluA3, and GluA4*

While GluA1 is referred to as the plasticity-promoting AMPAR subunit, GluA2- and GluA3-containing AMPAR appear to take place as AMPAR which consolidate these changes. GluA1/2 heteromers are abundant in principal cells of the hippocampus, comprising a majority of pyramidal cell AMPAR (Wenthold et al., 1996). Similar to GluA1 homomers, their trafficking is predominantly regulated by the presence of the GluA1 C-terminal, and is therefore considered to be activity regulated, participating in the plasticity-promoting induction of LTP (Isaac et al., 2007). The presence of the GluA2 C-terminal domain can permit exit from the ER through association with the PDZ domain protein, Protein Interacting With PRKCA 1 (PICK1) and CaMKII, however it may also regulate the retention of GluA2-containing AMPAR within endosomal compartments, permitting initial increases in GluA1-containing AMPAR at the cell surface, before release of GluA2-containing and replacement of CP-AMPA (Jaafari et al., 2012). Due to the presence of the edited Arginine residue, GluA2-containing AMPAR are predominately non-rectifying, and solely permeable to sodium (Na⁺) and potassium (K⁺). Therefore, the addition of GluA1/2 AMPAR is thought to promote NMDAR-dependent plasticity by contributing to increasing the size of the postsynaptic potential. Importantly, knockout of the GluA2 gene (*Gria2*), results in enhanced LTP, fully governed by CP-AMPA (Jia et al., 1996; Mainen et al., 1998; Meng et al., 2003). Interestingly, these animals express intact LTD, depotentiation, and basal synaptic transmission, until additional knockout of the GluA3 (*Gria3*) gene. Double *Gria2*^{-/-}/*Gria3*^{-/-} knockout animals show significantly reduced basal synaptic transmission and impaired LTD and depotentiation, while LTP remains enhanced (Meng et al., 2003). Although LTP is enhanced GluA2 knockout animals, reduced performance on spatial working memory and spatial reference learning tasks have also been observed (Shimshek et al., 2006)

As mentioned above, the presence of the GluA1 C-terminal domain governs the activity-dependent trafficking of GluA1/2-containing AMPAR during plasticity. Replacement of the GluA1 CTD with the CTD of GluA2 has been shown to impair LTP, while replacement of GluA2 CTD with that of GluA1 has been shown to impair NMDAR-dependent LTD (Zhou et al., 2018). Using genetic overexpression of *Gria1* and *Gria2*, Shi et al., (2001) has further examined the contribution of GluA1-3

in activity-dependent and constitutive trafficking. Following the induction of LTP, homomeric GluA1-containing AMPAR were shown traffic primarily to previously silent synapses. Overexpression of GluA2, and formation of GluA2 homomers showed synaptic delivery in the absence of activity, occurring constitutively. Importantly, this shows that the presence of the CTD of GluA1- and GluA2 AMPAR subunits dictates the trafficking characteristics of GluA1- and GluA2- containing AMPAR, such that GluA1 homomers and GluA1/2 heteromers are under primary control of the activity-regulated GluA1 CTD. On the other hand, AMPAR containing the GluA2 CTD and lacking the GluA1 CTD, such as GluA2 homomers and endogenous GluA2/3 heteromers are likely governed by constitutive trafficking to replace synaptic AMPAR. However, as GluA2 homomeric AMPAR do not occur naturally, GluA1/2-containing AMPAR may in fact dictate an activity-regulated replacement of existing AMPAR. This has been described by (Liu and Cull-Candy, 2000) wherein activity at GluA2-lacking CP-AMPAR promotes the replacement of these AMPAR by non-rectifying GluA2-containing AMPAR.

Similar to GluA1, GluA2 can undergo extensive post-translation modifications through phosphorylation occurring at s863 and s880 by PKC and t876 by Src family tyrosine kinases (Henley and Wilkinson, 2013). The phosphorylation state of many of these sites dictates the binding affinity of associated auxiliary proteins including SAP97, Glutamate Receptor Interacting Protein 1/2 (GRIP1/2), PICK1, postsynaptic density protein 95 (PSD95), and TARPy2 and γ 8 (Henley, 2003; Czöndör and Thoumine, 2013; Hanley, 2014b; Herguedas et al., 2019). Interestingly, synaptic activity through CP-AMPAR has been shown to facilitate the replacement of CP-AMPAR by disrupting their interaction with GRIP1/2 and driving GluA2-containing AMPAR to the extrasynaptic membrane in a manner dependent on PICK1 (Liu and Cull-Candy, 2005), and lateral diffusion to the synapse in a manner dependent on NSF (Gardner et al., 2005). These results indicate that expression of GluA2-containing AMPAR is a dynamic process, involving both activity-dependent and constitutive mechanisms.

While the role of GluA1- and GluA2-containing AMPAR are well documented, the role of GluA3-containing AMPAR remains rather enigmatic. Next to GluA1/2, GluA2/3-containing AMPAR comprise the second most abundant heteromeric AMPAR in cortical principal cells, yet comprise only 10-30% of GluA1 and GluA2 levels (Geiger et al., 1995; Wenthold et al., 1996; Tsuzuki et al., 2001). Relative to GluA1-containing AMPAR, GluA3-containing AMPAR increase in expression throughout the hippocampus during development (Ritter et al., 2002). Likewise, in adult rats, approximately 80% of spines in the lateral amygdala are immunoreactive for GluA3, commonly following the same proportion as the NMDAR subunit GluN1 (Radley et al., 2007). Together, these allude to a role of GluA3-containing AMPAR in synapse maturity and stabilization.

GluA3-containing AMPAR do not contribute to canonical LTP, LTP-associated insertion of AMPARs, nor contextual fear memory (Meng et al., 2003; Humeau et al., 2007). However, in GluA1-deficient mice, β -adrenergic signalling has been shown to convert low-activity GluA3-containing AMPAR into plasticity-promoting receptors in CA1 neurons, resulting in GluA3-dependent plasticity (Renner et al., 2017). Regardless, during basal conditions, GluA3-containing AMPAR may act to stabilize changes in AMPAR receptor surface expression through slow constitutive recycling and replacement of synaptic GluA1/2-containing AMPAR (Passafaro et al., 2001; Shi et al., 2001; Malinow and Malenka, 2002). Similar to GluA2, GluA3 shares binding domains for PICK1 and GRIP1/2 (Xia et al., 1999; Silverman et al., 2007; Hanley, 2014), which regulate trafficking to the cell surface and stabilization within the synapse. In response to both LTD-dependent and constitutive endocytosis, interactions of the GluA2 CTD with the PDZ-domain protein PICK1 has been shown to be required for removal of GluA2/3-containing AMPAR from the cell surface (Kim et al., 2001). Mimicking GluA2 s880 phosphorylation prevents interactions with GRIP1/2 and excludes GluA2/3-containing AMPAR from synapses, depressing transmission, and partially occluding LTD. On the other hand, preventing s880 phosphorylation reduces the extent of LTD, indicating that s880 phosphorylation may disrupt GluA2 and GRIP1/2 interactions, facilitate removal of these AMPAR from the synapse (Seidenman et al., 2003), and promote their trafficking to and from recycling endosomes (Mao et al., 2010). Interestingly, both basal and LTD-dependent interactions with PICK1, and GRIP1/2 require the activity of PKC (Daw et al., 2000; Xia et al., 2000). While GluA1-containing AMPAR are thought to occupy the synapse by lateral diffusion from perisynaptic and extrasynaptic stores, some evidence suggests GluA3-containing AMPAR are inserted directly into the PSD (Gerges et al., 2006), supported by electron microscopy observations that GluA3-containing AMPAR predominately occupy the PSD, and lie more centrally within the PSD than GluA1-containing AMPAR (Radley et al., 2007; Jacob and Weinberg, 2015).

Converse to GluA3, GluA4-containing AMPAR show the greatest expression during early development (Ritter et al., 2002; Henley and Wilkinson, 2016), expressed primarily in the cerebellum, but are absent from the majority of excitatory neurons in the adult brain (Schwenk et al., 2014; Pelkey et al., 2015). The CTD of GluA4 contains a PKA/PKC phosphorylation site at s842 (Esteban et al., 2003). During early development, phosphorylation of s842 regulates activity-dependent recruitment and stabilization of GluA4-containing AMPAR at the synapse (Gomes et al., 2007), and may also be regulated by TARPy2, γ 4 and γ 8 (Semenov et al., 2012; Pierce and Niu, 2019), as well as GSG1L (Keifer et al., 2017) auxiliary proteins. This period of development coincides with a period where PKA, but not CaMKII is required for hippocampal LTP (Yasuda et al., 2003), likely implicating a developmental

switch in activity-dependent AMPAR subunits. Alternatively, spontaneous synaptic activity has been shown to deliver GluA4-containing AMPAR to previously AMPA-silent synapses, allowing non-functional connections to be strengthened. These GluA4-containing AMPAR are later exchanged for GluA2 containing AMPAR in a manner requiring little neuronal activity (Zhu et al., 2000). However, following classical conditioning in freshwater pond turtles, GluA4 appears to show a predominant role in late phase consolidation of silent synapses (Mokin et al., 2007). Interestingly, parallels have been observed in the proportion of GluA4-containing AMPAR following spatial memory training in adult mice and classical conditioning in adult freshwater pond turtles, such that training increased both total and synaptic levels GluA4 (Keifer et al., 2008; Keihan Falsafi et al., 2012), while knockout of GluA4 impaired acquisition of spatial reference memory, with no effect on LTP or retention of spatial reference memory (Sagata et al., 2010).

1.4.3. *The Role of Calcium*

Following NMDAR activation, it has been accepted that the postsynaptic NMDAR-dependent influx of calcium initiates the essential signalling cascades required for the expression of NMDAR-dependent LTP. Synaptic potentiation has been observed following uncaging of a calcium-loaded calcium chelator Nitr-5 (Malenka et al., 1988), and alternatively, lowering the bath concentrations of calcium has been shown to selectively inhibit LTP (Dunwiddie and Lynch, 1979). Further, the kinetics of Ca^{2+} transients is tightly linked to the outcome of plasticity, such that differing outcomes of potentiation between cells can be predicted by the Ca^{2+} transients observed by each individually, thus the initial magnitude of postsynaptic Ca^{2+} increase is a critical variable in controlling the strength and duration of potentiation (Malenka, 1991b; Ismailov et al., 2004). Further, compartmentalization of Ca^{2+} transients have also been observed which may assist in the input specificity of LTP. Endogenous Ca^{2+} within dendritic spines is low, allowing for rapid changes in concentration, while diffusion across the spine neck is negligible, preventing the spread of Ca^{2+} -induced potentiation to neighbouring synapses (Sabatini et al., 2002). Crucially, Ca^{2+} gains its efficacy through the influence it has on downstream processes. Simply, Ca^{2+} , through its association with calmodulin, is the activity-dependent link between synaptic activity and downstream enzymatic activation (Eccles, 1983; Bliss and Collingridge, 1993; Suzuki, 1994; Malenka and Nicoll, 1999; Wu et al., 2006), and has therefore been defined as a key mediator in synaptic plasticity and potentiation.

1.4.4. Calcium/Calmodulin-dependent Kinase II

Following the discovery and identification of NMDAR and their role in plasticity, the field aimed to identify possible downstream targets of the NMDAR-dependent rise in intracellular Ca^{2+} . One of these targets was found to be the Ca^{2+} -dependent enzyme Ca^{2+} /calmodulin-dependent kinase II (CaMKII; Lisman et al., 2002). The major isoforms of the CaMKII gene consist of the α and β subunits which form dodecameric holoenzymes consisting of either one or both subunit types. An appealing property of this molecule is its ability to autophosphorylate target sites within itself to remain active (site t286 on CaMKII α subunits and t287 on CaMKII β subunits), even after intracellular Ca^{2+} has returned to baseline (Lisman, 1985). Mutation of this autophosphorylation site has been shown to not only prevent LTP but interfere with experience-dependent plasticity *in vivo* (Giese et al., 1998), while genetic CaMKII knockout mice showed deficiencies in the expression of LTP (Silva et al., 1992b) and impaired spatial memory (Silva et al., 1992a). Alternatively, introduction of active CaMKII into CA1 neurons potentiates the EPSC and occludes further LTP (Lledo et al., 1995). Thus, the activity of CaMKII has been proposed as one potential mechanism through which a cell or synapse may maintain a cellular correlate of 'memory-like' persistence (Lisman, 1994; Lisman et al., 2002). However, evidence shows that inhibition of CaMKII affects the induction of LTP and memory formation during contextual fear conditioning, but is not involved in maintenance of LTP, nor memory storage or retrieval *in vivo* (Buard et al., 2010). In line with this, stimulation of single dendritic spines has seen the activation and translocation of CaMKII to activated synapses within seconds following single synapse glutamate-uncaging or light-activation of channelrhodopsin-2 (Takao et al., 2005; Zhang et al., 2008; Lee et al., 2009), lasting for up to one hour post LTP-induction (Otmakhov et al., 2004). The rapid nature of CaMKII and its role in early LTP may be due to its abundant presence within the postsynaptic density (Kennedy et al., 1983; Petersen et al., 2003), forming complexes with GluN1, GluN2A, and GluN2B subunits of the NMDA receptor, regulating their association to synaptic scaffolding protein PSD-95 (Gardoni et al., 2006), as well as associating with other PSD proteins including densin-180 (Walikonis et al., 2001), synGAP (Oh et al., 2004), cytoskeletal proteins f-actin and α -actinin (Lin and Redmond, 2008; Jalan-Sakrikar et al., 2012), and the motor protein myosin Va (Costa et al., 1999), regulating trafficking to and from the synapse. The close association of CaMKII with these synaptic proteins and its localization within the PSD places CaMKII in prime position for incoming Ca^{2+} signalling (Gardoni et al., 1998; Leonard et al., 1999; Strack et al., 2000; Sanhueza et al., 2011), and a likely candidate for the regulation of synaptic processes during plasticity. Alternatively, CaMKII has also been shown to translocate from within dendritic spines towards NMDAR-potentiated synapses during LTP (Thalhammer et al., 2006). This mechanism may add an additional amplification

to existing synaptic CaMKII, increasing the specificity of potentiated synapses, as well as mediate the potentiation and growth of naïve synapses (Strack et al., 1997; Rongo, 2002; Tsui and Malenka, 2006; Lisman et al., 2012).

A primary mechanism through which CaMKII potentiates LTP is through the trafficking and regulation of cell surface and synaptic AMPAR. CaMKII regulates phosphorylation of GluA1 AMPAR subunits at the Ser-831 and s567 sites (Barria et al., 1997a; Barria et al., 1997b; Mammen et al., 1997; Lu et al., 2010), of which Ser-831 is shared with PKC (Roche et al., 1996), while PKA regulates Ser-845 phosphorylation (Diering et al., 2016). Importantly, a bidirectional regulation of these phosphorylation sites has been described during LTP and LTD, such that during basal activity, cell surface GluA1-containing AMPAR are phosphorylated at the PKA Ser-845 site. Following LTP, these AMPAR are further phosphorylated by CaMKII at Ser-831, while LTD removes Ser-845 phosphorylation and permits endocytosis (Lee et al., 2000). Interestingly, CaMKII-mediated phosphorylation has been found to enhance AMPAR activity through two primary mechanisms; firstly by increasing single channel conductance of existing AMPAR following Ser-831 phosphorylation (Derkach et al., 1999), and secondly, by enhancing synaptic targeting of extrasynaptic GluA1-containing AMPAR by s567 (Lu et al., 2010). Interestingly, CaMKII may further regulate AMPAR expression indirectly by phosphorylation of the AMPAR auxiliary protein TARPy2 (Hayashi et al., 2000; Opazo et al., 2010), promoting the trapping of extrasynaptic AMPAR within the synapse, likely through an increased association with PSD-95 (Ehrlich and Malinow, 2004b). The latter of these is thought to underlie a possible mechanism through which CaMKII may unsilence previously AMPAR-silent synapses (Poncer et al., 2002). Together, this evidence suggests both direct and indirect roles of CaMKII in promoting the induction of LTP (Diering and Huganir, 2018).

1.5. Messengers of Plasticity

Here, messengers of plasticity are defined as proteins or molecules which permit the action or regulation of proteins and processes which mediate plasticity. These proteins show distinct functions at the synapse, yet may comprise coinciding processes to regulate the induction, maintenance, and persistence of cellular memory. Many of the proteins described show clear evidence pertaining to the function, expression, and regulation of glutamate receptors, synaptic morphology, or related gene expression.

1.5.1. *The A-ζ of Protein Kinases*

Of the 250+ known protein kinases, only a few have been identified which contribute significantly to mechanisms of learning and memory. The idea that memory could be actively maintained by enzymatic activity was first established by Crick (1984), who proposed that persistently active enzymes could replace synaptic proteins necessary for maintaining changes that occur during learning (Crick, 1984). These kinases mediate changes in proteins by catalysing the addition of a phosphate group to specific protein substrates, which impact synaptic transmission through changes in ion channel expression, protein synthesis, and gene regulation (Giese and Mizuno, 2013). Of those shown to regulate synaptic plasticity, few have shown direct involvement with regards to the induction and maintenance of hippocampal LTP and LTD, through the regulation of glutamate receptors. Here, protein kinases A, C, and G will be discussed due to their direct roles in regulating AMPAR expression, protein synthesis, or immediate early gene (IEG) expression with relevant literature. Of note, PKB (also referred to as Akt), PKD, and PKN have also shown to play minor roles in the regulation of AMPAR expression (Pen et al., 2016; Zhao et al., 2019), and spine morphology (Dong et al., 2000; Taniguchi et al., 2001; Olayioye et al., 2013; Bencsik et al., 2015).

1.5.1.1. *Protein Kinase A*

Protein kinase A (PKA) is a tetrameric holoenzyme that consists of two catalytic and two regulatory subunits, initially identified in the 50s–60s (Sutherland and Rall, 1958; Walsh et al., 1968). Upon activation by Ca^{2+} , cyclic adenosine monophosphate (cAMP) binds PKA. The regulatory subunits dissociate from the catalytic subunits, and enable phosphorylation of target proteins. Interestingly, studies investigating mice with a genetic knockout of one of the catalytic subunits of PKA ($\text{C}\alpha$) shows

dramatic developmental impairments, significantly affecting growth and fertility in the few offspring which survive postnatally (Skålhegg et al., 2002). In contrast, knockout mice generated by ablation of the catalytic subunit $C\beta_1$ are phenotypically indistinguishable from wildtype littermates, with the only differences observed in the hippocampus, in which $C\beta_1$ knockout mice show impaired LTP, LTD, and depotentiation (Qi et al., 1996). These and additional findings have implicated PKA in both late phase LTP (Abel et al., 1997), and contextual fear conditioning (Bernabeu et al., 1997; Barad et al., 1998; Ahi et al., 2004; Isiegas et al., 2006). Interestingly, PKA expression may require protein synthesis, occurring between 1–6 hours post-training, placing its activity somewhere in the transition period between STP/E-LTP and L-LTP, and has been theorised to act in part as a ‘synaptic tag’ for capture of PRPs important for late phase LTP (Bernabeu et al., 1997; Bourtchouladze et al., 1998; Young et al., 2006).

Multiple targets of PKA phosphorylation have been identified, all of which play significant roles in mediating plasticity. Both NMDA and AMPA receptors have been shown to be tightly regulated by PKA activity (Greengard et al., 1991; Wang et al., 1991; Westphal et al., 1999; Skeberdis et al., 2006). PKA is associated with both NMDAR and AMPAR at the synapse through their affinity to PDZ-domain proteins PSD-95 and SAP97, and the formation of a complex with AKAP79/150 (Colledge et al., 2000). Importantly, another NMDAR binding protein, Yotiao, binds the calcineurin and protein phosphatase 1 (PP1) in close proximity to PKA (Westphal et al., 1999). Constitutive dephosphorylation of NMDAR by PP1 maintains low activity, whereas upon activation, PKA may phosphorylate PP1 to inhibit its activity, enhancing NMDAR currents and Ca^{2+} permeability (Michel and Scott, 2002; Skeberdis et al., 2006).

Further, PKA shows important roles in the regulation of cell surface GluA1-containing AMPAR, phosphorylating both Ser-831 and Ser-845 sites (Roche et al., 1996). Phosphorylation of Ser-845 is thought to enhance the trafficking of GluA1-containing AMPAR to the cell surface during both LTP (Ehlers, 2000; Esteban et al., 2003; Oh et al., 2006; Man et al., 2007), and synaptic upscaling during homeostatic plasticity (Diering et al., 2014). Importantly, opposing activity downregulates Ser-845 phosphorylated GluA1 from the cell surface, such that LTD or synaptic downscaling dephosphorylates GluA1 at Ser-845, removing GluA1-containing AMPAR from the synapse (Lee et al., 1998; Tavalin et al., 2002; Lee et al., 2003). Therefore, it is thought that maintenance of Ser-845 phosphorylation by PKA serves to maintain AMPAR at the synapse, likely through associations with AKAP79/150 and SAP97 (Diering et al., 2014). Interestingly, many of the associations between PKA and AKAP79/150 regulate the trafficking of CP-AMPA during LTP, LTD or homeostatic plasticity (Kim and Ziff, 2014; Zheng and Keifer, 2014; Sanderson et al., 2016), primarily by interrupting the association of

AKAP79/150 associated calcineurin, which inhibits CP-AMPA expression during basal activity (Sanderson et al., 2012; Purkey and Dell'Acqua, 2020). Of note, it has been proposed that both PKA and calcineurin exist in complex with AKAP79/150 and SAP97 on CP-AMPA, such that NMDAR-dependent LTD promotes GluA2-containing AMPAR removal and simultaneous PKA-dependent CP-AMPA insertion and translocation to the synapse. Low-frequency activity through synaptic CP-AMPA is thought to promote activation of tethered calcineurin activity and rapid removal of CP-AMPA from the synapse (Hell, 2016)

In addition to the role of PKA at the synapse, evidence suggests that PKA may play an additional role in regulating the activation of the cAMP response element-binding protein (CREB), a transcription factor with a crucial role in learning and memory (Impey et al., 1998; Athos et al., 2002; Abel and Nguyen, 2008; Kirschner et al., 2009). Importantly, the activation of CREB by PKA has been shown to regulate the expression of IEGs including *Arc*, *Zif268*, and *c-Fos* following synaptic activity (Didier et al., 2018), and LTP (Waltereit et al., 2001). In line with this, PKA has also been found to regulate the expression of long-term memories *in vivo* (Schafe et al., 1999; Schafe and LeDoux, 2000; Michel et al., 2011; Bollen et al., 2014). Therefore, the concerted regulation of both glutamate receptors and IEGs by PKA appears critical for the expression of many learning paradigms.

1.5.1.2. *Protein Kinase C*

In addition to PKA, protein kinase C (PKC) has been shown to regulate the expression of LTP and the formation of long-term memories. First isolated in the 80s, the PKC family consist of 10 isoenzymes, divided into three subgroups: conventional (α , β I, β II, and γ), novel (δ , ϵ , η , and θ) and atypical (λ and ζ ; Coussens et al., 1986; Jaken, 1996), each of which are generally activated by Ca^{2+} and diacylglycerol (DAG). The first evidence that PKC could be involved in the mechanisms underlying memory comes from a publication in the mid-80s which found that application of phorbol esters, which bind to and activate PKC, or intracellular injection of PKC in rat hippocampal slices elicited a long-lasting enhancement of synaptic transmission, counteracted by PKC inhibitors (Hu et al., 1987; Reymann et al., 1988). Interestingly, inhibition of PKC has been found to impair the induction but not maintenance of LTP (Malinow et al., 1989; Muller et al., 1990). This data indicates that PKC may be required for early-phase potentiation, however some evidence contradicts this (Colley et al., 1990).

Importantly, similar to PKA, PKC has been shown to play a role in the regulation of cell surface GluA1-containing AMPAR. PKC shares the GluA1 Ser-831 phosphorylation site with CaMKII (Diering et al., 2016). As mentioned previously, the scaffold protein AKAP79/150 regulates the binding of PKC and calcineurin to GluA1 through associations with the synaptic protein SAP97. Additionally,

AKAP79/150 also binds PKC in this complex, and this association is said to promote preferential access of PKC over CaMKII to the Ser-831 substrate, following LTP (Tavalin, 2008). Through this, the AKAP79/150-PKA complex acts to regulate the phosphorylation and expression characteristics of GluA1-containing AMPAR. In the presence of AKAP79/150, PKC phosphorylation of Ser-831 promotes the preferential expression of CP-AMPAR at the synapse (Summers et al., 2019) and enhances single channel conductance (Jenkins and Traynelis, 2012). PKC has also been found to regulate the expression of GluA2-containing AMPAR, such that phosphorylation at the GluA2 PKC site s880 releases GluA2 from GRIP and enhances its interaction with PICK1 leading to increased internalization (Chung et al., 2000). This role has been found necessary for the expression of LTD (Matsuda et al., 2000; Kim et al., 2001), yet dedepression may also be dependent upon the activity of PKC, thought to occur by placing internal s880-phosphorylated GluA2/3-containing AMPAR into a constitutive pool for insertion (Daw et al., 2000).

A persistently active, brain-specific isoform of PKC (PKM ζ), has been previously described as both necessary and sufficient for maintaining LTP. Application of the general PKC inhibitor chelerythrine chloride or the PKM ζ -specific myristoylated zeta-pseudosubstrate inhibitory peptide (ZIP) to hippocampal slices significantly impairs potentiation following HFS (Ling et al., 2002), and erases consolidated spatial memories (Pastalkova et al., 2006). One of the mechanisms employed by PKM ζ to enhance and maintain synaptic transmission is through its association with PICK1 and NSF. It is thought that PKM ζ enhances trafficking of GluA2/3-containing AMPAR to the cell surface by enhancing NSF-GluA2 binding and disrupting interactions between PICK1-GluA2 (Yao et al., 2008; Miguez et al., 2010). Interestingly, release of GluA2 from PICK1 via NSF has been shown necessary for the persistence of synaptic potentiation following CP-AMPAR-dependent LTP (Gardner et al., 2005), and therefore may describe a mechanism through which PKC (or PKM ζ) maintains memory persistence following CP-AMPAR-mediated LTP induction.

The inhibition of conventional (Abeliovich et al., 1993; Bonini et al., 2007), novel (Hongpaisan et al., 2013), and atypical (Serrano et al., 2008; Ren et al., 2013; Schuette et al., 2016) isoforms of PKC impair the expression of LTP, as well as alter aspects of spatial and contextual conditioning. These data indicate that PKC plays a varied role in the regulation of LTP and memory.

1.5.1.3. *Protein Kinase G*

Protein kinase G (PKG) is a cyclic guanosine monophosphate (cGMP)-dependent enzyme (also referred to as cGMP-dependent kinase, or cGK) activated by soluble guanylate cyclase (sGC) following stimulation by nitric oxide (NO), guanylate cyclase (sGC; Giese and Mizuno, 2013). There exists two

PKG genes (*PRK1* and *PRK2*) encoding PKG type I (PKG-I, consisting of α and β isoforms) and type II (PKG-II), both of which are ubiquitously expressed, especially in the hippocampus, as well as the cerebellum, neuromuscular junction end plates, and kidney (Wu et al., 2018b). Conventional and conditional PKG knockout mice show impairments in cerebellar LTD and motor learning (Feil et al., 2003), as well as an age-dependent impairment in hippocampal protein synthesis-dependent LTP (Kleppisch et al., 2003). Further, direct or indirect inhibition of PKG has been shown to impair hippocampal CA1 LTP (Frey et al., 1993; Zhuo et al., 1994; Lu and Hawkins, 2002; Monfort et al., 2004). Interestingly, the role of PKG was initially thought to occur primarily through the regulation of presynaptic mechanisms, supported by observations that bath application, but not postsynaptic whole-cell filling of the cGMP inhibitor Rp-8-Br-cGMPS inhibits LTP (Blitzer et al., 1995) while the cGMP analogue 8-Br-cGMP enhances synaptic transmission (Arancio et al., 1995), in a manner independent of NMDAR activation (Son et al., 1998).

While much evidence suggests a presynaptic mechanism, evidence also exists for a postsynaptic mechanism. Importantly, NMDAR are directly linked to the activation of the NO-cGMP-PKG pathway. Early observations found that glutamate increased NO and cGMP levels in a manner dependent on NMDAR activation (Garthwaite, 1985; Chalimoniuk et al., 1996). These observations were later supported by the physical interaction between the NO precursor NO synthase (NOS) and GluN2B subunits of the NMDAR, bridged by PSD-95 (Brenman et al., 1996; Christopherson et al., 1999; Sattler et al., 1999; d'Anglemont de Tassigny et al., 2007; D'Mello et al., 2011). This close association allows for rapid activation of NOS by Ca^{2+} and calmodulin (Hayashi et al., 1999), and thus rapid downstream stimulation of sGC, cGMP, and PKG (Denninger and Marletta, 1999). Disruptions of this complex impair fear conditioned memory formation (Li et al., 2018), while activation of the NO-cGMP-PKG pathway has been shown to be important for fear memory consolidation (Ota et al., 2008), object recognition (Furini et al., 2010), and place preference (Shen et al., 2012; Shen et al., 2014), the latter of which was found to be dependent on the activation of GluN2B-containing NMDAR and the trafficking of GluA1-containing AMPAR (Shen et al., 2016).

Importantly, early investigations examined the necessity of NO as a retrograde messenger, such that postsynaptic activation of NMDAR promotes NO production and diffusion to the presynaptic cell (Schuman and Madison, 1991). However, key roles have also been identified within the postsynaptic cell primarily through PKG activation (Hardingham and Fox, 2006; Rameau et al., 2007), and enhancement of AMPAR expression at the synapse. Importantly, GluA1 AMPAR subunits contain PKG phosphorylation sites within the CTD, at the PKA Ser-845 and CaMKII/PKC Ser-831 site (Roche et al., 1996; Lu and Roche, 2012; Seo et al., 2013; Mao et al., 2014; Diering and Huganir, 2018). In line with this, recent evidence has shown that PKG colocalizes with and binds with the CTD of GluA1 *in*

vitro and *in vivo*, at a site distinct from the phosphorylation site (amino acids 850–873), following activation of cGMP cLTP (Serulle et al., 2007). This interaction enhanced the phosphorylation of GluA1 by PKG at Ser-845 and promotes the delivery of GluA1-containing AMPAR to the cell surface. Moreover, these actions occur independently of PKA, and unlike PKA does not require the binding of anchoring proteins AKAP79/150 and SAP97). In pathologically driven hyperexcitable states, such as temporal lobe epilepsy (TLE), PKG has been found to be upregulated, and inhibition of PKG *in vivo* prevents hyperexcitability through an inhibition of synaptic delivery of CP-AMPA (Gu et al., 2018). These effects indicate that PKG may play a role in synaptic plasticity and LTP. In fact, application of nNOS, sGC, cGMP, or PKG inhibitors has been shown to significantly impair both the increase in mEPSC frequency following cLTP *in vitro* as well as the induction and persistence of LTP following TBS tetanisation *ex-* and *in-vivo* (4 pulses of 100 Hz at 5 Hz; Serulle et al., 2007). Inhibition of the PKG-GluA1 binding domain was found to be necessary for both the delivery of GluA1 to the cell surface following cLTP as well as the expression of LTP *in vivo*. Further, it has been shown that NO, cGMP and PKG promote the formation of new synapses and the trafficking of GluA1-containing AMPAR to the cell surface following cLTP (Wang et al., 2005). These findings have been further supported by the observation that enhancement of NO, cGMP or PKG increases the proportion of cell surface and synaptic CP-AMPA, while silencing of PKG decreases CP-AMPA expression (Incontro et al., 2013; Gu et al., 2018). Inversely, it has also been shown that activation of CP-AMPA induces a PKG-dependent increase in GluA1-containing AMPAR, and a small increase in GluA2-containing AMPAR (Tukey and Ziff, 2013), possibly indicating that PKG may play a role in the receptor subunit switch following activity at CP-AMPA (Liu and Cull-Candy, 2000; Plant et al., 2006). Further, NO activity may act as part of a downstream signalling cascade following CP-AMPA activation, to regulate LTP (Haj-Dahmane et al., 2017)

In research investigating the behavioural effects of NO-cGMP-PKG signalling, it has been shown that NMDAR signalling in the lateral nucleus of the lateral amygdala (LA) following auditory fear conditioning drives the expression of IEGs Arc, c-Fos, and Zif268, while selective inhibition of this pathway inhibited fear memory consolidation and likewise impaired IEG expression (Ota et al., 2010). Similarly, inhibition of the NO-cGMP-PKG pathway *in vitro* attenuates the expression of c-Fos, Zif268, Arc, and BDNF following activity-induced homeostatic upscaling (Gallo and Iadecola, 2011).

Interestingly, reduced levels of cerebrospinal fluid (CSF) cGMP correlates with severity of dementia and depression in AD patients (Hesse et al., 2017), and inhibition of the cGMP-degrading enzyme phosphodiesterase (PDE5), has been shown to result in long lasting amelioration of synaptic and memory abnormalities in APP/PS1 mice (Zhang et al., 2013), as well as reductions in levodopa-

induced dyskinesia 6-OHDA-lesioned rats (Picconi et al., 2011). These properties have identified PKG as a key kinase in regulating mechanism of learning and memory, as well as a potential therapeutic target for many neurodegenerative diseases and neurological disorders including Huntington's disease (Saavedra et al., 2013) Parkinson's disease (Picconi et al., 2010) Alzheimer's disease (AD; Puzzo et al., 2009), and major depressive disorder (Reiersen et al., 2011).

1.5.2. *Scaffold and Auxiliary Proteins*

More than one thousand proteins comprise the PSD, including neurotransmitter receptors, cell adhesion molecules, scaffold proteins, signalling enzymes, cytoskeleton proteins, and membrane trafficking proteins. The expression and synaptic localization of many of these proteins permit both basal transmission, as well as the full complement of synaptic plasticity. The major families of postsynaptic proteins are that of the membrane associate guanylate kinases (MAGUKs), which comprise PSD-93 and PSD-95 (Ehrlich and Malinow, 2004b; Ehrlich et al., 2007), and SAP97 and SAP102 (Elias and Nicoll, 2007), and that of the guanylate kinase-associated proteins (GKAPs) including GKAP, SAP90, PSD-95-associated protein 1 (SAPAP1), and discs large homologue-associated protein 1 (DLGAP1; Kim et al., 1997). Importantly, all of these scaffold proteins contain PDZ domains, capable of binding the CTD of NMDAR directly (Kornau et al., 1995; Niethammer et al., 1996), and indirectly to AMPAR through auxiliary proteins such as TARPy2 (Schnell et al., 2002; Nicoll et al., 2006). This association may be enhanced by scaffold and chaperone proteins such as AKAP79/150, PICK1, GRIP1/2, NSF, and the AP2 adaptor complex which act to regulate the binding of downstream protein kinases and phosphatases during plasticity events (Dong et al., 1997; Colledge et al., 2000; Tavalin et al., 2002; Collingridge et al., 2004; Gardner et al., 2005; Smith et al., 2006; Jaafari et al., 2012; Nair et al., 2013). These findings have brought forward the 'slot' and 'scaffold' hypotheses of LTP and LTD (Xu, 2011). Such that PSD MAGUKs, in association with TARPy2 (Bats et al., 2007), may mediate the maximum possible concentration of NMDAR and AMPAR at the synapse (Opazo et al., 2012). In fact, the formation of these 'slots' has been examined through the overexpression or knockout of PSD95 (El-Husseini et al., 2000), and to a lesser extent SAP102 (Schnell et al., 2002) and SAP97 (Schlüter et al., 2006). Overexpression of PSD-95 has been shown to selectively enhance basal synaptic transmission, mimic LTP (Ehrlich and Malinow, 2004), awaken previously silent synapses (Stein et al., 2003), and promote spine maturation (El-Husseini et al., 2000), while knockdown of MAGUKs reduces basal (Chen et al., 2015) and activity-driven (Ehrlich and Malinow, 2004) synaptic expression of both AMPAR and NMDAR, reduces *in vivo* LTP (Zhao et al., 2013), and impairs LTP-mediated spine morphology changes (Ehrlich et al., 2007). These observations indicate that scaffold

proteins are uniquely linked to the facilitation and regulation of synaptic plasticity through their associations to glutamate receptors and PSD proteins.

1.5.3. *Cytoskeletal Proteins*

A major aspect of cellular processes underlying plasticity includes the molecular and structural remodelling of the synapse, spine, dendrite, or major morphological changes to the entire cell (such as dendritogenesis and axonogenesis). In addition to changes in the postsynaptic potential following LTP, primarily governed through changes in the receptor content at the synapse, enhancements in potentiation are also shown to reflect changes in the postsynaptic morphology. Accordingly, plasticity-inducing stimulation has been shown to promote the formation of new dendritic spines (Parnavelas et al., 1973; Collin et al., 1997; McKinney et al., 1999; Wosiski-Kuhn and Stranahan, 2012), and the growth and stabilization of existing ones (Van Harreveld and Fifkova, 1975; Lee et al., 1980; Lendvai et al., 2000; Popov et al., 2004). Importantly, increases in spine size have been shown to be synapse specific (Jungenitz et al., 2018), correlates strongly with changes in AMPAR expression (Matsuzaki et al., 2001; Ganeshina et al., 2004; Matsuzaki et al., 2004), and are linked to *in vivo* behavioural learning, such as exposure to complex environments (Greenough and Volkmar, 1973), social isolation (Connor and Diamond, 1982), fear conditioning (Heinrichs et al., 2013; Xu et al., 2019), and working and spatial memory (Mahmmoud et al., 2015), indicating a strong correlation between memory formation and morphological changes to the synapse.

Many of these mechanisms involve the reorganization of the actin cytoskeleton (Lin et al., 2005; Korobova and Svitkina, 2010). Cellular actin exists in monomeric or globular (G-actin) and polymerized or filamentous (F-actin) forms. Importantly, F-actin remodelling and has been shown to regulate the trafficking, stabilization, and anchoring of AMPAR and NMDAR at the synapse (Allison et al., 1998; Mao et al., 2010), in addition to scaffolding proteins including PSD-95 (Pak et al., 2001; Mizui et al., 2005; Cingolani and Goda, 2008) and SAP97 (Waites et al., 2009; Hanley, 2014), while inhibition of F-actin stabilization has been shown to impair LTP (Kim and Lisman, 1999; Krucker et al., 2000). Seemingly counterintuitive, the Actin Depolymerizing Factor (ADF)/cofilin severs F-actin filaments, reducing the proportion of F-actin, but increasing the available pool of G-actin, creating actin nucleation sites and ultimately enhancing F-actin turnover. Inhibition of cofilin impairs AMPAR trafficking to the cell surface following LTP (Gu et al., 2010), reduces the surface motility of extrasynaptic AMPAR (Rust et al., 2010), restructures synaptic AMPAR nanodomains (Kerr and Blanpied, 2012), and results in impaired spatial memory performance (Rust et al., 2010).

An important aspect of AMPAR trafficking is the transport of AMPAR-containing vesicles across both large scale (soma to dendrite), as well as small scale (dendrite to synapse) distances. This is carried out primarily through associations between the F-actin cytoskeleton and myosin or kinesin motor proteins (Soldati and Schliwa, 2006). The best characterised of these are MyoV and MyoVI, which permit anterograde and retrograde directed movement, respectively (Hartman et al., 2011). MyoVI has been shown to associate with SAP97 and AP2 to promote the endocytosis of GluA1-containing AMPAR (Wu et al., 2002; Osterweil et al., 2005), while MyoVa, a subclass of MyoV proteins, can bind directly to the GluA1 C-terminus, and is necessary for the delivery of AMPAR to the cell surface during LTP (Correia et al., 2008). Conversely, MyoVb appears necessary for the delivery of Rab11-positive recycling endosomes into spines following LTP (Wang et al., 2008).

1.5.4. *Immediate Early Genes*

In addition to synaptic changes, mediated in part by interactions between glutamate receptors and spine scaffold and structure proteins, additional regulators of plasticity have been linked to strongly synaptic activity. These proteins include IEGs, defined as class of genes that show rapid upregulation in response to signals such as neurotransmitters and growth factors. Included in these are the transcription factors early growth response protein 1 (ERG-1, also known as Zif268), and the Jun (c-Jun, JunB, JunD) and Fos (c-fos, FosB, FosB2) families (Bahrami and Drabløs, 2016), as well as effector IEGs Homer (Vazdarjanova et al., 2002), Rheb (Yamagata et al., 1994), Narp (Tsui et al., 1996), β -A activin (Andreasson and Worley, 1995), and activity-regulated cytoskeletal-associated protein, Arc (Lanahan and Worley, 1998). While both transcription factor IEGs and effector IEGs are rapidly upregulated by synaptic activity, the contribution of transcription factor IEGs is indirect, involving the regulation of other genes, while effector IEGs appear to directly modify cellular function. Much of the literature surrounding IEGs has investigated their role in neuronal ensembles and memory traces. In the hippocampus, many spatial, and working memory paradigms induce strong transcription and expression of IEGs in select populations of task-specific neurons (Vann et al., 2000; Hall et al., 2001; Xie et al., 2014). Of these, Arc has been shown to elicit control of many aspects mentioned above, including F-actin reorganization, AMPAR trafficking, and gene transcription.

1.5.4.1. Activity-Regulated Cytoskeletal-Associated Protein, Arc

Originally discovered by (Lyford et al., 1995) and (Link et al., 1995) Arc mRNA was initially shown to be rapidly and specifically upregulated at activated synapses following high frequency stimulation (HFS; Wallace et al., 1998; Steward and Worley, 2001). The expression of Arc mRNA and the synthesis of Arc protein has been further shown to require Ca²⁺, PKA, CaMKII, mitogen activated protein kinase (MAPK), eukaryotic elongation factor 2 kinase (eEF2K), and CREB signalling (Park et al., 2008; Kumar et al., 2012), driven by activation of ionotropic, metabotropic, and enzyme-linked receptors, including NMDAR (Bloomer et al., 2008), nicotinic acetylcholine receptors (α 7nAChR; Kristensen et al., 2007), mGluR (Xia et al., 1996; Kumar et al., 2012), platelet-derived growth factor receptors (PDGFR), and tropomyosin receptor kinase B (TrkB; Yin et al., 2002; Kuipers et al., 2016).

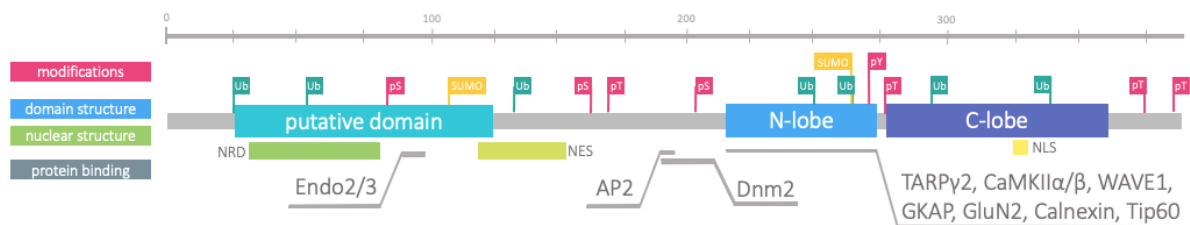


Figure 1-12 | Schematic diagram of Arc protein properties. Post-translational modifications include: phosphoserine (pS, ■), phosphothreonine (pT, ■), phosphotyrosine (PY, ■), ubiquitinated lysine (Ub, ■), SUMOylated lysine (SUMO, ■). Key sites include the nuclear retention domain (NRD, ■), nuclear export signal (NES, ■), and the nuclear localization signal (NLS, ■) within putative domain (■) and N- (■) and C-lobes (■). Dnm2 = dynamin-2, endo2/3 = endophilin-2/3. Scale bar = amino acids. Structure based of (Nikolaienko et al., 2018).

Following synthesis, Arc protein has been shown to associate with the cytoskeletal proteins F-actin, MAP2, Drebrin-A, and WASP-family verprolin-homologous protein (WAVE1), components of the clathrin-mediated endocytic mechanism, endophilin-3 (Endo3), dynamin-2 (Dnm2), and the clathrin adaptor complex AP2 (Fujimoto et al., 2004; Moga et al., 2004; Chowdhury et al., 2006; Rial Verde et al., 2006), the AMPAR auxiliary protein TARPy2, the PSD proteins GKAP, α and β isoforms of CAMKII, and NMDAR subunits GluN2A and GluN2B, and Notch1 (Zhang et al., 2015), the histone acetyltransferase Tip60 (Wee et al., 2014), the endoplasmic reticulum protein, Calnexin (Myrum et al., 2017), as well as presenilin-1 (PSEN1) as part of the γ -secretase complex (Figure 1-12). Through these associations, Arc has been linked to the regulation of cytoskeleton restructuring, gene expression, and the regulation and expression of both GluA1 (Chowdhury et al., 2006) and GluA2-containing (Rial Verde et al., 2006) AMPAR. This later function appears dependent on Arc's ability to interact with endophilin-3 and dynamin-2, indicating that Arc has the ability to actively promote the endocytosis of

GluA1 and GluA2-containing AMPARs from the cell membrane in an activity regulated manner. Through this, it is thought that Arc mediates the expression of LTP, LTD and homeostatic plasticity.

The induction of Arc synthesis upon synaptic activation, localization to active dendrites, association with key synaptic proteins, and regulation of cell surface AMPAR expression makes it a prime candidate for investigating the mechanisms underlying learning and memory. Due to this, previous publications have provided strong evidence for the necessity of Arc protein synthesis in the expression of LTP induction and consolidation. By negating the effects of Arc protein through conditional knockout (cKO; Plath et al., 2006) *in vivo* (in the DG) and *ex vivo* (in the CA1), or infusion of antisense oligodeoxynucleotides (ODNs; Guzowski et al., 2000; Messaoudi et al., 2007) *in vivo* (DG), these groups provided initial evidence that both persistent and acute blockade of Arc function alters the expression of LTP. Primarily, all groups found a significant deficit in the persistence of late phase LTP, lasting between 90 minutes to 5 days following acute (Messaoudi et al., 2007), and persistent (Guzowski et al., 2000) ODN treatment, respectively. In both cKO and persistent ODN experiments, blockade of Arc protein expression impaired spatial memory (Guzowski et al., 2000; Plath et al., 2006), as well as context fear conditioning, conditioned taste aversion, and object recognition in cKO mice (Plath et al., 2006). Interestingly, this work has been recently examined through a comprehensive approach of Arc KO and cKO mice (Kyrke-Smith et al., 2020), utilizing both HFS and TBS LTP induction protocols. Here, the authors describe a lack of dependence of Arc expression on the persistence of LTP in both KO and cKO mice using both HFS and TBS induction protocols. The authors note differences in anaesthetic regime and Arc knockout strategy, which may account for differences in the expression of LTP.

Importantly, in Arc cKO (Plath et al., 2006) and KO (Kyrke-Smith et al., 2020) mice, but not ODN infused rats, the initial induction of LTP was significantly enhanced, exceeding that of wild-type (WT) mice by 50% (Plath et al., 2006), before rapidly returning to baseline by 90 minutes in the case of (Plath et al., 2006). This may reflect differential regulation of basal levels of cell surface AMPAR following persistent and acute blockade of Arc. Such that, the delivery of AMPAR following synaptic activity in cKO/KO mice may result in the accumulation of AMPAR at the extrasynaptic membrane, priming the induction of LTP. Acute blockade of Arc by ODN 5-90 minutes before the induction of LTP minutes (Guzowski et al., 2000; Messaoudi et al., 2007) may not be sufficient to expand these extrasynaptic pools (Kennedy and Ehlers, 2011).

Importantly, the observed differences in the necessity of Arc protein in the regulation of late-phase LTP, may also be due to the expression and requirement of CP-AMPA. Due to due to Arc's role in receptor endocytosis it is thought that the increase in potentiation observed by both Plath et al., (2006) and Kyrke-Smith et al., (2020) may be due to increased expression and availability of

extrasynaptic CP-AMPA. Overexpression of Arc has been shown to decrease cell surface expression of CP-AMPA (Lanté et al., 2011; DaSilva et al., 2016; Scheyer et al., 2018), and may permit the insertion of CI-AMPA (Wall et al., 2018). If the induction protocol used by Plath et al., (2006; *in vivo*: 6 series of 6 trains of 6 stimuli at 400 Hz, 200 ms, *ex vivo*: 200 pulses at 1.5 Hz + postsynaptic depolarization) is sufficient to induce the induction of CP-AMPA in these animals, but not the induction protocol used by Kyrke-Smith et al., 2020; 4 trains of 10 bursts at 5Hz containing 4 stimuli at 100Hz), LTP in absence of Arc may saturate synaptic AMPAR and impair the removal of CP-AMPA, preventing the exchange for GluA2-containing AMPAR and impairing the persistence of LTP (Liu and Cull-Candy, 2000). Alternatively, it is possible the induction protocol used by (Kyrke-Smith et al., 2020) induced CP-AMPA dependent LTP, and the increase in both induction and persistence *ex vivo* and increased induction *in vivo* may result from LTP governed solely by CP-AMPA, due to impaired endocytosis of CP-AMPA.

In addition to mediating aspects of LTP, Arc also plays a role in the regulation of LTD. Arc cKO mice show reductions in the extent of both the induction and persistence of LTD *in vivo* (Plath et al., 2006), acute siRNA-mediated blockade of Arc prevents the maintenance, but not induction of LTD (Park et al., 2008; Waung et al., 2008). This mechanism appears more directly linked to impairments in the endocytosis of both GluA1- and GluA2/3-containing AMPAR as overexpression of Arc occludes LTD through a mechanism requiring the removal of GluA2/3-containing AMPAR (Rial Verde et al., 2006), while knockdown of Arc protein impairs mGluR-mediated endocytosis of GluA1- and GluA2/3-containing AMPAR. Interestingly, while NMDAR may be required for the induction of Arc following LTP (Bloomer et al., 2008; Yilmaz-Rastoder et al., 2011), NMDAR-dependent LTD appears to function independent of Arc function (Rial Verde et al., 2006), and in fact may negatively regulate Arc mRNA (Yilmaz-Rastoder et al., 2011). It is thought that past activity, such as novel environment exposure, induces dendritic transport of Arc mRNA and primes neurons for local synthesis of Arc protein during mGluR-mediated LTD (Jakkamsetti et al., 2013). Importantly, Steward et al., (2015) posit that if increased Arc activity is linked to the endocytosis of AMPAR, strong Arc expression following high periods of synaptic activity, such as electroconvulsive stimulation (ECS; Lyford et al., 1995; Steward and Worley, 2001) should result in a rundown of synaptic efficacy *in vivo* during the period of high Arc expression. Interestingly, this group found that following ECS, strong activation of Arc expression did not result in a depression of synaptic responses (Steward et al., 2015). This work indicates that Arc may play a more complex role in the maintenance of synaptic transmission.

Lastly, Arc has also been implicated in the mechanisms of homeostatic scaling through its removal of GluA1- and GluA2-containing AMPARs from the synapse and cell surface. In primary hippocampal cell

cultures, experimentally induced inactivity with the sodium channel blocker tetrodotoxin (TTX), or increased activity with the GABA_A antagonist bicuculline has been shown to result in increased and decreased surface GluA1 AMPAR expression, respectively. Overexpression or knockout of Arc protein occludes these homeostatic scaling responses, such that overexpression of Arc decreases basal expression of GluA1 AMPARs and impairs synaptic downscaling, while knockout of Arc increases basal cell surface GluA1, preventing the upscaling of AMPAR following activity blockade (Shepherd et al., 2006). Conversely, Arc has also been found to selectively reduce synaptic GluR2/3 AMPARs (Rial Verde et al., 2006). Here, reductions in AMPAR transmission, following overexpression of Arc in organotypic hippocampal slices, were occluded by expression of the GluR2 C-terminal tail, preventing removal from the cell surface. Biotinylation of cell surface proteins saw a reduction in GluA2, with no effect on surface GluA1.

Following these findings, authors note that the disparities between outcomes observed by Shepherd et al., (2006) and their own observations, and posit that differences in the recycling dynamics of GluA1- and GluA2-containing AMPAR in cell cultures versus organotypic slices may be responsible. Slow recycling of GluA1-containing compared to GluA2/3-containing AMPAR in hippocampal slice cultures may explain the selectivity for GluA2/3 over GluA1-containing AMPAR, while GluR1-containing AMPAR recycling is much faster in primary cultured neurons. Further, cultured neurons obtained from young animals may differ in the expression of subunit composition compared to tissue obtained from adult animals. The expression of GluA1-containing CP-AMPAR is higher in tissue obtained from young animals than that in adult tissue (Takemoto et al., 2017). Therefore, internalization of AMPAR may arise from the expression or availability of AMPAR for endocytosis, rather than selectivity governed by Arc itself, and thus conclusions from overexpression and knockout studies must be interpreted from the perspective of the system in which it is examined.

Additionally, Arc has also been found to be necessary for synapse-specific homeostatic scaling, by mediating the synaptic upscaling of GluA1-containing AMPARs (Béïque et al., 2011). Here, chronic inactivation of glutamate release from the single presynaptic terminals showed a homeostatic increase in CP-AMPAR. However, within Arc-KO cells, these synapses fail to promote this upregulation in synaptic AMPARs. It is thought that this may occur through an occlusion-like mechanism, such that Arc may be required for enhancing the trafficking of GluA1 to the synapse. Alternatively, persistent Arc expression may be required for the formation and maintenance of internal AMPAR reserve pools (Béïque et al., 2011).

Regardless, following the observed interactions of Arc with AMPAR regulatory proteins and Arc's proposed regulation of both GluA1- and GluA2-containing AMPAR, the following mechanism has been proposed (Hanley, 2018; Wall and Corrêa, 2018; Figure 1-13);

- 1) GluA1- and GluA2-containing AMPAR at the synapse are bound to PSD-95 via TARPy2. Following LTD stimulation, dephosphorylation of TARPy2 disrupts the association with PSD-95 while Ca^{2+} enhances GluA2-PICK1 binding (Citri et al., 2010). Alternatively, following LTP, phosphorylation of TARPy2 enhances PSD-95 binding (Tomita et al., 2005).
- 2) Arc protein associates with the AP2 complex, which binds GluA1 via PSD-95-bound TARPy2 (Matsuda et al., 2013), or GluA2 via PICK1, at the plasma membrane (Lee et al., 2002; Biou et al., 2008; Garafalo et al., 2015; DaSilva et al., 2016). This selectivity may define the differential recruitment of activity driven GluA1-containing and CP-AMPAR, and more stable GluA2/3-containing AMPAR populations.
- 3) Calcineurin enhances AP2-PICK1 binding, and AP2 recruits clathrin to the membrane to initiate the formation of the clathrin-coated pit (CCP) assembly. AP2-PICK1 interaction disrupts GluA2-PICK1. Formation of the CCP decreases the binding affinity of AP2 and Arc and this complex dissociates (Kelly et al., 2014).
- 4) Dissociation of Arc from AP2 frees the same binding motif used by dynamin-2 as well as binding endophilin. The binding of dynamin-2 and endophilin-3 promotes the scission of the endocytic vesicle containing the AMPAR (Sundborger et al., 2011).

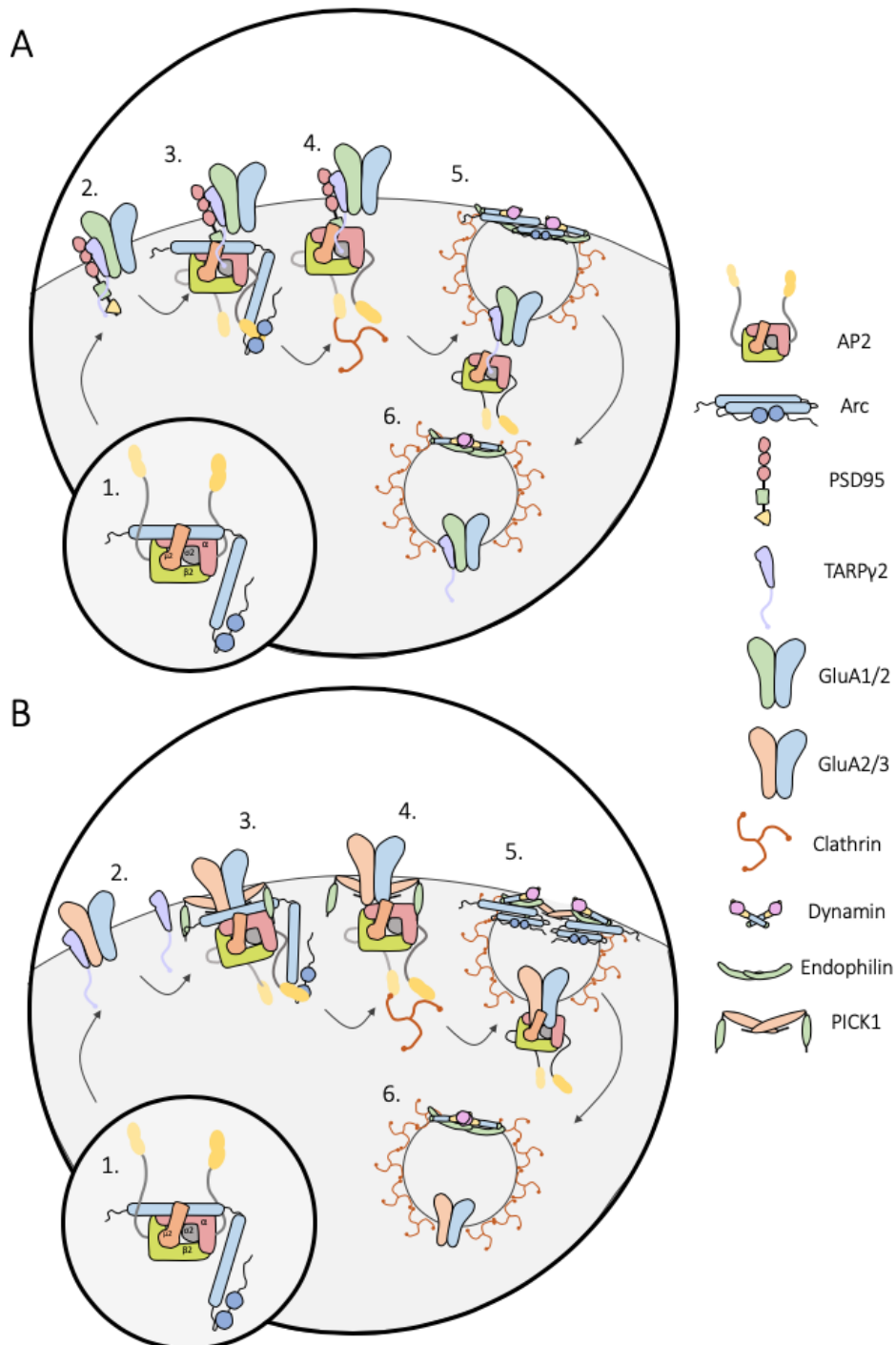


Figure 1-13 | Regulation of GluA1 and GluA2 endocytosis by Arc. Arc has been hypothesised to differentially regulate cell surface GluA1 and GluA2-containing AMPAR expression through proposed protein-protein interactions.

- A) Arc regulates GluA1-containing AMPAR. 1) Following activity, Arc binds AP2. 2) GluA1 binds PSD-95 via TARPy2. 3) AP2 binds GluA1 via TARPy2. AP2 recruits clathrin and initiates formation of the clathrin-coated pit (CCP). 5) Arc dissociates and binds dynamin and endophilin to enable scission of the CCP from the membrane. 6) GluA1-bound vesicle is then internalized.
- B) Arc regulates GluA2-containing AMPAR. 1) Following activity, Arc binds AP2. 2) TARPy2 dissociates from GluA2, PICK1 binds GluA2. 3) Arc-AP2 binds PICK1. 4) Arc dissociates from AP2, AP2 recruits clathrin. 5) Arc binds dynamin and endophilin to enable scission of the CCP from the membrane. 6) GluA2-containing vesicles are internalized.

In addition to regulating synaptic AMPAR, Arc expression may also play an important role in the dynamic regulation of morphological plasticity (Figure 1-14). As previously shown by Messaoudi et al., (2007), infusion of Arc antisense ODNs into the rat dentate gyrus 2 hours post-HFS impaired the persistence of LTP. This effect was found to be dependent on Arc-mediated phosphorylation of cofilin. Dephosphorylation of cofilin allows for nucleation and polymerization of F-actin filaments by Arp2/3 (Smith et al., 2013), promoting trafficking of AMPAR to the cell surface (Wang et al., 2013), while phosphorylation of cofilin inhibits F-actin polymerization, consolidating spine growth, and stabilizing synaptic AMPAR, following activity (Fukazawa et al., 2003; Chen et al., 2007; Gu et al., 2010; Calabrese et al., 2014). Interestingly, within one hour following HFS, Arc has been previously found to undergo SUMOylation, a post-translational modification involving the addition of a small ubiquitin-like modifier (Nair et al., 2017). This SUMOylation promotes the association of a complex with the F-actin binding protein Drebrin-A in synaptoneurosomal and cytoskeletal fractions *in vivo*. Drebrin-A has been previously shown to be important in regulating actin stabilization (Hayashi and Shirao, 1999; Kojima and Shirao, 2007; Ivanov et al., 2009; Mikati et al., 2013) by promoting phosphorylation and inhibition of cofilin activity (Grintsevich and Reisler, 2014). The binding of SUMOylated Arc protein to Drebrin-A is thought to promote the dephosphorylation of cofilin and polymerization of F-actin. Therefore, Arc may regulate actin dynamics in a two-step manner, through both SUMOylated and non-SUMOylated functions. Firstly, within one hour, a fraction of the total pool of newly synthesised Arc undergoes SUMOylation, associates with Drebrin-A and exits the spine head (Koganezawa et al., 2017), permitting dephosphorylation and activation of cofilin. In turn, cofilin promotes F-actin polymerization, growth of the actin cytoskeleton, trafficking of AMPAR to the cell surface, and induction of LTP. Secondly, within 2 hours, the return of Drebrin-A to the spine promotes phosphorylation and deactivation of cofilin, stabilizing the F-actin cytoskeleton and anchoring synaptic AMPAR. Supporting this idea is the observation that SUMOylated Arc has been found to be required for the upscaling of AMPAR following inactivity (Craig et al., 2012), possibly by promoting the trafficking of AMPAR to the cell surface (Henley and Wilkinson, 2013; Figure 1-14).

Interestingly, SUMOylated Arc does not coprecipitate with CaMKII α , CaMKII β , PSD-95 and dynamin-2, unlike non-modified Arc (Nair et al., 2017). Therefore, it is possible this modification allows for distinction between separate mechanisms such that spine expansion during early phase LTP, may occur concurrently or independently to Arc's endocytosis of AMPARs and spine stabilization following periods of high activity (Craig et al., 2012; Hanley, 2014). Furthermore, Huang et al., (2007) have shown that following HFS, local inhibition of actin polymerization by infusion of a Rho kinase inhibitor blocked Arc mRNA localization to the activated dendritic lamina. These results likely indicate a positive feedback, wherein locally translated Arc is initially SUMOylated, associating with Drebrin-A

and enhancing F-actin polymerization. This in turn may allow localization of *Arc* mRNA to activated synapses, where non-modified *Arc* binds CaMKII α , CaMKII β , PSD-95 and dynamin-2 to regulate consolidation of LTP and LTD.

Interestingly, *Arc* may play an additional role in the trafficking of GluA4-containing AMPAR to the synapse during classical conditioning (CC), in freshwater pond turtles (*Pseudemys scripta elegans*). Here, CC has been found to increase GluA4-containing AMPAR at the synapse (Mokin and Keifer, 2004), as well as enhancing the rapid colocalization and co-immunoprecipitation of *Arc* with both actin and GluA4-containing AMPAR (Mokin et al., 2006). This data is thought to describe a role for *Arc* in the synaptic targeting of GluA4-containing AMPAR during CC (Mokin et al., 2007), through an association with the actin cytoskeleton and the selective localization of GluA4-containing AMPAR to previously silent synapses (Mokin et al., 2007).

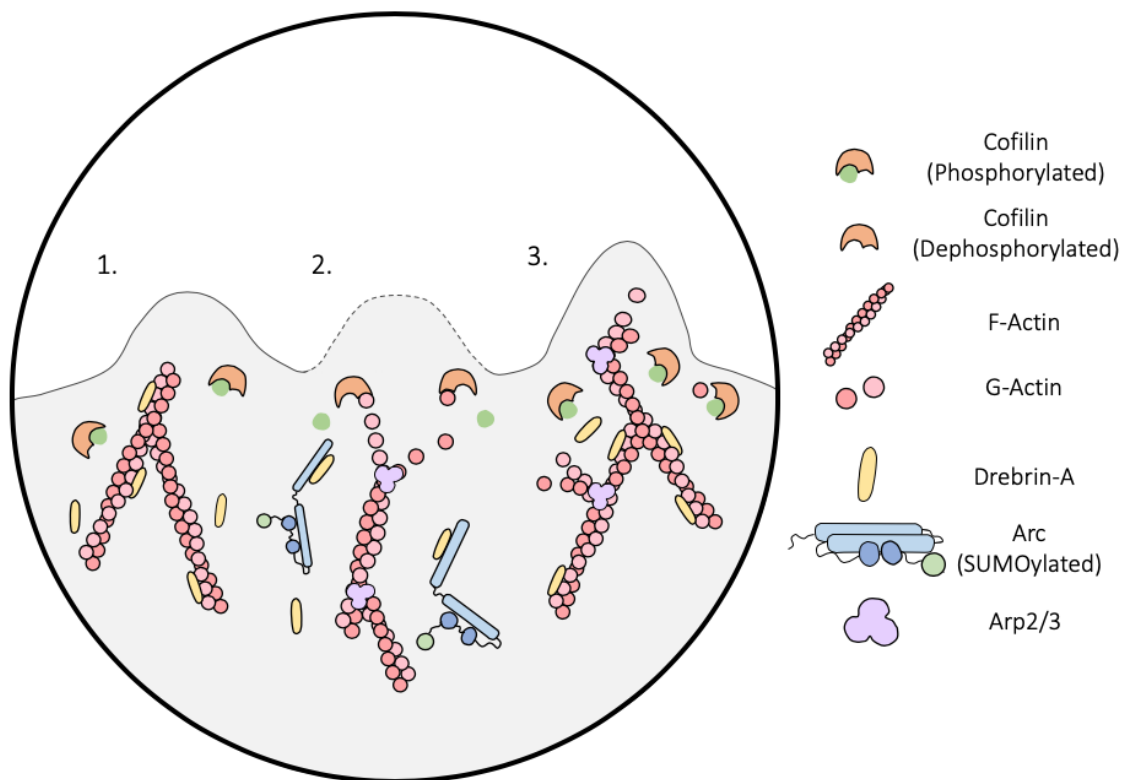


Figure 1-14 | *Arc* aids in growth of the cytoskeleton during plasticity events. 1) During basal stimulation, an equilibrium exists between F-actin growth and decay. Drebrin-A remains bound to– and stabilizes– f-actin, cofilin is phosphorylated and inactive. 2) Following stimulation, SUMOylated *Arc* binds to, and releases, Drebrin-A from F-actin. This dissociation promotes dephosphorylation and activation of cofilin. Dephosphorylated cofilin is free to bind and destabilize F-actin. Severing and debranching of F-actin into monomeric G-actin promotes actin nucleation and elongation by increasing availability of filament ends, via Arp2/3. 3) Unbound from SUMOylated *Arc*, Drebrin-A returns to the spine, inhibits cofilin's actions and stabilizes the F-actin cytoskeleton.

Arc's ability to regulate and modify the actin cytoskeleton may in turn influence the formation and growth of spines. Increasing Arc expression in cultured hippocampal neurons has been shown to increase spine density by increasing the proportion of mature, thin and filopodia spines, decreasing the proportion of immature stubby spines (Peebles et al., 2010; Enriquez-Barreto et al., 2014). Conversely, Arc knockout mice show decreased spine density, further supporting Arc's role in activity regulated spine development (Huang et al., 2007; Bramham et al., 2008). Impairing Arc's ability to internalize GluA1-containing AMPAR, by overexpression of mutant Arc lacking the endophilin-3 binding domain (amino acids Δ 91–100), failed to replicate Arc's increase in thin and filopodia spines. Therefore, this alteration in spine morphology may be driven, in part, by Arc's ability to simultaneously drive endocytosis of GluA1 AMPARs and regulate growth of the cytoskeleton (Peebles et al., 2010). Interestingly, previous work has shown that GFP-tagged Arc mRNA localizes stably and selectively to the base of stubby, thin, and mushroom spines by means of a mechanism which is not dependent on synaptic activity (Dynes and Steward, 2012). This may indicate that under conditions of basal activity docked Arc mRNA is selective for these spine types. Alternatively, synaptic activity has also been shown to simultaneously drive mRNA decay, eliminating Arc mRNA from inactive dendritic domains (Farris et al., 2014). This mechanism may allow or enhance the selective localization of Arc mRNA to active synapses, such that Arc mRNA may dock at the base of many spine types, but depending on the stimulation paradigm, mRNA is driven towards translation or degradation.

As well as localization within dendrites and regulation of the synaptic assembly, Arc has shown additional subcellular localization within the nucleus, concentrated in puncta associated with promyelocytic leukaemia (PML) bodies, which are known to regulate gene transcription (Bernardi and Pandolfi, 2007). Here it has been proposed to regulate nuclear gene transcription (Eskiw and Bazett-Jones, 2002; Bloomer et al., 2008), involving the down regulation of GluA1 (*Gria1*) transcription (Korb et al., 2013). Thus, rapid upregulation of Arc may result in internalization of GluA1-containing AMPAR, in addition to reduced synthesis of GluA1 AMPAR subunits. Further, within the nucleus, Arc has been shown to interact with the histone-acetyltransferase, Tip60, a subunits of chromatin remodelling (Wee et al., 2014). This interaction has been shown to promote PML recruitment to enhance acetylation of histones. This finding indicates that Arc may also be involved in promoting learning induced gene-expression (Park et al., 2013). However, in response to acute cocaine administration, nuclear Arc expression appears to suppress chromatin remodelling and gene expression (Salery et al., 2017). These data may suggest that during periods of high activity, Arc acts primarily to reduce synaptic activity and gene expression, dampening down the network to maintain the expression of Hebbian plasticity.

Finally, while Arc has shown strong associations with AMPAR expression, and gene transcription, recent work has identified a novel role for Arc protein through shared properties with retroviral Gag proteins (Dodonova et al., 2019). Due to these similarities, Arc has been found to form virus-like capsids, capable of encapsulating and transporting functional RNA and protein between cells in endosomal-derived extracellular vesicles, in both cultured hippocampal rat neurons (Pastuzyn et al., 2018) and *Drosophila* neuromuscular junction (Ashley et al., 2018), therefore suggesting Arc can modulate synapse-, cell-, and network-wide plasticity.

1.6. Modulators of Plasticity

A final level in the dynamic control of plasticity includes molecules which act to modulate immediate synaptic transmission, or prime synapses for future strengthening or weakening. Much research has examined the mechanisms through which neurotrophins, hormones, and neuropeptides enhance the expression of LTP and LTD. In general, these modulators permit the synthesis, expression, or regulation of mediators and messengers of plasticity, but are not directly involved in the full expression of canonical LTP or LTD.

Here, I have defined neurotrophic molecules as modulators which share seemingly closely related mechanisms of action with a specific focus on the regulation of LTP and memory, and have been implicated in the pathophysiology of neurodegenerative disorders and neurological diseases. Based on previously established criteria (McAllister et al., 1999), Table 1-1 outlines a range of molecules with defined implications in plasticity. These criteria include:

1. Neurotrophic molecules and their cognate receptors must be expressed in the right places and at the right times for the form of synaptic plasticity being considered.
2. Expression and secretion must be activity dependent.
3. Must regulate aspects of neuronal function which change activity in neural circuits, including synaptic function, membrane excitability, and neuronal morphology and connectivity.

Table 1-1 | Identification of molecules involved in neuronal plasticity

<i>Classification</i>	<i>Abbreviation</i>	<i>Definition</i>	<i>Evidence for involvement in plasticity</i>
<i>Neurotrophins</i>	NGF	Nerve growth factor	(Sastry et al., 1988; Conner et al., 2009)
	BDNF	Brain-derived neurotrophic factor	(Cunha et al., 2010; Panja and Bramham, 2014; Solinas et al., 2019)
	NT-3	Neurotrophin 3	(Arvanov et al., 2000)
	A β	Amyloid- β	(Khan et al., 2010; Parihar and Brewer, 2010; Palmeri et al., 2017; Lazarevic et al., 2017 ; Gulisano et al., 2019)
	sAPP α	Secreted amyloid precursor protein α	(Clarris et al., 1994; Small et al., 1994; Ring et al., 2007; Young-Pearse et al., 2008; Taylor et al., 2008; Weyer et al., 2011; Hick et al., 2015; Klevanski et al., 2015; Richter et al., 2018; Mockett et al., 2019)
	sAPP β	Secreted amyloid precursor protein β	(Furukawa et al., 1996b; Barger and Harmon, 1997;_Chasseigneaux et al., 2011)
<i>Neuroipoietic factors</i>	CNTF	Ciliary neurotrophic factor	(Stoop and Poo, 1996)
<i>Hematopoietic factors</i>	GCSF	Granulocyte colony-stimulating factor	(Diederich et al., 2009)
	IL-1, 2, 6, 11	Interleukins 1, 2, 6, 11	(Ross et al., 2003; Xiong et al., 2003; Chirila et al., 2014)
<i>Growth factors</i>	EFG	Epidermal growth factor	(Kopec et al., 2015),
	FGF	Fibroblast growth factors	(Wozniak et al., 2007)
	TNF	Tumour necrosis factors, α and β	(Stellwagen and Malenka, 2006; Liu et al., 2017)
<i>Neuropeptides</i>	ACTH	Adrenocorticotropic hormone	(Seidenbecher et al., 1993; Scantlebury et al., 2017)
	CGRP	Calcitonin gene-related peptide	(Wu et al., 2018a)
	CCK	Cholecystokinin	(Yasui and Kawasaki, 1995; Chen et al., 2019)
	CRF	Corticotropin-releasing factor	(Wang et al., 2000b; Blank et al., 2002)
	ENK	Enkephalin	(Bramham and Sarvey, 1996; Roberts et al., 1997)
	GAL	Galanin	(Sakurai et al., 1996; Badie-Mahdavi et al., 2005)

Catecholamines
, hormones

NPY	Neuropeptide Y	(Whittaker et al., 1999; Sajdyk et al., 2008)
NT	Neurotensin	(Amano et al., 2008)
NRG1	Neuregulin-1	(Kwon et al., 2008; Jedlicka et al., 2015)
SOM	Somatostatin	(Baratta et al., 2002; Chen et al., 2009)
SP	Substance P	(Kato and Yoshimura, 1993; Dasgupta et al., 2017)
VP	Vasopressin	(van den Hooff et al., 1989; Chafai et al., 2012)
VIP	Vasoactive intestinal polypeptide	(Cunha-Reis et al., 2014)
Ach	Acetylcholine	(Luo et al., 2008; Mitsushima et al., 2013; Takkala and Woodin, 2013)
Epi	Epinephrine	(Kuba and Kumamoto, 1986; Kumamoto and Kuba, 1987)
GH	Growth hormone	(Mahmoud and Grover, 2006; Molina et al., 2012)
NE	Norepinephrine	(Izumi and Zorumski, 1999; Maity et al., 2015)
DA	Dopamine	(Li et al., 2003; Swant and Wagner, 2006)
5-HT	Serotonin	(Villani and Johnston, 1993; Hu et al., 2004; Mlinar et al., 2015)

1.6.1. Brain-Derived Neurotrophic Factor

One of the most acknowledged neuromodulators in the field of plasticity is the brain-derived neurotrophic factor (BDNF). BDNF belongs to a family of growth factors alongside nerve growth factor (NGF), neurotrophins-3, 4, 5 and 6 (NT-3-6). BDNF synthesis occurs through both activity-regulated and constitutive pathways. Interestingly, BDNF exists as one of the numerous mRNA transcripts present in the dendrites, and is capable of undergoing activity-dependent local translation (An et al., 2008). Similar to many neurotrophins, BDNF is initially synthesised as a precursor protein (preproBDNF) in the endoplasmic reticulum (Figure 1-15). Following cleavage, proBDNF is transported to the Golgi and sorted into either constitutive or regulated secretory vesicles (Greenberg et al., 2009). It is here that proBDNF can be converted into

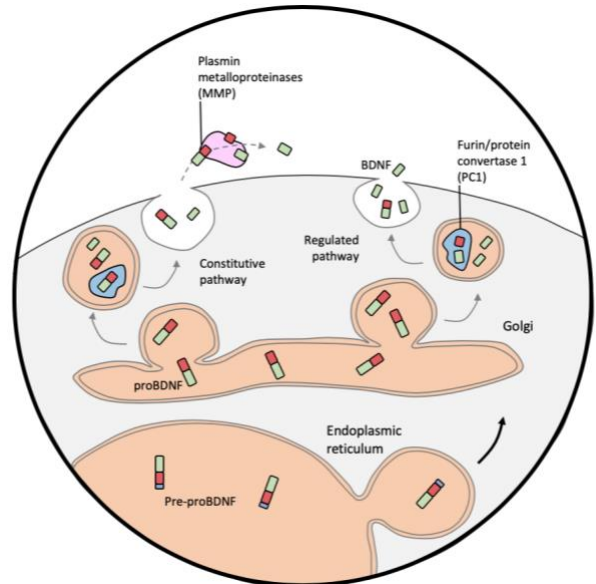


Figure 1-15 | Production and release of BDNF. Pre-proBDNF is synthesised and processed in the endoplasmic reticulum. ProBDNF is transported to the Golgi to be sorted. From here, ProBDNF is processed by furin or protein convertase 1 (PC1) into mature BDNF before release into the extracellular space or by plasmin metalloproteases (MMP) following release from the cell.

mature BDNF in the trans-Golgi network, by endoproteases such as furin, or in the immature secretory granules by proprotein convertases such as protein convertase 1 (PC1). Alternatively, following secretion proBDNF can be converted to mature BDNF by plasmin and matrix metalloproteinases present extracellularly.

BDNF acts through the tropomyosin receptor kinase B (TrkB), eliciting activation of downstream signalling cascades including Ras, MAPK, PKC, CaMKII, PI3K and PLC- γ (Sasi et al., 2017). Through these, BDNF mediates many neurotrophic processes, including neurogenesis (Lian et al., 2016; Liu and Nusslock, 2018), neuroprotection (Hofer and Barde, 1988), and cellular excitation and synaptic plasticity (Kang and Schuman, 1995; Kafitz et al., 1999). While proBDNF has been implicated in the facilitation of LTD (Woo et al., 2005), mature BDNF has been shown to enhance both E-LTP and L-LTP. Importantly, heterozygous and homozygous BDNF knockout mice show impaired maintenance of LTP (Korte et al., 1995), able to be rescued by virus-mediated perfusion of BDNF (Korte et al., 1996; Patterson et al., 1996). Interestingly, in conditions wherein the activity-dependent secretion of BDNF is inhibited, the maintenance, but not induction, of LTP is impaired (Sakata et al., 2013). While these past experiments have examined BDNF-mediated potentiation in response to tetanic stimulation, acute application of BDNF (25 minutes) to hippocampal slices has been shown to gradually enhance synaptic transmission in the dentate gyrus in the absence of tetanisation, or NMDAR activation (Ying et al., 2002). This enhancement of synaptic transmission was found to plateau within 3–4 hours post-BDNF, persisting without decrement for at least 15 hours. Further, this effect was found to be dependent on the early activity of MAPK, promoting CREB phosphorylation within 15 minutes and Arc transcription and translation within 3 hours (Messaoudi et al., 2002; Ying et al., 2002; Kuipers et al., 2016). Inhibition of BDNF by TrkB-targeted antibodies 45 minutes before the induction of LTP, or 10 minutes, 2- and 4-hours following the induction of LTP significantly attenuated the expression and maintenance of LTP *in vivo*. Application of TrkB-targeted antibodies 8- and 10-hours post-LTP induction did not significantly attenuate LTP persistence, indicating that BDNF may have an effective window in which it acts (Panja and Bramham, 2014).

In order to enhance the maintenance of LTP, it is thought that BDNF promotes the local synthesis of PRPs at the site of synaptic activity (Zhang and Poo, 2002; Leal et al., 2014). This mechanism has been described to mediate the synaptic tag and capture of PRPs during heterosynaptic plasticity. In conjunction with PKM ζ , BDNF has been shown to enhance mGluR-primed LTP, converting a weak heterosynaptic LTP into a protein synthesis dependent, non-decaying LTP. Interestingly, although BDNF has been shown to coordinate a protein synthesis-dependent maintenance of LTP (Sajikumar and Korte, 2011), application of BDNF minutes after TBS stimulation has been shown to rescue an anisomycin-induced impairment in LTP maintenance (Pang et al., 2004).

This has been thought to occur through the protein synthesis-independent activation of PKM ζ (Mei et al., 2011), suggesting PKM ζ may act downstream of BDNF signalling.

Both pre- and postsynaptic mechanisms have been described in BDNF-mediated induction and maintenance of LTP. BDNF has been shown to enhance presynaptic transmission (Gottschalk et al., 1998), likely by enhancing the synthesis of presynaptic vesicle proteins (Tartaglia et al., 2001), and the number of docked vesicles (Tyler and Pozzo-Miller, 2001). Postsynaptically, BDNF enhances the transcription, translation and trafficking of GluN1, GluN2A-, and GluN2B NMDAR (Caldeira et al., 2007), as well as the GluA1-containing CP-AMPA (Smith et al., 2005; Li and Wolf, 2011; Fortin et al., 2012). The incorporation of CP-AMPA has been shown to occur within 60 minutes, and was found to be dependent on mammalian target of rapamycin (mTOR), CaMKII, and protein synthesis (Caldeira et al., 2007).

1.6.2. *APP: A Multifaceted Control of Plasticity*

The APP protein is a lipid membrane bound protein 695-770 amino acids in length, belonging to the family of proteins including the amyloid precursor-like proteins (APLP1 and APLP2) in mammals and the amyloid precursor protein-like protein (APPL) in drosophila (Figure 1-16). APP exists in 8 isoforms, 3 of which are the most common: the APP695 is predominantly expressed in the CNS, while APP751 and APP770 forms, are more ubiquitously expressed (Bayer et al., 1999). Initially, full-length APP was understood to play a crucial role in regulating cell processes involved in metabolism and development, throughout the CNS, as well as kidney, heart, muscle, and lung tissue (Tanaka et al., 1989). APP knockdown mice show significant reductions in body weight, grip strength, locomotion and impaired synaptic transmission, as well as a susceptibility to epileptic seizures (Zheng et al., 1995). Further, in the CNS, APP is widely believed to be functionally involved in neuronal development, cell signalling, and homeostasis (Young-Pearse et al., 2007; O'Brien and Wong, 2011).

Within the CNS, APP is present in both excitatory and inhibitory neurons (Liao et al., 2016) at both pre- and postsynaptic terminals, as well as within glial cells including astrocytes and microglia (LeBlanc et al., 1996; Wang et al., 2009). Following synthesis and sorting in the ER and Golgi, APP is delivered to both axons (Koo et al., 1990) and dendrites (Das et al., 2013) by fast anterograde trafficking, mediated by kinesin-driven transport (Kamal et al., 2000). Following trafficking, both constitutive and activity-dependent processing permit cleavage of secreted metabolites (Figure 1-17). The processing of APP by α -, β -, and γ -secretases determines the outcome of the amyloidogenic versus the non-amyloidogenic pathway. Following trafficking from the trans-Golgi network, APP is transported to the cell surface. Here, APP may be proteolyzed directly by A disintegrin and metalloproteinase (ADAM10) α -secretase to generate the N-terminal secreted amyloid precursor

protein- α (sAPP α ; Figure 1-16). Alternatively, a small population of cell surface APP may be processed by the β -site amyloid precursor protein-cleaving enzyme 1 (BACE1), releasing sAPP β (Wang et al., 2018). Cleavage at the β -secretase site releases an APP fragment 16 amino acids shorter than sAPP α ,

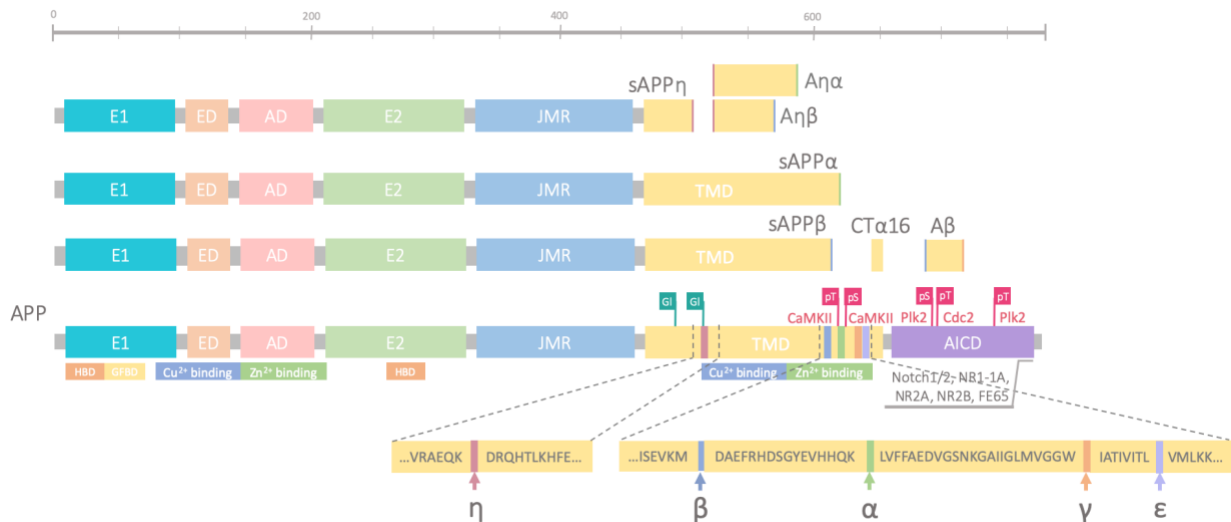


Figure 1-16 | Structure and domains of the Amyloid Precursor Protein. Schematic diagram depicts the APP protein and primary metabolites, as well as sites of α - (red), β - (blue), γ - (green), ϵ - (orange), and η (purple)-secretase activity. Post-translational modifications include: phosphoserine (pS, red), phosphothreonine (pT, pink), glycosylation (Gl, green). Heparin-binding domain (HBD, orange), growth factor binding domain (GFBD, yellow), Zn²⁺- (green) and Cu²⁺- (blue) binding domains. E1 (cyan), ED (orange), AD (pink), E2 (green), juxtamembrane region (JMR, blue), transmembrane domain (TMD, yellow), APP intracellular domain (AICD; purple). Scale bar = amino acids. Structure based on (Nikolaienko et al., 2018).

and these 16 amino acids (CT α 16) have been shown to mediate many of the differences between the two peptides (Richter et al., 2018; Morrissey et al., 2019b).

The dwell time of APP at the cell surface is short (Lorenzen et al., 2010). Unprocessed, full-length APP, or remaining C-terminal fragments following α - and β -secretase activity (generating α and β CTFs, respectively), may be reinternalized in clathrin-coated pits into late endosomes or lysosomes containing both BACE1 and γ -secretase proteases. Here, unprocessed APP may undergo both β -secretase and γ -secretase processing to release sAPP β , A β , and AICD, while α - and β -CTFs may also undergo further γ -secretase processing releasing p3, and APP intracellular domain (AICD), and A β , and AICD, respectively (O'Brien and Wong, 2011). Both p3 and AICD have been proposed to be involved in a range of intracellular signalling cascades, such as gene transcription, and neurite development, as well as caspase-mediated cell death signalling (Müller et al., 2008; Chow et al., 2010; Frykman et al., 2010; Zhou et al., 2012). This processing permits the production of sAPP α to preclude A β generation by cleavage and secretion at the plasma membranes (Nitsch et al., 1993; Lammich et al., 1999). Following generation of A β , A β fragments undergo lysosomal degradation or release into the extracellular space via vesicle recycling (Schroeder and Koo, 2005), or packaging into extracellular

vesicles (Sardar Sinha et al., 2018; Figure 1-17). Recently, alternative proteases have been identified which cleave APP to generate sAPP η (Willem et al., 2015) and CTF- ϵ (Eggert et al., 2004). Generation of the N-terminal product sAPP η by membrane-bound matrix metalloproteinases such as MT5-MMP (η -secretase) also releases CTF- η fragments A $\eta\alpha$ and A $\eta\beta$, via α - and β -secretase, respectively. Conversely, the ϵ -secretase cleavage occurs in close proximity to γ -secretase and likely promotes release of the intracellular domain of APP following α , and β -secretase activity (De Strooper et al., 2010).

While processing of APP has been shown to occur constitutively, the release of both A β and sAPP α have also been linked directly to synaptic activity (Cirrito et al., 2003). Due to this, the naturally high metabolic activity of the hippocampus and closely associated cortices appear preferentially targeted for increased APP processing (Del Turco et al., 2016). During activity increased presynaptic vesicle fusion during neurotransmitter release, and clathrin-mediated endocytosis during vesicle recycling, promotes the delivery and internalization of APP, permitting A β generation and release. Alternatively, PKC-dependent activity has been shown to enhance cell surface expression of APP (Hung et al., 1993), promoting α -secretase activity, and inhibiting A β production (Skovronsky et al., 2000).

1.6.3. *Amyloid Beta*

Amyloid beta (A β) was first isolated as the principal component of amyloid deposits in the brain and cerebral vasculature of AD and Down's Syndrome (DS) patients (Masters et al., 1985). While A β has been shown to form peptides ranging from 39-43 residues in length, the primary forms are A β 40 and A β 42, produced by γ -secretase cleavage. It is through these two forms arise from poor specificity for the cleavage site (Li et al., 2000), while mutations in the γ -secretase complex protein PS1 (*PSEN1*) drive γ -secretase towards A β 42 production (Wolfe, 2007). The presence of the longer C-terminal tail of A β 42 is thought to promote aggregation into higher order molecules, and the formation of extracellular A β plaques (Jarrett et al., 1993). Due to this, a consistent feature of AD pathology is an increased ratio of A β 42/40, suggesting a shift in balance of these products is a critical step in AD pathogenesis

A β has been widely understood as a key regulator of the neurodegeneration observed in AD. The presence of extracellular A β -containing plaques and intracellular hyperphosphorylated Tau protein and accumulation of neurofibrillary tangles (Spillantini et al., 1990). These dystrophies are thought to occur downstream of aberrant A β signalling, promoted by sporadic or genetic factors contributing to the pathogenesis of AD (Ricciarelli and Fedele, 2017). These changes, mediated in

large by A β , have been linked to the loss of excitatory synapses (Lue et al., 1999), impairments in memory and LTP (Shankar et al., 2008; Faucher et al., 2016), and neuritic dystrophy (Pike et al., 1992), ultimately leading to cell death (Banerjee et al., 1997) and atrophy of the CNS (Whitwell, 2010). Notably, in animal models expressing mutated forms of APP or PS1, deficits in synaptic composition and transmission are present before the emergence of plaques by several months (Hsia et al., 1999). At the synapse, oligomeric A β has been shown to bind in close proximity to synapses (Lacor et al., 2004; Koffie et al., 2009), and impair synaptic density in a radial manner from A β plaques (Hsieh et al., 2006; Spiers-Jones et al., 2007; Birnbaum et al., 2015). These oligomers have been further shown to impair the induction and maintenance of LTP (Freir et al., 2001; Shankar et al., 2008), enhance LTD (Li et al., 2009), and reduce cell surface levels of GluN1 and GluN2B NMDAR subunits (Snyder et al., 2005; Kurup et al., 2010), as well as synaptic GluA1, (Almeida et al., 2005), and GluA2 (Liu et al., 2010) AMPAR subunits. From this, it is posited that small A β oligomers provide a majority of the neurotoxicity evident in AD, with A β plaques providing diffuse stores of these peptides.

This research provides strong evidence that A β acts to promote pathological dysregulation of synapses, however under conditions in which high concentrations of A β are present. Converse to this, a non-pathological role of A β has also been identified at lower, physiological levels. At concentrations reflective of those present in the healthy brain (Rozmahel et al., 2002; Phinney et al., 2003; Pawlik et al., 2004), mounting evidence suggest that A β shows characteristics of a canonical neurotrophin. Such that APP, and thus A β , as well as β - and γ -secretases are expressed throughout the hippocampus (Hébert et al., 2004; Del Turco et al., 2016; Meakin et al., 2018) and cortex (Satoh et al., 2012; Bergström et al., 2016), from early in development throughout adulthood (Yusof et al., 2019; Bergström et al., 2016). Further, as mentioned above, the generation of A β is activity dependent, with extracellular release tightly linked to vesicle fusion and recycling (Cirrito et al., 2003), and A β has shown promise in positively modulating neuronal function, such as enhancing synaptic transmission, cell excitability, and promoting plasticity.

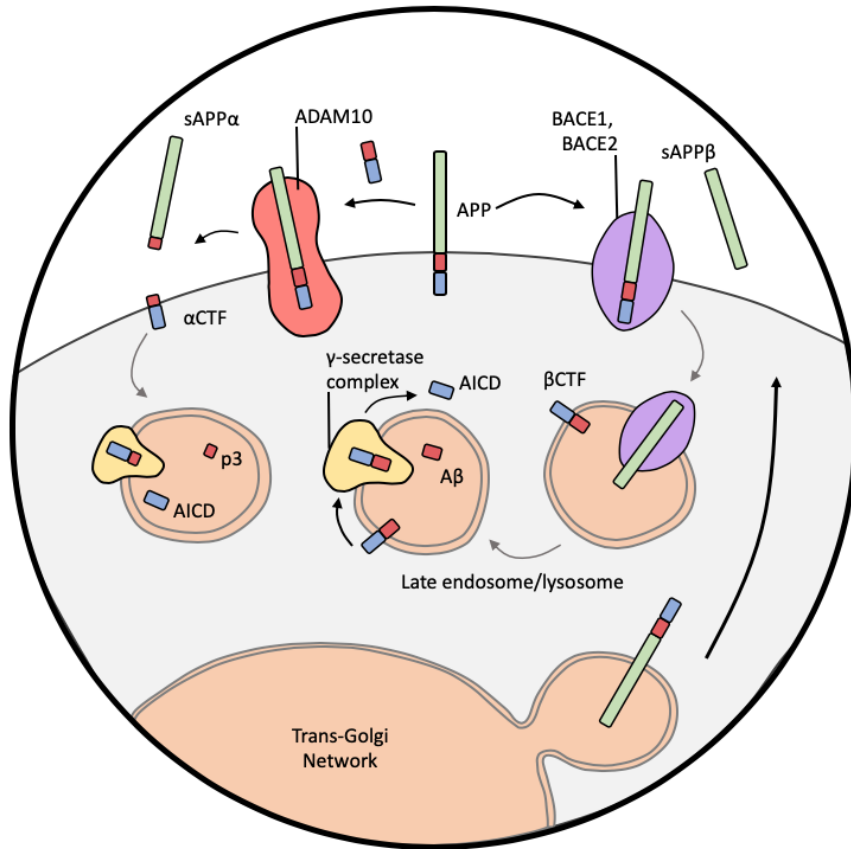


Figure 1-17 | Stylized diagram of APP processing. In the non-amyloidogenic pathway, APP is trafficked towards the plasma membrane where it is cleaved by α -secretase, generating soluble APP alpha (sAPP α) and α -secretase C-terminal fragment (α -CTF). Full length APP is internalised by clathrin-dependent endocytosis. APP, BACE1 and BACE2 converge in early endosomes. The amyloidogenic pathway then results in APP cleavage into soluble APP β (sAPP β) and β -secretase C-terminal fragment (β -CTF; also known as C99). Both non-processed, full-length APP and sAPP β can be reinserted into the plasma membrane through recycling endosomes. Final γ -cleavage of APP generates the APP intracellular domain (AICD) and amyloid β (A β) peptides.

It has been previously shown that inhibition of A β degradation enhances mEPSC responses through an enhancement in presynaptic vesicle release (Abramov et al., 2009; Lazarevic et al., 2017). Likewise, picomolar concentrations of A β enhances neuronal neurotransmission (Puzzo et al., 2008), and spontaneous astrocytic calcium transients (Lee et al., 2014), both in a manner dependent on the activation of α 7nACh receptors. Further, cGMP-induced LTP has been found to be dependent on A β through a mechanism which increases APP/BACE-1 convergence in lysosomes (Palmeri et al., 2017). In line with this, recent work has highlighted a role of A β in the conversion of E-LTP to a protein synthesis-dependent L-LTP, as well as increasing phosphorylation of CREB and CaMKII and increasing BDNF levels, in a manner dependent on the NO/cGMP/PKG cascade and α 7nAChR activation (Gulisano et al., 2019). Interestingly, A β may act in a concentration- and aggregation-dependent manner to gate α 7nAChR activity. Such that, at picomolar concentrations, monomeric A β promotes α 7nAChR

activation (Dineley et al., 2002; Dougherty et al., 2003; Wu et al., 2007; Puzzo et al., 2008), while nanomolar concentrations (Liu et al., 2001; Pettit et al., 2001; Grassi et al., 2003) and oligomeric A β (Kroker et al., 2013) inhibit the activation of α 7nAChRs (Wang et al., 2000a; Lasala et al., 2019). Lastly, depletion of A β *in vivo* has been shown to result in impaired performance on both reference and fear conditioning-based tasks (Puzzo et al., 2008; Garcia-Osta and Alberini, 2009). Taken together, these data provide evidence for a role of A β in regulating memory formation at physiological concentrations, while significantly impairing synaptic plasticity and neuronal health at greater concentrations (Figure 1-18). These dual mechanisms displayed by A β may provide insight into why many of the drug treatments aiming to reduce or eliminate A β in AD fail (Lista et al., 2015; Morley and Farr, 2016).

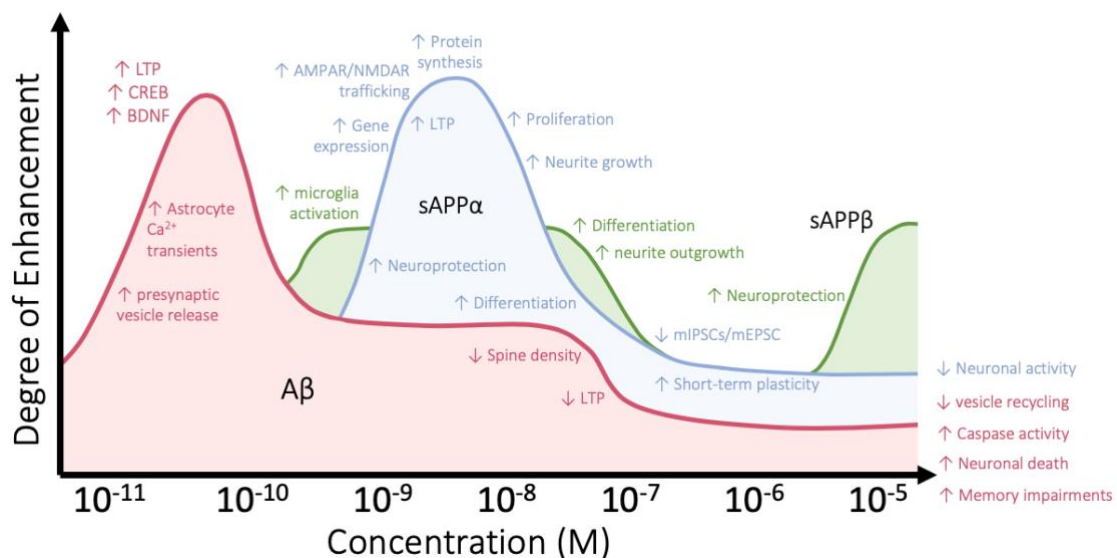


Figure 1-18 | Hormetic relationship between APP metabolites and the expression of key neurotrophic mechanisms. A β (■), sAPP β (■), and sAPP α (■) show distinct concentration-dependent regulation of cellular processes, with minimal overlap. Many of the positive effects of A β - and sAPP α are present at low picomolar and nanomolar concentrations, respectively. sAPP α begins to inhibit neuronal active at high nanomolar concentrations, while A β becomes detrimental to plasticity and cell health at high nanomolar and micromolar concentrations. Effective sAPP β concentrations appear at low nano- and micromolar concentrations. Concentrations are presented as a log of molar (M) concentration.

1.6.4. sAPP α

A facet of the APP protein which has arisen throughout the course of its research is its role in promoting neurotrophic support during development, as well as contributing to the regulation of plasticity. Research examining acute and chronic application or knockout of APP have provided

significant evidence that APP mediates many aspects of central and peripheral nervous system function. Initial observations found that knockout of APP resulted in reduced peripheral motor function (Zheng et al., 1995; Zheng et al., 1996; von Koch et al., 1997), defective CNS neuronal migration (Herms et al., 2004), reduced neuronal morphology and synaptic transmission (Zheng et al., 1995; Zheng et al., 1996; Dawson et al., 1999), and impaired spatial memory performance (Müller et al., 1994). Around this time the N-terminus of APP was identified to contain growth factor-like structure (Rossjohn et al., 1999), containing heparin-binding, and cysteine-rich domains. Animal models lacking the expression of N-terminal APP, but retaining the amyloidogenic C-terminal domain, show extensive gliosis, impaired spatial memory performance, and reduced LTP magnitude (Nalbantoglu et al., 1997). Importantly, many of the deficits displayed by knockout or mutation of the endogenous APP gene, could be rescued with acute application of sAPP α , restoring brain and body weight, as well as motor deficits and synaptic transmission and spatial memory (Ring et al., 2007). Importantly, application of sAPP β was insufficient to rescue the increased lethality of APP-KO mice, nor the associated motor deficits (Li et al., 2010). While sAPP β has been shown to regulate aspects of neurite outgrowth (Chasseigneaux et al., 2011), neural differentiation (Freude et al., 2011), and neuroprotection (Furukawa et al., 1996b; Barger and Harmon, 1997), mounting evidence suggests sAPP α mediates many of the neurotrophic and plasticity-enhancing effects present in APP, at lower effective concentrations (see Figure 1-18). Crucially, in many neurological and neurodegenerative disorders, the expression and regulation of sAPP α appears altered and may contribute significantly to the pathology of the disease.

1.6.4.1. *sAPP α as a Biomarker*

As part of the pathology which arises in AD and associated pathologies, the amyloid cascade hypothesis further posits that there is a clear shift in the processing of APP towards the amyloidogenic pathway, and away from the non-amyloidogenic pathway (Selkoe and Hardy, 2016). AD is a multifactorial disease, consisting of both familial (fAD) and sporadic (sAD) forms (Barykin et al., 2017). A minority of AD cases present with fAD, with a predominantly early-onset, driven primarily by the inheritance of mutations in *APP*, *ADAM10*, *PSEN1*, and *PSEN2* (Bertram et al., 2010). Most cases (90%) present as the more complex sAD, arising from a combination of environment and lifestyle factors (Piaceri et al., 2013), as well as genetic predisposition associated with the $\epsilon 4$ allele of the Apolipoprotein E gene (*APOE*), in approximately 20% of sAD cases (Ertekin-Taner, 2010). *APOE* has been described to regulate the metabolism and clearance of A β from the CNS (Verghese et al., 2013), and therefore has been implicated in contributing to A β -mediated pathology. Importantly, both fAD

and sAD have been hypothesised to arise, in part, as a result of the amyloid cascade hypothesis. Such that mutations which directly influence APP processing in fAD or A β clearance in sAD alter A β expression in the CNS. Logically, if a therapeutic is administered before the deposition and accumulation of A β , which opposes the further deposition of A β or counteracts early dysfunction, a therapeutic such as this would be expected to delay onset or severity of the disease. However, a caveat of this arises such that the period before detrimental cognitive decline, but possible to be detected physiologically, must be defined.

Due to this, many studies have attempted to measure the metabolites of APP processing, including sAPP α , sAPP β , total sAPP, and A β 40/42, from blood, plasma, and cerebral spinal fluid (CSF) from human patients, aiming to detect onset or manifestation of neurodegenerative diseases, including AD. Much of the research examining the expression of APP metabolites in AD has focused on A β , finding strong correlations between levels of A β 40/42 with Mini-Mental State Examination (MMSE) scores (Struyfs et al., 2015) and disease progression (Bibl et al., 2012; Janelidze et al., 2016), in both sAD (Portelius et al., 2010) and fAD (Portelius et al., 2012). Studies examining the concentration of sAPP α in AD patients have however been somewhat inconsistent. This may have arisen partially through discrepancies in the methodology, including MMSE scores, heterogeneity of the disease, comorbid conditions, specificity and sensitivity of the assays and cross-reactivity of antibodies, and differences in sampling, processing, and storage of samples. One study in particular was conducted on patients scoring greater than 20 on the MMSE. Of those patients with CSF characteristics of AD, many demonstrated high CSF levels of sAPP α and sAPP β (Lewczuk et al., 2010). However, comparing this to studies which have found a significant decrease in sAPP α while using less strict exclusion criteria, the increased levels of APP metabolites may be indicative of patients with typically higher cognitive ability (scoring > 20) despite presence of pathological AD characteristics, or those in an early stage of the disease progress (Prior et al., 1991; Van Nostrand et al., 1992; Sennvik et al., 2000; Colciaghi et al., 2002; Rosen et al., 2012). Notably, in studies which concluded little to no change in AD patients CSF levels of sAPP α and sAPP β , the antibodies used failed to distinguish between sAPP α and sAPP β and thus measured total sAPP (Palmert et al., 1990; Hock et al., 1998). This limits the conclusions drawn as many recent studies suggest unchanged sAPP β with decreased sAPP α (Prior et al., 1991; Van Nostrand et al., 1992; Sennvik et al., 2000).

Furthermore, differences may arise in the aetiology of the disease. In patients with fAD mutations such as those affecting APP (Swedish APP KM670/671NL) and ADAM10 (Q170H and R181G), there are significant decreases in CSF levels of sAPP α (Lannfelt et al., 1995; Kim et al., 2009), which is further correlated with poor performance on neuropsychological tests that assess intelligence, verbal and visuospatial functions, memory, and attention (Almkvist et al., 1997). A similar

trend is seen in patients possessing one or two copies of the $\epsilon 4$ allele of APOE, suggesting risk factors for sAD may also affect the processing and expression of sAPP α (Olsson et al., 2003; Thordardottir et al., 2017). Importantly, while the levels of sAPP α significantly decrease in fAD, and in moderate-to-severe AD (Lannfelt et al., 1995; Almkvist et al., 1997), it appears many studies have not found significant changes in the early stages of sAD and mild cognitive impairment (MCI; Perneczky et al., 2011; Rosen et al., 2012; Brinkmalm et al., 2013; Perneczky et al., 2013; Araki et al., 2017), compared to sAD patients in advanced stages of the disease (Rosén et al., 2012). This indicates that direct genetic alterations in APP processing may influence biofluid levels of sAPP α to a greater, more detectable level than in sAD. Interestingly, reduced CSF concentrations of sAPP α are also evident in other conditions, including cerebrovascular and neurodegenerative diseases such as stroke (Selnes et al., 2010), amyotrophic lateral sclerosis (ALS; Selnes et al., 2010; Steinacker et al., 2011), bipolar disorder (Jakobsson et al., 2013; Rolstad et al., 2015), and idiopathic normal pressure hydrocephalus (Miyajima et al., 2013), therefore changes in the levels of sAPP α in these conditions may indicate a critical clinical evaluation is necessary to rule out comorbid diseases which may interfere with the specificity of an AD diagnosis.

1.6.4.2. *sAPP α as a Neuroprotective Molecule*

Following the observations that APP can regulate copper- (White et al., 1999), iron- (Maynard et al., 2002; Duce et al., 2010), zinc-, and manganese- (Needham et al., 2014) homeostasis, levels of glucose and insulin (Needham et al., 2008), as well as provide anticoagulant functions with regards to thrombosis (Henry et al., 1998; Xu et al., 2009), it was becoming clear that sAPP α may also demonstrate neuroprotective and neurotrophic functions. sAPP α has since been shown to protect against a battery of insults including traumatic brain injury (TBI; Pierce et al., 1996; Chen et al., 2004; Thornton et al., 2006; Loane et al., 2009; Corrigan et al., 2012; Siopi et al., 2013; Plummer et al., 2016), hypoglycemia and glutamate toxicity (Mattson et al., 1993; Furukawa et al., 1996b; Ryan et al., 2013), and proteasomal deficiency-induced cell stress and apoptosis (Copanaki et al., 2010; Kundu et al., 2016). While many of these assays examine sAPP α 's ability to counteract apoptosis or apoptosis-related pathways, a 2016 study examined the effects of transient hypoxia on electrical activity at the network and cellular level, in APP-KO mouse tissue. Relative to wild-type (WT) mice, in APP-KO mice hypoxia-induced impairments were exacerbated, including increased intracellular Ca^{2+} , faster loss of function, higher incidence of spreading depression, and much slower recovery upon reoxygenation (Hefter et al., 2016). Importantly, these deficits could be abrogated following selective expression of sAPP α or blockade of L-type calcium channels. These results indicate that sAPP α contributes much of

its neuroprotective functions to calcium homeostasis. Of interest, many of the neuroprotective effects including activation of nuclear factor-kappa B (NF κ B) DNA-binding activity, calcium homeostasis, and K⁺-channel activation, occur as part of the cGMP pathway (Furukawa et al., 1996a; Furukawa and Mattson, 1998). Further, *in vivo* studies have corroborated this research, finding that during transient hippocampal ischemia, administration of sAPP α significantly ameliorated neuronal loss (Smith-Swintosky et al., 1994), consistent with findings that APP-KO and BACE-KO mice show increased mortality as a result of cerebral ischemia (Koike et al., 2012). Similarly, APP-KO mice appear more vulnerable to TBI, but show reduced cell death, and axonal deficits, and improved motor outcomes following intracerebroventricular administration of sAPP α or peptides derived from it (Corrigan et al., 2014), indicating an endogenous role of sAPP α during injury. Importantly, sAPP α has also been shown to provide neuroprotection against A β -induced toxicity (Goodman and Mattson, 1994; Barger and Mattson, 1996b; Gralle et al., 2009; Milosch et al., 2014), by promoting an upregulation in neuroprotective genes such as transthyretin and insulin-like growth factor-2 (Stein et al., 2004). sAPP α may also directly regulate the expression of A β , by binding to and inhibiting of BACE1 directly, reducing the production of A β (Obregon et al., 2012; Peters-Libeu et al., 2015). These observations further support the hypothesis that dysregulation of APP processing exacerbates A β -mediated pathology through an impairment in sAPP α -mediated neuroprotection.

1.6.4.3. *sAPP α as a Putative Treatment*

The rise of the amyloid cascade hypothesis has largely driven by efforts to minimize levels of A β in the brain. This has led to clinical trials aimed at reducing A β action directly or inhibiting its production. Among the anti-A β therapeutic approaches, the most extensively developed is that of immunotherapy—direct targeting of endogenous A β protein through administration of exogenous monoclonal antibodies (van Dyck, 2018). While many attempts have reached phase 1 (Ostrowitzki et al., 2012; Landen et al., 2013; Sevigny et al., 2016) or 2 (Salloway et al., 2009; Rinne et al., 2010; Farlow et al., 2012) of clinical trials, many have also made it through to phase 3 (Doody et al., 2014; Salloway et al., 2014). However, all cases have failed to meet their primary end points, with no significant changes to disease progression or cognition in the face of major problems with safety. Because of this, indirect targets of A β generation have been sought. The β -secretase enzyme BACE1 has been shown to be significantly increased in AD patients (Fukumoto et al., 2002; Fukumoto et al., 2004), and significantly correlated with A β load (Li et al., 2004), and has therefore been targeted as a target of potential therapeutics. Early investigations found BACE1 inhibitors to provide significant ameliorations to brain A β levels (Lai et al., 2012; Stamford et al., 2012; Bernier et al., 2013; Forman et

al., 2013; Eketjäll et al., 2016) while increasing sAPP α levels (Martenyi et al., 2012; Willis et al., 2012). However, many of these trials failed to provide significant ameliorations in cognitive or functional decline (Hawkes, 2017; Egan et al., 2018), likely due to little benefit in reducing A β late in the disease progression, and off-target effects (Lahiri et al., 2014).

Due to sAPP α 's innate role in combating neurodegeneration, whilst providing trophic support, it is only logical to approach treatment against neurodegeneration from the standpoint of enhancing either direct CNS concentrations of sAPP α , or upregulating endogenous mechanisms which do so. Perhaps surprisingly, recent investigations into FDA-approved drugs marketed towards improving symptoms present during mild-moderate AD, has shown a unique link to APP physiology. Cholinesterase inhibitors Rivastigmine, Phenserine, and Donepezil have been shown to significantly decrease A β *in vitro* (Lahiri et al., 2007; Takada-Takatori et al., 2019), *in vivo* (Ray et al., 2020), and in CSF of AD patients (Maccacchini et al., 2012). Additionally, Rivastigmine has been found to inhibit A β generation through a mechanism which enhances ADAM-9, -10, and -17 α -secretase activity, and thus simultaneously enhance sAPP α production. This effect was found to be robust when assayed in rat neuronal PC12 cells, primary human brain cultures, 3 \times transgenic (APPKM670/671NL, PS1M146V, MAPTP301L) mice, as well as post-mortem human brain samples from those with AD and treated with Rivastigmine. The action of these drugs is spurred by the cholinergic hypothesis of AD, which posits that cholinergic hypofunction mediates the cognitive decline present in AD, and augmentation of this may be beneficial, by either enhancing activity of the endogenous acetylcholine (ACh) or by exogenous agonists (Fisher, 2012). Results from animal research provides support for this as high concentrations of A β impair α 7nAChR activation (Liu et al., 2001; Pettit et al., 2001; Grassi et al., 2003), which negatively affect the induction of LTP (Kroger et al., 2013), but can be rescued by co-application of competitive agonists of α 3 β 4 (Nery et al., 2013) and α 4 β 2- and α 7nAChRs (Kroger et al., 2013). Importantly, activation of α 4 β 2-, and α 3- and α 7-containing nAChR (Nitsch et al., 1992; Mousavi and Hellstrom-Lindahl, 2009), as well as m1- and m3-containing muscarinic AChRs (mAChRs; Nitsch et al., 1996), enhances the release of sAPP α while simultaneously attenuating A β production, indicating that A β itself may drive positive feedback regulation at physiological levels and may be an avenue worth exploring therapeutically.

1.6.4.4. *sAPP α as a Promoter of Plasticity*

In addition to promoting neuroprotection, APP has been shown to contribute to the growth of neurons, promoting the formation and strengthening of synapses and enhancing plasticity. APP-null and APP-silenced mice show significant reductions in the proportion of synaptophysin-positive

presynaptic terminals, impaired induction and maintenance of hippocampal LTP (Seabrook et al., 1999; Taylor et al., 2008), in addition to prominent reductions in total neurite length, dendritic branching, reduced spine density and reduced spine head volume (Ring et al., 2007; Hick et al., 2015). As research has continued, sAPP α has begun to prove itself as not only a key facilitator of neuroprotection but as a neurotrophic and plasticity-enhancing protein, also. Early observations found that APP-null and APP-silenced (through antibody targeting) mice showed prominent reductions in the proportion of synapses (Seabrook et al., 1999), reductions in total neurite length, dendritic branching, reduced spine density and reduced spine head volume (Lee et al., 2010b; Tyan et al., 2012), as well as significant reductions in the induction and persistence of hippocampal LTP (Ring et al., 2007; Weyer et al., 2011; Hick et al., 2015), and impaired performance on hippocampal-dependent memory tasks (Klevanski et al., 2015). Importantly, many of these impairments are able to be rescued by acute application or viral knock-in of sAPP α or the C-terminal 16 amino acid APP_{672–688} peptide (CT α 16), but not the sAPP β fragment (Ring et al., 2007; Weyer et al., 2011; Hick et al., 2015; Klevanski et al., 2015), indicating that many of the synaptic functions provided by APP may arise by sAPP α -driven mechanisms. In fact, sole application of sAPP α to hippocampal tissue has been shown to promote neurite (Clarris et al., 1994; Small et al., 1994), and axonal outgrowth (Young-Pearse et al., 2008), primarily produced through the presence of heparin-binding site at residues APP_{96–110} (Small et al., 1994), APP_{319–335} containing the amino sequence RERMS (Ninomiya et al., 1994), or the APP_{328–332} motif alone (Jin et al., 1994). In line with this, overexpression of human APP (Mucke et al., 1996; Lee et al., 2010b), or the α -secretase ADAM10 (Bell et al., 2008) has been shown to increase the proportion of cholinergic, glutamatergic and GABAergic synapses, accompanied by increases in surface and total GluA2, but not GluA1-containing AMPAR (Lee et al., 2010b). Further, using time-lapse two-photon in vivo microscopy, spine density was found to remain unaltered in APP-KO mice, however these mice showed significant deficits in spine turnover, affecting spine formation and elimination, as well as environmental enrichment-dependent increase in spine density. Interestingly, the latter was found to be rescued by application of exogenous D-serine (Zou et al., 2016), indicating that APP, or sAPP α may mediate astrocyte and D-serine homeostasis to regulate these changes. Together, these results indicate a crucial role of autocrine or paracrine signalling of sAPP α in the formation and maintenance of spines, necessary for learning-induced plasticity.

In addition to altering morphological plasticity, sAPP α has been shown to also facilitate functional physiological outcomes. Early experiments showed that application of sAPP α to acute hippocampal slices shifts the frequency of the LTD induction, such that low frequency, LTD-inducing stimulation (LFS, 1Hz) was insufficient to induce LTD following pre-treatment with sAPP α . Alternatively, sAPP α was also shown to enhance HFS-induced (100Hz) LTP by 50% (Ishida et al., 1997),

in a manner dependent on cGMP, and likely PKG. Similarly, inhibition of endogenous sAPP α by antibody targeting, or inhibition of α -secretase by TAPI-1, significantly reduces LTP in the dentate gyrus of adult rats *in vivo* (Taylor et al., 2008), as well as impairing spatial memory. These results have been so-far linked to an increase in NMDAR currents (Moreno et al., 2015), however this is contested (Furukawa and Mattson, 1998), while more recent work has linked the activation of α 7nAChRs in sAPP α - and CT α 16-mediated enhancements of LTP (Richter et al., 2018; Morrissey et al., 2019a).

sAPP α 's ability to enhance synaptic potentiation, in both *in-* and *ex-vivo* preparations, is further evident by sAPP α 's effect on behaviour. Intracerebral administration of antibodies targeted towards residues 672–688 of APP has been shown to impair performance on inhibitory avoidance in rats (Doyle et al., 1990), and passive avoidance in chicks (Mileusnic et al., 2000). Similarly, inhibition of α -secretase impairs spatial water-maze memory in rats (Taylor et al., 2008), similar to complete knockout of APP (Ring et al., 2007). Importantly, these deficits could be restored by either acute administration (Taylor et al., 2008) or genetic overexpression (Ring et al., 2007) of sAPP α . Further, these memory-enhancing effects have been found to be applicable in rescuing amnesia- (Meziane et al., 1998), A β - (Mileusnic et al., 2004), AD- (Fol et al., 2016), TBI- (Corrigan et al., 2012), and aging-induced memory impairments (Xiong et al., 2017). Further, acute treatment of sAPP α , but not sAPP β , is capable of protecting against oligomeric A β -induced spine loss (Tackenberg and Nitsch, 2019), while both sAPP α and CT α 16 have been shown to rescue impairments in LTP in an AD mouse model (Fol et al., 2016; Morrissey et al., 2019a). Interestingly, evidence from human studies, show in both AD and Bipolar Disorder (BD), cerebrospinal fluid concentrations of sAPP α have been found to be significantly lower than healthy controls (Zhang et al., 2011; Jakobsson et al., 2013; Rolstad et al., 2015). In addition, decreased sAPP α is significantly correlated with decreased cognitive performance on attention and speed in those with BD.

While many strides have been made in understanding how sAPP α promotes LTP and concomitant modulations to memory and behaviour, many of the underlying mechanisms remain unsubstantiated. sAPP α has been previously shown to enhance both *de novo* transcription and translation (Ryan et al., 2013; Mockett et al., 2019), with transcription thought to be mediated through NF κ B (Barger and Mattson, 1996a). The outcomes of this appear to mediate extensive gene expression, much of which regulates neuroprotection through cell survival, inflammatory, anti-apoptotic, and neurogenic responses (Stein et al., 2004; Aydin et al., 2011; Demars et al., 2011).

sAPP α has been further shown to regulate translational processes by directly regulating protein synthesis. Application of sAPP α (1, 10 nM; 25 min) but not sAPP β has been shown to enhance

synaptodendritic protein synthesis in rat hippocampal synaptoneurosomes (Claasen et al., 2009), independent of transcription. This effect was found to be dose-dependent and dependent on the activity of CaMKII, MAPK, and PKG. Interestingly, the degree of protein synthesis enhancement was significantly affected by age, such that old (22–23-month-old) rats increased protein synthesis approximately 15% less than young (8-12 weeks) counterparts. More recently, sAPP α has been shown to enhance LTP in a concentration- and protein synthesis-dependent manner (Mockett et al., 2019) as well as requiring trafficking of proteins from the Golgi to the cell surface. Importantly, this enhancement of LTP was found to be specific to sAPP α , as LTP remained unaffected by sAPP β . Further, sAPP α was found to concomitantly increase cell surface levels of GluA1 but not GluA2 AMPAR subunits, in a concentration (0.3, 1 nM)-dependent manner and dependent on CaMKII, PKG and activation of NMDAR. Similarly, sAPP α also increased cell surface levels of GluN1, in a concentration (1 nM)- and CaMKII-dependent manner. Further, in primary hippocampal cell culture, sAPP α (1 nM, 2 hr) was found to enhance *de novo* synthesis of GluA1, but not GluA2 AMPAR subunits (Mockett et al., 2019). Interestingly, the enhancement of LTP is able to be recapitulated by application of as little as three amino acids found within the E2 APP328-330 domain of sAPP α (Morrissey et al., 2019a), referred to as the RER peptide, as well as CT α 16 (Morrissey et al., 2019b), in a concentration- and protein synthesis-dependent manner.

Together, these results define many likely mechanisms through which sAPP α , and associated peptides, may promote the expression of synaptic plasticity and memory. This work has established gene expression, protein synthesis, and glutamate receptor trafficking as key processes mediating these changes, yet the underlying details remain largely unknown. To date, no study has examined the effect of sAPP α on the expression of IEGs such as Arc and the relationship to cell surface expression of AMPAR. The regulation of these processes is critical to the expression of LTP, and therefore would provide important insights into the regulation of memory in both health and disease. This thesis aims to extend the current understanding of the mechanisms underlying sAPP α -mediated plasticity by investigating AMPAR trafficking and Arc protein in hippocampal neurons. We hypothesise that sAPP α regulates the enhancement of LTP, in part through the insertion of newly synthesised GluA1-containing CP-AMPAR at the cell surface. Moreover, we hypothesise that the expression of these AMPAR would be regulated by the expression and function of the IEG Arc.

Chapter 2: Materials and Methods

2.1. Primary Neuronal Culture Preparation

All experimental protocols conducted in New Zealand were approved by the University of Otago Animals Ethics Committee and conducted in accordance with New Zealand Animal Welfare Legislation under the ethics approval ET18/15.

The preparation of primary hippocampal cultures followed a modified protocol based on Banker and Goslin, (1998), Banker and Cowan, (1977) and Kaech and Banker, (2006), and refined by Dr. Tet-Woo Lee and Dr. Megan Elder. Antibiotics were not used for experiments examining the expression of glutamate receptors but were present for the examination of Arc protein. All instruments were autoclaved and all liquids were filter sterilized prior to use. Aseptic techniques were employed at all times. Glass bottom culture dishes (50 mm, 14 mm glass, MatTek Corporation, #P35G-1.5-14-C), 6 well plastic dishes (Corning, #3516), 96-well assay plates (Corning, #3603), or 175 cm² flasks (Sigma, #CL55431306) were coated overnight with Poly-D-Lysine (PDL; 100-200 µg/mL, Sigma), rinsed with autoclaved sterilised Milli-Q ultrapure water (MQ), and left to dry in a Herasafe KS Class II Biological Safety Cabinet (Thermofisher).

2.1.1. *Dissection*

Two Sprague-Dawley rat pups (male or female, postnatal day (PD) 0-1) were sourced from a breeding colony maintained at the Hercus Taieri Resource Unit by the University of Otago. Pups were decapitated with a sharp pair of scissors (Fine Science Tools, #14060-09), and heads were submerged in a 100 x 20 mm petri dish (Corning, #430591) containing ice-cold dissection media (DM; in mM: 82 Na₂SO₄, 30 K₂SO₄, 5.8 MgCl₂, 0.252 CaCl₂, 1 4-(2-hydroxyethyl)-1-piperazineethanesulfonic acid (HEPES), 20 glucose, 0.001% Phenolred in MQ, adjusted to pH 7.4) and moved to a sterile laminar flow cabinet (Esco).

The skin and skull were cut along the midline to the nose, and laterally to the eyes in a 'T' shape using a small pair of scissors (Figure 2-1A-D). Using forceps (Fine Science Tools, #91197-00), the skull was peeled back to expose the brain, which was carefully removed following the severing of the optic tracts and cranial nerves using a small iris spatula (Fine Science Tools, #91110-13). The brain was transferred to a dish of fresh, chilled DM. A pair of forceps with extra fine angled tips (Fine Science

Tools, #91110-10) was used to separate the midbrain and forebrain, sever the corpus callosum, and separate the hemispheres. The meninges and blood vessels were removed from the lateral surface of the hemisphere and the olfactory bulb and cerebellum were removed using a curved Iris spatula (Figure 2-1E-I). Any midbrain and meninges from the medial aspect were removed using forceps, exposing the hippocampus (Figure 2-1J). The hippocampi were inverted from the cortex and removed from the surrounding tissue by carefully pinching away the cortex. Any remaining cortical tissue was carefully removed from the hippocampus and transferred to a 15 mL Falcon® conical tube containing ice-cold DM (Figure 2-1K-M). For the dissociation and culture of cortical tissue, remaining midbrain tissue was removed and the cortex was cut into smaller pieces, and transferred to ice-cold DM (Figure 2-1N-Q)

2.1.2. *Dissociation and Plating of Primary Neurons*

Following dissection, the hippocampi were incubated in cysteine-activated papain (2.64 mM L-Cysteine (Sigma #168149), 3 % Papain (Sigma, #19001-73-4) in DM, NaOH was added to return to pH 7.4) for 15 min at 37 °C to initiate dissociation of the extracellular matrix. This incubation was repeated with fresh papain solution for an additional 15 min before tissue was thoroughly washed (4 x, 30 s) with ice-cold DM to arrest the protease action. Cells were then manually dissociated by trituration in warm neuronal growth media (NGM; 97 % Neurobasal A media, 2 % B27 supplement and 1 % Glutamax-100; Life Technologies), and any remaining tissue was allowed to settle during incubation on ice (3 min). The supernatant was removed and centrifuged (70 x g, 4 °C, 5 min) to pellet the dissociated cells, which were resuspended in warm NGM and counted using Trypan blue staining in a hemocytometer. Cells were plated at a density of 40,000 cells/cm² (40,000 total) on MatTek dishes for immunofluorescence, 67,500 cells/cm² (20,000 total) in 96-well plates, and 31,500 cells/cm² (300,000 total) or 63,000 cell/cm² (600,000 total) in 6-well plates for RNA or protein extraction, respectively. Cells were maintained at 37 °C (5 % CO₂) in a Heracell™ VIOS 160i CO₂ Incubator (ThermoFisher).

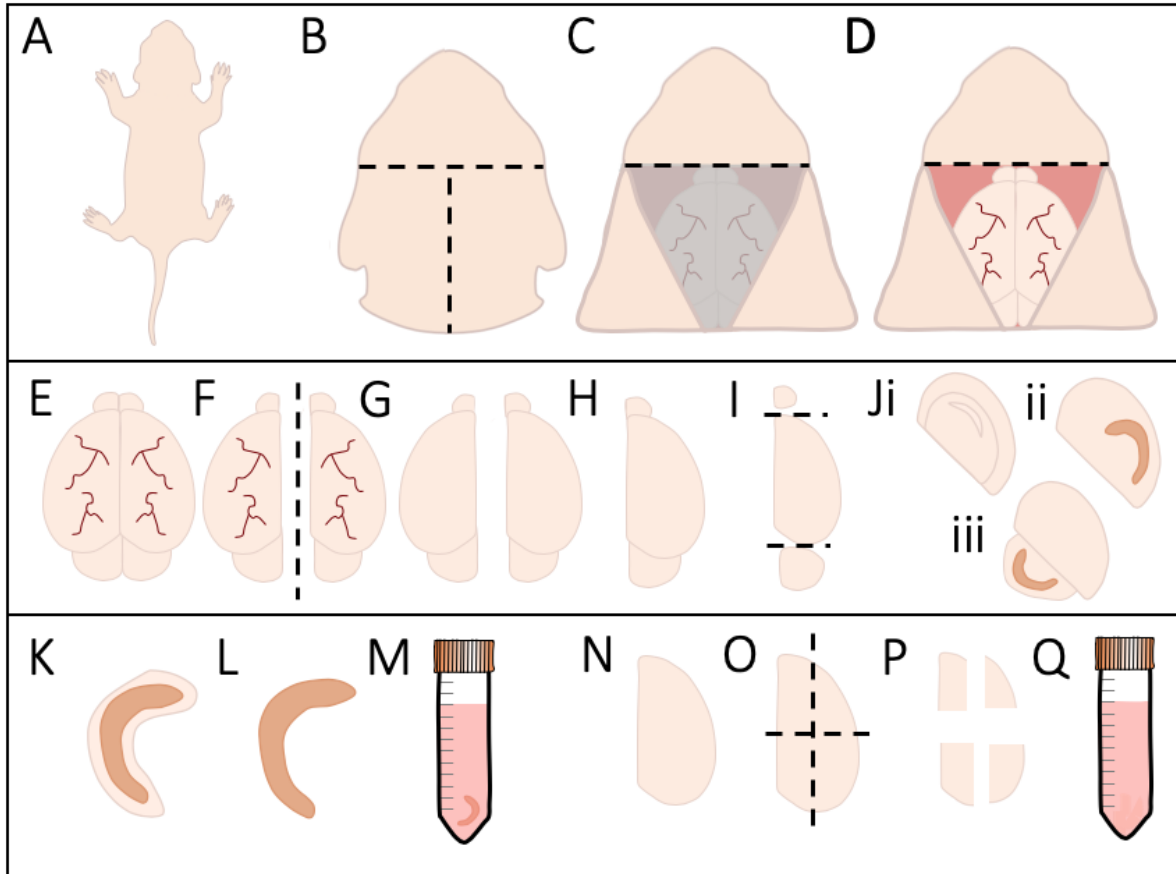


Figure 2-1 | Hippocampal and cortical dissection. A) Sprague-Dawley rat pups (PD 0-1) are decapitated. B-C) Skull is exposed by T-shaped cut down the midline, D) and the skull is removed to access the brain. E) The brain is removed and placed in ice-cold dissection media. F) The two cortical hemispheres are separated medially through the corpus callosum and G-H) the meninges are removed from the lateral surface of the cortex. I) The olfactory bulb and cerebellum are removed from each hemisphere, and Ji) the cortex is turned onto the lateral face, Jii) midbrain tissue is removed, and the hippocampus is exposed. Any remaining meninges in the hippocampal fissure and on the face of the hippocampus are removed and Jiii) the hippocampus is inverted and separated from the cortex by pinching with forceps. K-L) Any excess tissue is removed from the hippocampus and M) all hippocampi are placed in 10 mL of ice-cold DM. For cortical cultures, N) remaining neocortex tissue is quartered (O-P) and Q) placed in 10 mL of ice-cold DM.

2.1.3. *Production of Conditioned Media for Cell Culture Maintenance*

Following plating, cultures were supplemented with conditioned media at four hours post-plating and 4 days *in vitro* (DIV 4). This media consisted of NGM that had been supplemented with media from healthy cultures comprised primarily of cortical neurons or glial cells, which contained secreted factors to support the growth of primary hippocampal cultures (Conde Guerri et al., 1989; Figure 2-2). For the curation of conditioned media, neuronal cells were plated in a 75 cm² flask coated with PDL (100 µg/mL) and maintained in NGM, with weekly feeding with NGM. Approximately 80% of the media was harvested every four days after DIV 7. For glial conditioned media, glial cells were dissociated from cortical tissue, resuspended, and plated in Minimal Essential Media (MEM; 87 % minimum essential medium (Gibco), 10 % fetal bovine serum (Gibco) and 3 % glucose (1.1 mM), supporting glial but not neuronal growth, in uncoated 175 cm² flasks. On DIV 1, the flask was shaken to loosen microglial attachments and remaining unhealthy neurons. The media was changed for fresh MEM to remove cell debris, and again on DIV 3 and DIV 5. On DIV 7, only glial cells remained and the MEM was replaced with NGM to support further glial cell growth and proliferation. Glial conditioned media was harvested every four days from DIV 11. Media from both flasks was harvested for up to 40 days, or until the cells appeared less healthy as determined visually by increasing debris or fragmented neuronal projections. Following collection, the media was centrifuged (69.5 x g, 5 min) to pellet any cellular debris and the supernatant was stored at -20 °C prior to use.

Primary hippocampal cultures were supplemented at 4 hr and 4 days post-plating with conditioned media (80 % NGM, 15 % glial media and 5 % neuronal media prepared, as described in section 2.1.3. *Production of Conditioned Media for Cell Culture Maintenance*) and maintained with weekly supplements of NGM for 21–27 DIV.

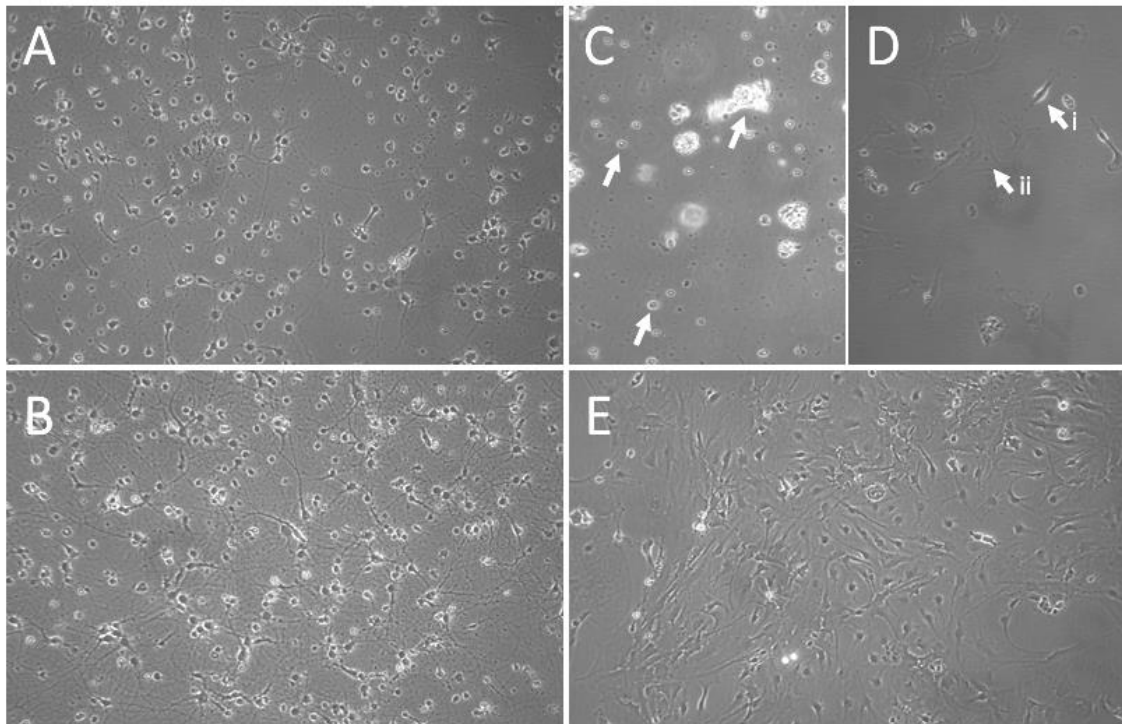


Figure 2-2 | Growth of neurons and proliferation of glia. Representative phase contrast images of A) DIV5 and B) DIV 12 neuronal flask cultures. On DIV 1 C) glial flasks show cellular debris and dead cells (arrows), removed by shaking. D) By DIV5 remaining neurons present as small cell bodies with retracting neurites (arrow, i), astrocytes begin to expand in size and multiply in number (arrow, ii). E) By DIV 12 glial cells cover most of the flask surface.

2.2. Adult Primary Neuronal Culture Preparation

2.2.1. Dissection

C57/Bl6 mice and C57/Bl6 mice containing the Swedish APP mutation (APP_{swe}: KM670/671NL) and PS1 exon 9 deletion (PS1 Δ exon9), male or female (9 months) were sourced from a breeding colony maintained at the Hercus Taieri Resource Unit by the University of Otago. Mice received an injection of pentobarbital (200 mg/kg, i.p.) before decapitation by guillotine. Brains were removed and chilled in ice-cold and oxygenated modified artificial cerebrospinal fluid (aCSF) for which sucrose was substituted for NaCl (composition in mM: sucrose 210, glucose 20, KCl 2.5, NaH₂PO₄ 1.25, NaHCO₃ 26, CaCl₂ 0.5, MgCl₂ 3, pH 7.4 when gassed with 95% O₂-5% CO₂). Brains were then transferred to 100mm x 20mm petri dishes, containing ice-cold DM, and moved to a sterile laminar flow cabinet (Esco). Henceforth, adult mouse brains were obtained similar to that for primary neuronal cultures obtained from young animals (see section 2.1.1. *Dissection*). However, unlike young tissue the removal of meninges proved more difficult and therefore, for the most part, remained intact to avoid unnecessary damage to the cortical tissue underneath. Following the removal of the hippocampus, brainstem, and cerebellum, cortical tissue was diced into fine pieces and stored on ice in a 15 mL Falcon® tube containing DM for transport.

2.2.2. Dissociation and Plating of Primary Neurons

Dissociation and plating of cortical tissue followed a similar protocol as for young tissue (see 1.1.2. *Dissociation and plating of primary neurons*). Cells were plated at a density of 40,000-56,000 cells/cm² (40,000-56,000 total) on MatTek dishes. Following plating, cells were left to settle for 15 minutes to ensure attachment, before washed with warm NGM, and replaced with 1 mL conditioned media containing 10 ng/mL human basic fibroblast growth factor (bFGF; Thermofisher, #13256029). On DIV 4 cultures were supplemented with 1 mL NGM containing 10 ng/mL bFGF. Henceforth cells were fed weekly with NGM.

2.3. Experimental Procedures

2.3.1. Immunocytochemistry

For a list of drugs and antibodies used in these experiments, see Table 2-1 and Table 2-2, respectively.

2.3.1.1. Treatment of Primary Cultures

Recombinant human sAPP α and sAPP β were produced as per Turner et al., (2009) by Dr. Megan Elder in the Tate lab. In brief, sAPP α and sAPP β constructs were stably integrated into cultured HEK 293T cells (American Type Culture Collection). Both sAPP α and sAPP β were secreted and purified from the culture media, and purification of proteins were assessed by a single band on an SDS polyacrylamide gel as analysed by Coomassie Blue staining, and by Western analysis. This preparation has been validated in a variety of studies *in vivo* and *in vitro* including electrophysiological and behavioural investigations (Turner et al., 2007; Taylor et al., 2008; Ryan et al., 2013; Mockett et al., 2019). Both sAPP α and sAPP β were diluted into stock solutions in 0.1x PBS, and diluted in culture media or artificial cerebrospinal fluid (aCSF) for the final working concentration.

For experiments examining the effect of sAPP α or sAPP β on the expression of targets of interest, cells were incubated in 0.1-1 nM sAPP α diluted in existing media for the length of treatment. Following this period, the culture media was aspirated and cells were fixed in 4 % paraformaldehyde (PFA) in phosphate buffered saline (PBS; 1.37 M NaCl, 27 mM KCl, 43 mM Na₂HPO₄•7H₂O, 14 mM KH₂PO₄) containing MgCl₂ (1 mM), CaCl₂ (0.1 mM), and sucrose (PBS-MCS; 155.42 mM), for 20 min at room temperature (RT). Here, the inclusion of sucrose aids in maintaining an isotonic solution, preserving the cell membrane during fixation (Cheng et al., 2019), as well as maintaining structural integrity of internal organelles (Kisselev and Goldberg, 2005; Danchenko et al., 2019).

Table 2-1 | Catalogue of inhibitors and antagonists used throughout immunocytochemical and immunohistochemical experiments.

<i>Drugs (Inhibitors)</i>	<i>Target</i>	<i>Concentration (Stock, mM; working, μM)</i>	<i>Pre-Incubation (min)</i>	<i>Details</i>
Anisomycin	Translation	50; 40	30	Sigma, #A9789
Actinomycin-D	Transcription	10; 40	15	Tocris, #1229
KN62	CaMKII	5; 10	15	Tocris, #1277
PD98059	MAPK	50; 50	0	Tocris, #1213
KT5823	PKG	5; 10	0	Tocris, #1289
Chelerythrine Chloride	PKC	10; 1	30	Tocris, #1330
H-89 Dihydrochloride	PKA	2; 10	30	Calbiochem, #371963
Rapamycin	mTOR	0.86; 0.001	30	Tocris, # 1292
Sodium Fluoride	Serine/Threonine phosphatases	0.5; 1000	15	Sigma #S7920
Phenylmethylsulfonyl Fluoride	Serine/Threonine phosphatases	10; 100	15	Sigma, #P-7626
Okadaic Acid	Serine/Threonine phosphatases	10; 1	15	Tocris, #1136
<i>Drugs (Antagonists)</i>	<i>Target</i>	<i>Concentration (Stock, mM; working, μM)</i>	<i>Pre-Incubation (min)</i>	<i>Details</i>
α -Bungarotoxin	α 7nAChR	0.01; 0.001	30	Abcam, #AB120542
IEM-1460	GluA2-lacking AMPA	100; 100	50	Abcam, #AB141507
D(-)-2-Amino-5- Phosphonopentanoic Acid	NMDAR	50; 50	30	Sigma, #A8054
CPG 55845 Hydrochloride	GABA _B	25; 50	30	Tocris, #1248
ANA-12	TrkB	10; 100	30	Tocris, #4781
\pm A-Methyl-4- Carboxyphenylglycine	mGluR _{II/III}	25; 500	30	Sigma, #M-4796

2.3.2. Primary Antibody Probe

To examine whole cell (total) expression of a protein of interest, cells were permeabilized using 0.5% Triton X-100 in PBS (15 min); this step was omitted prior to probing only the surface-bound fraction of a target protein. In order to prevent nonspecific binding to target proteins, blocking buffer was applied to cells in preparation for probing with primary antibodies (4 % normal goat serum in PBS; NGS), for 1-hour at RT or overnight at 4 °C. Antibodies were diluted in blocking buffer and applied for

1.5 hours (FUNCAT-PLA, BioPLAy, PLA) or 2 hours (Immunocytochemistry, Immunohistochemistry, 4. *Antibody Specificity*) at RT or overnight at 4 °C. Unbound and excess antibody was removed by washing the cells in PBS (3 x 5 min).

2.3.3. *Secondary antibody probe*

Primary antibodies were detected using corresponding fluorescent-labelled secondary antibodies diluted in blocking buffer (30 min, RT). The nuclear stain DAPI was routinely included in the secondary antibody incubation (1 µg/µL) unless otherwise stated. Unbound antibody was washed from the cells with PBS (3 x 5 min), and cells were imaged immediately in PBS (pH 7.4).

Table 2-2 | Catalogue of primary and secondary antibodies used in immunocytochemistry (IC), immunohistochemistry (IH), western blot (WB), FUNCAT-PLA (F-PLA), BioPLAy (B), and PLA (PLA).

<i>1°</i>	<i>Antigen</i>	<i>Host species</i>	<i>Dilution</i>	<i>Use</i>	<i>Details</i>
	α Tubulin	Mouse	1:10000	WB	Abcam, AB7291
	Arc	Rabbit	1:1000	IC, IH, WB	Synaptic Systems, 156003
	Biotin	Mouse	1:1000	F-PLA, B	Sigma, B7653
	Biotin	Rabbit	1:1000	IC	Abcam, AB53494
	GFAP	Mouse	1:1000	IC	Abcam, AB10062
	GluA1 (c-terminal)	Rabbit	1:1000	IC, F, B, F-PLA, WB	Abcam, AB31232
	GluA1 (N-terminal)	Mouse	1:250	IC, WB, PLA	Merk Millipore, MAB2263
	GluA2 (C-terminal)	Rabbit	1:500	I, F-PLA	Merk Millipore, AB1768-I
	GluA2 (N-terminal)	Mouse	1:500	IC, B, F-PLA, PLA	Abcam, 133477
	GluA2 (N-terminal)	Rabbit	1:500	IC, B, F-PLA, PLA	Thermofisher, 32-0300
	GluA3 (N-terminal)	Mouse	1:500	IC, B, F-PLA, PLA	Thermofisher, 32-0400
	MAP2	Guinea Pig	1:1000; 1:500	IC, IH, B, F-PLA, PLA	Synaptic Systems, 188004; Abcam, AB11267
	pCREB (Ser133)	Rabbit	1:500	IH	Cell Signalling, 9198
	Prox1	Mouse	1:1000	IC	Abcam, AB33219
	Synapsin-1	Mouse	1:1000	ICC	Synaptic Systems, 106011
	Tau	Rabbit	1:500	I	Sigma-Aldrich, SAB5500182
<i>2°</i>	<i>Fluorophore</i>	<i>Host Species</i>	<i>Dilution</i>	<i>Use</i>	<i>Details</i>
	Alexa fluor 405	Goat anti-mouse	1:1000	IC	Invitrogen, A31553
	Alexa fluor 488	Goat anti-mouse	1:500	IC	Thermofisher, A11001
	Alexa fluor 488	Goat anti-Guinea Pig	1:1000	IC, IH, F-PLA, B, PLA	Thermofisher, A11073
	Alexa fluor 488	Goat anti-rabbit	1:1000	IC	Invitrogen, A11034
	Alexa fluor 555	Goat anti-mouse	1:1000	IC	Invitrogen, A21424
	Alexa fluor 555	Goat anti-rabbit	1:1000	IC, IH	Invitrogen, A21429
	Alexa fluor 647	Goat anti-mouse	1:500	IC	Invitrogen, A21236
	IRDye680	Goat anti-rabbit	1:10000	WB	LI-COR, 926-32210
	IRDye800	Goat anti-mouse	1:10000	WB	LI-COR, 926,32220
	PLA ^{MINUS}	Donkey anti-mouse	1:10	F-PLA, B, PLA	Sigma-Aldrich, DUO92004
	PLA ^{PLUS}	Donkey anti-rabbit	1:10	F-PLA, B, PLA	Sigma-Aldrich, DUO92002
<i>Miscellaneous</i>					
	DAPI	-	1:1000 (1 μ g/ μ L)	IC, IH, F-PLA, B, PLA	ThermoFisher, D1306
	Duolink Detection Reagent Texas Red	-	1:5	F-PLA, B, PLA	Sigma-Aldrich, DUO92008

2.3.4. *Fluorescent Non-Canonical Amino Acid Tagging– Proximity Ligase Assay (FUNCAT-PLA)*

The detection of newly synthesised protein with FUNCAT-PLA was conducted in accordance with published protocol from (Dieterich et al., 2010) and adapted for current experiments. All steps carried out at RT were conducted at 21-22 °C in a temperature-controlled bench-top incubator (Benchmark Scientific, H2200-HC). Cultures used for FUNCAT-PLA experiments were between DIV21-27. The methionine analogue L-Azidohomoalanine (AHA, 4 mM; Click Chemistry Tools, #1066) was prepared in methionine-free Neurobasal A (Gibco, custom product) supplemented with 2% B27 and 1% Glutamax.

2.3.4.1. *Treatment and Incorporation of AHA*

Following visual assessment of cell health, dishes were randomly assigned to treatment groups for each experiment. Following the removal of existing media, treatment dishes received 1 nM sAPP α (diluted from 320 nM stock) in 4 mM AHA (prepared as described in section 2.3.4 *Fluorescent Non-Canonical Amino Acid Tagging– Proximity Ligase Assay (FUNCAT-PLA)*). Control groups received only AHA-containing NGM for the length of the treatment. Following the incubation period, the cultures were immediately washed three times in PBS-MC (pH 7.4, RT) then fixed in 4 % PFA in PBS-MCS (20 min, RT). Cells were incubated in blocking buffer (4 % normal goat serum in PBS, 1 hr at RT), and then washed twice in PBS pH 7.8 (2 x 10 min, RT) to slowly raise the pH in preparation for the click reaction.

2.3.4.2. *Click Reaction*

The detection of the AHA-containing, newly synthesised proteins, is made possible through addition of an alkyne-bearing biotin moiety. This moiety can be covalently attached to the azide-bearing AHA through a copper(I)-catalysed [3+2] azide-alkyne cycloaddition or 'click chemistry' (see Figure 2-3). The click reaction mixture was prepared immediately prior to application to the cells. The mixture was comprised of 200 μ M Tris (1-benzyl-1H-1,2,3-triazol-4-yl)methyl amine (TBTA triazole ligand, Aldrich), 500 μ M Tris(2-carboxyethyl)phosphine hydro-chloride (TCEP, Thermo Scientific), 25 μ M Biotin-PEG4-alkyne (Biotin alkyne, Aldrich) and 200 μ M CuSO₄ in PBS pH 7.8. All reagents were dissolved sequentially through vigorous vortexing after the addition of each component from stock solutions.

Immediately following preparation, 1000 μL of 'click mix' was added to each dish, and incubated overnight at RT.

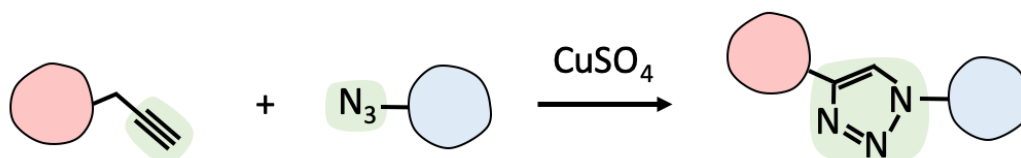


Figure 2-3 | Copper-catalysed azide-alkyne cycloaddition (CuAAC). An alkyne-bearing biotin (●) can be covalently attached to the azide-bearing AHA (●) via a Copper-catalysed click-chemistry reaction.

2.3.4.3. *Detection of Newly Synthesized Proteins*

Following the 'click'-mediated labelling of newly synthesized cell surface proteins with a biotin moiety, FUNCAT-PLA was employed to visualise their expression and location (Figure 2-4). Cells were washed with PBS (pH 7.8, 2 x 10 min), permeabilized with 0.5 % Triton X-100 in PBS (15 min, RT), and incubated in blocking buffer (1 hr, RT). Cells were then probed with primary antibodies against biotin, MAP2, and the target protein (GluA1 or GluA2; refer Table **2-2**; Appendix 4. *Antibody Specificity*), in blocking buffer (1.5 hr, RT). Following incubation, unbound antibody was removed by washing with PBS (3 x 5 min) prior to addition of proximity ligation assay (PLA) probes.

2.3.4.4. *Proximity Ligation Assay (PLA)*

Detection of newly synthesized proteins was carried out using proximity ligation assays (PLA; Figure 2-4). The probes used in PLA recognize the constant region of the primary antibody or antibodies. The maximum proximity of these antibodies for successful ligation has been cited as ≤ 16 nm (Trifilieff et al., 2011) to ≤ 40 nm (Bagchi et al., 2015). Once in proximity, the DNA strands attached to the probes participate the generation of a concatemeric 'rolling circle amplification' product, when exposed to the appropriate substrates and enzymes. A dilution (1:10) of Donkey PLA⁺ and PLA⁻ probes (Duolink, Sigma-Aldrich; see Table **2-2**) was prepared in blocking buffer containing anti-guinea pig 488 secondary antibody (1:1000) and DAPI (1:1000), where possible. This mixture was applied to the cells (37 °C, 1 hr) in a humidified chamber; the dishes were placed on a metal tray surrounded by wet paper towels, double-sealed in two zip-lock bags. Following incubation, the cells were washed using Wash Buffer A (0.01 M Tris base, 0.15 M NaCl, 0.05 % Tween 20, pH 7.4; 4 x 5 min, RT; Duolink,

Sigma-Aldrich) prior to the addition of ligation mixture (containing circularization oligomers complementary to those conjugated to the PLA probes, and T4 ligase (1 U/ μ L) diluted in MQ according to manufacturer's instructions; 30 min, 37 °C; in a humidified chamber).

Binding of PLA⁺ and PLA⁻ probes permits the ligation of the circularization oligomers, forming the basis of the rolling circle amplification process. Following this, the ligation reaction mixture was washed from the cells using Wash Buffer A (4 x 5 min, RT) prior to addition of the amplification solution (containing fluorophore-labelled (λ_{ex} 594 nm; λ_{em} 624 nm) nucleotides for the rolling circle reaction, and Phi29 polymerase (10 U/ μ L), diluted in MQ according to Duolink's instructions; 100 min, 37 °C, in a humidified chamber). Following amplification, cells were washed in Wash Buffer B (0.2 M Tris-HCl, 0.1 M NaCl, pH 7.5; 2 x 10 min, RT; Duolink, Sigma-Aldrich) in order to arrest the polymerase reaction. Excess Tris-HCl was washed from the cells using PBS (pH 7.4), and the cells were then post-fixed to support the stability of the PLA signal (4 % PFA in PBS, 20 min), washed (4 x 5 min, PBS, pH 7.4) and stored in PBS (4 °C). The resultant fluorescent signal is approximately 500 nm and can be effectively detected using fluorescence microscopy.

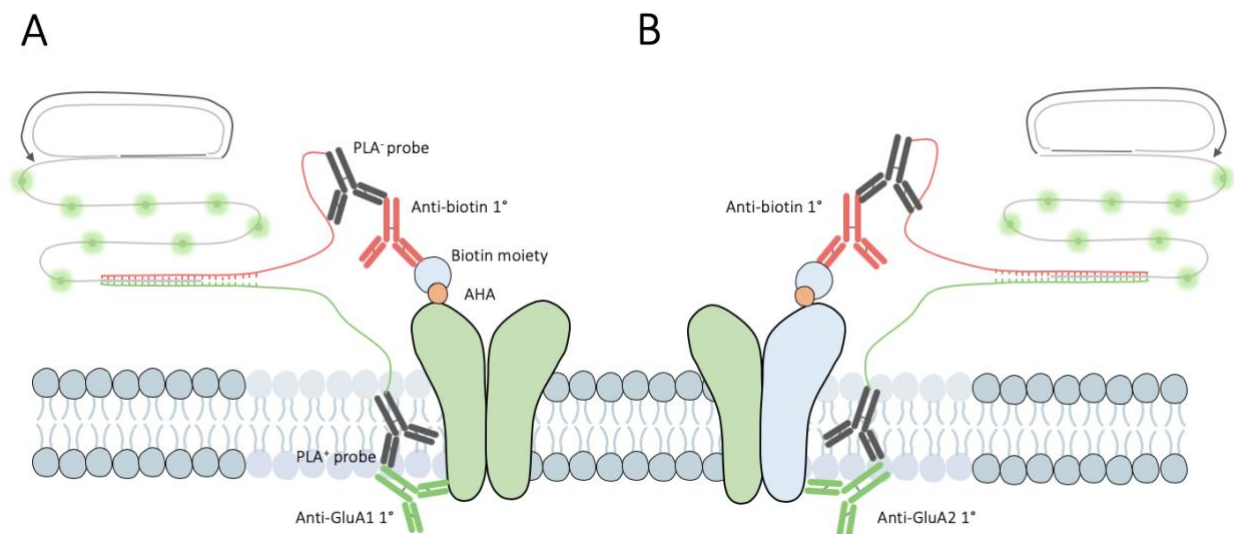


Figure 2-4 | Schematic diagram of FUNCAT-PLA experimental design. Newly synthesised cell surface A) GluA1 or B) GluA2 proteins are targeted by incubation with AHA (●) and 'click'-mediated addition of a biotin moiety (●). Following permeabilization of the plasma membrane (●), primary anti-biotin (●) and A) anti-GluA1 or B) anti-GluA2 antibodies (●) are added, followed by PLA⁺ and PLA⁻ probes (●). Incubation of PLA probes with appropriate ligation and amplification reagents allows for formation of the rolling circle amplification and addition of fluorescent probes (●).

2.3.5. *Detection of Cell Surface Proteins Using BioPLAy*

For the detection of cell surface receptors, we employed a novel technique, which incorporates biotinylation of surface proteins with proximity ligation assays (BioPLAy; Figure 2-5). All steps carried out at RT were conducted at 21-22 °C in a temperature-controlled bench-top incubator (Benchmark Scientific, H2200-HC). All PBS used was at pH 7.4, and cultures were used for experiments between DIV21-DIV27.

2.3.5.1. *Treatment*

Following a visual assessment of cell health, dishes were randomly assigned to treatment groups for each experiment. Following the removal of existing media, treatment dishes received 1 nM sAPP α (diluted from 320 nM stock in NGM) diluted in NGM. Control groups received only NGM for the length of the treatment.

2.3.5.2. *Biotinylation*

In order to isolate the cell surface fraction of GluA1-containing AMPAR, the cell-impermeant Sulfo-NHS-SS-Biotin was applied following treatments. Immediately prior to application, EZ-Link Sulfo-NHS-SS-Biotin (2.5 mg/mL; ThermoFisher Scientific, #21331) was dissolved in PBS-MC (1 mL, RT). Culture media was aspirated from the experimental dishes and the dissolved biotin conjugate was added to each dish on ice (10 min, 4 °C), to arrest biological processes, including those involved in receptor endo- and exocytosis. Excess biotin was washed from the cells using ice-cold PBS-MC (3 x, quickly). The cells were immediately fixed in 4 % PFA in PBS-MCS (20 min, RT).

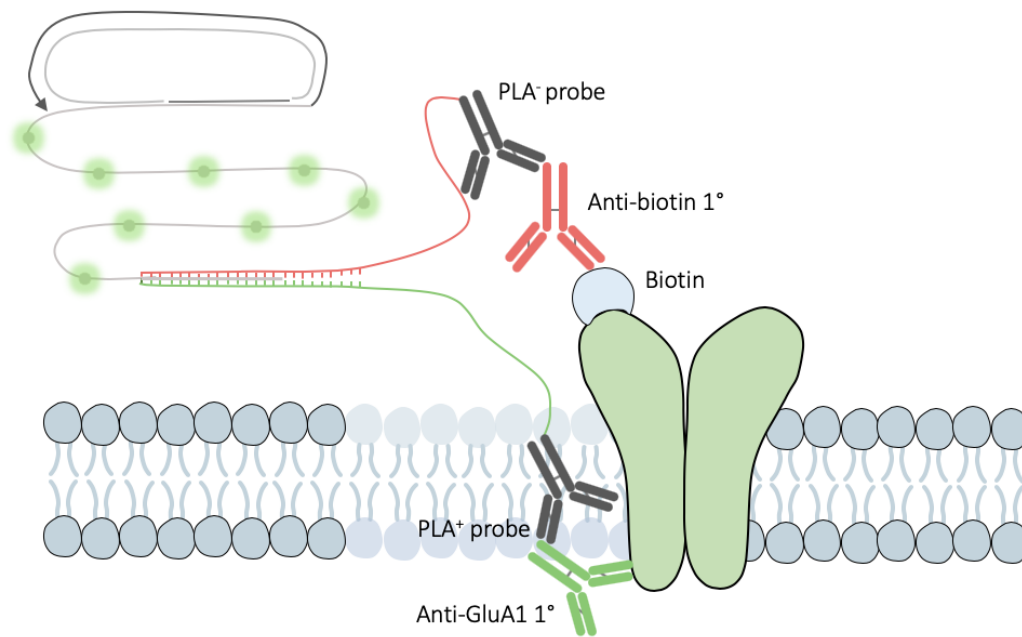


Figure 2-5 | Schematic diagram of BioPLAY experimental design. Cell surface GluA1 proteins are targeted by addition of Sulfo-NHS-SS-Biotin (●). Following permeabilization of the plasma membrane (●) primary anti-biotin (●) and anti-GluA1 (●) antibodies are added, followed by PLA⁺ and PLA⁻ probes (●). Incubation of PLA probes with appropriate ligation and amplification reagents allows for formation of the rolling circle amplification and addition of fluorescent probes (●).

2.3.5.3. Proximity Ligation Assay (PLA)

Proximity ligation assay was performed as described in section 2.3.4.4. *Proximity Ligation Assay (PLA)*. Briefly, the cells were permeabilized in 0.5 % Triton X-100 in PBS (15 min, RT), and incubated in blocking buffer (4 % normal goat serum in PBS, 1 hr at RT, or overnight at 4 °C). Following this, all dishes were incubated with the primary antibodies of interest (1.5 hr, RT; refer Table **2-2**). Cells were then washed (PBS pH 7.4, 3 x 5 min) and incubated in PLA⁺ and PLA⁻ probes (1:10 in blocking buffer) with the addition of Alexafluor 488-bound goat anti-Guinea pig secondary antibody (1:1000) and DAPI (1 µg/µL; 1 hr, 37 °C, in a humidified chamber). Unbound probes were washed with Wash Buffer A (4 x 5 min, RT). Dishes were incubated with the ligation mixture (30 min, 37 °C, in a humidified chamber), and washed with Wash Buffer A (4 x 5 min, RT) prior to incubation with the amplification reaction mixture (100 min, 37 °C, in a humidified chamber). Cells were then washed in Wash Buffer B (2 x 10 min, RT) The cells were finally washed (3 x 5 min) and imaged immediately in PBS (pH 7.4).

2.3.6. *Detection of Cell Surface Receptor Subunit Dimers (PLA)*

Similar to BioPLAy (see section 2.3.6. *Detection of Cell Surface Proteins Using BioPLAy*), PLA-only implements surface labelling of AMPA receptor subunits with epitope-specific antibodies to allow for formation of 'rolling circle amplification' product upon addition of appropriate PLA probes.

2.3.7. *Treatment*

Treatment of experimental cultures was carried out as described in section 2.3.5.1. *Treatment*. In brief, treatment dishes received 1 nM sAPP α (diluted from 320 nM stock), in NGM following aspiration of existing media from the dishes. Control groups received NGM-only for the length of the treatment.

2.3.8. *Addition of Antibodies*

Immediately prior to application, cells were washed (PBS-MC; 3 x, quickly) and immediately fixed in 4% PFA in PBS-MCS (20 min, RT). For experiments investigating GluA1/2-containing AMPAR (Figure 2-6A), using both C-terminal and N-terminal antibodies, cells were incubated in blocking buffer (4 % normal goat serum in PBS, 1 hr at RT), probed with the N-terminal antibody (1.5 hr, RT), washed (PBS pH 7.4, 3 x 5 min), and subsequently permeabilized with 0.5 % Triton X-100 in PBS (15 min, RT). Cells were then probed with the C-terminal antibody in addition to guinea pig anti-MAP2 for visualization of neuronal structure (1.5 hr, RT) and washed (PBS pH 7.4, 3 x 5 min).

For experiments utilizing two N-terminal antibodies, such as those investigating GluA2/3-containing AMPAR (Figure 2-6B), permeabilization was omitted and cells were incubated in blocking buffer (4 % normal goat serum in PBS, 1 hr at RT) followed by incubation of primary antibodies (1.5 hr, RT). Following this, cells were washed (PBS, pH 7.4; 3 x 5 min), permeabilized (0.5 % Triton X-100 in PBS, RT; 15 min) and incubated in blocking buffer again (4 % normal goat serum in PBS, 1 hr at RT) before addition of anti-MAP2 for visualization of neuronal structure (1.5 hr, RT).

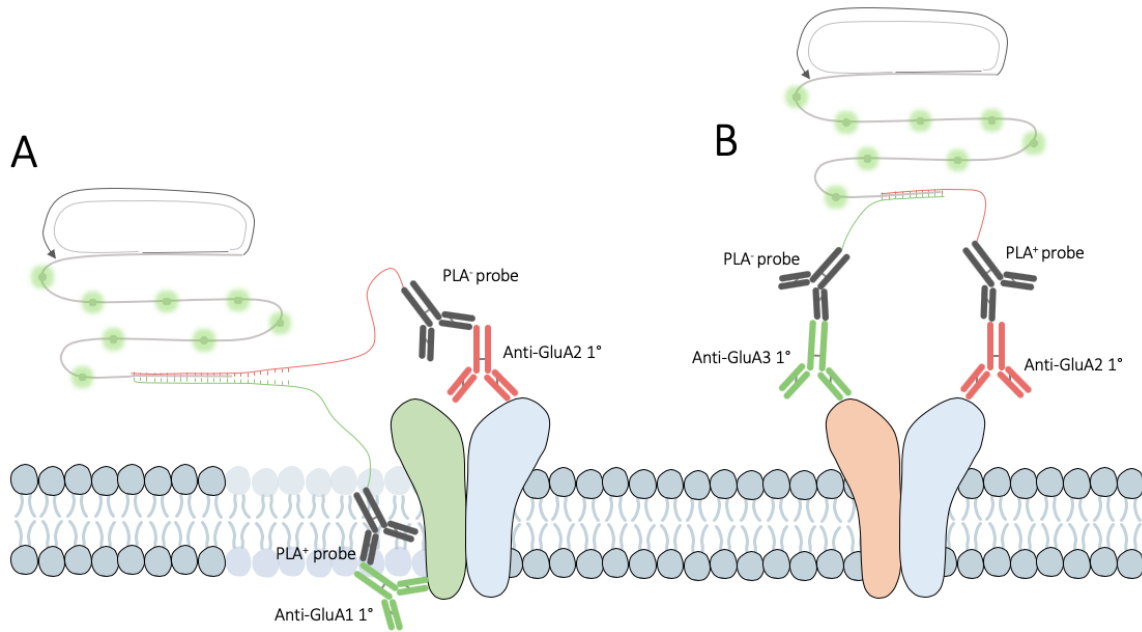


Figure 2-6 | Schematic diagram of A) GluA1/2 and B) GluA2/3 PLA experimental design. A) Cell surface GluA1/2 AMPAR were targeted by addition of N-terminal GluA2 antibody (●) before permeabilization of the plasma membrane (●). Following permeabilization C-terminal primary anti-GluA1 (●) are added. B) Cell surface GluA2/3 AMPAR were targeted by addition of N-terminal GluA2 (●) and N-terminal GluA3 (●) antibodies, before permeabilization. Both GluA1/2 and GluA2/3 AMPAR complexes were targeted by application of PLA⁺ and PLA⁻ probes (●). Incubation of PLA probes with appropriate ligation and amplification reagents allows for formation of the rolling circle amplification and addition of fluorescent probes (●).

2.3.9. Proximity Ligation Assay

Proximity ligation assay was performed as previously described in sections 2.3.4.4. *Proximity Ligation Assay (PLA)* and 2.3.5.3. *Proximity Ligation Assay (PLA)*. In brief, cells were incubated in PLA⁺ and PLA⁻ probes (1:10 in blocking buffer) with the addition of Alexafluor 488-bound goat anti-Guinea pig secondary antibody and DAPI (1:1000; 1 hr, 37 °C; humidified chamber). Unbound probes were washed with Wash Buffer A (4 x 5 min, RT). Dishes were incubated with the ligation mixture (30 min, 37 °C; in a humidified chamber), and washed with Wash Buffer A (4 x 5 min, RT) prior to incubation with the amplification reaction mixture (100 min, 37 °C, in a humidified chamber). Cells were then washed in Wash Buffer B (2 x 10 min, RT) and probed with DAPI (1 µg/µL, 10 min). The cells were finally washed (3 x 5 min) and imaged immediately in PBS (pH 7.4).

2.3.10. Treatment of Cultures With siRNA

To investigate the effect of siRNA knockdown of Arc protein following sAPP α treatment, we employed treatment of cultures with Accell™ Arc siRNA (1 μ M) targeted to the open reading frame (ORF) of the Arc gene (see Table 2-3). Cells were pre-treated with Arc siRNA for 1 hour before co-incubation \pm sAPP α (1 nM, 2 hr) and AHA (4 mM). Cells were processed for FUNCAT-PLA (see section 2.3.4. *Fluorescent Non-Canonical Amino Acid Tagging– Proximity Ligase Assay (FUNCAT-PLA)* or Immunocytochemistry (see section 2.3.1. *Immunocytochemistry*). Alongside this, the non-targeting (NT) control siRNA was used to assess effects, if any, of the addition of small molecules in the interpretation of results. Additionally, to assess efficacy of Accell™ siRNA expression in our cultures we employed the Accell™ Red non-targeting control siRNA (1 μ M; Table 2-3). This siRNA contains a fluorophore conjugated to a non-targeting sequence, able to be visualized by conventional epifluorescence microscopy. Cultures were pre-treated for 1 hour, followed by an additional 2 hours in line with experimental treatment lengths. Cells were processed for immunocytochemistry for markers of cell structure (MAP2, DAPI) under dark conditions to maintain fluorescence signal.

All Accell™ siRNA were prepared in a 1x siRNA reconstitution buffer consisting of (in mM): KCL 300, MgCl₂ 1, HEPES 30, and pH'd to 7.3-7.6 by addition of 2M KOH. All reagents were prepared in RNase-free water and sterile filtered. siRNA were reconstituted in 1x siRNA reconstitution buffer and incubated at 37 °C with gentle rocking for 70 min. Reconstituted siRNA were aliquoted and stored at -20°C until needed. For treatment of cultures, siRNA were further diluted to a working concentration of 1 μ M in NGM \pm AHA alongside treatment conditions.

Table 2-3 | Summary table of siRNA and their targets used in FUNCAT-PLA experiments.

<i>Target</i>	<i>Target Sequence</i>	<i>Molecular Weight (g/mol)</i>	<i>Extinction Coefficient (L/mol⁻¹cm⁻¹)</i>	<i>Details</i>
ARC	CUGCAGUACAGUGAGGGUA	13,511.8	346,388	Dharmacon, A-080172-15-0020
NON-TARGETING	UGGUUUACAUGUGUCGACUAA	13,400	150,000	Dharmacon, D-001910-01-20
<i>Target</i>	<i>Target Sequence</i>	<i>Fluorophore</i>	<i>Absorption/Emission</i>	<i>Details</i>
RED NON-TARGETING	UGGUUUACAUGUGUCGACUAA	DY-547	557/570 nm	Dharmacon, D-001960-01-05

2.4. Reverse Transcriptase Quantitative Polymerase Chain Reaction (RT-qPCR)

2.4.1. RNA Isolation and Purification

For the quantification of mRNA from culture, cells were treated as per Section 2.3.1.1. *Treatment of Primary Cultures*. Total RNA was extracted from cortical cell cultures prepared in 6-well plates at a density of 31,500 cells/cm². Tissue was lysed by using 350 µl Buffer RL (Norgen Biotek Corp., #17200) directly in the culture plate and gentle swirling for 5 min at RT. Tissue was transferred to an RNase-free microcentrifuge tube to which 200 µl ethanol was added. RNA was bound to RNA-binding spin columns (Norgen Biotek Corp., #17200) by centrifugation for 1 min at 3,500 x *g*. This was followed by an on-column DNA removal, by passing 400 µl of Wash Solution A through the column by centrifugation (1 min, RT, 14,000 x *g*), followed by 100 µl RNase-free DNase solution, centrifugation (1 min, RT, 13,000 x *g*). This was repeated three times before incubation (15 min, 25–30°C) and centrifugation for a final time (2 min, RT, 13,000 x *g*) to thoroughly dry the resin. Purified RNA was eluted by addition of Elution Solution A (50 µl; Norgen Biotek Corp., #17200) to the column, centrifugation (2 min, RT, 200 x *g*, followed by 1 min, 13,000 x *g*) and collection in an RNase-free microcentrifuge tube kept on ice. A second elution of 50 µl was performed as above into a separate collection tube.

2.4.1.1. RNA Quality and Quantification

Using a Nanodrop ND-1000 v3.8.1 Spectrophotometer and associated software (ThermoFisher Scientific), 2 µl of RNase-free water was pipetted onto the measurement pedestal and used as a blank measure. Following this, 2 µl of RNA sample was pipetted onto the pedestal, measured, and the pedestal cleaned. This was repeated for both primary and secondary elution separately. The quality of each of the RNA samples can be determined primarily by the A260/A280 ratio, wherein a ratio of approximately 1.8–2.0 indicates a ‘pure’ RNA sample, free of contaminants such as proteins, salts, or phenol. Following a ‘pure’ reading from each of the elution samples, both primary and secondary elution were combined and a final quality and concentration report was generated using the Nanodrop system, resulting in approximately 100 µl of ‘pure’ RNA.

2.4.1.2. Primer Design

For the quantification of RNA following treatment, the following primers were designed using Primer-BLAST (<https://www.ncbi.nlm.nih.gov/tools/primer-blast/>; see Table 2-4), under the conditions that the primer must span an exon-exon junction and was specific for rat. Primers were hence selected based on specific amplification of the gene of interest, the T_m of each primer were within 5°C of each other, and the percentage of guanine (G) or cytosine (C) present was between 40% and 60%. Candidate primers were also checked for primer dimerization (binding with itself), repeats (nucleotide sequences repeating), and hairpin binding, features which may affect primer efficiency during the RT-qPCR reaction.

Table 2-4 | Summary table of primer sequence pairs used in RT-qPCR experiments.

<i>Gene Target</i>	<i>Forward Primer</i>	<i>T_m</i> (°C)	<i>Reverse Primer</i>	<i>T_m</i> (°C)
ZIF268	5'-GGG AGC CGA GGG AAC AA-3'	58.2	5'-CGT TAT TCA GAG CGA TGT CAG AA-3'	54.8
HPRT	5'-TGA CAC TGG TAA AAC AAT GCA-3'	52.8	5'-GGG AGC CGA GCG AAC AA-3'	58.2
ARC #1	5'-AGC AGA ATC AGA GAT GGC CG-3'	57.2	5'-TGA ATC ACT GCT GGG GGC-3'	58.0
ARC #2	5'-GAC TTG ATT GAG CTG GGG CT-3'	57.5	5'-TAT GAA TCA CTG CTG GGG GC-3'	57.3

2.4.1.3. cDNA Synthesis

cDNA libraries were created from the total RNA extracted from cultured cortical neurons ($n = 1-4$ wells per condition, 4-5 experimental replicates) using SuperScript III RT (Invitrogen). Following the manufacturer's instructions for a 20 μ l reaction volume, Master Mix I was made by adding 1 μ l Oligo(dT)₂₀ (50 μ M) and 1 μ l dNTP mix (10 mM) to a 0.6 mL RNase-free microcentrifuge tube. Master Mix II contained 4 μ l 5X First Strand Buffer, 1 μ l dithiothreitol (DTT; 0.1 mM), 1 μ l RNaseOUT (40 U/ μ l), and 1 μ l SuperScript III RT (200 U/ μ l). Following this, 5 ng of total RNA was added to an RNase-free tube followed by Nuclease-free H₂O for a total volume of 11 μ l. This was then heated at 65°C for 5 min via thermocycler, and incubated on ice for 1 min. 7 μ l of Master Mix II was then added and mixed via pipette. cDNA samples were stored at -20 °C prior to use.

2.4.1.4. SYBR Green mRNA Assays

To test the efficiency of each primer, 5 μ l of cDNA from each test sample was combined and serially diluted with RNase-free H₂O at 1:1, 1:5, 1:25, and 1:125. Following qPCR amplification and data acquisition, the triplicates were averaged and concentrations were converted to log₁₀ values and graphed onto a scatter plot. A line of best fit, as determined by Excel 2011 (Microsoft), was generated giving an m and an R² value. A primer set was determined to be efficient using the equation $E = 10^{-1/m} \times 100$, and with an R² value greater than 0.90. In certain cases, the highest or lowest value was removed as they may affect the line of best fit, due to PCR inhibition or low concentrations of RNA, respectively. Primers were also deemed efficient by the melting curves generated following the PCR to identify a specific amplification is occurring (Figure 2-7). The presence of a singular peak indicated a single RNA product had been amplified while a double peak indicated nonspecific amplification or primer dimers. Due to this, Arc primer #2 was not used for any experiments.

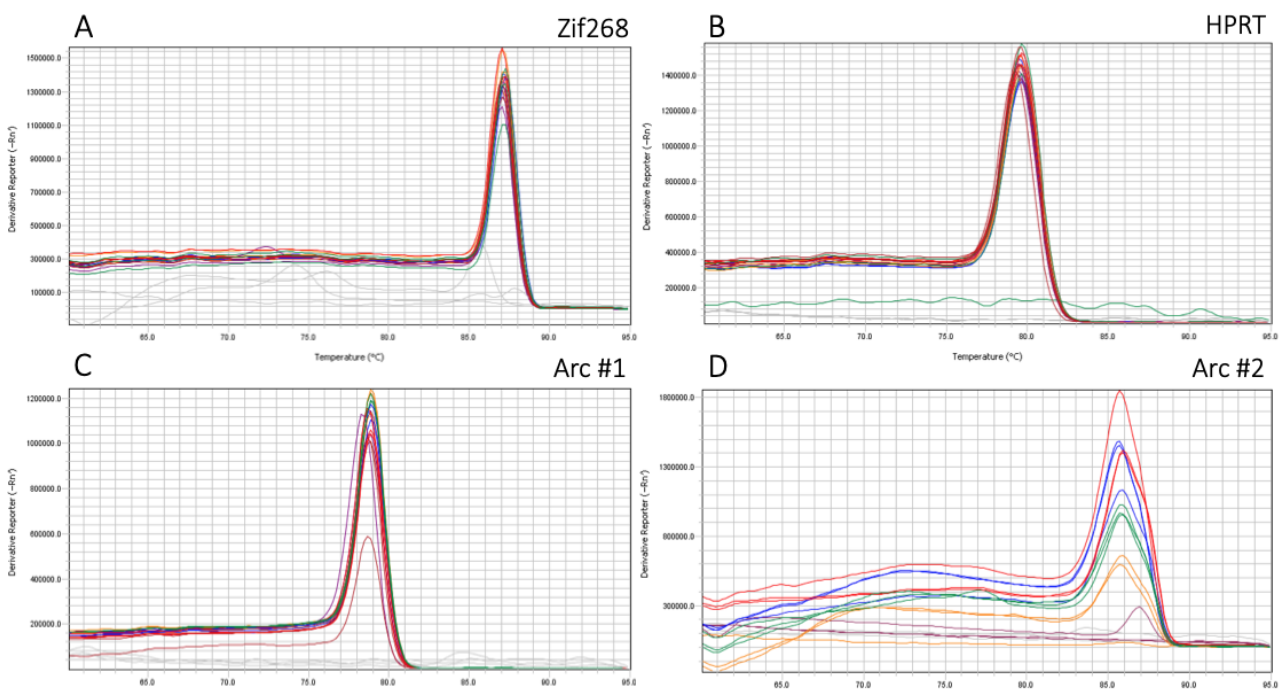


Figure 2-7 | Melt curve plots. Graphs show A) Zif268, B) HPRT, C) Arc #1, D) Arc #2, E) Gria1, F) Gria2, and G) Gria3. Axes show the derivative reporter ($-Rn'$) plotted against temperature ($^{\circ}$ C).

2.4.2. Reverse-Transcriptase Quantitative Polymerase Chain Reaction (RT-qPCR)

Each primer was tested at a 1:25 dilution and each condition was tested in triplicate. On a 96-well plate (Roche, #0472962001), each well contained 3 μ l cDNA and 7 μ l of a premade master mix consisting of 1 μ l Forward Primer (5 μ M), 1 μ l Reverse Primer (5 μ M) and 5 μ l SYBR Green Master Mix (ThermoFisher Scientific, #4309155). Using a LightCycler 480 and its associated software, setting the sample volume to 10 μ l, each plate underwent a pre-incubation program at 95°C for 5 min. Following this, an amplification program with a quantification analysis involved 40 cycles of 95°C for 30 s, 60°C for 30 s and 72°C for 30 s. Following amplification, a melting curve analysis was carried out with 95°C for 15 s, 60°C for 1 min, followed by continuous ramp at 0.05 °C/s up to 95°C before cooling to 40°C and holding for 30 s (Figure 2-8)

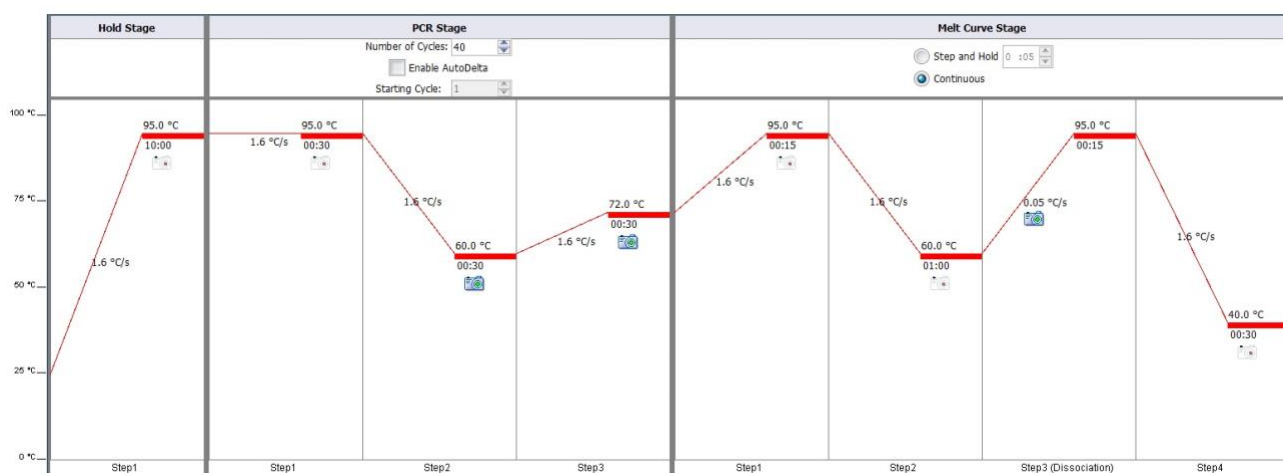


Figure 2-8 | Experimental setup of RT-qPCR amplification and quantification cycles. Image shows progress of RT-qPCR experiments during hold stage, PCR, stage, and melt curve stage. Red line indicates rate of degree change (°C/s), holding temperature (°C) and holding duration (min).

2.4.3. Western Blot

Western blotting was utilised to validate the binding of antibodies to a target of the expected size as the proteins of interest, to be used in immunocytochemical- and PLA-based experiments.

2.4.3.1. *Protein Extraction and Sample Preparation*

Primary hippocampal cultures were grown for protein harvesting on Poly-D-lysine coated wells of a 6-well plate, and harvested at DIV24-27. The cell layer was washed (PBS-MC, pH 7.4), scraped from the well and collected by centrifugation (14,000 x *g*, 5 min, 4 °C). The pellet was washed with PBS and centrifuged again before the cells were lysed and homogenised in buffer (1 mM EGTA, 1 mM EDTA, 0.1 mM PMSF, 1 x Complete, 1 % Triton-X, 10 % SDS, 10 µM KN62 in PBS). The samples were sonicated (Bandelin Sonorex Digital Ultrasonic bath; 2 min, RT), and centrifuged (20 min, 14 000 x *g*, 4 °C). The supernatant was collected, and the pellet was re-homogenised. Protein was quantified using the BCA assay and stored at - 80 °C until use.

2.4.3.2. *Gel Electrophoresis and Transfer*

SDS-Polyacrylamide resolving gels (9% Bis-Acrylamide (Bio-Rad), 0.5 mM SDS, 0.05% TEMED, 0.05% APS buffered with 0.37 M Tris-HCl) were cast in NOVEX 1 mm gel cassettes (ThermoFisher). The gels were sealed with water overnight at 4 °C. Stacking gels (5% acrylamide, 0.5 mM SDS, 0.1% TEMED, 0.05% APS buffered with 0.125 M Tris-HCl) were cast, and the gels were left at RT for 20 min. NOVEX cassettes were locked into a NOVEX X-cell Surelock Minicell system (Invitrogen). Inner and outer chambers of the box were filled with sufficient running buffer (192 mM glycine, 0.1% SDS buffered with 25 mM Tris-HCl) to cover the wells in the gels. The prepared samples were pipetted into the wells alongside a molecular weight rainbow marker (Amersham, GE Healthcare Life Sciences). Electrophoresis was conducted at 125 V for 2 hr, or until the dye front reached the base of the gel. The separated proteins were then transferred to nitrocellulose membranes (Amersham Protran 0.45 µm NC, GE Healthcare Life Science) using NOVEX X-cell II blotting modules (Invitrogen). The transfer was carried out at 100 mAmp for 2 hr, using transfer buffer (96 mM glycine, 10 % methanol buffered with 12 mM Tris-HCl).

Following transfer, blocking buffer was applied to the membranes (Odyssey blocking buffer; Li-Cor; 1 hr, RT). Primary antibodies were diluted in 0.1 % BSA, 0.1 % NGS in PBS with 0.1% Tween, and membranes were probed overnight at 4 °C with gentle rocking. The following day, unbound antibody was removed using PBS-Tween (4 x 5 min) and the membranes were incubated with the appropriate secondary antibodies in PBS-Tween (1 hr, RT, gentle rocking). Unbound antibody was washed using PBS-Tween (4 x 5 min) and the membranes were washed in PBS, before being allowed to dry on filter paper prior to scanning. Protein was detected using the LI-COR Odyssey Infrared Fluorescence Imaging system. Image capture was carried out using Image Studio. The brightness and contrast levels of captured images were adjusted for image presentation.

2.5. Preparation of Acute Hippocampal Slices for Electrophysiology and Biochemical Experiments

All experimental protocols were approved by the University of Otago Animals Ethics Committee and conducted in accordance with New Zealand Animal Welfare Legislation under the ethics approval DET19/16. All experiments conducted on acute tissue were prepared from young adult male Sprague-Dawley rats (4-6 weeks), as described previously (Mockett et al., 2019).

2.5.1. *Acute Hippocampal Slice Preparation*

Rats were deeply anaesthetised with ketamine (100 mg/kg, i.p.) and decapitated by guillotine. The brains were removed and chilled in ice-cold and oxygenated modified artificial cerebrospinal fluid (aCSF) for which sucrose was substituted for NaCl (composition in mM: sucrose 210, glucose 20, KCl 2.5, NaH₂PO₄ 1.25, NaHCO₃ 26, CaCl₂ 0.5, MgCl₂ 3, pH 7.4 when gassed with 95% O₂-5% CO₂). Following removal, the brain was transferred to an ice-cold dissection platform (Figure 2-9A,B). Hemispheres were separated and cerebellum were removed. Ice-cold aCSF was applied throughout to ensure the tissue remained cold and rigid. Using a razor blade, a cut through the forebrain (at the point of the middle cerebral artery) was made, and the hemisphere was flipped onto the cut face, exposing the midbrain (Figure 2-9C-E). Midbrain tissue was removed using a flat spatula, revealing the medial surface of the hippocampus. The tissue was rolled onto the lateral surface of the cortex. The flat spatula was then used to slide beneath the hippocampus, carefully flipping it out above the cortical tissue, lateral surface facing up (Figure 2-9F-H). The hippocampus was separated from the cortex and two 45° cuts were made at each end, loosening the hippocampus from remaining cortical tissue (Figure 2-9I). From here the ventral portion of the hippocampus was removed. Area CA3 was removed by removal of the lower 1/10th of the remaining dorsal hippocampus, in order to increase the signal-to-noise ratio of recordings by reducing the amount of spontaneous activity (Dumas et al., 2018; Figure 2-9J,K). From here, the hippocampal tissue was glued gently to the vibratome mounting platform with the lateral surface facing out and the dorsal surface facing up. Hippocampi were dissected at a thickness of 400 µm, using a vibroslicer (Leica, VT1000; Figure 2-9L-N). Slices were transferred to a porous, transparent membrane in an incubation chamber, and maintained at the interface between air and standard aCSF (in mM: NaCl 124, KCl 3.2, NaH₂PO₄ 1.25, NaHCO₃ 26, CaCl₂ 2.5, MgCl₂ 1.3, D-glucose 10, equilibrated with carbogen 95% O₂-5% CO₂; 32°C). Slices remained here for 30 minutes before transfer to RT for an additional 90 minutes (Edwards and Konnerth, 1992; Lein et al., 2011).

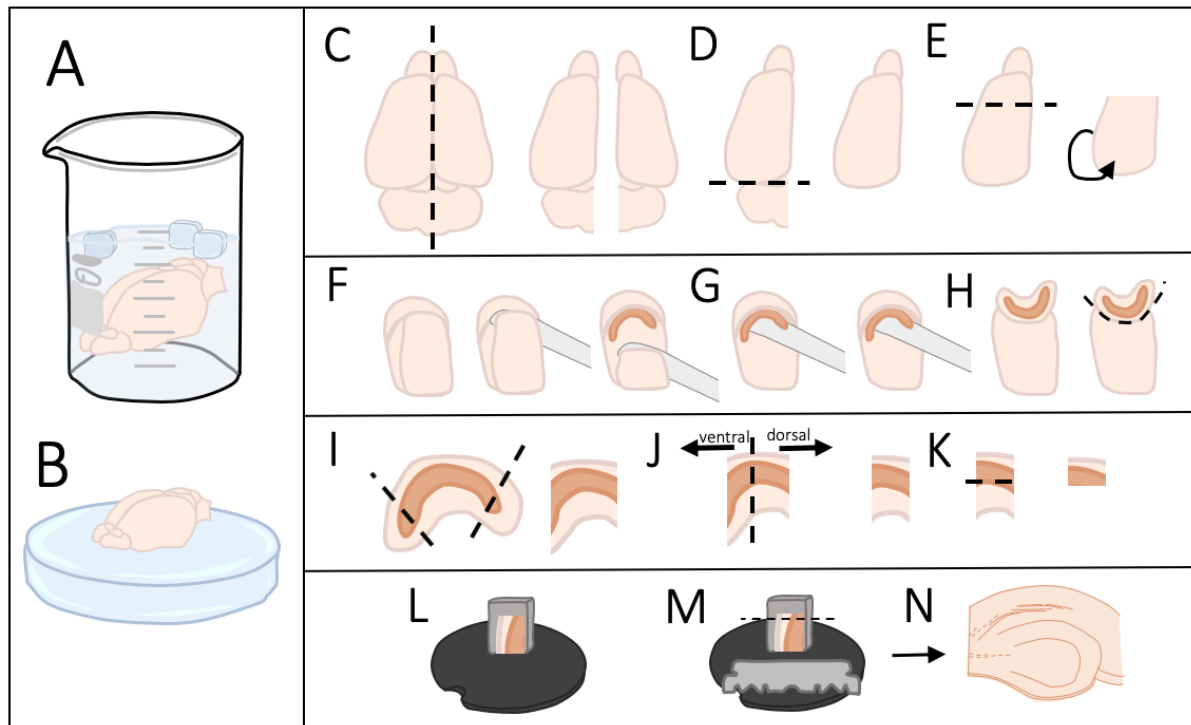


Figure 2-9 | Acute transverse hippocampal slice dissection. Following decapitation and removal of the brain, A) brains are transported in oxygenated ice cold modified aCSF and transferred to B) a chilled dissection platform. C) Hemispheres are separated and D) the cerebellum is removed. E) The forebrain is removed by a vertical slice at the point of the middle cerebral artery. Remaining hemisphere is flipped onto the cut face. F) Midbrain tissue is removed, revealing the hippocampus. G) Using the spatula, the hippocampus is carefully flipped and H) separated from the remaining cortex. I) Additional tissue at the end of the hippocampus are removed by two 45° cuts, J) followed by removal of the most ventral aspect. K) The CA3 area is removed from the remaining dorsal tissue by vertical slice of approximately the lower 1/10th of the remaining tissue. L) The ventral surface is glued to the vibratome mounting platform M-N) and 400 μ m transverse sections are cut.

2.5.2. Immunohistochemistry

sAPP α and other drug treatments were subsequently applied in warmed aCSF for 15 minutes or 2 hours. When studying inhibitor effects on sAPP α treatment, slices were pre-incubated for 30 minutes with the inhibitors (α BGT, 10 nM; APV, 50 μ M) before subsequent co-incubation with sAPP α for 2 hours. When studying the effects of sAPP α treatment on phosphorylated CREB (pCREB) expression, slices were co-incubated with inhibitors of serine/threonine-protein phosphatases (Sodium Fluoride (NaF), 1 mM; Phenylmethylsulfonyl Fluoride (PMSF), 100 μ M; Okadaic acid, 1 μ M). Following treatment, slices were washed in PBS-MC (pH 7.4) and subsequently fixed in 4% PFA in PBS-MCS (pH 7.4) overnight at 4°C. Following fixation, slices were washed in PBS (pH 7.4) and embedded in Agarose (3 %; Roche). 400 μ m slices were resliced to 50 μ m sections using a vibroslicer (Vibratome 1500, Warner instruments). Slices were stored in PBS (pH 7.4) at 4°C until use. For immunohistochemical

analysis, slices were permeabilized with 0.5 % Triton X-100 in PBS (pH 7.4; 10 min). Slices were then blocked in 4% normal goat serum in PBS (pH 7.4) for 1-hour at RT. Slices were incubated with primary antibodies of interest (overnight, 4 °C), washed (3 x 10 min; PBS, pH 7.4) and incubated in appropriate secondary antibodies (1 hr, RT), followed by 3 x 10 min washes (PBS, pH 7.4). All steps were performed with gentle agitation. Slices were mounted on coverslips (Histobond) in AquaPolymount mounting media (Polysciences) for imaging.

2.5.3. *Field Potential Electrophysiology*

Hippocampal slices were obtained from young adult male Sprague-Dawley rats (4-6 weeks) as previously described in section 2.5.1. *Acute Hippocampal Slice Preparation*. Briefly, rats were deeply anaesthetised with ketamine (100 mg/kg, i.p.) and decapitated by guillotine. The brains were removed the hippocampus was separated from surrounding cortical tissue. Area CA3 was removed and the hippocampi were dissected at a thickness of 400 μm , using a vibroslicer (Leica, VT1000; Figure 2-9). Slices were transferred to a porous, transparent membrane in an incubation chamber, and maintained at the interface between air and standard aCSF. Slices remained here for 30 minutes before transfer to RT for an additional 90 minutes.

Following recovery, slices were transferred to the recording chamber containing recirculating aCSF (95% O₂, 5% CO₂; 32.5 °C), superfused continuously at a rate of 2 mL/min. Baseline field excitatory postsynaptic potentials (fEPSPs) were elicited in area CA1 by stimulation of the Schaffer collateral-commissural pathway at 0.017 Hz (diphasic pulses, 0.1 ms half-wave duration) using a teflon-coated 50 μm tungsten wire monopolar electrode (A-M Systems Inc, Carlsborg, WA). Evoked responses were recorded with a glass microelectrode filled with aCSF (1.9-2.9 M Ω) and placed in stratum radiatum of area CA1 (approximately 300 μm from stimulating electrode; Figure 2-10). During periods of baseline recording the stimulation intensity was adjusted to elicit a fEPSP with an initial slope value of 40% of the maximum elicited when delivering 200 μA of current. Drugs, including sAPP α (1 nM) and IEM-1460 (100 μM), were bath-applied by switching to an identical preheated and oxygenated aCSF solution that contained the compound of interest. IEM-1460 was delivered 20 minutes prior to, and during, sAPP α administration and continued 10 min post-TBS. Non-saturated LTP was induced by applying a half-maximal train of standard theta burst stimulation (TBS; 5 trains of 5 pulses at 100 Hz delivered at 200 ms intervals) at baseline stimulus intensity (Raymond et al., 2000; Mockett et al., 2019).

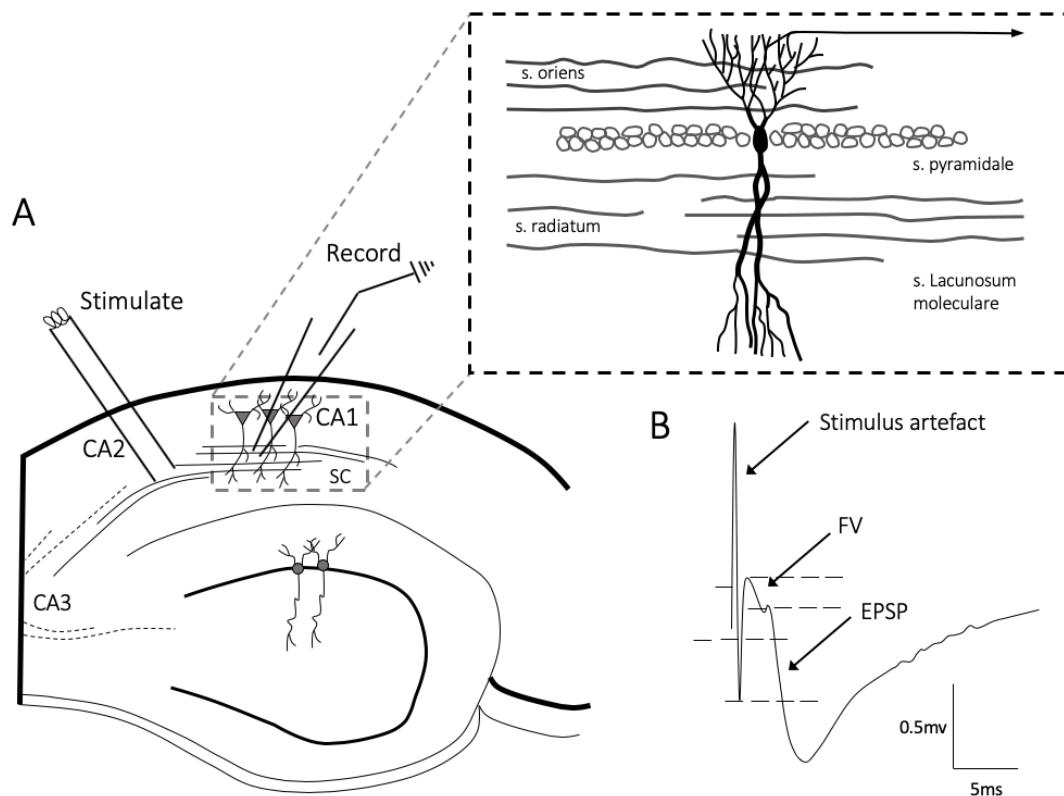


Figure 2-10 | Hippocampal slice diagram. A) Illustration of a transverse hippocampal section used in electrophysiological experiments. Inset image shows magnification of area stimulation and recording area CA1. s. = stratum. B) Representative extracellular waveform. Electrical stimulation of CA1 Schaffer collaterals elicits a stimulus artefact, followed by a presynaptic population spike or fibre volley (FV). The slope of the negative-going field excitatory postsynaptic potential (EPSP) corresponds to depolarising synaptic currents.

2.6. Microscopy and data analysis

2.6.1. Sample Choice and Blinding

The primary criterion for the selection of cells for imaging was the presence of a healthy appearance and proximity to neighbouring cells. Health was determined by MAP2 immunofluorescence with an absence of dendritic fragmentation or swelling. Additionally, DAPI-stained nuclei were examined for signs of fragmentation or condensation (refer Appendix 2. *Cell health*). Cells were selected which were not completely isolated from neighbouring cells but presented clearly traceable, unobstructed dendrites. Oftentimes cells closest to the outer edge of the dish were selected due to these criteria. A minimum of ten cells per dish was selected in this manner for imaging.

2.6.2. *Light Microscopy*

For experiments examining the expression of a protein using immunofluorescence, images were acquired using an Olympus IX71 inverted light microscope using a 40x/0.6-N.A objective (LUCPLFLN). The images were captured using a Hamamatsu Orca-AG camera (C4742-80-12AG) in 1024 x 1024 pixel 8-bit mode and saved as .tif files.

2.6.3. *Image Analysis*

To quantify immunofluorescence, neurons were outlined using ImageJ (refer Appendix 1.1. *Quantifying Arc protein expression in primary hippocampal neurons*). An 'integrated intensity/neuronal area' value was generated for each cell and somatic compartment, including all dendrites up until intersection with neighbouring dendrites. This value was corrected for average background fluorescence by subtracting average background fluorescence. Dendritic fluorescence was determined by subtracting corrected somatic values from whole cell values. For the analysis of primary and secondary dendrites, gray values were sampled at 0.5 μm increments, and the averages were binned into 50- and 25 μm segments, respectively. Statistical analysis was achieved by averaging each dendritic segment per cell, for a total cell average. For experiments examining pCREB expression in acute hippocampal slices (refer Appendix 1.2. *Quantifying pCREB protein in primary hippocampal slices*), DAPI was used to define a 'mask' around the nuclear layer and pCREB was measured as 'integrated intensity/DAPI area.' For experiments examining Arc expression in acute hippocampal slices (refer Appendix 1.2.1. *Quantifying Arc Protein Signal in Hippocampal Slices*), area CA1 was defined by a square area adjacent to the hippocampal fissure (encompassing both the pyramidal cell layer and stratum radiatum) and an integrated intensity/area' value was generated for each slice.

To quantify the PLA signal within the cultured neurons, a custom made ImageJ script created by Maximilian Heumüller (Max Planck Institute for Brain Research, Frankfurt) was used (tom Dieck et al., 2015; refer Appendix 1.3. *Quantifying PLA signal in primary hippocampal neurons*). In brief, images were separated into single channel images and the PLA signal threshold was manually defined by averaging the optimal value for several images. This value was applied to the PLA channel, and the area of the punctate signal was measured. The PLA signal was expressed relative to neuronal size as defined by the MAP2 signal which was manually outlined and isolated. The MAP2 mask was dilated by 2 pixels to encompass signal present in spines. For experiments examining the somatic signal, the analysis was conducted as above except that the somatic compartment was manually isolated from dendrites and surrounding cells. The somatic analysis for BioPLAy and PLA for the detection of subunit

dimers included a step to remove PLA detected within the nucleus, as these experiments showed non-specific PLA signal. In order to analyse the dendritic PLA signal, all traceable dendrites to the main neuron were measured 50 μm proximal from the soma, and straightened with the 'straighten' plug-in in ImageJ, and the PLA signal was analysed as above.

To analyse the proximity of PLA signal to the synaptic marker synapsin-1, the ImageJ plugin Just Another Colocalization Plugin (JACoP) was used (refer Appendix 1.4. *Quantifying Colocalization of PLA Signal Within Synapses*). In brief, images were separated into single channel images and the proximal 50 μm of MAP2 and PLA signal was isolated. Average PLA and synapsin-1 signal threshold values were determined for all treatment groups and applied within the JACoP plugin. In order to determine colocalization, the Mander's overlap coefficient was used to generate a value proportionate to the level of overlap of PLA on synapsin-1 signal. Here, a value of -1 indicates negative correlation, 0 indicates no correlation and +1 indicates a positive correlation. In addition, the proximity of PLA puncta to synapsin-1 signal was determined by manual measurements of the centre of each PLA puncta (determined by the brightest pixel) to the centre of mass of the nearest synapsin-1 puncta. PLA puncta within 0-2, 2-4, and > 4 μm from the synapsin-1 centre of mass were considered synaptic, extrasynaptic, and non-synaptic, respectively.

2.6.4. *Statistical Analysis*

For RT-qPCR data, data exhibited a normal distribution (Shapiro–Wilk normality test), significance was assessed using Student's t-tests where $p < 0.05$ was accepted as significantly different. Data were normalized to the control gene HPRT and expressed relative to no-drug control.

Statistics for all immunocytochemistry experiments were performed using Kruskal–Wallis one-way ANOVA followed by Dunn's multiple comparisons test. Normal distribution of data was determined (D'Agostino and Pearson omnibus normality test). Outliers within the raw data sets were detected using the Grubb's test. Data for all slice work exhibited a normal distribution (Shapiro–Wilk normality test). Experiments examining pCREB expression were analysed by use of Student's t-tests, and experiments analysing Arc protein expression were analysed using one-way ANOVA followed by Šidák's multiple comparisons test. Data are expressed as fold change relative to control values.

For electrophysiology experiments, the baseline response value was calculated by averaging the responses over the final 10 min before LTP induction. All responses throughout the recording were normalised to the baseline value before application of IEM-1460 and expressed as a percentage of baseline. Normal distribution of data was determined by D'Agostino and Pearson omnibus normality test. Statistical differences between experimental groups was performed on data

normalised to the average of baseline 10 minutes before TBS, and determined by one-way ANOVA with Tukey's multiple comparisons tests, where appropriate.

To observe the effect of treatment on the expression of proteins at the cell surface, data were normalised to the experimental control condition. Outliers within the raw data sets were detected using the Grubb's test, and identified candidates were removed if significantly different from the data set, following visual analysis of the PLA channel. For all data sets, D'Agostino and Pearson omnibus normality tests were used to determine whether the data was normally distributed. Data from ≥ 3 experiments was amalgamated and significance was by assessed one-sample t-tests (relative to a theoretical mean of 1) or Mann-Whitney two-tailed u-tests (Girard et al., 2007; Boos and Stefanski, 2013; tom Dieck, et al., 2015). For data examining the proportion of proteins within synaptic domains, normality was determined by Shapiro-Wilk normality test. Significance was assessed by two-way ANOVA and Šidák's multiple comparisons effect.

Chapter 3: Results

3.1. *Characterization of Primary Hippocampal Cultures*

Previous research investigating the mechanisms of learning and memory have utilized primary hippocampal and cortical cultures as a means of isolating neurons for analysis of biological properties related to cellular structure and function. A common procedure for producing these cultures involves the manual dissection and isolation of cortical or subcortical structures from rodent or murine pups, dissociation of the cellular profile, and incubation and maintenance of plated cells for up to four weeks or longer (Banker and Goslin, 1998). Comparisons of *in vitro* cell cultures to the likes of *ex vivo* tissue sections have been continually present throughout the literature as ongoing research is performed with both preparations. While brain sections have been regarded as an exceptional preparation for maintaining local synaptic circuitry and preserving brain architecture (Cho et al., 2007), primary cultures have shown an increasing advantage as a convenient and viable technique for simulating the molecular microenvironment of complex *in vivo* tissue, and allowing greater spatial resolution (Millet and Gillette, 2012). This thesis aimed to examine the regulation and expression of IEGs and glutamate receptors in primary hippocampal neurons in culture, in response to the neurotrophic protein, sAPP α . Therefore, before these experiments begin, we first aimed to describe the cellular and molecular environment present in these cultures.

3.1.1. *Growth and Development*

Primary hippocampal cultures were prepared from PD 0-1 rat pups and maintained in culture for 21–27 DIV prior to use (refer section 2.1. *Primary Neuronal Culture Preparation*). While synaptic development has been shown to occur within a week *in vitro*, full maturation and complexity of both pre- and post-synaptic complements does not occur until > 21 days *in vitro* (Dotti et al., 1988; Fletcher et al., 1991; Fletcher et al., 1994; Grabrucker et al., 2009). Development of cultures was documented as the cells matured using phase contrast microscopy. In accordance with previous studies (Banker and Cowan, 1977; Dotti et al., 1988; van Spronsen et al., 2013), immediately following plating, cells were observed as small spherical bodies beginning to adhere to the Poly-D-lysine coated glass coverslip (Figure 3-1A). By DIV 2, cell bodies began to produce minor processes with many extending primary projections. Over the following 7 days, dendritic arborization increased in size and complexity (Figure 3-1B), and throughout the next two weeks cells continued to project dendrites and axons (Figure 3-1C), increasing the complexity of the network and covering a majority of the culture surface (Figure 3-1D).

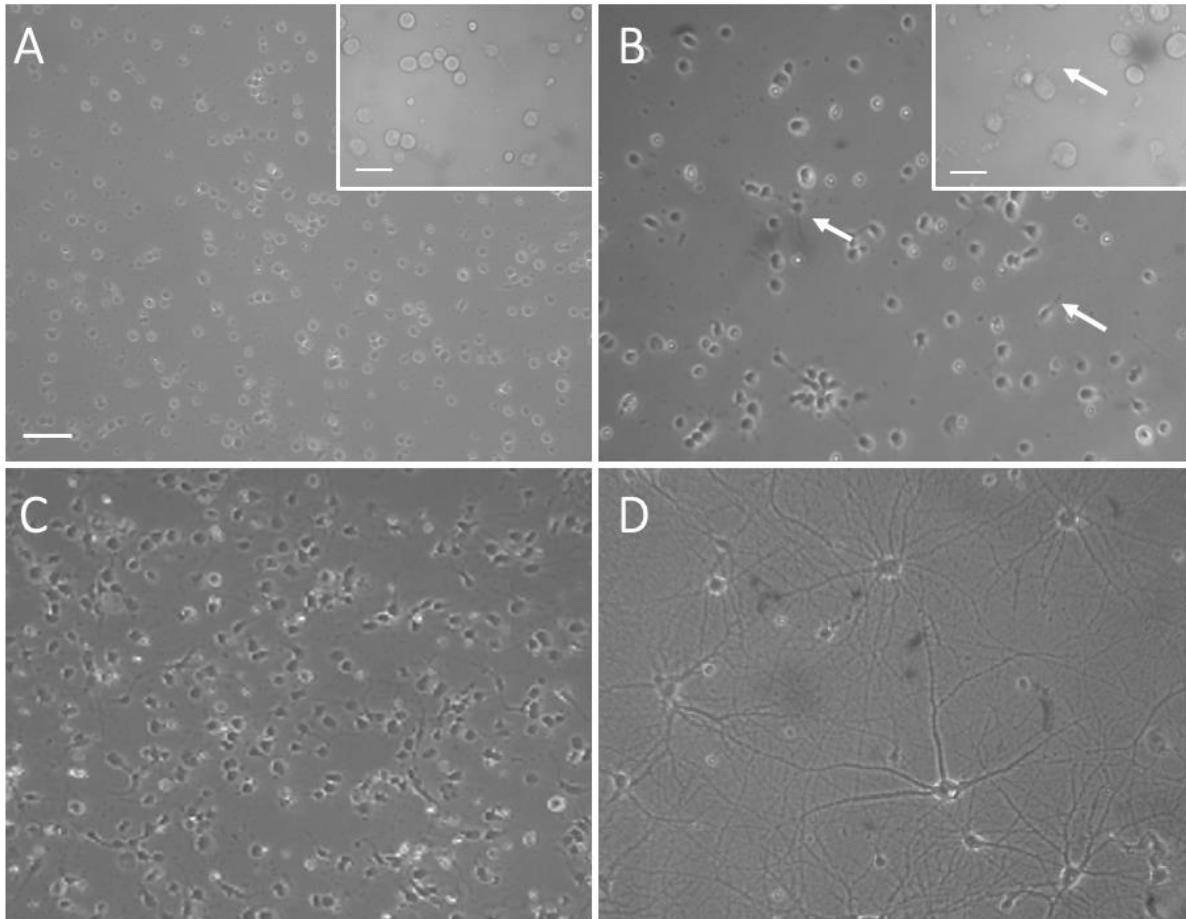


Figure 3-1 | Temporal development of hippocampal cells in primary culture. Phase contrast images of primary hippocampal cells in culture (at a density of 4×10^4 cells/cm²) imaged at various time points following initial plating. Seeded cell bodies (A, upper right inset) begin to send out primary projections and minor neurites by DIV 2 (B, indicated by white arrows), and by DIV 7 have produced multiple projections (C). By DIV 24, a dense and complex arborization of dendrites is seen extending from a large soma (D). Scale bar = 100 μ m (10 x), scale bar (inset images) = 50 μ m (A), 20 μ m (B; 40 x).

3.1.2. *Immunofluorescent Detection of Primary Neuron Development*

In addition to examining cell development by phase contrast microscopy, it is also possible to observe development by probing cells for key proteins using immunocytochemistry. This method allows for finer observation of neuronal growth by examining key proteins in cells of interest. By probing for the neuron specific protein microtubule-associated protein 2 (MAP2; Caceres et al., 1984), we are able to distinguish MAP2-positive immunofluorescence concentrated in the soma of neurons at the instant of cell plating (0 hours; Figure 3-2A; Bernhardt and Matus, 1984). At this stage, it is expected that cells develop a lamellipodia around the circumference of the cell body (Dotti et al., 1988), containing predominantly actin filaments. By 24-48 hours we can begin to distinguish MAP2- and tau-positive minor neurites (Figure 3-2B-C). These neurites appear cylindrical, yet have expanded, flattened, growth cones at their tips. Once established these minor neurites appear rather stable, with many continuing to develop (Dotti et al., 1988).

As is common for hippocampal neurons in culture, by 72 hours the primary axon arose as a branch from a short process which had dendritic characteristics, including MAP2-immunoreactivity. This tau-positive axon differentiates and can be marked as the establishment of neuronal polarity (Yogev and Shen, 2017; Figure 3-2D). This polarity can be observed through a marked increase in its growth rate, a decrease in MAP2-immunoreactivity, and an increase in tau-immunoreactivity. From this stage on, the primary axon grows rapidly, while minor processes begin to elongate and take on the appearance of dendrites. This development continues throughout DIV 3-8 (Figure 3-2E-G), while dendrites continue to grow and develop, however at a slower rate than axons (LeBrasseur, 2005; Polleux and Snider, 2010).

By DIV 14 additional axons can be observed as branching collaterals emerging from the primary axonal process. Around this time, increased observations of *en passant* boutons are possible, as axons began to make close associations with neighbouring dendrites. Many of these associations appear as bulb-like protrusions from the axonal process, likely indicating the presence of presynaptic boutons, and either the formation of immature synapses or the presence of mature synapses (Reilly et al., 2011; Schedin-Weiss et al., 2016; Chéreau et al., 2017; Figure 3-2G). By DIV 21-24, neurons reach full dendritic and axonal arborization and growth begins to plateau (van Spronsen et al., 2013; Sahu et al., 2019; Figure 3-2H). Associations between axons and dendrites appear to become more refined, increasing in number along greater lengths of the dendrite (Figure 3-2F).

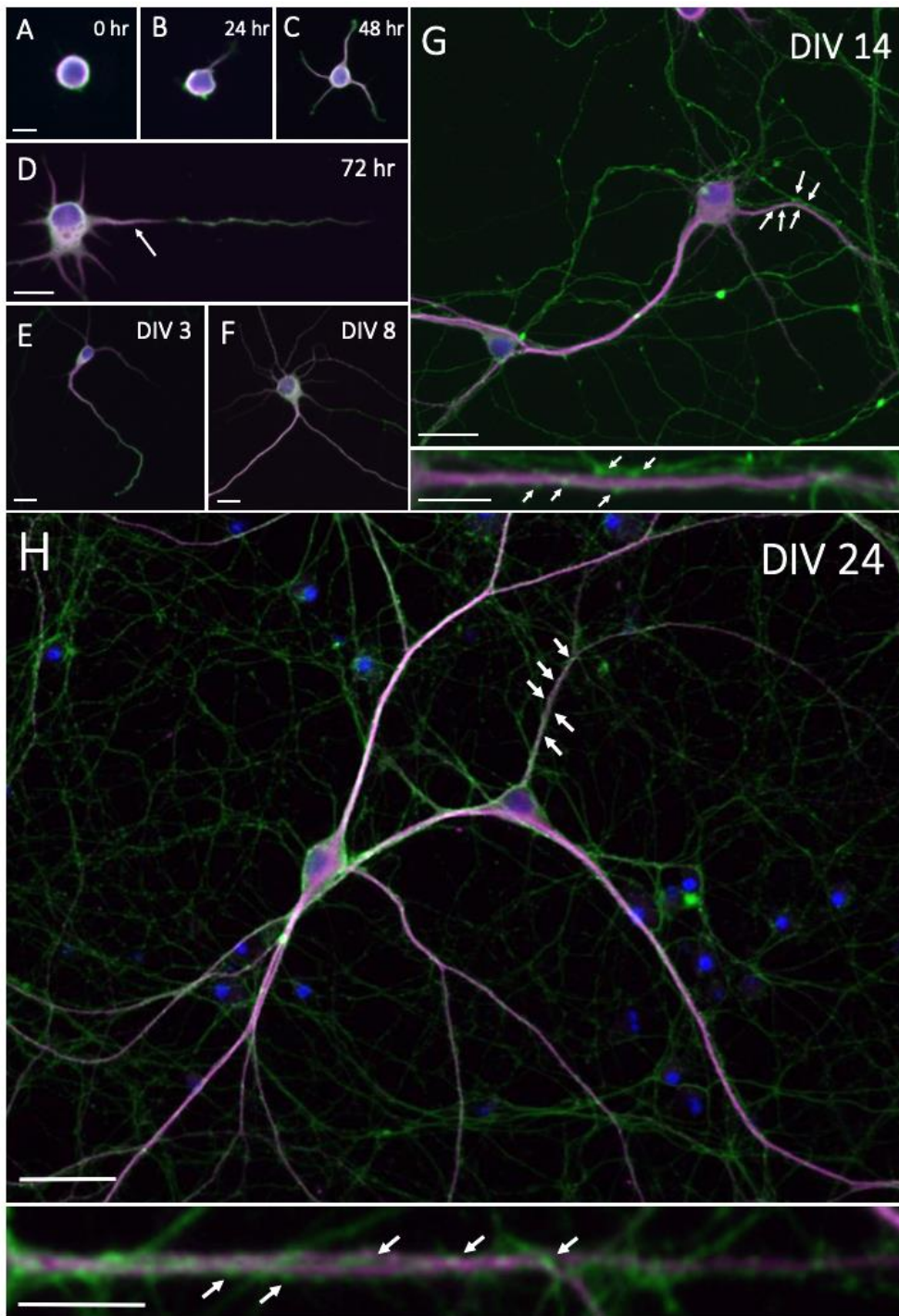


Figure 3-2 | Temporal development of MAP2- and Tau-positive neurites. Immunocytochemistry images of primary hippocampal cells in culture (40×100 cells/cm²) imaged at various time points following initial plating. Seeded cell bodies (A) begin to send out a MAP2-positive neurite within 24 hours (B). Additional neurites form within 48 hours, becoming tau-positive (C). A primary neurite becomes primarily tau-positive by 72 hours developing into an axon (D) and MAP2-positive axon-initial segment (arrow). By DIV 3 MAP2-positive and tau-positive neurites extend to become dendrites and axon, respectively (E). By DIV14 the formation of *en passant* boutons is observable (arrows, G). Inset image shows magnified section of dendritic and axonal proximity. Dendritic and axonal growth continues through DIV 24, with the persistence of *en passant* boutons (arrows, H). Inset image shows magnified section of dendritic and axonal proximity. Arrows indicate close associations of tau-positive axons and MAP2-positive dendrites. Images show neurons (MAP2, ■), nucleus (DAPI, ■), and axons (Tau, ■). $n = 1$. Scale bars = 20 μm (A-F), 50 μm (G-H), inset image = 10 μm .

3.1.3. Cellular Populations Within Primary Hippocampal Cell Cultures

In order to further understand the cell types present within our primary hippocampal co-cultures, we probed our cultures with immunocytochemical markers of cell type-specific proteins. While our experimental investigations will focus primarily on the expression of proteins in neurons, it is important to note that in healthy co-cultures such as those produced using our protocol, a mixture of both neuronal and glial cells will be present. Due to the proliferative capability of glial cells, left long enough, co-cultures will become overgrown with glial cells, an occurrence which may obscure or otherwise affect downstream analysis of molecular changes (Lauer et al., 2002), thus it was important to establish the expression of these cell types before downstream analysis. Many methods have been developed to circumvent this, including addition of the anti-mitotic drugs such as cytarabine (Ara-C), a pyrimidine antimetabolite additive that acts to inhibit DNA synthesis and thus the division of proliferative cells such as glia (Delivopoulos and Murray, 2011). However, methods such as these have been shown to have adverse effects on neurons (Wallace and Johnson, 1989; Martin et al., 1990). It is well established that the presence of glia *in vitro* and *in vivo* is necessary for the development and function of neurons (Helmuth, 2001; Ullian et al., 2001). Specifically, several astrocyte-derived signals have been described as essential for the induction of neuronal neuritogenesis and synaptogenesis (Mauch et al., 2001; Medina and Taberner, 2002; Haydon and Carmignoto, 2006; Barker et al., 2008; Bertrand et al., 2011; Yates, 2012). Our protocol for the culturing of primary hippocampal neurons involves the maintenance of cultures in serum-free Neurobasal-A media and B27 supplement which support the growth and development of neurons but does not directly support glial proliferation (Brewer et al., 1993). Therefore, in order to provide an initial support of glial cell growth, within the first four days, co-cultures were supplemented with conditioned media derived from glial-only cultures (refer Section 2.1.3. *Production of Conditioned Media for Cell Culture Maintenance*). Cultures were also supplemented with a small percentage of media from neuronal and glial co-cultures, in order to account for any secreted factors that may require the presence of both cell types. This allows for initial proliferation and support from glial cells, after which media supplementation comes solely from Neurobasal-A media, B27 and GlutaMAX only. This method has been shown to enhance survival of neurons in co-culture (Conde Gueri et al., 1989; Shi et al., 2013).

Here, we have probed our primary hippocampal cultures (DIV21-24) with immunocytochemical markers such as MAP2, or the glial fibrillary acidic protein (GFAP), present in astrocytic cells (Eng et al., 2000). These markers have been shown to be reliable indicators of neuron and astrocyte morphology, respectively, through their continued expression *in vitro* (Caceres et al., 1984; Sofroniew and Vinters, 2010). As shown by Figure 3-3, our primary hippocampal cell cultures show distinct populations of both MAP2- (Figure 3-3A,C) and GFAP-positive (Figure 3-3B-C) cells,

expressing typical neuronal and glial cell morphology (Müller et al., 2015). While the ratio of astrocytes per neuron has been shown to be 1:1.5 in the rodent hippocampus (Keller et al., 2018), this method provided a 1:1 ratio of neurons to astrocytes by DIV24 (cell counts of MAP2- and GFAP-positive cells; $n = 1$ experiment), similar to previous observations in culture (Dawes et al., 2018; Gunhanlar et al., 2018). In line with observations described in the literature, these co-cultures appeared to form close associations with GluA1-positive neurons (Figure 3-3D), which may indicate the formation of *in vitro* tripartite synapses (Todd et al., 2013; Robertson et al., 2014).

In addition to this, we have further identified subpopulations of granule cells within our neuronal population (Figure 3-3E). This population was isolated visually by use of antibodies against the granule cell specific transcription factor Prospero Homeobox 1 (Prox1; Lavado et al., 2010; Iwano et al., 2012), and indicates that our cultures contain distinct populations of Prox1-positive and -negative neurons. Identification of these populations provides information which may supplement downstream analysis and interpretation of results. Prox1-positive neurons accounted for 30% of MAP2-positive neurons in our cultures (cell counts of PROX1-negative and PROX1-positive cells; $n = 1$ experiment), with the remaining 70% of neurons able to be attributed to excitatory and inhibitory populations, similar to past observations (Soumier et al., 2009; Digilio et al., 2015). Interestingly, observations from past literature have shown population estimates of almost 1:1 granule to pyramidal cells when obtained from young postnatal (PD 0) mouse pups (Wu et al., 2015). While curious, this may arise from developmental differences between species.

Furthermore, as shown in Figure 3-3A, MAP2 staining shows continuous and robust signal, indicating the presence of a healthy neuron. In unhealthy neurons, MAP2 expression is fragmented in the dendrites and can take on a 'beads on a string' appearance due to cellular 'blebbing' of the membrane, a reliable indicator of cell stress (Charras, 2008; Appendix Figure A-15). Alternatively, unhealthy astrocytes have been shown to be double-stained by both GFAP and MAP2, and represents a permanent change in reactive astrocytes (Geisert et al., 1990; Schinstine and Iacovitti, 1996). In addition to this, the use of the nuclear stain 4',6-diamidino-2-phenylindole (DAPI) can be used to identify cell bodies, as well as the presence of a fragmented, condensed, or swollen nuclei, also an indication of poor health or cell stress (Dini et al., 1996). While few unhealthy cells are to be expected in long-term maintenance of primary cultures, cultures consistently had a very low level of unhealthy cells as determined by the above criteria.

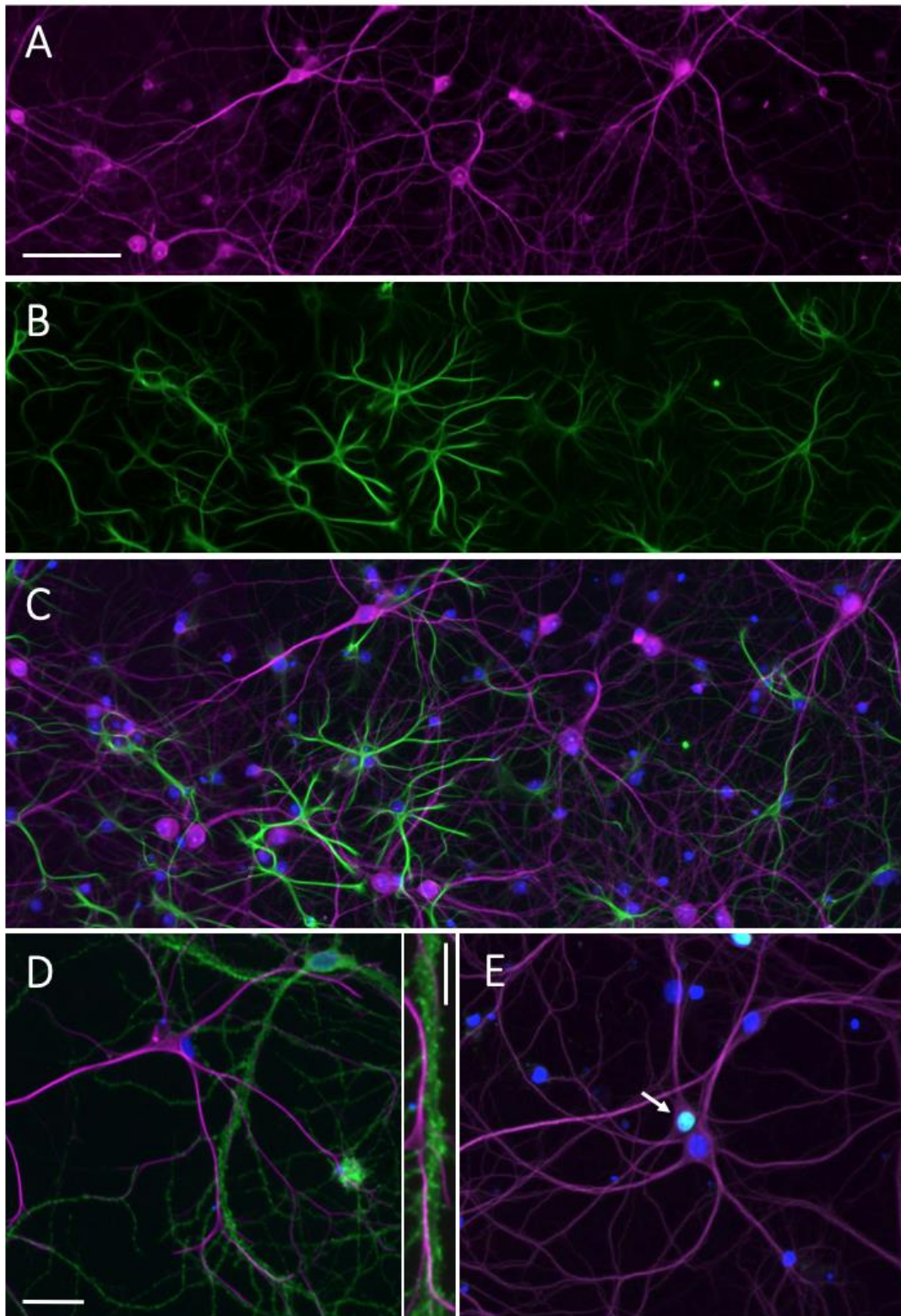


Figure 3-3 | Primary Hippocampal cultures contain Glial and Neuronal populations. Representative images show A) MAP2-positive neurons (■), B) GFAP-positive astrocytes (■), C) the close association between neurons and astrocytes throughout the cultures, and D) close associations with GluA1-positive dendrites (GFAP, ■; GluA1, ■). D) Populations of Prox1-positive (arrow) granule cells are present in our hippocampal cultures (MAP2, ■; Prox1, ■, DAPI, ■). $n = 1$ experiment. Scale bars = 100 μm (A-C), 50 μm (D-E), inset images = 10 μm .

3.1.4. *Identification of Pre- and Post-Synaptic Markers of Mature Synapses in Neuronal Cultures*

Synaptic transmission is a fundamental property of neurons, including those grown in culture (Vogt et al., 1995; Maximov et al., 2007). Communication between cells occurs primarily at synapses, which consist of pre- and postsynaptic domains separated by a 10–20 nm wide extracellular space, called the synaptic cleft. The most direct approach for the visualisation of synapses is the use of immunocytochemical markers for both pre- and postsynaptic proteins (Biederer and Scheiffele, 2007). Presynaptic proteins such as synaptophysin-1, a vesicle-associated protein present along axons (Fletcher et al., 1991; Di Liegro et al., 1995; Kwon and Chapman, 2011), and the postsynaptic excitatory glutamate receptor subunits GluA1 and GluA2, are reliable markers of mature and active postsynaptic domains (Pickard et al., 2000; Jacob and Weinberg, 2015). Single- and dual-labelling of these proteins in culture allows for visualisation of synapses via conventional fluorescence microscopy (Pickard et al., 2000; Verstraelen et al., 2018). At this resolution, dual labelling of pre- and postsynaptic proteins results in the coalescence of fluorescent signals, at points at which both proteins are present in close proximity (approximately 200-500 nm; Huang et al., 2009; Dzyubenko et al., 2016). Therefore, while single-labelling immunofluorescence can give an indication of protein content within a cell, dual-labelling of synaptophysin-1 and GluA1 or GluA2 gives an indication of pre- and postsynaptic terminals in close contact.

By one-week *in vitro* cells will begin to produce endogenous action potentials and synapses will begin to form, alongside the presence of immature dendritic spines (Dichter et al., 1983; Basarsky et al., 1994; Papa et al., 1995). From DIV8, hippocampal neurons grown in culture express the GluA1 protein (Zhang et al., 2017) and contribute to synaptic currents (Shi et al., 2010). From DIV8 onwards, spines continue to mature and the number of both excitatory and inhibitory synapses continues to increase (Grabrucker et al., 2009), as the length and number of dendrites also increases (Harrill et al., 2015). By DIV 21 a majority of synapses contain dual immunoreactivity for pre- and postsynaptic proteins (Grabrucker et al., 2009), reaching a relatively stable plateau.

Here, we probed our cultures (DIV 8) for GluA1, and found a small but notable presence of GluA1 protein within both the soma and dendrites (Figure 3-4A). We further examined GluA1 (Figure 3-4B) and GluA2 (Figure 3-4C) in DIV 21 hippocampal neurons which were present to a greater extent in both somatic and dendritic compartments, in line with previous observations (Richmond et al., 1996). DIV 21-27 neurons were also found to be positive for the presynaptic marker synaptophysin-1 (Figure 3-4D), which colocalized with both GluA1 (Figure 3-4E) and GluA2 (Figure 3-4F), indicating the presence active synapses in our cultures.

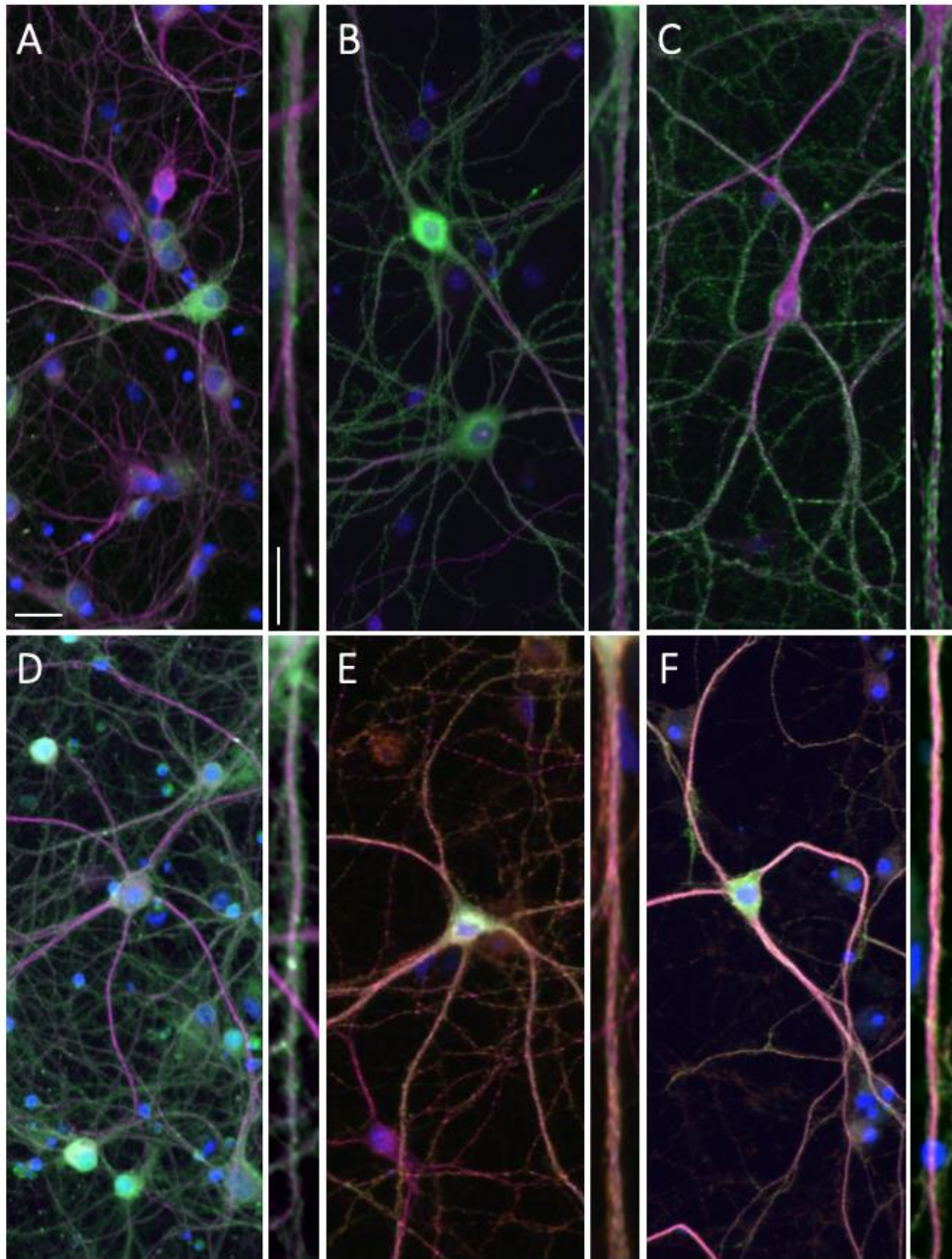


Figure 3-4 | Development of synapses in vitro. Representative images show hippocampal neurons stained for A) GluA1 (■, DIV 8), B) GluA1 (■, DIV 21-27), C) Synaptophysin-1 (■, DIV 21-27), D) GluA2 (■, DIV 21-27), E) the colocalization of both synaptophysin-1 (■) and GluA1 (■), and F) the colocalization of both synaptophysin-1 (■) and GluA2 (■). All images show neuronal architecture with MAP2 (■) and DAPI (■). $n = 1$ experiment. Scale bar = 50 μm , inset images = 20 μm

3.2. *Observations from the Culturing of Adult Cortical Mouse Neurons*

The culturing of tissue from both embryonic and early postnatal rodents has been shown to result in successful growth of both neuronal and glial populations. While the use of young tissue provides an easy and effective means to isolate primary neurons, these developmental stages may not accurately represent later stages of development or disease progression. However, successful culturing of neurons from adult animals has been historically difficult, and at times described as impossible, yet few groups have found success in isolating neurons and glia (Brewer, 1997; Eide and McMurray, 2005; Brewer and Torricelli, 2007; Sun et al., 2017), dorsal root ganglia (Mollá et al., 2017), and neural progenitor cells (Palmer et al., 1999; Ray and Gage, 2006; Babu et al., 2007) from adult tissue.

Here we aimed to establish a protocol for the preparation of adult neuronal cultures. Primary cortical cultures were prepared from 9-month-old wild-type (WT) and APP^{swe}/PS1 Δ E9 C57/BL6 (APP/PS1) mice and maintained in culture for 9-14 days DIV prior to use. Adaptions were made to our current protocol for culturing postnatal neurons (refer section 2.2 *Adult Primary Neuronal Culture Preparation*; Eide and McMurray, 2005; Brewer and Torricelli, 2007).

3.2.1. *Growth and Development of Adult Neuronal Cultures*

Similar to cultures derived from early postnatal tissue, development of adult neuronal cultures was documented as the cells matured using phase contrast microscopy. In line with observations from Eide and McMurray, (2005) and Brewer and Torricelli, (2007), immediately following plating, cells were observed as small spherical bodies and pyramidal soma, beginning to adhere to the poly-D coated glass coverslip (Figure 3-5A). After roughly 5-7 days adult cellular 'colonies' appeared (Figure 3-5B), and continued to extend processes (Figure 3-5C). Some neuron-like cells were observed clustering together with glia (Figure 3-5D), however without confirmation by use of immunocytochemical markers, these observations are purely morphological. While some groups have reported maintenance of adult cortical neurons for as long as 3 weeks (Ross et al., 2018), by DIV 14, neurons began to deteriorate, appearing as clusters of bright spheres, indicating detachment from the glass coverslip and cell death. The youngest cultures (DIV 9) were thus fixed and prepared for immunocytochemistry.

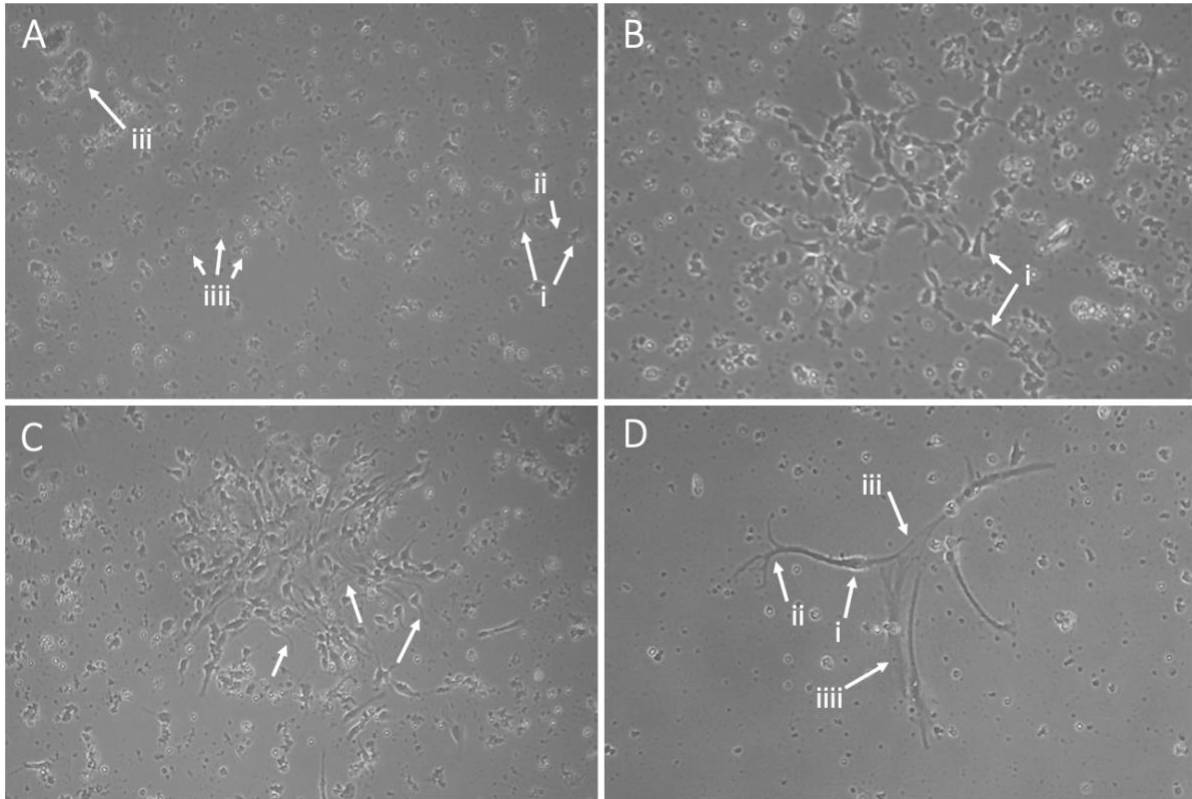


Figure 3-5| Adult mouse culture growth and development. A) By DIV 3, cultures begin to show the presence of neurons (i) with immature neurites (ii). DIV 3 cultures also show some cellular debris (iii), and many unadhered dead cells (iiii). B) by DIV 5 ‘colonies’ of cells can be observed with neurons and small neurites (i). C) these colonies continue to grow and neurites continue to extend and develop into identifiable dendrite-like branches (white arrows). Neuron development and the presence of glia is more obvious in D) smaller colonies where neurons (i) show multi-branching dendrites (ii) and axons (iii), in close proximity to fusiform shaped astrocytes (iiii). *n* = 1 experiment. Scale bar = 50 μ m.

3.2.2. *Cellular Populations in Adult Primary Cortical Cultures*

In line with our previous work, utilizing neuronal tissue obtained from PD 0-1 rat pups, we aimed to examine the populations of neurons and astrocytes in our adult mouse cultures. Immunocytochemistry was used targeting the neuronal marker MAP2 and the astrocyte marker GFAP. Here the addition of DAPI was used as an indicator of nuclear bodies present in culture which may not also express positive for MAP2 or GFAP. Through this, we observed conservation of the 'colonies' seen via phase contrast microscopy. Interestingly, in dishes double labelled for GFAP and MAP2, majority of the colonies were positive for GFAP with few MAP2-positive neurons present. Astrocytes showed typical morphology for those cultured from adult tissue (Sun et al., 2017), with a majority adopting polygonal/fusiform or flat shaped cell bodies, although some astrocytes formed monopolar or bipolar morphology. A majority of neurons present showed a typically small soma, with 1-2 MAP2-positive primary projections (Figure 3-6).

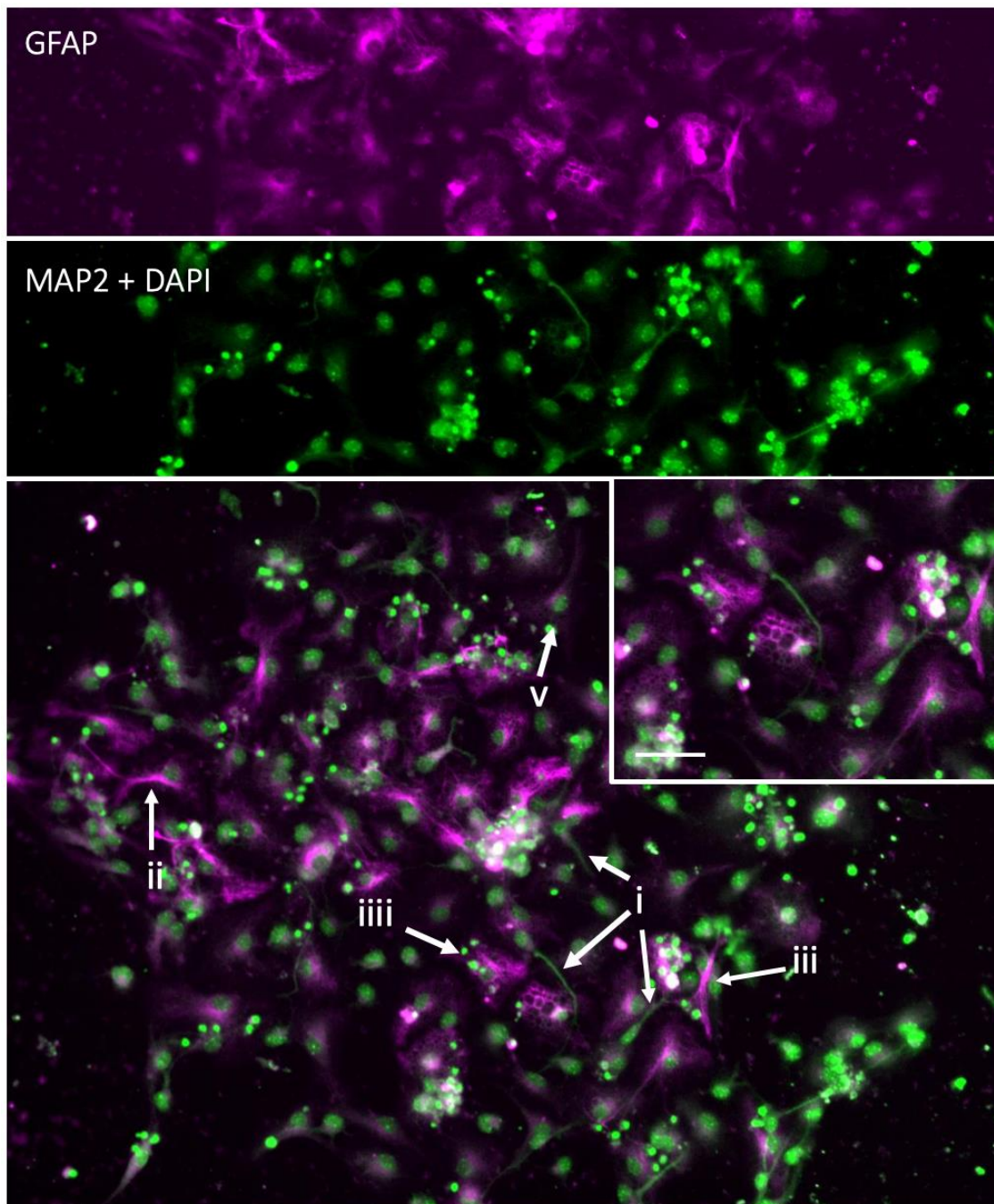


Figure 3-6| Cellular populations in adult cortical cultures. Immunocytochemistry showed populations of i) MAP2- and DAPI-positive neurons (■), and GFAP-positive (■) ii) monopolar, iii) bipolar, iiiii) polygonal, and v) flat astrocytes (DIV 9). Inset image shows digital magnification of neurons and astrocytes. *n* = 1 experiment. Scale bar = 50 μ m.

3.2.3. *Cultured Wild-Type and APP/PS1 Adult Mouse Neurons Express GluA1*

Secondary to examining the presence of cell populations within our adult mouse cultures, we further aimed to examine whether the cells present in our cultures express appropriate glutamate receptors. GluA1 is present in the mouse cerebral cortex and associates strongly with immunocytochemical markers for neurons (Carino et al., 2012; Maheshwari et al., 2012), glial cells (Bender et al., 2020), and reactive astrocytes (Hefferan et al., 2007). Importantly, past observations have shown high immunoreactivity for pre- and postsynaptic markers synapsin-1 and PSD-95, respectively, by 3 weeks *in vitro* (Ross et al., 2018), indicating adult-derived neurons are capable of maintaining the regeneration of synapses in culture.

As mentioned in section 3.1.4. *Identification of Pre- and Post-Synaptic Markers of Mature Synapses in Neuronal Cultures*, neurons obtained from embryonic or young postnatal animals have previously been shown to express synaptic markers, including GluA1, from 8 days onwards (Richmond et al., 1996). Here, we have obtained cells from much older tissue, with perhaps slower regenerative abilities than younger tissue, and maintained for only 9 days *in vitro*. In face of this, when examining GluA1 expression under permeabilized conditions, our cultures showed many GluA1- and MAP2-positive cells in cultures obtained from both WT and APP/PS1 transgenic tissue (Figure 3-7). Importantly, while many MAP2-positive cells appeared morphologically neuronal, a majority MAP2 staining expressed as showing astrocyte morphology, indicating the likely presence of GluA1-positive reactive astrocytes (Geisert et al., 1990; Schinstine and Iacovitti, 1996)

Here we aimed to establish a protocol for the preparation of adult neuronal cultures. In line with past literature, we have further described the difficulties in isolating cells for co-culture of neurons and glia. While we were successful in the isolation of MAP2- and GFAP-positive cells, the identity of these cells would require greater validation than the techniques used here. Additionally, as previously observed (Brewer, 1997), the use of Neurobasal A medium for preparation of adult neurons can sometimes result in the release of neuronal DNA following osmotic shock, possibly promoting the death of neurons in these preparations. Future attempts should aim to optimize the osmolarity of medium used to isolate adult neurons in order to promote the longevity of neurons in these cultures. For these reasons, these cultures were not ultimately used for the experimental drug treatments described throughout this thesis. However, the observations provided by this work highlights considerations when attempting this approach and provide an early proof-of-concept for future directions.

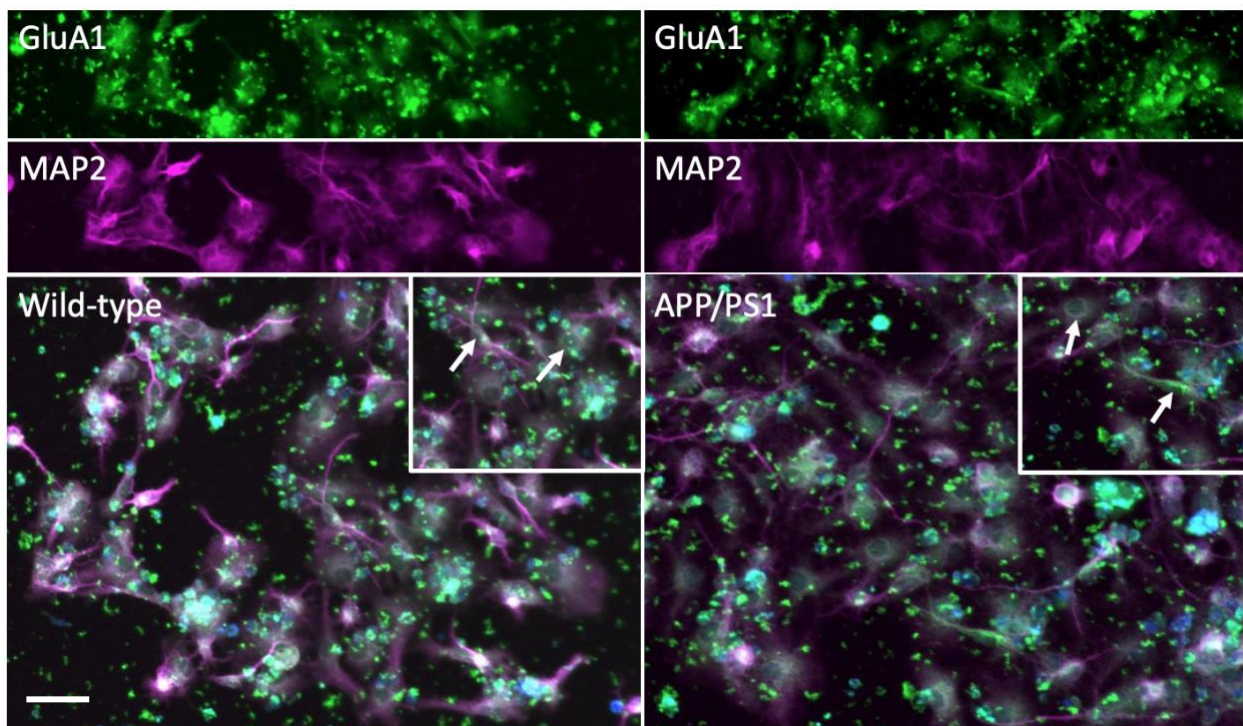


Figure 3-7 | GluA1-positive cells. Immunocytochemistry showed populations of double labelled cells (DIV 9) positive for both GluA1 (■) and MAP2 (■) in tissue obtained from A) wild-type, and B) APP/PS1 transgenic mice. Upper panels show GluA1, middle panels show MAP2, and lower panels show combined GluA1 and MAP2 channels. Inset images show magnification of combined channels, arrows indicate clear GluA1-positive neurons. $n = 1$ experiment. Scale bar = 50 μm .

Chapter 4

4.1. *Examining Arc Expression in Response to sAPP α*

Historically, IEGs, and specifically Arc, has been a proven method for effectively measuring plasticity or the activation of synapses in both *in vitro* (Das et al., 2018) and *in vivo* assays of plasticity (Grinevich et al., 2009; Steward et al., 2018). Additionally, Arc has shown direct links to the expression of AMPA receptors in governing the regulation of plasticity (Rial Verde et al., 2006; Shepherd et al., 2006; Shepherd and Bear, 2011). It is recognized that both endogenous (Taylor et al., 2008) and exogenous (Richter et al., 2018) sAPP α promotes the regulation of plasticity and the expression of AMPAR (Mockett et al., 2019; Martinsson et al., 2019). Therefore, due to the inherent activity-regulated properties of Arc, initial experiments sought to utilize this, allowing for assessment of upstream and downstream processes governing sAPP α 's control of plasticity and AMPAR expression in culture.

All data presented here, including additional experiments and observations is available by publication in Frontiers of Molecular Science, as part of the research topic Advances in Biomedical and Molecular Neuroscience (Livingstone et al., 2019), and can be found at <https://doi.org/10.3389/fnmol.2019.00198>.

4.1.1. *sAPP α Facilitates an Increase in Arc and Zif268 mRNA Expression*

Previous work has identified networks of genes associated with the treatment of hippocampal slices with sAPP α (1nM), including rapidly-induced transcription factors *JunB*, *c-Fos*, and importantly *Zif268* (Minatohara et al., 2016). Therefore, we aimed to examine whether sAPP α (1 nM) promoted an increase in *Arc* mRNA expression in primary cortical cell cultures, in a time-dependent manner, using reverse transcription quantitative polymerase chain reaction (RT-qPCR). As a positive control we also examined the expression of *Zif268*, previously shown to increase in expression following sAPP α (1 nM, 15 min) in organotypic hippocampal slices (Ryan et al., 2013), and further linked to the regulation of *Arc* mRNA *in vivo* (Penke et al., 2011). As a negative control we also examined the transcription factor Specificity Protein 2 (*SP2*; Suske, 1999). Here, we found that treatment with sAPP α facilitated a slowly developing increase in the levels of *Arc* mRNA (Figure 4-1). No significant change was found in either *Arc* or *Zif268* mRNA at 15 or 30 min of sAPP α incubation (*Arc*: 15 min: 1.27 ± 1.00 , $p = 0.35$; 30 min: 1.14 ± 0.28 , $p = 0.49$; *Zif268*: 15 min: 0.96 ± 0.45 , $p = 0.28$; 30 min: 1.30 ± 0.68 , $p = 0.30$). However, following 60- and 120-min exposure the levels of both *Arc* (60 min: 2.29 ± 1.32 , $p = 0.01$; 120 min: 2.69 ± 1.53 , $p \leq 0.0001$) and *Zif268* (60 min: 1.78 ± 1.02 , $p = 0.01$; 120 min: 1.38 ± 0.57 , $p = 0.04$; Figure 4-1)

mRNA increased significantly relative to no-drug controls. This effect was found to slowly diminish with time as both *Arc* and *Zif268* were reduced by 240 minutes (*Arc*: 1.57 ± 1.15 , $p = 0.04$; *Zif268*: 1.43 ± 0.86 , $p = 0.05$) and eliminated by 24 hours (*Arc*: 1.051 ± 0.14 , $p = 0.45$; *Zif268*: 0.94 ± 0.043 , $p = 0.32$). No significant change was found in *SP2* following any length of treatment (15 min: 1.049 ± 0.1501 , $p = 0.19$; 30 min: 1.063 ± 0.15 , $p = 0.17$; 60 min: 1.15 ± 0.24 , $p = 0.10$; 120 min: 1.18 ± 0.094 , $p = 0.06$; 240 min: 0.94 ± 0.043 , $p = 0.33$; 24 hr: 1.032 ± 0.14 , $p = 0.21$).

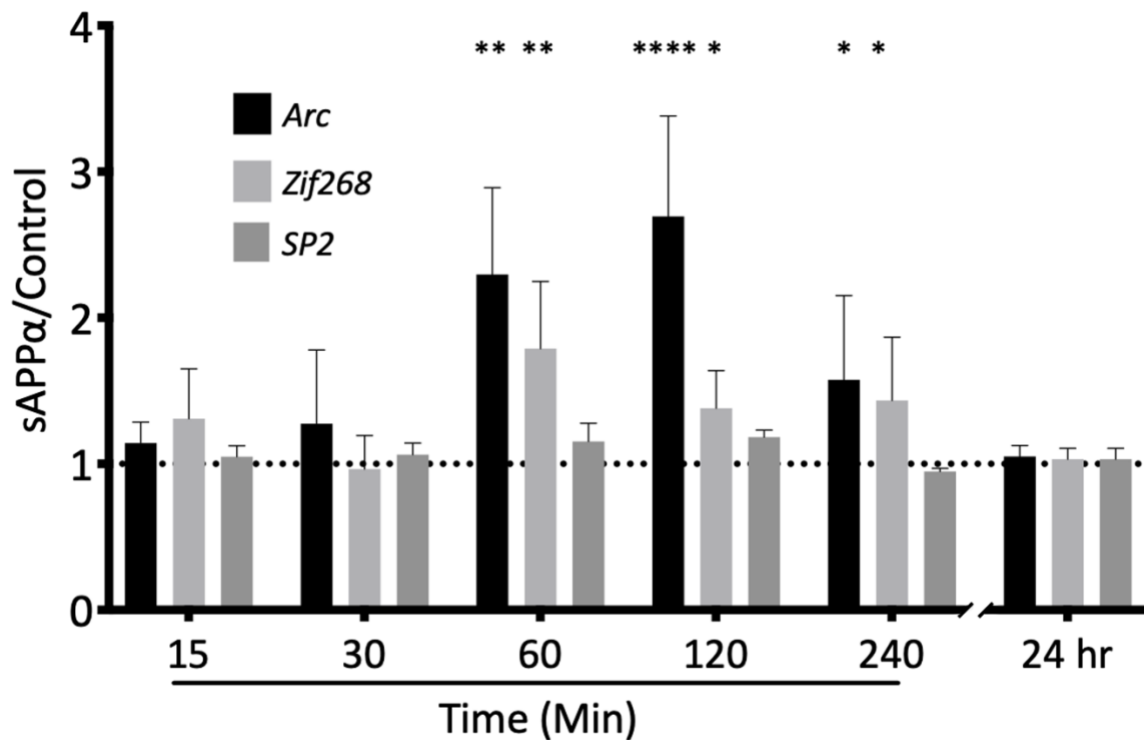


Figure 4-1 | sAPP α promotes the transcription of *Arc* and *Zif268* mRNA. RT-qPCR showed that sAPP α (1 nM) promotes an increase in the expression of *Arc* and *zif268* mRNA in primary cortical cells in culture at 60, 120 min ($n = 5$ wells), and 240 min ($n = 4$ wells) relative to no-drug controls ($n = 9$ wells). Normality was detected by Shapiro-Wilk normality test. All data are expressed as mean \pm SEM from ≥ 4 experiments. No significant change was detected at 15 ($n = 5$ wells) or 30 ($n = 5$ wells) min, nor 24 h ($n = 4$ wells), nor was there a significant change in the negative control gene *SP2* ($n = 4$). Students t -tests; * $p \leq 0.05$, ** $p \leq 0.01$, **** $p \leq 0.0001$.

4.1.2. *sAPP α Facilitates an Increase in Arc Protein Expression*

Previous research has shown a strong association between the increased expression of *Arc* mRNA and its rapid, activity- and experience-dependent translation (Steward et al., 1998; Steward et al., 2015). Interestingly, induction of *Arc* transcription leads to an increase in dendritic *Arc* mRNA, by active transport to sites of synaptic activity. In this sense *Arc* stands out from other immediate early genes which do not show this pattern of dendritic expression (Maroteaux et al., 2014), or such rapid activity-dependent transport (Steward et al., 1998). Therefore, examinations of both somatic and dendritic accumulation of *Arc* protein may give important insights into the regulation of plasticity by sAPP α . Thus, in order to examine *Arc* protein expression in our primary hippocampal neurons, we utilized immunocytochemistry and examined *Arc* expression in both somatic and dendritic compartments. Further, while evidence from our RT-qPCR data suggest a peak of *Arc* mRNA expression at 2 hours, this is reflected by past observations in behavioural learning paradigms (Hossaini et al., 2010; Lonergan et al., 2010; Soulé et al., 2012), and following synaptic activity (Chotiner et al., 2010) and BDNF treatment (El-Sayed et al., 2011). Therefore, we selected this timepoint for the examination of *Arc* protein following sAPP α treatment. Here, we found that sAPP α (1 nM, 120 min) increased both somatic (1.35 ± 0.46 , $p \leq 0.0001$) and dendritic (1.92 ± 0.81 , $p = 0.0003$) *Arc* protein expression relative to controls (Figure 4-2A,C,F,G). Similarly, 0.1 nM sAPP α significantly increased dendritic *Arc* expression (1.35 ± 0.05 , $p = 0.0002$), but it did not significantly affect somatic *Arc* protein expression (1.15 ± 0.39 , $p = 0.24$; Figure 4-2A-B,F,G).

While many plasticity-enhancing properties have been found of sAPP α , the β -secretase product, sAPP β has shown few comparative properties. sAPP β differs from sAPP α by 16 C-terminal amino acids, and has been described as 100-fold less effective in ameliorating excitotoxicity and attenuating glucose deprivation compared to sAPP α (Furukawa et al., 1996), is unable to protect against oligomeric A β -induced spine loss (Tackenberg and Nitsch, 2019), and does not enhance LTP (Mockett et al., 2019). Therefore, we next examined the effect of sAPP β treatment (0.1 nM, 1 nM; 120 min) and found, in contrast to sAPP α , that neither 0.1 nM nor 1 nM sAPP β significantly increased dendritic *Arc* protein (0.1 nM: 0.97 ± 0.49 ; 1 nM: 0.92 ± 0.45 , $p \geq 0.99$; Figure 4-2A,D,F,G). Interestingly, while 0.1 nM sAPP β did not affect *Arc* protein expression in the soma (0.91 ± 0.34 , $p \geq 0.99$), 1 nM sAPP β resulted in a small but significant decrease in somatic *Arc* expression (0.82 ± 0.38 , $p = 0.03$; Figure 4-2A,E,F). Thus, the enhancement of *Arc* expression appears to be specific to sAPP α .

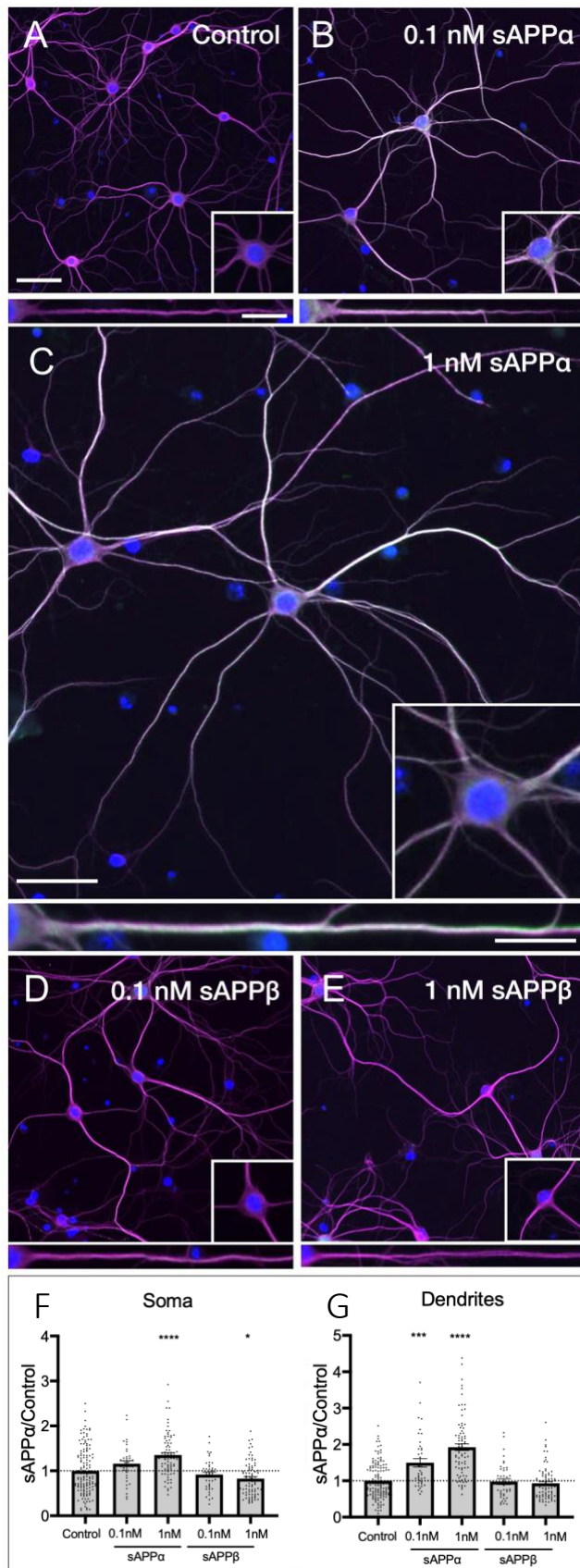


Figure 4-2 | sAPP α promotes Arc protein expression in a concentration-dependent manner. Representative images showing Arc protein levels in **A)** no drug control ($n = 140$ cells), **B)** 0.1 nM sAPP α ($n = 40$ cells), **C)** 1 nM sAPP α ($n = 80$ cells), **D)** 0.1 nM sAPP β ($n = 40$ cells) and **E)** 1 nM sAPP β -treated ($n = 80$ cells) primary hippocampal neurons. **F)** Average data showing 1 nM sAPP α promotes an increase, and 1 nM sAPP β a modest decrease in Arc protein expression in the soma. **G)** Average data showing 0.1 and 1 nM sAPP α promotes an increase in dendritic Arc protein. All data are expressed as mean \pm SEM from ≥ 4 experiments. Normality was detected by D'Agostino and Pearson omnibus normality tests, and significance was calculated using a Kruskal-Wallis one-way ANOVA with Dunn's multiple comparisons test on raw data. * $p = 0.0378$, *** $p = 0.0002$, **** $p \leq 0.0001$. Representative images show neuronal soma, dendrites (MAP2; \square), Arc protein (\blacksquare), nuclei (DAPI; \blacksquare) and magnified somatic (inset, bottom right) and dendritic compartments. Scale bars = 50 μm (A-B,D-E), 100 μm (C); lower panels = 10 μm .

4.1.3. *sAPP α Promotes an Increase in Arc Protein Throughout Primary and Secondary Dendrites*

Following the observation that sAPP α (0.1 nM, 1 nM; 120 min) enhanced dendritic arc protein expression, we further aimed to validate these findings and extend this analysis, by assessing fluorescence intensity levels and distribution of Arc protein throughout the dendrites— a method previously employed Gumy et al., (2017). This assessment validated the finding that sAPP α (1 nM, 120 min) promotes an increase in Arc protein expression throughout the dendrites, as dendritic Arc expression was found to be significantly increased throughout the initial 50 μ m (control: 40.06 ± 14.93 ; 0.1 nM sAPP α : 63.82 ± 20.1 , $p \leq 0.0001$; 1 nM sAPP α : 62.04 ± 22.6 , $p \leq 0.0001$; Figure 4-3), middle 50 μ m (control: 32.43 ± 15.69 ; 0.1 nM sAPP α : 52.91 ± 25.57 $p = 0.0005$; 1 nM sAPP α : 52.89 ± 22.29 , $p \leq 0.0001$) and final 50 μ m segment of primary dendrites (control: 27.09 ± 11.58 ; 0.1 nM sAPP α : 43.72 ± 22.3 , $p \leq 0.0001$; 1 nM sAPP α : 48.09 ± 24.17 , $p = 0.0311$; Fig. 3A; Gilbride, 2016). Increased Arc expression in secondary dendrites was observed in the initial 25 μ m (control: 32.54 ± 13.55 ; 0.1 nM sAPP α : 45.22 ± 19.61 , $p = 0.01$; 1 nM sAPP α : 43.73 ± 21.08 , $p = 0.01$) and middle 25 μ m dendritic segment (control: 27.03 ± 14.08 ; 0.1 nM sAPP α : 37.64 ± 15.19 , $p = 0.002$; 1 nM sAPP α : 36.63 ± 17.49 , $p = 0.004$), however Arc expression was not significantly altered in the final 25 μ m of secondary dendrites (control: 24.85 ± 12.25 ; 0.1 nM sAPP α : 31.99 ± 13.06 , $p = 0.26$; 1 nM sAPP α : 30.06 ± 14.26 , $p = 0.06$). While Arc expression has been previously shown to extend to distal dendrites (de Solis et al., 2017), the results observed here may indicate that signals regulating Arc expression or Arc protein itself fails to reach distal dendrites within the 2-hour window. Alternatively, this may indicate that processes of protein degradation may have already begun (Farris et al., 2014).

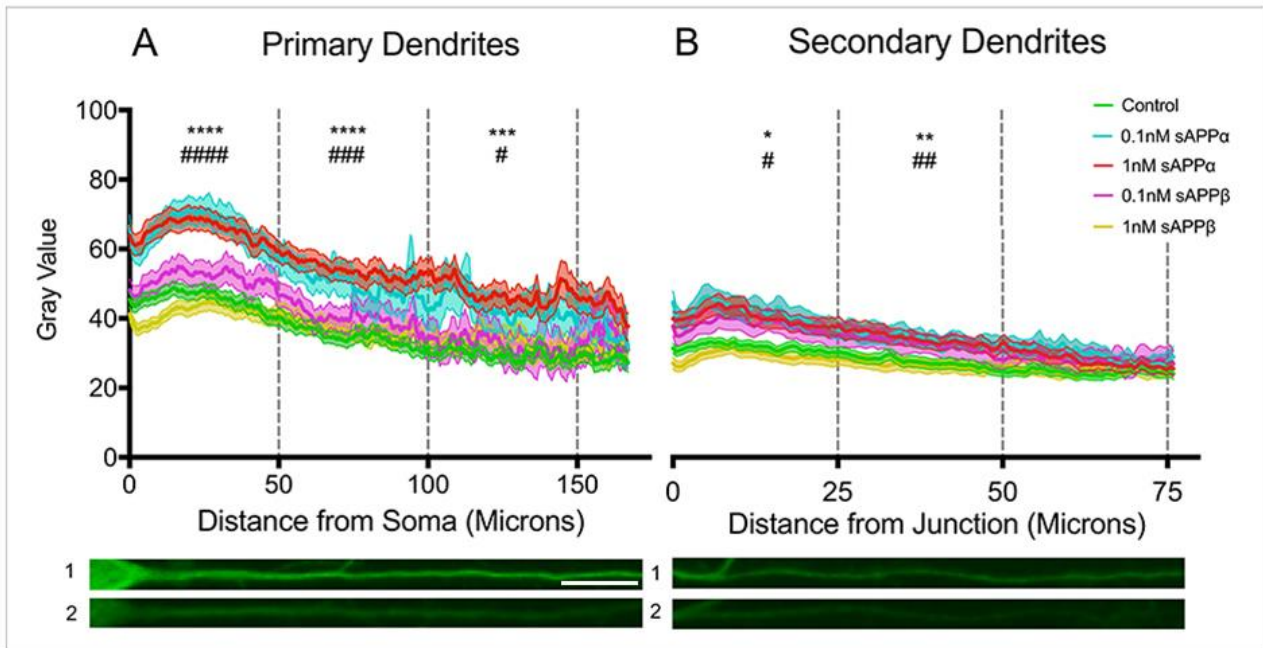


Figure 4-3 | Arc protein expression increases throughout primary and secondary dendrites. Average fluorescent intensity of Arc expression throughout (A) primary and (B) secondary dendrites (mean \pm SEM, $n = 40-141$). Significance was determined by averaging dendritic gray value within each cell and is expressed per treatment group within (A) 50 and (B) 25-micron bins. Representative fluorescence images illustrate Arc protein expression (■) within primary (A1,2) and secondary (B1,2) dendrites in the presence of 1 nM sAPP α (A1, B1) or no drug (A2, B2). Asterisks (*) and hashes (#) indicate significance found between control and 1 nM and 0.1 nM sAPP α , respectively. Data are expressed as raw gray value (solid line) \pm SEM (shaded area). All data are expressed as mean \pm SEM from ≥ 4 experiments. Normality was detected by D'Agostino and Pearson omnibus normality tests, and significance was calculated using a Kruskal–Wallis one-way ANOVA with Dunn's multiple comparisons test on raw data. */# $p \leq 0.05$ **/# $p \leq 0.005$ ***/### $p = 0.0005$, ****/#### $p \leq 0.0001$. Scale bar = 50 μm . Data was analysed with help from honours student Courtney Westlake.

4.1.4. *Arc Protein Expression is Transcription- and Translation-Dependent*

As shown by section 4.1.1. *sAPP α Facilitates an Increase in Arc and Zif268 mRNA Expression*, sAPP α (1 nM) enhances the expression of Arc mRNA in primary cortical neurons. Likewise, sAPP α (1 nM, 120 min) enhances the expression of Arc protein in both the soma and dendrites of cultured hippocampal neurons. To examine the relationship between these two events, we aimed to further examine whether the expression and localization of Arc would be otherwise affected by inhibition of both *de novo* transcription and translation in primary hippocampal neurons. Here, we found that sAPP α -induced Arc protein expression in both somatic (2.24 ± 1.830 , $p \leq 0.0001$) and dendritic (1.99 ± 1.45 , $p \leq 0.0001$) compartments was blocked by co-application of the transcription inhibitor actinomycin-D (Act-D; 10 μ M; soma: 0.81 ± 0.68 ; dendrites: 0.95 ± 0.61 , respectively; $p \leq 0.0001$; Figure 4-4A-C,E-F). Additionally, co-application of the translation inhibitor anisomycin (Aniso; 40 μ M) also eliminated the effect (soma: 0.62 ± 0.30 ; dendrites: 0.84 ± 0.41 , $p \leq 0.0001$; Figure 4-4A,B,D-F). These effects indicate that Arc protein expression at 2 hours is fully dependent on both *de novo* transcription and translation of mRNA and protein. These results reflect those observed by past literature examining the dependence of Arc transcription and translation during BDNF (Messaoudi et al., 2002; Zheng et al., 2009), dopamine (Fosnaugh et al., 1995), and nicotine (Schochet et al., 2005) treatment, as well as synaptic activity (Link et al., 1995; Lyford et al., 1995). Together, these findings add evidence to support the hypothesis that sAPP α promotes both Arc transcription and translation.

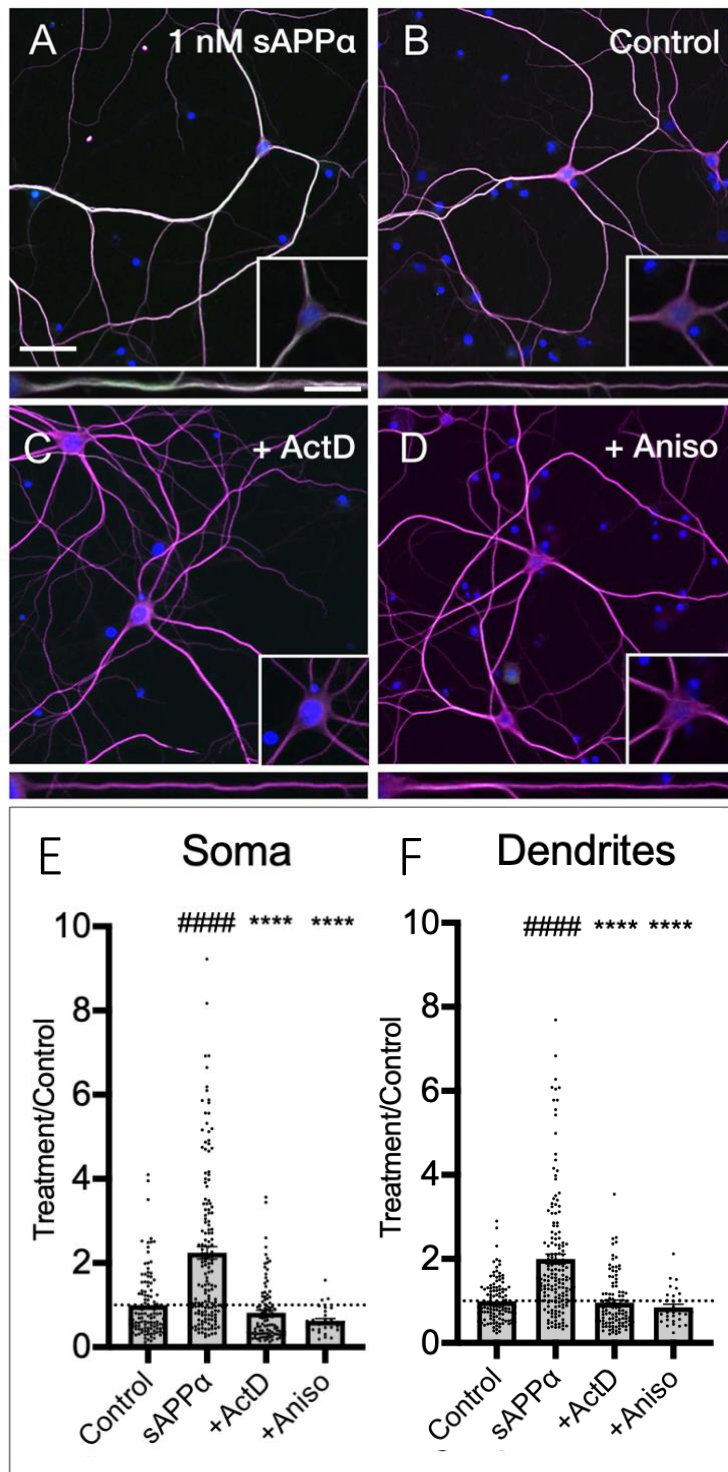
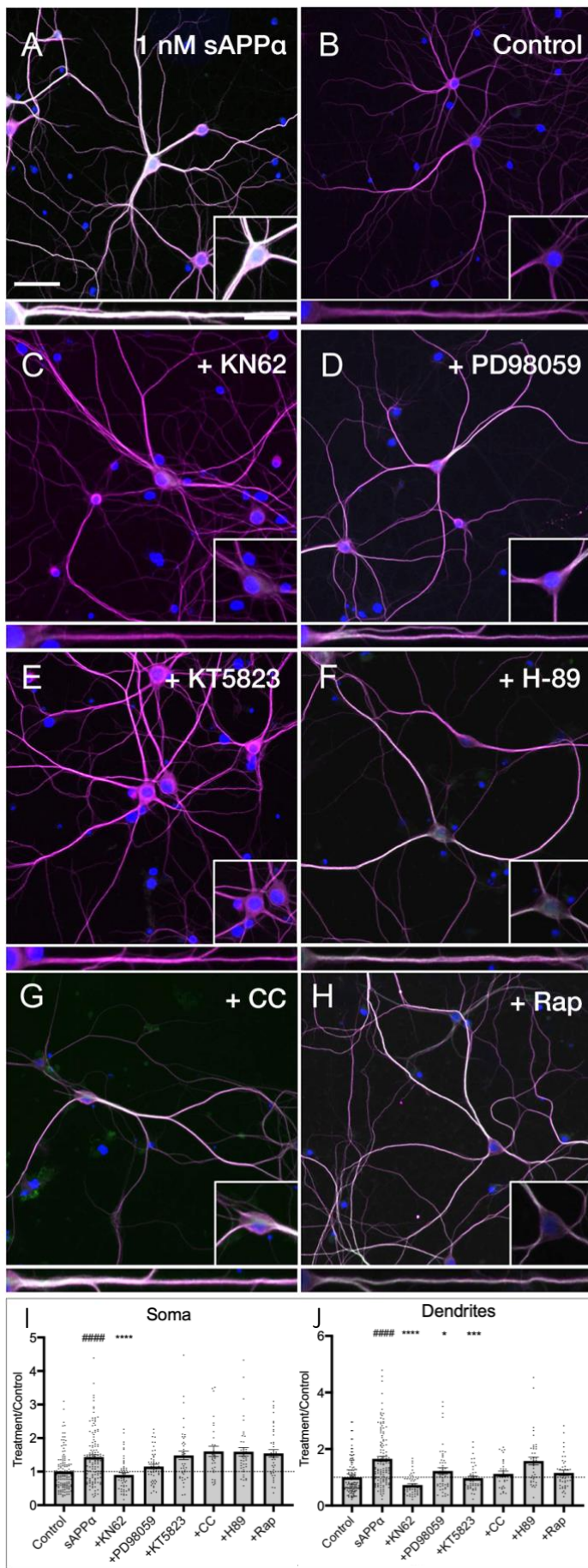


Figure 4-4 | Arc protein expression is prevented by inhibitors of transcription and translation. Representative images showing Arc protein levels in **A**) sAPPα (1 nM, 120 min, $n = 157$ cells) and **B**) no drug control ($n = 115$ cells) conditions. sAPPα-mediated Arc expression is inhibited with co-application of **C**) Actinomycin-D ($n = 104$ cells) or **D**) Anisomycin ($n = 30$ cells) in the **E**) soma and **F**) dendrites of hippocampal neurons. All data are expressed as mean \pm SEM from ≥ 4 experiments. Normality was detected by D'Agostino and Pearson omnibus normality tests, and significance was calculated using a Kruskal–Wallis one-way ANOVA with Dunn's multiple comparisons test on raw data. Hashes (#) indicate significance between control and sAPPα-treated; asterisks (*) indicate significance between sAPPα- and inhibitor-treated; ****/#### $p \leq 0.0001$. Representative images show neuronal soma, dendrites (MAP2; \square), Arc protein (\square), nuclei (DAPI; \square) and magnified somatic (inset, bottom right) and dendritic compartments. Scale bars = 50 μ m (A-D); lower panels = 10 μ m.

4.1.5. *Arc Protein Expression is Dependent on CaMKII/MAPK/PKG Signalling*

Previous research has identified CaMKII, MAPK, and PKG as key downstream kinases in the regulation of cell surface GluA1 (Mockett et al., 2019), and the enhancement of synaptodendritic protein synthesis (Claassen et al., 2009). Here, we sought to determine if the translation or subcellular distribution of Arc protein utilizes similar processes. As well as this we aimed to extend our assay to examine protein kinases likewise linked to the regulation of Arc protein, synaptic plasticity, or protein synthesis, such as PKA, PKC, and mammalian target of rapamycin (mTOR; Waltereit et al., 2001; Boehm et al., 2006; Wang and Proud, 2006). Here, primary hippocampal cultures were incubated with sAPP α in the presence or absence of inhibitors for 2 hours with or without pre-treatment (refer Table 2-1. *Catalogue of Inhibitors and Antagonists used Throughout Immunocytochemical and Immunohistochemical Experiments*).

Accordingly, we found that sAPP α -mediated Arc protein expression was significantly reduced following inhibition of CaMKII in the soma (0.90 ± 0.48 , $p \leq 0.0001$; Figure 4-5A,B,C,I). Arc protein expression in the soma was otherwise unaffected by inhibitors of MAPK (1.15 ± 0.46 , $p = 0.47$; Figure 4-5A,B,D,I), PKG (1.48 ± 0.82 , $p \leq 0.99$; Figure 4-5A,B,E,I), PKC (1.60 ± 0.83 , $p \leq 0.99$; Figure 4-5A,B,F,I), PKA (1.5 ± 0.80 , $p \geq 0.99$; Figure 4-5A,B,G,I) or mTOR (1.54 ± 0.71 , $p \leq 0.99$; Figure 4-5A,B,H,I). Furthermore, dendritic Arc protein expression was significantly reduced through inhibition of CaMKII (0.72 ± 0.34 , $p \leq 0.0001$; Figure 4-5A,B,C,J), MAPK (1.22 ± 0.80 , $p = 0.0428$; Figure 4-5A,B,D,J), and PKG (0.97 ± 0.45 , $p \leq 0.0001$; Figure 4-5A,B,E,J), however remained unaffected by inhibitors of PKA (1.57 ± 0.88 , $p \geq 0.99$; Figure 4-5A,B,F,J), PKC (1.12 ± 0.51 , $p = 0.0875$; Figure 4-5A,B,G,J), and mTOR (1.15 ± 0.58 , $p = 0.0511$; Figure 4-5A,B,H,J). Given these results, and that of past research, it seems likely these processes may contribute to the transcription, translation, and localization of Arc in both the soma and dendrites following sAPP α treatment.



4.1.6. *Dendritic Arc Protein Expression is Dependent on Activation of NMDA- and α 7nACh Receptors*

Despite many studies, the cell surface receptor or receptors which transduce signals downstream of sAPP α are yet to be conclusively identified, though candidates have emerged. These include NMDAR, α 7nAChR, sorting-related receptor with A-type repeats (SORLA), gamma aminobutyric acid receptors (GABA_B), and membrane-bound APP itself (Rice et al., 2017; Hartl et al., 2013; Milosch et al., 2014; Richter et al., 2018; Mockett et al., 2019). Here, we pharmacologically inhibited likely candidates mediating sAPP α 's plasticity-promoting effects and observed the effect on Arc protein levels (Figure 4-6). We found that application of antagonists targeting GABA_B (CPG55845; 50 μ M), TrkB (ANA-12; 100 μ M), or mGluRI/II receptors (MCPG; 500 μ M) had no significant effect on dendritic Arc protein expression (Figure 4-6A,B,I) following sAPP α treatment (1 nM, 120 min; CPG55845: 2.79 ± 1.08 , $p \geq 0.99$, Figure 4-6C,I; ANA-12: 2.78 ± 1.29 , $p \geq 0.99$, Figure 4-6D,I; MCPG: 2.29 ± 1.27 , $p \geq 0.99$, Figure 4-6E,I). However, Arc protein expression was significantly reduced following antagonism of NMDA receptors by APV (50 μ M; 1.67 ± 0.78 , $p = 0.01$; Figure 4-6F,I) and α 7nACh receptors with α -bungarotoxin (α BGT, 10 nM; 1.61 ± 1.18 , $p = 0.0138$; Figure 4-6G,I). Combined antagonism of NMDA and α 7nACh receptors completely abolished sAPP α -mediated Arc expression (0.78 ± 0.49 , $p \leq 0.0001$; Figure 4-6H,I). Previous work has established a coupling between NMDA- and α 7nACh Receptors (Li et al., 2012; Li et al., 2013), promoting a synergism of activity (Aramakis et al., 1998; Bali et al., 2017; Bali et al., 2019). Due to this, these results may suggest a novel mechanism whereby synergistic action between NMDA and α 7nACh receptors govern an enhancement in sAPP α -mediated Arc protein expression.

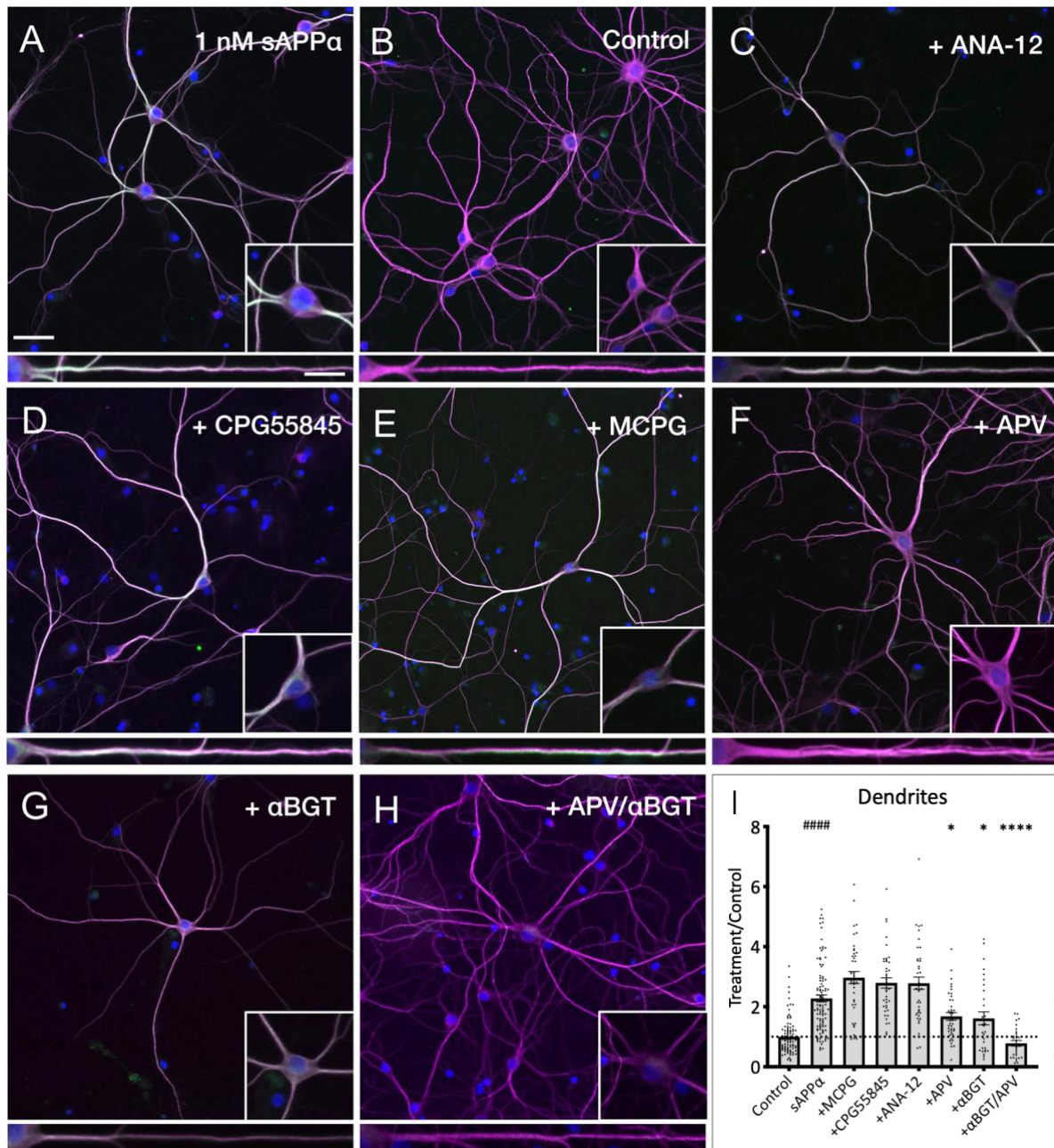


Figure 4-6 | Arc protein expression is dependent on NMDA and α 7nACh receptors. Representative images showing A) sAPP α (1 nM, 120 min, $n = 80$ cells) promotes and increase in the expression of Arc protein in cultured hippocampal neurons relative to B) no drug controls ($n = 80$ cells). Co-incubation of sAPP α with C) ANA-12 ($n = 40$ cells), D) CPG55845 ($n = 40$ cells), and E) MCPG ($n = 40$ cells) had no effect on sAPP α -induced Arc expression. Co-incubation with F) APV ($n = 40$ cells), or G) α BGT ($n = 30$ cells) significantly reduced Arc protein expression, while co-incubation with both H) APV and α BGT ($n = 30$ cells) fully eliminated this effect in the I) dendrites. Outliers were removed from each experiment prior to amalgamation using Grubb's tests, and normality was detected by D'Agostino and Pearson omnibus normality tests. All data are expressed as mean \pm SEM from ≥ 3 experiments. Significance was calculated using a Kruskal–Wallis one-way ANOVA with Dunn's multiple comparisons test on raw data. Hashes (#) indicate significance between control and sAPP α treated; asterisks (*) indicate significance between sAPP α - and antagonist-treated; * $p \leq 0.05$, #### $p = 0.0001$, **** $p \leq 0.0001$. Representative images show neuronal soma, dendrites (MAP2; \square), Arc protein (\square), nuclei (DAPI; \square) and magnified somatic (inset, bottom right) and dendritic compartments. Scale bars = 50 μ m (A-D); lower panels = 10 μ m.

4.2. *sAPP α Increases CREB Phosphorylation and Arc Protein in Acute Hippocampal Slices*

So far, this thesis has described sAPP α 's ability to enhance Arc protein expression *in vitro*, in a manner dependent on CaMKII, MAPK, PKG signalling and activation of NMDAR and α 7nAChRs. Previous work has shown that the enhancement of LTP and cell surface GluA1 by sAPP α is likewise dependent on these processes (Richter et al., 2018; Mockett et al., 2019). Additionally, Arc expression throughout hippocampal areas CA1 (Penke et al., 2011; Jakkamsetti et al., 2013; Gao et al., 2018), CA3 (Rosi et al., 2005; Chawla et al., 2018a; Chawla et al., 2018b; Hudgins and Otto, 2019), and dentate gyrus (Messaoudi et al., 2007; Ramirez-Amaya et al., 2013; Kuipers et al., 2016) have been shown to be important for many functional outcomes of memory. Thus, the question remains whether sAPP α promotes an equally significant increase in Arc protein expression in acute hippocampal slices, as observed in primary hippocampal neurons.

Here, we aimed to extend our analyses to examine Arc expression in acute hippocampal slices, as well as further validate the relationship between NMDAR and α 7nAChR activation following sAPP α treatment, by inhibition of these receptors and examination of phosphorylated Ca²⁺/cAMP-response element-binding protein (pCREB), a signalling event strongly associated with NDMAR activity (Xia et al., 1996; Sala et al., 2000; Valera et al., 2008; de Oliveira Coelho et al., 2013; Zhou et al., 2013). We hypothesised that in addition to enhancing Arc protein expression, sAPP α (1 nM, 15 min) would enhance the expression of pCREB in the cell body layer of area CA1 and the dentate gyrus of the hippocampus. Within area CA1 of acute hippocampal slices (Figure 4-7A), we found that sAPP α (1 nM, 15 min) significantly increased pCREB levels (2.08 ± 0.60 , $p = 0.01$; Figure 4-7B,C,G), supporting a role for NDMAR activity. Further, we found that sAPP α (1 nM, 120 min) significantly increased Arc expression (1.55 ± 0.22 , $p = 0.02$; Figure 4-7D,E,H) and that this effect was attenuated by co-incubation with NMDA and α 7nACh antagonists APV (50 μ M) and α BGT (10 nM; 1.08 ± 0.18 , $p = 0.042$; Figure 4-7F,H), validating the observations from primary hippocampal cultures.

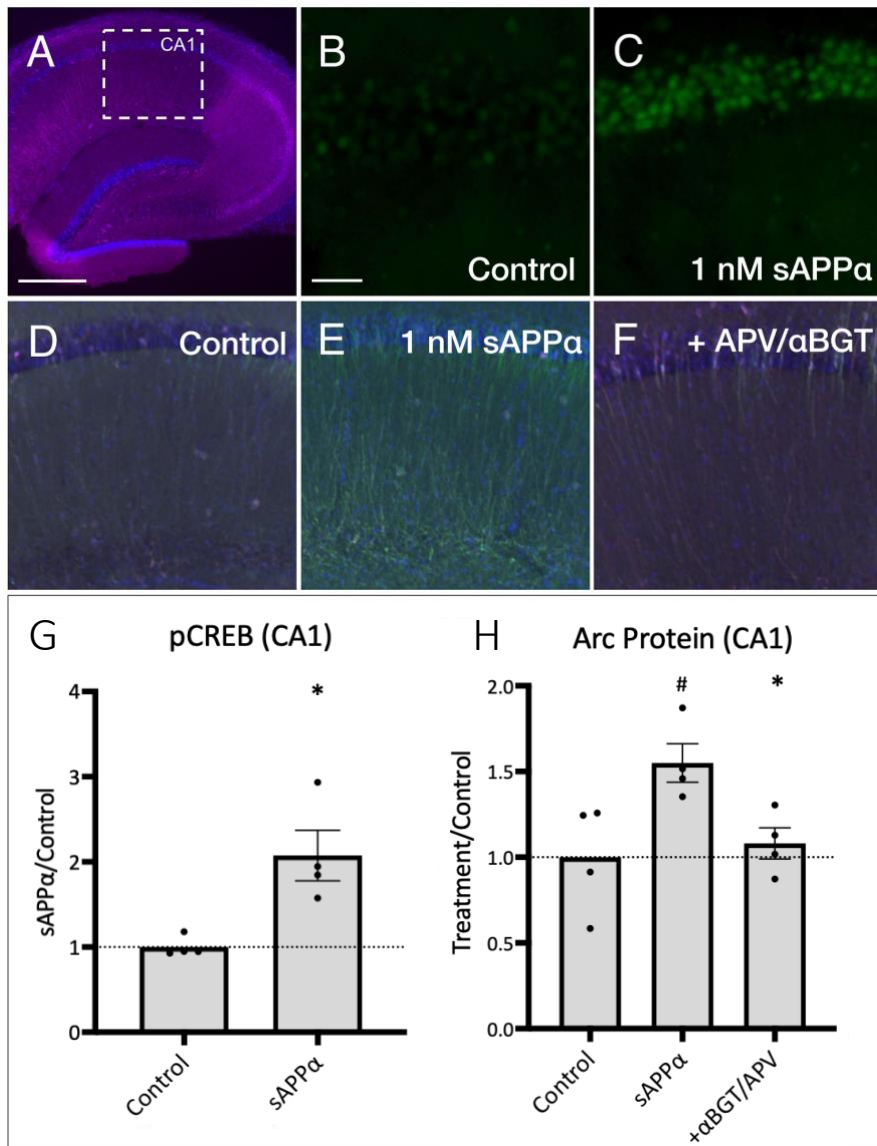


Figure 4-7 | sAPP α increases CREB phosphorylation and Arc protein in acute hippocampal slices. A) A representative transverse section of an acute hippocampal slice, with a sub-region of area CA1, used for quantitative analysis, outlined by a white dotted box (MAP2 (■); nuclei: DAPI (■)); imaged at 4x magnification; scale bar = (500 μ m). Relative to B) no drug controls ($n = 3$ rats, 4 slices), C) incubation of slices with sAPP α (1 nM, 15 min, $n = 2$ rats, 4 slices) increased pCREB (■; imaged at 20x magnification; scale bar = 100 μ m) in the PCL of CA1. Relative to D) no drug controls ($n = 3$ rats, 4 slices), E) incubation of slices with sAPP α (1 nM, 2 hr, $n = 3$ rats, 4 slices) significantly increased Arc protein expression (■; imaged at 4x magnification) in area CA1. Co-incubation of sAPP α with F) APV and α BGT ($n = 3$ rats, 4 slices) attenuated this effect. Normality was detected by Shapiro–Wilk normality tests. All data are expressed as mean \pm SEM. Significance of pCREB (G) and (H) Arc protein expression was calculated by G) student’s t-test, and H) one-way ANOVA with Šidák’s multiple comparisons test on raw data. Hashes (#) indicate significance between control and sAPP α -treated; asterisks (*) indicate significance between sAPP α - and antagonist-treated; # $p \leq 0.05$, * $p = 0.04$. PCL = pyramidal cell layer.

4.2.1. *Trend in CREB Phosphorylation and Arc Protein Expression in the Dentate Gyrus of Acute Hippocampal Slices*

Given the involvement of both pCREB and Arc protein expression in synaptic activity in the dentate gyrus (Schulz et al., 1999; Bramham et al., 2010), we further sought to expand our analysis to examine expression of pCREB and Arc in the hilus of the dentate gyrus of acute hippocampal slices. Converse to results observed in area CA1, we found a small but non-significant increase in pCREB in the hilus of the dentate gyrus (1.17 ± 0.058 , $p = 0.0858$; Figure 4-8A-C). Likewise, Arc protein in the DG showed a small increase in expression (sAPP α : 1.15 ± 0.18 , $p = 0.6953$; APV/ α BGT: 0.98 ± 0.13 , $p = 0.6610$; Figure 4-8H) but did not reach significance, reflecting a similar trend to pCREB expression.

Interestingly, while many publications have described the induction of Arc protein within the dentate gyrus following spatial exploration (Ramirez-Amaya et al., 2013), LTP (Messaoudi et al., 2007), and BDNF treatment (Kuipers et al., 2016), these results may be due to the sensitivity of our analysis. The relatively small sample size, as well as the large variation in control groups examining both pCREB (coefficient of variation (CV): control: 27.26%, sAPP α : 4.96%) and Arc (CV: control: 33.71%, sAPP α : 16.21%, APV/ α BGT: 13.28%) protein expression may have contributed to the observed lack of effect within these analyses. Alternatively, we have shown that this effect requires the activation of both α 7nAChR and NMDAR. While the presence of NMDAR in the dentate gyrus is unquestioned (Bernabeu and Sharp, 2000; Dalby and Mody, 2003; Wright and Jackson, 2014), evidence suggests an absence of α 7nAChR-containing excitatory granule cells in these neurons (Frazier et al., 2003). While synergistic activation of α 7nAChR and NMDAR is required for Arc expression (see section 4.1.6. *Dendritic Arc Protein Expression is Dependent on Activation of NMDA- and α 7nACh Receptors*), it may be expected that sAPP α would not induce the full complement of Arc protein expression in this paradigm. The small but non-significant increase in pCREB (Figure 4-8A-C) and Arc protein (Figure 4-8H) in the dentate gyrus may reflect the NMDAR component of this.

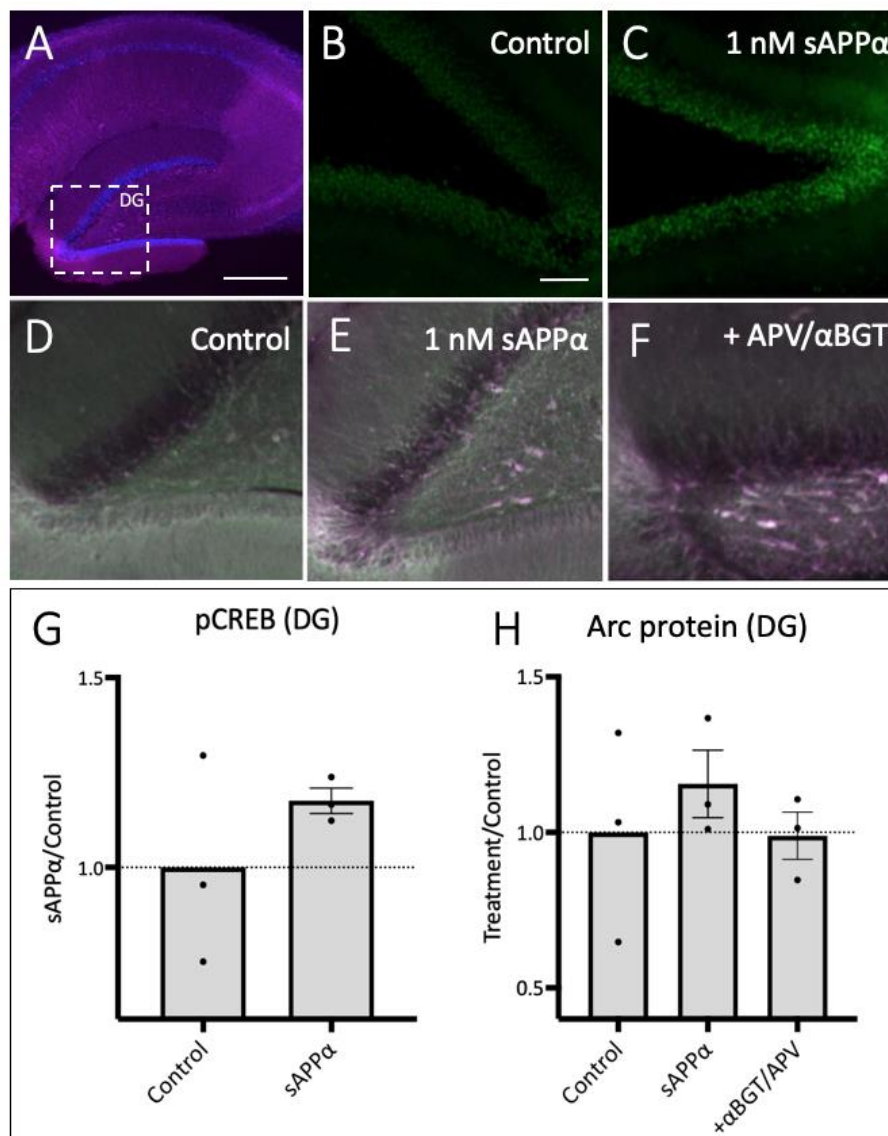


Figure 4-8 | sAPP α does not significantly increase pCREB or Arc protein in the hilus of the dentate gyrus in acute hippocampal slices. Representative transverse sections of A) acute hippocampal slices in the hilus of the dentate gyrus (MAP2 (■); nuclei: DAPI (■); imaged at 4x magnification). Relative to B) no drug controls ($n = 2$ rats, 3 slices), incubation of slices with C) sAPP α (1 nM, 15 min, $n = 2$ rats, 3 slices) did not significantly increase pCREB relative to controls, as assessed by student's t-test (■; imaged at 20x magnification). Relative to D) no drug controls ($n = 2$ rats, 3 slices), E) incubation of slices with sAPP α (1 nM, 120 min, $n = 2$ rats, 3 slices) did not significantly increase Arc protein expression (■; imaged at 20x magnification) in the DG. Similarly, co-incubation of sAPP α with F) APV and α BGT ($n = 2$ rats, 4 slices) did not affect Arc protein expression. All data are expressed relative to control, as mean \pm SEM. Normality was detected by Shapiro–Wilk normality tests, and significance was assessed by H) student's t-test and H) one-way ANOVA with Šidák's multiple comparisons test on raw data. Scale bars = 500 μ m (A), 100 μ m (B-D).

4.2.2. *Increases in Arc Protein is Specific to Area CA1 and Does Not Occur in Area CA3*

Following the observation that Arc protein expression increases in area CA1 in response to sAPP α -treatment, we further examined Arc protein expression in area CA3 of acute hippocampal slices. Here, we found no significant increase in Arc protein relative to control (sAPP α : 1.55 ± 0.22 , $p = 0.6343$; APV/ α BGT: 1.080 ± 0.18 , $p = 0.9630$; Figure 4-9).

While these data may reflect the relatively small sample size, these observations may also arise through differences in the anatomical and molecular structure of synapses terminating in area CA3, compared to those in CA1 and the DG. LTP at CA3 mossy fibre synapses occurs through primarily presynaptic means, independent of postsynaptic NMDAR activation (Harris and Cotman, 1986; Lysetskiy et al., 2005), postsynaptic Ca²⁺ influx (Zalutsky and Nicoll, 1990), and may not involve an AMPAR component (Bliss et al., 2003). Interestingly, α 7nAChR may play a unique role in enhancing synaptic activity at these synapses through their enhancement of presynaptic Ca²⁺ currents and neurotransmitter release (Gray et al., 1996; Radcliffe et al., 1999; Sharma and Vijayaraghavan, 2003; Sharma et al., 2008; Grybko et al., 2010). Regardless, it appears sAPP α may enhance Arc expression and synaptic plasticity independent from these mechanisms.

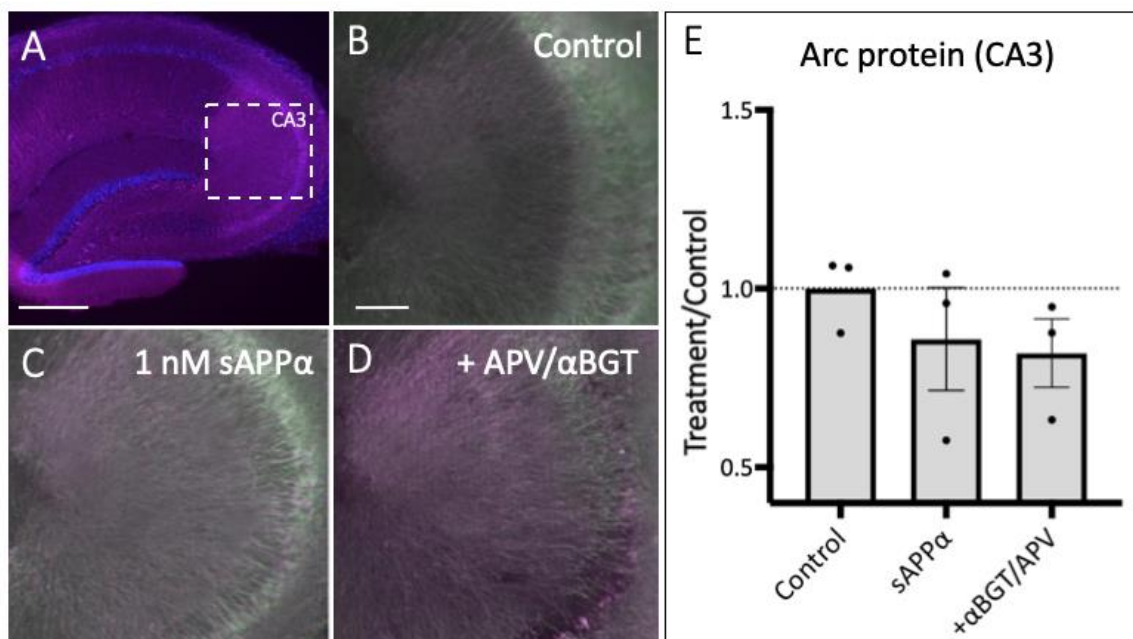


Figure 4-9 | sAPP α does not increase Arc protein in area CA3. A) Representative transverse sections of acute hippocampal slices in area CA3 (MAP2 (■); nuclei: DAPI (■); imaged at 4x magnification). In area CA3, relative to B) no drug controls ($n = 2$ rats, 3 slices), incubation of slices with C) sAPP α (1 nM, 120 min, $n = 2$ rats, 3 slices) did not significantly increase Arc protein relative to controls, similarly D) APV and α BGT significantly alter Arc protein expression. Normality was detected by Shapiro–Wilk normality tests. E) Data are expressed relative to control, as mean \pm SEM. Significance was assessed by one-way ANOVA with Šidák’s multiple comparisons test on raw data. Representative images show MAP2 (■), and Arc protein (■), imaged at 20x magnification. Scale bars = 500 μ m (A), 100 μ m (B-D).

4.3. Summary

The work described in this chapter aimed to characterise the expression of the IEG Arc in cultured hippocampal neurons, which was enhanced following incubation with sAPP α (1 nM, 120 min). This expression was paired with an increase in Arc and *Zif268* mRNA in a time dependent manner. In line with published research examining the role of sAPP α in protein synthesis and trafficking of GluA1, the expression of Arc protein in both somatic and dendritic neuronal compartments was found to be differentially regulated following inhibition of CaMKII, MAPK, and PKG. Further, we have defined a novel role for the synergistic activity of NMDA- and α 7nACh receptors, in mediating this effect. Replicating these experiments in area CA1 of acute hippocampal slices validated the dependency on NMDA- and α 7nACh receptors in the expression of Arc protein, and was found to be coupled to the expression of pCREB, indicating a necessary role of NMDAR activation as a downstream signalling event. Interestingly, both the increase in pCREB and Arc protein was found to be specific to area CA1, as no significant change was present in area CA3 nor the hilus of the dentate gyrus. Importantly, these experiments are limited due to the lack of inhibitor or antagonist-only controls as well as the use of only one inhibitor per kinase. Previous work has shown that inhibitors of CaMKII, PKG, MAPK and protein synthesis, as well as the NDMAR antagonist APV have little to no effect on glutamate receptor trafficking and phosphorylation (Mockett et al., 2019), while both NMDAR and α 7nACh receptors have been shown to provide little to spontaneous synaptic currents in culture (Hefft et al., 1999; Hmaied et al., 2002). However, these experiments cannot rule out any drug-only effects on baseline kinase or receptor activity nor draw conclusions on the specificity of the kinases targeted.

Regardless, these results support the hypothesis that sAPP α enhances both the synthesis and the dendritic expression of Arc protein. While this may indicate a role of Arc in mediating the expression of the sAPP α -mediated enhancement of LTP, further experiments are required to link the function of Arc to the regulation of plasticity following sAPP α treatment.

Chapter 5

5.1. *The Role of Calcium-Permeable AMPAR (CP-AMPA) in sAPP α -Mediated Enhancement of LTP*

Previous work has shown that sAPP α (1 nM, 30 min) enhances both the induction and persistence of LTP, and increases cell surface levels of GluA1-, but not GluA2-containing AMPAR, in a protein synthesis-dependent manner following mild TBS (Mockett et al., 2019). This specific increase of GluA1 on the cell surface suggests a role for GluA1-containing homomeric AMPAR in regulating sAPP α -enhanced LTP. This chapter aimed to examine the hypothesis that sAPP α (1 nM, 30 min) may enhance synaptic transmission by enhancing the expression of GluA1-containing AMPAR at the synapse.

Here, we sought to test this hypothesis by taking advantage of the susceptibility of GluA1 homomeric CP-AMPA to blockade by polyamine-containing inhibitors such as N,N,N-trimethyl-5-[[tricyclo[3.3.1.1^{3,7}]dec-1-ylmethyl]amino]-1-pentanaminium bromide hydrobromide (IEM-1460; Schlesinger et al., 2005). IEM-1460 contains a positively-charged polyamine tail and hydrophobic adamantane head, blocking the ion channel of GluA2-lacking AMPAR in a voltage-dependent manner (Twomey et al., 2018), with a relatively high affinity, reversibility (Samoilova et al., 1999) and specificity to GluA2-lacking Ca²⁺-permeable AMPAR (Samoilova et al., 1999). Experiments utilized an LTP-inducing stimulation protocol which enhances synaptic transmission, but is non-saturating (half-maximal train of standard TBS: 5 trains of 5 pulses at 100 Hz delivered at 200 ms intervals) as per Mockett et al, (2019).

5.1.1. CP-AMPA Contribute a Small Fraction of Basal Synaptic Transmission

Importantly, previous research has shown that only 8% of total AMPA receptor complexes exist as homomeric GluA1 in CA1/CA2 hippocampal pyramidal neurons, under basal conditions (Wenthold et al., 1996). Due to this, previous observations have shown that administration of CP-AMPA antagonists has little-to-no effect on basal CA1 synaptic transmission (Plant et al., 2006; Sutton et al., 2006; Adesnik and Nicoll, 2007; Park et al., 2016), indicating a lack of synaptic CP-AMPARs, or levels below the sensitivity of detection.

To first examine the role of CP-AMPA in basal synaptic transmission in our preparation, acute hippocampal slices (400 μm) were prepared from young adult male Sprague-Dawley rats (4-6 weeks), and transferred to a recording chamber (refer section 2.5.1. *Acute Hippocampal Slice Preparation*). Following the establishment of a stable baseline for 20 minutes (Figure 5-1A), IEM-1460 (100 μM , 50 min) was applied to slices and baseline responses were measured. Here we found that application of IEM-1460 (20 min) resulted in a modest, but significant reduction in baseline responses ($94.62 \pm 3.82\%$ of baseline, $p = 0.0002$, $n = 12$; Figure 5-1B). An additional 30 minutes of IEM-1460 further reduced baseline transmission (average decrease of 8.3%) relative to initial baseline values, however this did not reach significance ($91.70 \pm 6.71\%$ of baseline, $p = 0.0573$; Figure 5-1B). While previous publications have utilized IEM-1460 to investigate the role of CP-AMPA in various applications across a range of concentrations (30-200 μM), those utilizing IEM-1460 at similar concentrations to the current study did not report any significant effects on baseline transmission. This may result from many factors including animal species, *in vivo* versus *ex vivo*, differences in slice preparations, and importantly, the age of the animal used (Gray et al., 2007; Asrar et al., 2009; Sanderson et al., 2016; Suyama et al., 2017).

We further aimed to examine whether treatment of hippocampal slices with sAPP α would affect baseline responses. Here we found that sAPP α (1 nM, 30 min) did not significantly alter baseline responses from initial values ($99.73 \pm 5.35\%$, $p = 0.4070$). Importantly, these results indicate that sAPP α treatment alone does not involve the direct potentiation of synaptic transmission, indicating that translocation of AMPAR into the synapse may require additional stimulation.

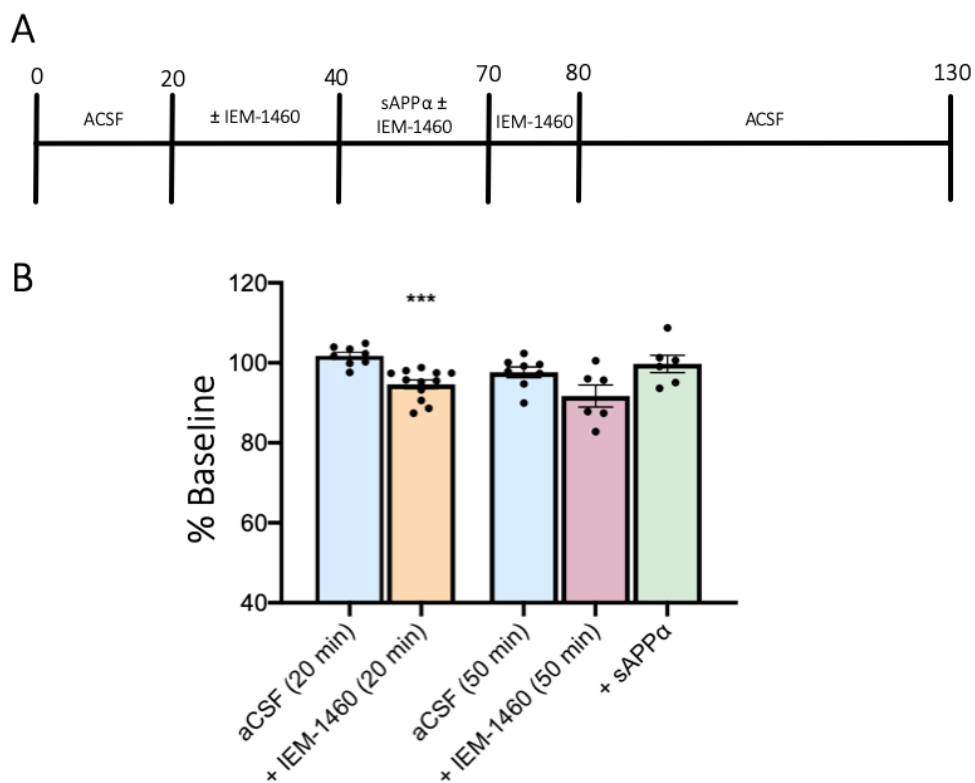


Figure 5-1 | Reduction in basal synaptic transmission following CP-AMPA blockade. A) Representative schematic of the experimental design, values represent time points (min) of key events during the recording period. B) Data showing averaged fEPSP measurements as percentage from initial baseline values following 20 minutes of IEM-1460 (●) and an equivalent 20 minutes of aCSF (20 min aCSF; ●), or an additional 30 minutes IEM-1460 (●), and 30 minutes of sAPPα treatment (●), and an equivalent 30 minutes of aCSF (50 min aCSF; ●) in control ($n = 8$ slices), IEM-1460 treated ($n = 12$ slices), sAPPα-treated ($n = 6$ slices) conditions from 6-8 animals. Data from multiple experiments following 20 min of IEM-1460 treatment were pooled. All data were measured as an average of the final 10 minutes of baseline stimulations at each interval, relative to percent of baseline in the presence of aCSF only. Normality was determined by Shapiro-Wilk normality test, and significance was calculated using an Student's t-test. Asterisks (*) indicate significance between antagonist-treated and control, *** $p \leq 0.001$.

5.1.2. *CP-AMPA Do Not Contribute to LTP Following a Mild Theta-Burst Stimulation Protocol*

In order to establish whether CP-AMPA are involved in the enhancement of LTP following sAPP α treatment and mild TBS, the contribution of CP-AMPA to LTP elicited by our mild TBS protocol alone needed to be established. As previously described (refer section 2.5.1. *Acute Hippocampal Slice Preparation*), hippocampal slices were prepared from young adult male Sprague-Dawley rats (4-6 weeks), maintained in an incubation chamber for 120 minutes, and transferred to a recording chamber. Following the establishment of a stable baseline for 20 minutes, acute hippocampal slices were treated with the CP-AMPA antagonist IEM-1460 (100 μ M; 50 min) to ensure extrasynaptic, perisynaptic and trafficked AMPAR were inhibited prior to TBS. Perfusion of IEM-1460 continued 10 minutes post-TBS after which the recording chamber was switched back to standard aCSF for the remainder of the recording. Here we have examined the enhancement of synaptic transmission as an average of the first (early LTP) and final (late LTP) 10 minutes following TBS.

As shown by Figure 5-2., application of IEM-1460 (100 μ M, 50 min) had no significant effect on the magnitude of either early (control: $52.10 \pm 17.53\%$ of baseline, $n = 8$; IEM-1460: $59.66 \pm 17.00\%$ of baseline, $n = 6$, $p = 0.9399$) or late (control: $32.79 \pm 17.39\%$ of baseline; IEM-1460: $28.44 \pm 10.31\%$ of baseline, $p = 0.9873$) potentiation following TBS, supporting past research (Adesnik and Nicoll, 2007; Gray et al., 2007; Asrar et al., 2009). Thus, we can conclude that CP-AMPA do not normally play a significant role in the potentiation of synaptic transmission following a mild TBS protocol, and therefore conclusions drawn following treatment of slices with sAPP α may be attributed to mechanisms employed by sAPP α .

5.1.3. *CP-AMPA Contribute to the Initial Enhancement of sAPP α -LTP*

Here, we aimed to first replicate previous observations that sAPP α (1 nM, 30 min) enhances both E- and L-LTP following TBS (Mockett et al., 2019), and further examine the role of CP-AMPA in mediating this effect. LTP was elicited in area CA1 of hippocampal slices in the presence or absence of sAPP α (1 nM) 30 minutes before application of TBS. To examine the role of CP-AMPA in sAPP α -mediated LTP, slices were pre-treated with IEM-1460 (100 μ M) for 20 minutes, in addition to co-treatment with sAPP α (1 nM) for 30 minutes, and 10 minutes post-TBS stimulation in the absence of sAPP α .

As shown in Figure 5-2, relative to control slices, pre-incubation with sAPP α (1 nM, 30 min) enhanced both early (control: $52.1 \pm 17.53\%$, $n = 8$; sAPP α : $126.2 \pm 33.20\%$ of baseline, $n = 6$, $p \leq 0.0001$; Figure 5-2C,D) and late (control: $32.79 \pm 17.39\%$; sAPP α : $90.33 \pm 15.91\%$ of baseline, $p = 0.0014$; Figure 5-2C,E) phase LTP, confirming previously observed enhancements described by Mockett et al., (2019). Co-application of IEM-1460 with sAPP α significantly inhibited this sAPP α -mediated early potentiation relative to sAPP α -treatment alone ($84.19 \pm 28.76\%$ of baseline, $n = 6$, $p = 0.0334$; Figure 5-2C,D). Wash-out of IEM-1460 resulted in the recovery of potentiation, returning potentiation to a level comparable to sAPP α -induced enhancement ($69.39 \pm 38.22\%$ of baseline, $p = 0.4784$; Figure 5-2C,E), which was significantly different from control slices ($p = 0.0438$). These results indicate that the initial potentiation of sAPP α -enhanced LTP is due to the rapid incorporation of functional CP-AMPA at the synapse. The return of potentiation following washout may indicate that these AMPAR persist at the synapse throughout the recording duration, however these experiments do not rule out the possibility of potentiation mediated by GluA2-containing AMPAR.

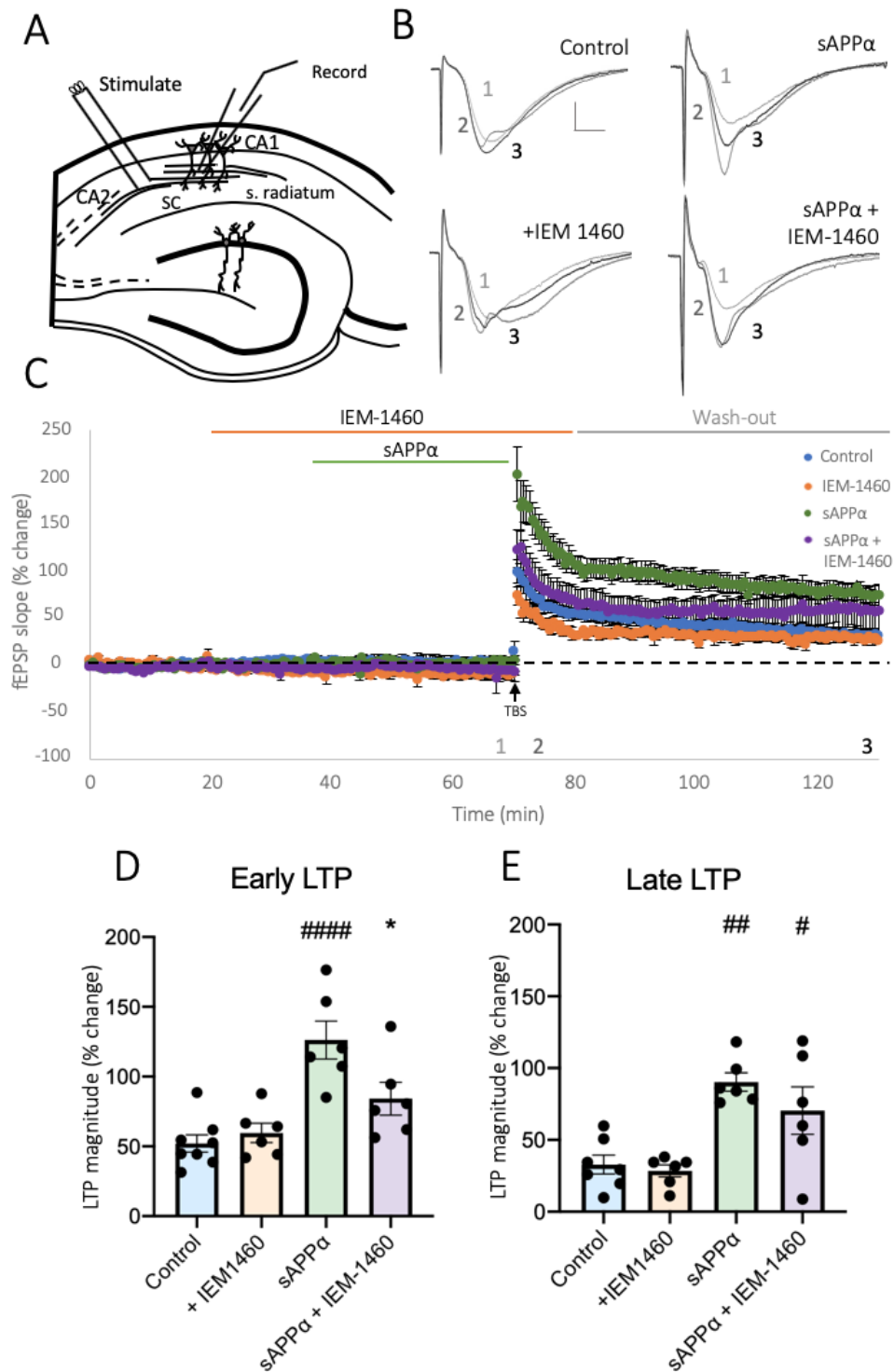


Figure 5-2 | Early phase sAPP α -enhanced LTP is dependent on activation of CP-AMPA. A) Representative schematic of transverse hippocampal slices showing positioning of stimulation and recording electrodes in area CA1. B) Representative field excitatory postsynaptic potential (fEPSP) traces taken at the end of baseline recording (1), upon TBS (2), and 60 min post-TBS (3). Scale bar = 1 mV, 5 s. C) Average traces of control slices, receiving only a mild TBS (5 bursts at 5 Hz, 5 pulses at 100 Hz/burst; ●, $n = 8$ slices), IEM-1460 (100 μ M; ●, $n = 6$ slices), sAPP α (1 nM, ●, $n = 6$ slices) and sAPP α + IEM-1460-treated (●, $n = 6$ slices) conditions. All conditions are normalised to the average of baseline 10 minutes before application of IEM-1460, and all data are presented as mean % change \pm SEM. Data shows summary histograms for D) early and E) late potentiation following TBS. Data are averaged from the first (D) and final (E) 10 minutes potentiation post-TBS for each experimental group relative to baseline, averaged 10 minutes before TBS. * $p = 0.0334$, # $p = 0.0438$, ### $p = 0.0014$, #### $p \leq 0.0001$. Normality was detected by Shapiro-Wilk normality test. Significance was assessed by one-way ANOVA with Tukey's multiple comparisons tests. Hashes (#) indicate significance between control and sAPP α -treated; asterisks (*) indicate significance between sAPP α - and antagonist-treated. SC = Schaffer collaterals, s. radiatum = Stratum radiatum.

5.2. Summary

The results described in this chapter aimed to examine the contribution of CP-AMPA to mild TBS-induced LTP, as well as LTP enhanced by sAPP α treatment (1 nM, 30 min). Additionally, we aimed to assess the effect of the CP-AMPA antagonist IEM-1460 on baseline responses, before the induction of LTP. Here, we found a small, but significant effect of IEM-1460 on baseline synaptic transmission in our acute hippocampal slices. Further, we have provided evidence for a dependency of CP-AMPA activity during the induction of sAPP α -primed LTP. Conversely, LTP induced by mild TBS alone was not dependent on the expression of these AMPARs. These results support the hypothesis that sAPP α primes LTP through the expression of CP-AMPA. Importantly, sAPP α treatment alone does not appear to enhance the synaptic expression of these AMPAR as baseline synaptic transmission remained unaltered. Thus, these results may indicate that sAPP α sequesters CP-AMPA at perisynaptic or extrasynaptic domains prior to the induction of LTP. Due to past observations that sAPP α (1 nM, 30 min) enhances trafficking of GluA1-containing AMPAR to the cell surface (Mockett et al., 2019), it is possible that the origin of these AMPAR may be from internal stores, but lateral diffusion from extrasynaptic sites cannot be ruled out. Regardless, these results describe a key role of CP-AMPA in the induction of sAPP α -mediated LTP.

Chapter 6

6.1. *sAPP α Regulates the Dynamic Control of AMPA Receptors at the Cell Surface*

Previous work from our laboratory, using acutely prepared hippocampal slices, has shown that sAPP α (1 nM, 30 min) increases cell surface expression of GluA1- but not GluA2- containing AMPAR in a manner dependent on protein synthesis (Mockett et al., 2019). Additionally, work from primary hippocampal cultures has provided evidence that sAPP α (1 nM, 120 min) enhances cell surface GluA1 in a protein synthesis-dependent manner (Elder, et al., 2017). Further, in Chapter 5 (refer section 5.1.3. *CP-AMPA Contribute to the Initial Enhancement of sAPP α -LTP*) we have provided evidence that these GluA1-containing AMPAR are Ca²⁺-permeable and facilitate the induction of LTP. This chapter aims to expand these observations with specific examination of somatic and dendritic cell surface AMPAR populations. In addition to this, we have extended the treatment window in order to observe the occurrence and persistence of cell surface AMPAR populations across time. In order to investigate both total and *de novo* populations of cell surface AMPAR, we employed the newly developed techniques FUNCAT-PLA and BioPLAy (Elder, 2017) with fluorescence microscopy.

6.1.1. *sAPP α Promotes the Rapid and Persistent Expression of Cell Surface GluA1 in the Soma and Dendrites of Primary Hippocampal Neurons*

We first aimed to examine total populations of cell surface GluA1-containing AMPAR using BioPLAy (refer section 2.3.5. *Detection of Cell Surface Proteins Using BioPLAy*). This technique allows for isolation of proteins present at the cell surface via biotinylation and subsequent PLA. Using BioPLAy, cell surface GluA1 was found to increase in the soma following 30-minute sAPP α treatment (4.41 ± 4.73 ; $p \leq 0.0001$) compared to control, followed by a small increase 2 hours later (1.65 ± 1.44 ; $p = 0.0199$; Figure 6-1A). Conversely, dendritic cell surface GluA1 was found to significantly increase within 30 minutes (2.60 ± 1.84 ; $p \leq 0.0001$), and increase to a greater extent following 2-hour sAPP α treatment (6.64 ± 8.99 ; $p \leq 0.0001$; Figure 6-1B). Together, these data suggest that sAPP α promotes rapid cell surface expression of GluA1 subunits at the soma and dendrites. These AMPAR, with time, may be trafficked to dendrites via surface diffusion. Alternatively, rapid somatic cell surface expression may be followed by internalisation, transport to dendrites and exocytosis at the dendritic cell surface. While these experiments do not address whether these subunits are newly made or derived from activation of internal pools, these observations extend the results from acute tissue, with an additional level of temporal and spatial resolution.

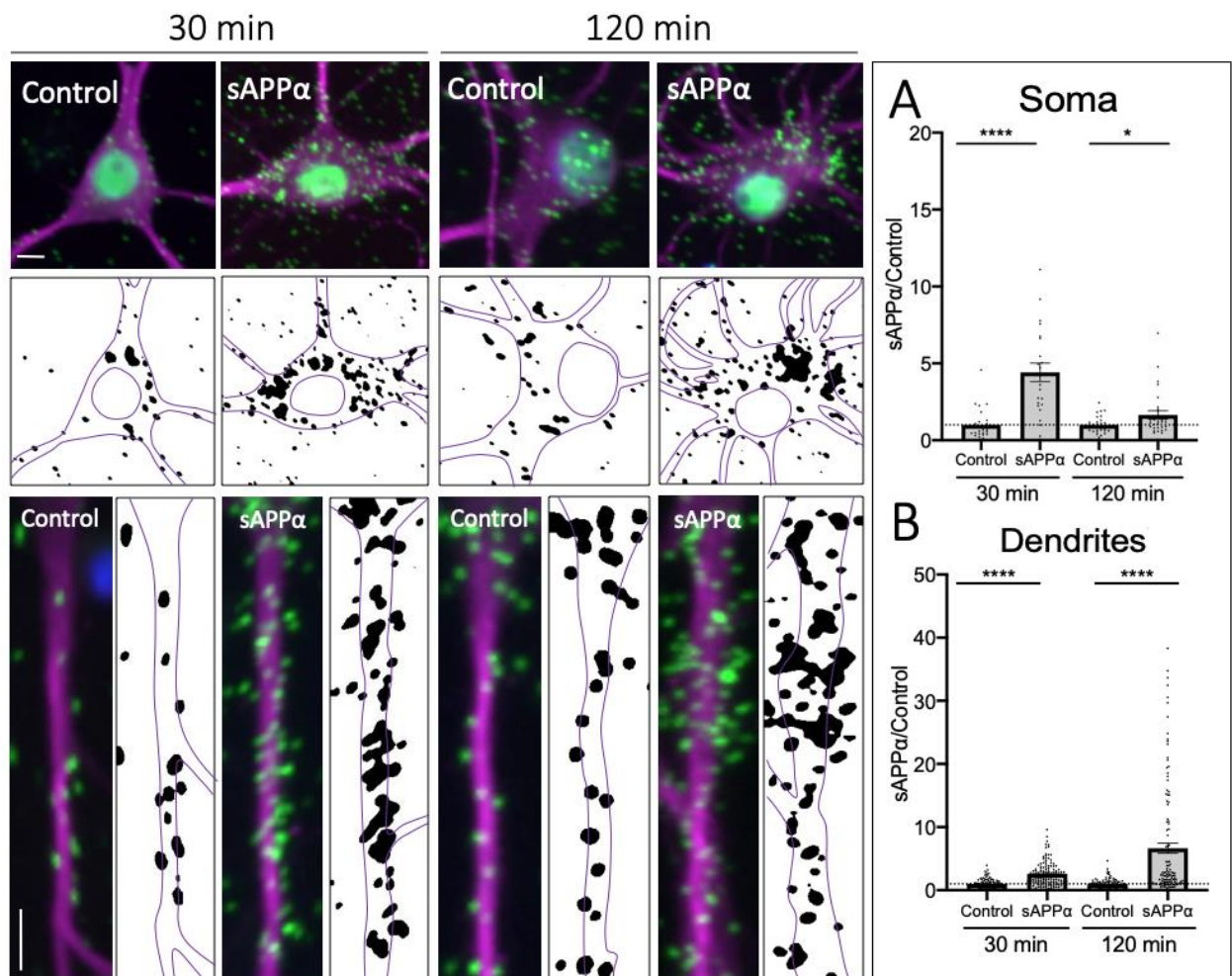


Figure 6-1 | sAPP α enhances cell surface expression of GluA1. Representative images showing cell surface GluA1 levels in the soma (top panels) and dendrites (lower panels) from 30 minute (left) and 120 minute (right) controls and sAPP α treated conditions. A) Average data showing 1 nM sAPP α (30, 120 min) promotes an increase in the soma ($n = 30$ cells), B) Average data showing 1 nM sAPP α (30, 120 min) promotes an increase in the dendrites ($n = 104-128$ dendrites). Outliers were removed from each experiment prior to amalgamation using Grubb's tests, and normality was detected by D'Agostino and Pearson omnibus normality tests. All data are expressed relative to control, as mean \pm SEM from 3 experiments. Significance was assessed by student's t-test, * $p = 0.0199$, **** $p \leq 0.0001$. Representative images show neuronal soma (upper panels) and dendrites (lower panels); MAP2; \square , GluA1; \blacksquare , DAPI; \blacksquare Scale bars = 10 μ m.

6.1.2. *sAPP α Promotes the Rapid and Transient Trafficking of de novo GluA1-Containing AMPAR to the Somatic and Dendritic Cell Surface*

Previous work in acute hippocampal slices has shown that the rapid increase in cell surface expression of GluA1, following sAPP α -treatment is dependent on protein synthesis (Mockett et al., 2019). This finding suggests the dependence on protein synthesis may arise from either the need to rapidly synthesize GluA1 subunits for subsequent trafficking to the cell surface, or the synthesis of chaperone or scaffolding proteins to aid the trafficking and anchoring of pre-existing, GluA1-containing AMPAR at the cell surface. Alternatively, the protein synthesis component of this may require aspects of both. Therefore, we hypothesised that sAPP α may enhance the rapid synthesis and cell surface expression of GluA1-containing AMPAR in primary hippocampal cultures. To address this, we utilized FUNCAT-PLA under detergent-free conditions.

We found that 30 minutes of sAPP α treatment (1 nM) significantly increased cell surface *de novo* GluA1 in the soma (2.018 ± 2.60 ; $p = 0.0039$; Figure 6-2A) and dendrites (3.97 ± 10.62 ; $p = 0.0009$; Figure 6-2B) of cultured hippocampal neurons. However, following 2 hours of sAPP α treatment, there was no detectable change in *de novo* somatic (0.83 ± 1.11 ; $p = 0.265$; Figure 6-2A) or dendritic (0.86 ± 3.51 ; $p = 0.673$; Figure 6-2B) GluA1. Indeed, GluA1 was significantly decreased relative to 30 minutes of sAPP α treatment in both the soma ($p = 0.0058$) and dendrites ($p = 0.0005$). These results suggest that sAPP α rapidly induces *de novo* synthesis of GluA1 subunits, which are trafficked to the cell surface by 30 minutes, but are later internalized within 2 hours of treatment.

Of note, is the large standard deviation especially apparent within the dendrites. As a vast majority of the data points for both control and sAPP α -treated groups were zero, the data were not normally distributed (as assessed by D'Agostino & Pearson normality test). However, as all groups expressed a median value of zero, a non-parametric test was deemed an inaccurate representation of the data. Thus, the use of parametric student's t-test is considered appropriate when the sample size is large (Girard et al., 2007; Dieterich et al., 2010; Boos and Stefanski, 2013; Zhang et al., 2015; tom Dieck, et al., 2015). Additionally, calculated variance of our data appears extremely high, however the similar means of experimental groups supports the similar spread of data generated following statistical analysis (CV: control (30 min): 401.3%, sAPP α (30 min): 267.2%, control (120 min): 302.6%, sAPP α (120 min): 406.8%). The variance in our data may be explained by the heterogeneous nature of neuronal cell types present in the primary cell cultures. While we focused on MAP2-positive neurons, this level of analysis does not distinguish between excitatory or inhibitory neurons or indeed pyramidal cells vs. granule cells. Thus, our data may reflect the intrinsic cell-to-cell variability in factors including gene expression, synapse number, receptor abundance, and excitability (Nusser et al., 1998; McAllister et al., 2000; Cullen et al., 2010; Biffi et al., 2013; Pelkmans et al. 2013; Zoli et al., 2018; Osorio et al., 2019).

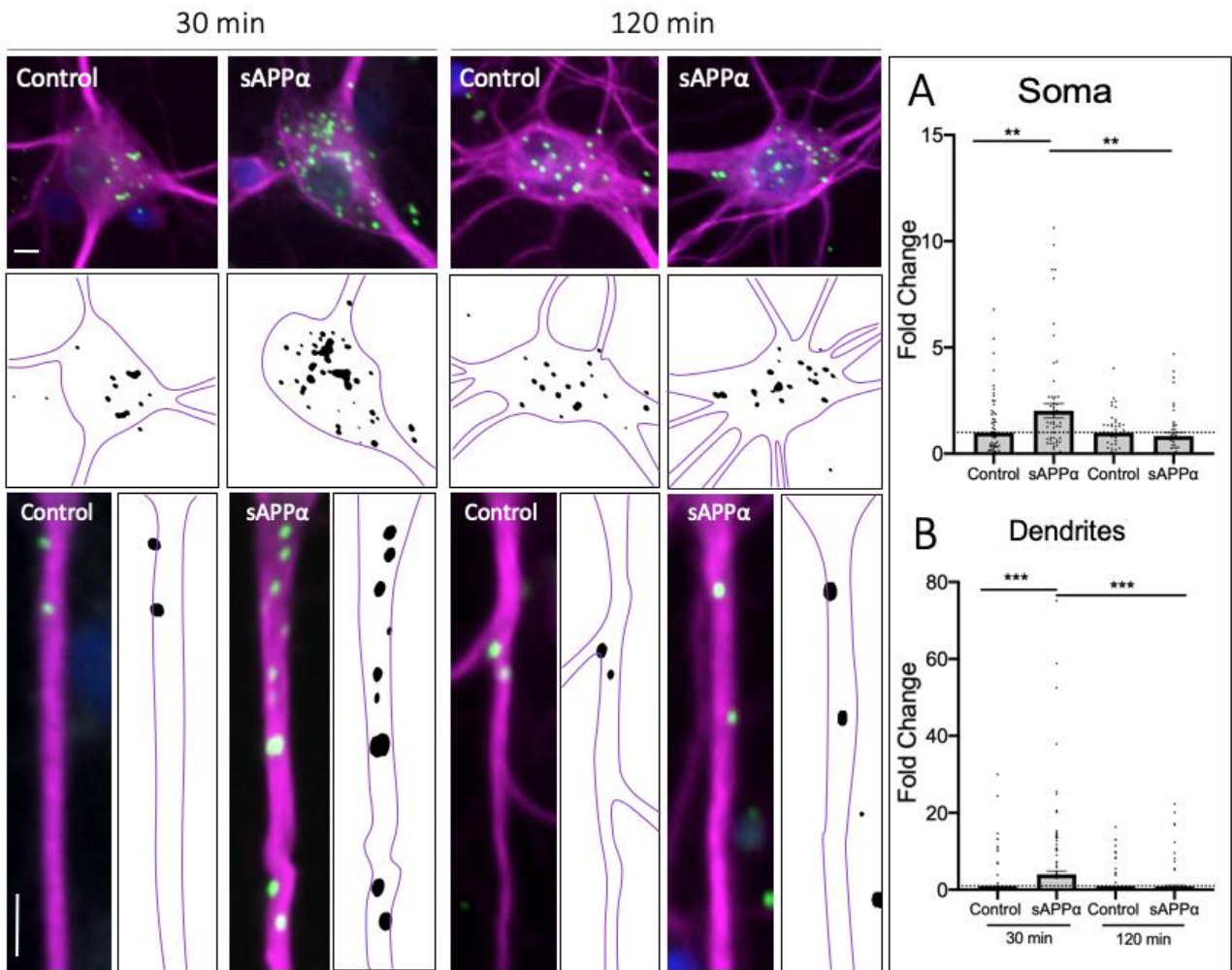


Figure 6-2 | Rapid increase in cell surface *de novo* GluA1 following treatment. Representative images showing cell surface *de novo* GluA1 levels in the soma (top panels) and dendrites (lower panels) from 30 minute (left) and 120 minute (right) control and sAPPα-treated conditions. A) Average data showing 1 nM sAPPα promotes an increase in the soma ($n = 50-71$ cells) following 30- but not 120-min. B) Average data showing 1 nM sAPPα (30 min) promotes an increase in *de novo* GluA1 at the dendritic cell surface follow 30- but not 120- minute treatments ($n = 104-128$ dendrites). Outliers were removed from each experiment prior to amalgamation using Grubb's tests, and normality was detected by D'Agostino and Pearson omnibus normality tests. All data are expressed relative to control, as mean \pm SEM from 3 experiments. Significance was assessed by student's t-test. $**p \leq 0.01$, $***p \leq 0.001$. Representative images show neuronal soma (upper panels) and dendrites (lower panels; MAP2; $\color{magenta}\blacksquare$, GluA1; $\color{green}\blacksquare$, DAPI; $\color{blue}\blacksquare$) Scale bars = 10 μm .

6.1.2.1. *sAPP α Enhances the Extrasynaptic, but not the Synaptic Population of de novo Cell Surface GluA1*

Following the observations that sAPP α (1 nM, 30 min) significantly increases *de novo* cell surface GluA1, we further sought to determine the synaptic localization of these AMPAR. Here, we have used the presynaptic marker synapsin-1 to determine the proportion of synaptic, extrasynaptic, and non-synaptic *de novo* GluA1-containing AMPAR identified by FUNCAT-PLA at the cell surface (Figure 6-3A, B).

Synaptic overlap of GluA1 puncta was determined using Mander's overlap coefficient (MOC, Figure 6-3C). Here, we found no significant difference between control and sAPP α -treated (1 nM, 30 min) conditions (control: 0.35 ± 0.29 , sAPP α : 0.31 ± 0.23 ; $p = 0.7038$; Figure 6-3C), indicating that sAPP α treatment does not increase the proportion of synaptic GluA1, reflecting the observed lack of effect of sAPP α on basal synaptic transmission in acute hippocampal slices (refer section 5.1.1. *CP-AMPA Contribute a Small Fraction of Basal Synaptic Transmission*). Due to this, we next sought to determine the proportion of synaptic, extrasynaptic and non-synaptic cell surface *de novo* GluA1 puncta relative to the proximity of synapsin-1-positive synapses. Here, we have defined synaptic, extrasynaptic, and non-synaptic PLA as 0-2, 2-4, and $> 4 \mu\text{m}$ from the closest synapsin-1 centre of mass, respectively (refer section 2.6.3. *Image analysis* and Appendix 1.4. *Quantifying Colocalization of PLA Signal Within Synapses*). Here, we observed a shift in the frequency of *de novo* GluA1 present at synapses following sAPP α treatment, increasing the proportion of GluA1 puncta 2-4 μm proximal to the synapse (Figure 6-3D). Expanding on this, we found a significant increase in the number of *de novo* GluA1 at extrasynaptic sites (control: 1.22 ± 0.089 ; sAPP α : 1.92 ± 0.14 ; $p = 0.0003$), however no change was detected at synaptic (control: 1.28 ± 0.10 , sAPP α : 1.34 ± 0.12 ; $p = 0.9872$), or non-synaptic (control: 1.52 ± 0.094 , sAPP α : 1.44 ± 0.10 ; $p = 0.9655$) sites (Figure 6-3E). These results suggest that sAPP α rapidly enhances the extrasynaptic pool of *de novo* GluA1-containing AMPAR within the dendrites.

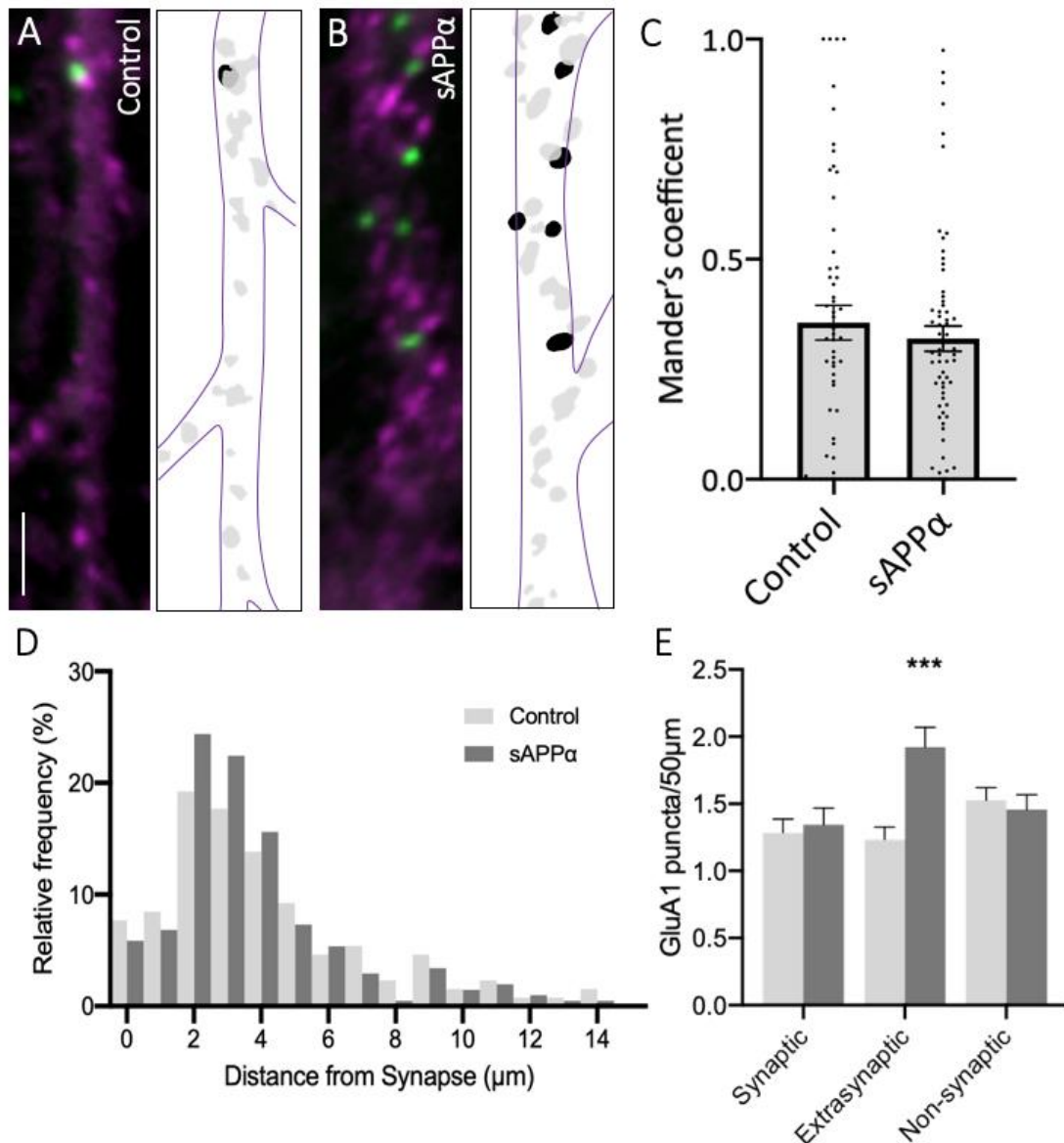


Figure 6-3 | sAPP α enhances *de novo* GluA1 at the extrasynaptic membrane. Representative images showing *de novo* cell surface GluA1 in A) control and B) sAPP α -treated conditions. Representative images show dendrites (50 μ m; synapsin-1; \square , GluA1; \square). Scale bar = 10 μ m. C) No significant difference was observed in the Mander's overlap coefficient following sAPP α -treatment (1 nM, 30 min; $n = 20$ cells, 58-65 dendrites). Significance was assessed by Mann-Whitney two-tailed u -test. D) Frequency histogram of the distribution of *de novo* GluA1 puncta in relevance to synapsin-1 immunofluorescence. Distances were calculated for individual PLA puncta with respect to the closest synapsin-1 centre of mass. Synaptic PLA showed overlapping centres within 0-2 μ m, puncta within 2-4 μ m were considered extrasynaptic, and puncta beyond 4 μ m were considered non-synaptic ($n = 58-65$ dendrites, 130-205 puncta). E) Quantification of GluA1 puncta abundance at the synaptic, extrasynaptic, and non-synaptic membrane ($n = 58-65$ dendrites, 130-205 puncta). Normality was determined by Shapiro-Wilk normality test. Significance was assessed by two-way ANOVA and Šidák's multiple comparisons, *** $p \leq 0.0005$.

6.1.3. *Rapid Decrease in Dendritic de novo Cell Surface GluA2 Following sAPP α Treatment*

So far, we have shown that sAPP α (1 nM, 30 min) enhances the cell surface population of *de novo* GluA1. Previously we have shown that expression of total *de novo* GluA2 decreases within the dendrites of neurons following sAPP α treatment, in primary hippocampal neurons (1 nM, 120 min; Elder, 2019), while cell surface GluA2 is unaffected by treatment in acute hippocampal slices (30 min; Mockett et al., 2019). Together, these observations indicate that sAPP α may enhance the cell surface expression of *de novo* GluA1 homomeric receptors, in a manner which may restrict the synthesis or trafficking of GluA2. To further these findings, we sought to examine the expression of *de novo* GluA2 on the cell surface across time, in both somatic and dendritic compartments. Here, we provide evidence that *de novo* cell surface GluA2 remains unaffected by sAPP α -treatment at the soma, following both 30-minute (0.86 ± 1.08 , $p = 0.654$) and 120-minute (1.32 ± 1.22 , $p = 0.148$; Figure 6-4A) treatments. Interestingly, 30-minute treatments showed an early decrease of *de novo* cell surface GluA2 at the dendritic cell surface (0.54 ± 1.45 , $p = 0.009$), returning to control levels within 120 minutes (1.92 ± 9.13 , $p = 0.395$; Figure 6-4B). From this, we can infer that sAPP α may inhibit or otherwise restrict the early expression of *de novo* GluA2 from the cell surface while specifically upregulating the expression of *de novo* GluA1. Previous research has shown that the restriction of GluA2 trafficking by auxiliary proteins such as PICK1 permits the expression of GluA1-containing CP-AMPA (Hanley et al., 2002; Hanley, 2007; Makuch et al., 2011). Further, we have previously shown that sAPP α (1 nM, 15 min) promotes the expression of the microRNA (miRNA) mir-30 (Ryan et al., 2013), which has been linked to the downregulation of GluA2 in the hippocampus (Song et al., 2019). Together, these results indicate that sAPP α may act to upregulate extrasynaptic *de novo* GluA1-containing homomeric AMPAR in a manner which does not require the association with *de novo* GluA2, further supporting our hypothesis that sAPP α enhances the expression of homomeric GluA1-containing CP-AMPA.

Similar to data described in section 6.1.2. *sAPP α Promotes the Rapid and Transient Trafficking of de novo GluA1-Containing AMPAR to the Somatic and Dendritic Cell Surface*, a vast majority of the data points within the dendrites for both control and sAPP α -treated groups were zero. Due to the large sample size, a parametric student's t-test is considered appropriate (Girard et al., 2007; Boos and Stefanski, 2013; Zhang et al., 2015; tom Dieck, et al., 2015). Calculated variance of our data showed a similar variance across treatment groups (control (30 min): 100.8%, sAPP α (30 min): 178.3%, control (2 hr): 108.0%, sAPP α (2 hr): 92.1%), indicating that while the data were not normally distributed, data were similarly variable across treatment conditions.

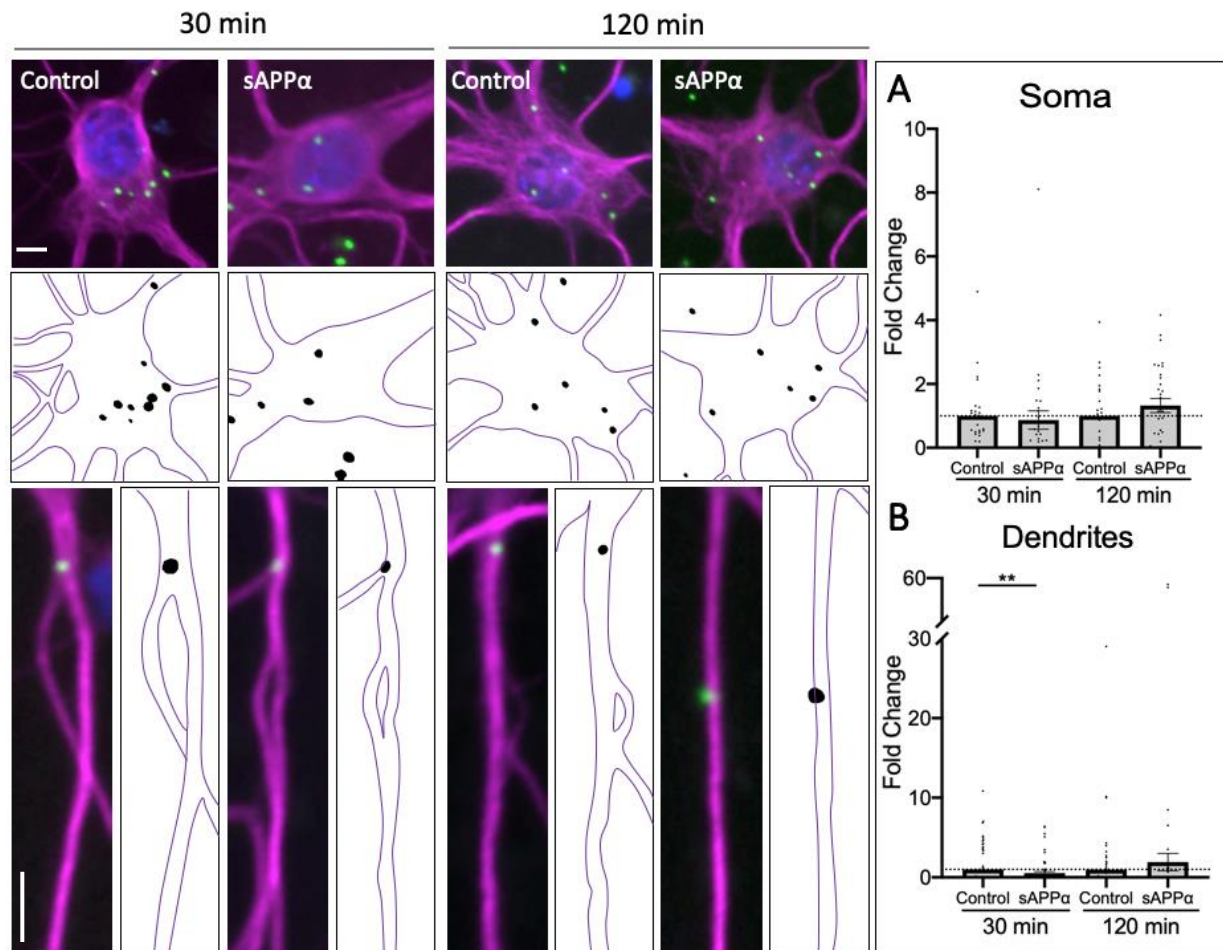


Figure 6-4 | Rapid decrease in *de novo* cell surface GluA2 following treatment. Representative images showing cell surface *de novo* GluA2 levels in the soma (top panels) and dendrites (lower panels) from 30 minute (left) and 120 minute (right) controls and sAPP α treated conditions. A) Average data showing 1 nM sAPP α does not affect somatic ($n = 25-31$ cells) *de novo* GluA2. B) Average data showing 1 nM sAPP α (30 min) significantly decreases dendritic *de novo* GluA2 ($n = 71-76$ dendrites). All data are expressed relative to control, as mean \pm SEM from 3 experiments. Outliers were removed from each experiment prior to amalgamation using Grubb's tests, and normality was detected by D'Agostino and Pearson omnibus normality tests. Significance was assessed by student's t-test, $**p \leq 0.01$. Representative images show neuronal soma (upper panels) and dendrites (lower panels; MAP2; \square , GluA1; \square , DAPI; \square) Scale bars = 10 μ m.

6.1.4. *Accell™ Arc siRNA Inhibits Somatic and Dendritic sAPP α -Dependent, but not Basal, Arc Expression*

As described above, we have shown that *de novo* GluA1 increases rapidly at the cell surface within 30 minutes of sAPP α treatment, however returning to baseline levels within 2 hours. These results infer a mechanism through which sAPP α promotes the delayed removal of *de novo* GluA1-containing AMPAR previously delivered to the cell surface. Further, we have previously shown that sAPP α (1 nM, 120 min) enhances Arc protein expression in primary hippocampal neurons (refer section 4.1.2. *sAPP α Facilitates an Increase in Arc Protein Expression*; Livingstone et al., 2019). Due to Arc's close relationship to the internalization of GluA1-containing AMPAR (Shepherd et al., 2006), we hypothesised that Arc may be responsible for the removal of *de novo* GluA1 from the cell surface at a later time-point. In order to examine the expression of *de novo* GluA1 following treatment with the Accell™ Arc antisense siRNA, we first aimed to assess Arc protein expression using immunocytochemistry following treatment of cultures with the Arc siRNA during both basal and sAPP α -stimulated conditions (refer section 2.3.10. *Treatment of Cultures With siRNA* and Appendix 3. *Accell™ siRNA Specificity*). Additionally, we have used the control non-targeting (NT) siRNA with no homology to any known rat gene to assess specificity of the Arc siRNA. In order to ensure effective uptake of siRNA and inhibition of ongoing synthesis, cultures received pre-treatment of siRNA in addition to co-treatment alongside sAPP α .

Following pre-treatment with siRNA (1 μ M, 60 min), primary hippocampal cultures were co-treated with either Arc or NT siRNA (1 μ M, 120 min), in the presence or absence of sAPP α (1 nM). Treatment of Arc or NT siRNA alone had no significant effect on Arc protein expression in either the soma (Arc siRNA: 0.78 ± 0.53 , $p \geq 0.99$; NT siRNA: 1.11 ± 0.48 , $p = 0.0509$; Figure 6-5A) nor dendrites (Arc siRNA: 1.26 ± 0.67 , $p = 0.8774$; NT siRNA: 1.28 ± 0.47 , $p = 0.7561$; Figure 6-5B) relative to control. As shown in 1.3 *sAPP α facilitates an increase in Arc protein expression*, sAPP α treatment (1 nM, 120 min) enhanced both somatic (2.05 ± 1.43 , $p = 0.0306$; Figure 6-5A) and dendritic (2.33 ± 1.39 , $p = 0.0010$; Figure 6-5B) Arc protein expression. This effect was consistent following co-treatment with sAPP α and the NT siRNA (soma: 1.59 ± 1.003 , $p = 0.0198$; dendrites: 1.98 ± 0.81 , $p = 0.0022$), and no significant difference was detected between sAPP α -treated and sAPP α + NT siRNA in either the soma (sAPP α : 2.05 ± 1.43 , sAPP α + NT siRNA: 1.59 ± 1.003 , $p \geq 0.9999$ or dendrites (sAPP α : 2.33 ± 1.39 , sAPP α + NT siRNA: 1.98 ± 0.81 , $p \geq 0.9999$). However, co-treatment of sAPP α with the Arc siRNA significantly reduced Arc protein expression in both the soma (0.72 ± 0.27 , $p = 0.0100$) and dendrites (1.16 ± 0.68 , $p = 0.0066$) relative to sAPP α -treatment alone, and was not significantly different from control in either compartment ($p \geq 0.99$). Together, these results indicate that the Accell™ siRNA system effectively inhibits *de novo* Arc synthesis in our primary hippocampal cultures.

It is interesting to note that application of the Arc siRNA did not affect basal Arc protein levels. Arc transcription and translation is low under basal conditions (Korb et al. 2011), and therefore small changes from baseline may not be detected by our analyses.

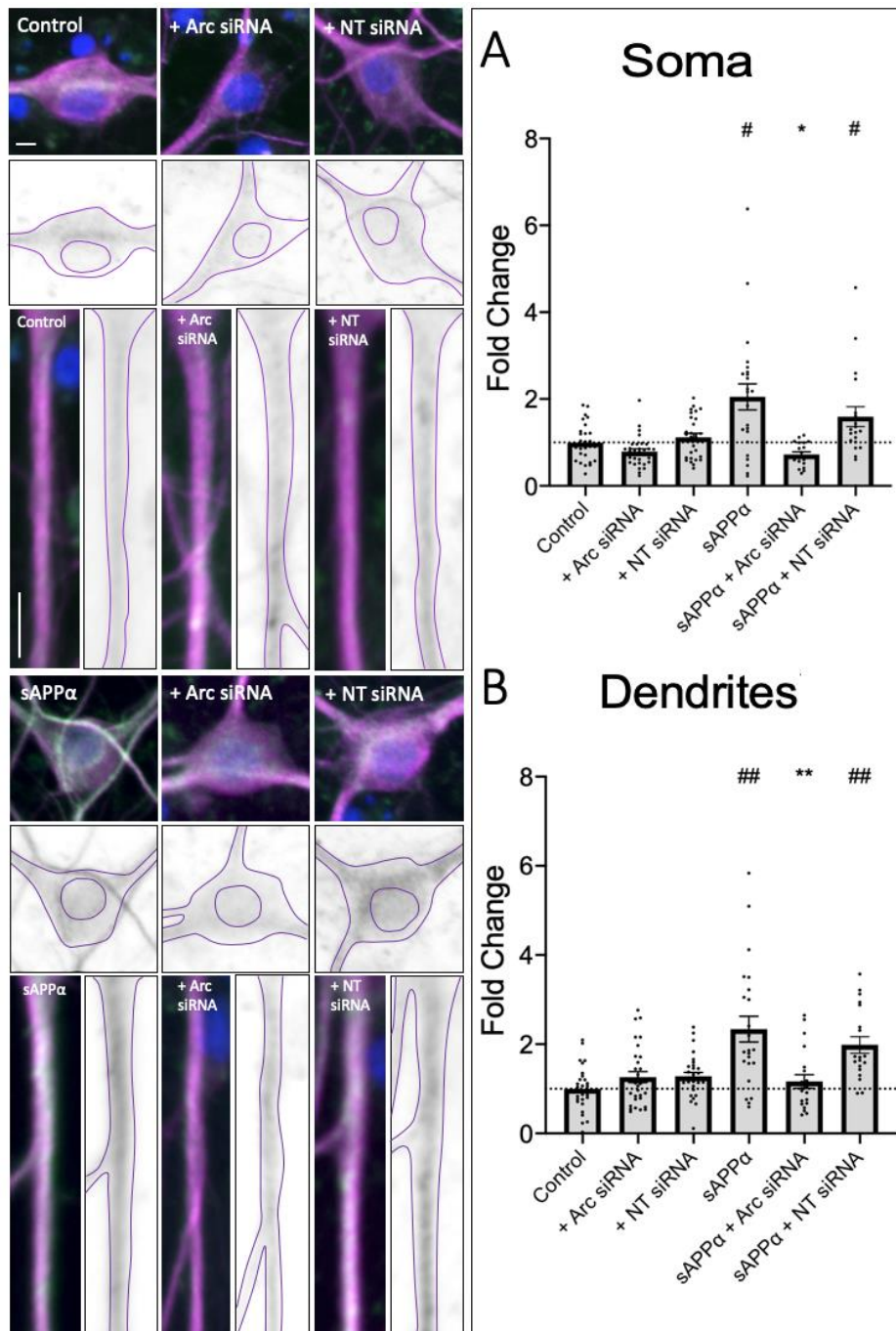


Figure 6-5| sAPP α -promoted Arc expression is affected by Accell™ Arc siRNA. Representative images show Arc protein levels the soma (upper panels) and dendrites (lower panels) in control and sAPP α -treated primary hippocampal neurons \pm co-treatment with Arc siRNA or non-targeted (NT) control siRNA. In both the A) soma and B) dendrites ($n = 19-30$ cells), sAPP α treatment significantly enhanced Arc expression in sAPP α -only and sAPP α + NT siRNA conditions. This effect was inhibited by co-treatment with the Arc siRNA. Outliers were removed from each experiment prior to amalgamation using Grubb's tests, and normality was detected by D'Agostino and Pearson omnibus normality tests. Significance was calculated using a Kruskal–Wallis one-way ANOVA with Dunn's multiple comparisons test on raw data, and expressed as fold change relative to the experimental control from 3 experiments. Hashes (#) denote significant difference from control, asterisks (*) denote significant difference from sAPP α -treated. #/* $p \leq 0.05$ **/## $p \leq 0.005$. Representative images show neuronal soma, dendrites (MAP2; \square), Arc protein (\blacksquare), nuclei (DAPI; \blacksquare). Scale bars = 10 μ m.

6.1.5. Internalization of *de novo* GluA1 is Dependent on Arc Expression

Following the confirmation that treatment of hippocampal cultures with *Accell*[™] siRNA inhibits sAPP α -stimulated Arc protein expression, we have employed siRNA knockdown of *de novo* Arc protein to assess whether inhibition of Arc protein synthesis results in the persistence of *de novo* cell surface GluA1 expression, as labelled by FUNCAT-PLA, in hippocampal neurons grown in primary hippocampal cultures.

Firstly, as expected, sAPP α treatment for 2 hours resulted in no change in either somatic (0.73 ± 0.88 , $p = 0.118$) nor dendritic (0.85 ± 1.56 , $p = 0.374$) expression of *de novo* cell surface GluA1, relative to control conditions (see section 6.1.2. *sAPP α Promotes the Rapid and Transient Trafficking of de novo GluA1-Containing AMPAR to the Somatic and Dendritic Cell Surface*). However, in the presence of Arc siRNA (preincubation: 1 μ M, 60 min, followed by co-incubation with sAPP α : 1 nM, 120 min), we observed a significant increase in the expression of *de novo* GluA1 at both the somatic (1.55 ± 2.010 , $p = 0.0043$; Figure 6-6A) and dendritic (4.14 ± 6.67 , $p \leq 0.0001$; Figure 6-6B) cell surface, relative to sAPP α -only conditions. These results suggest that following the rapid expression of *de novo* GluA1 at the cell surface, *de novo* GluA1-containing AMPAR are endocytosed as a result of Arc synthesis.

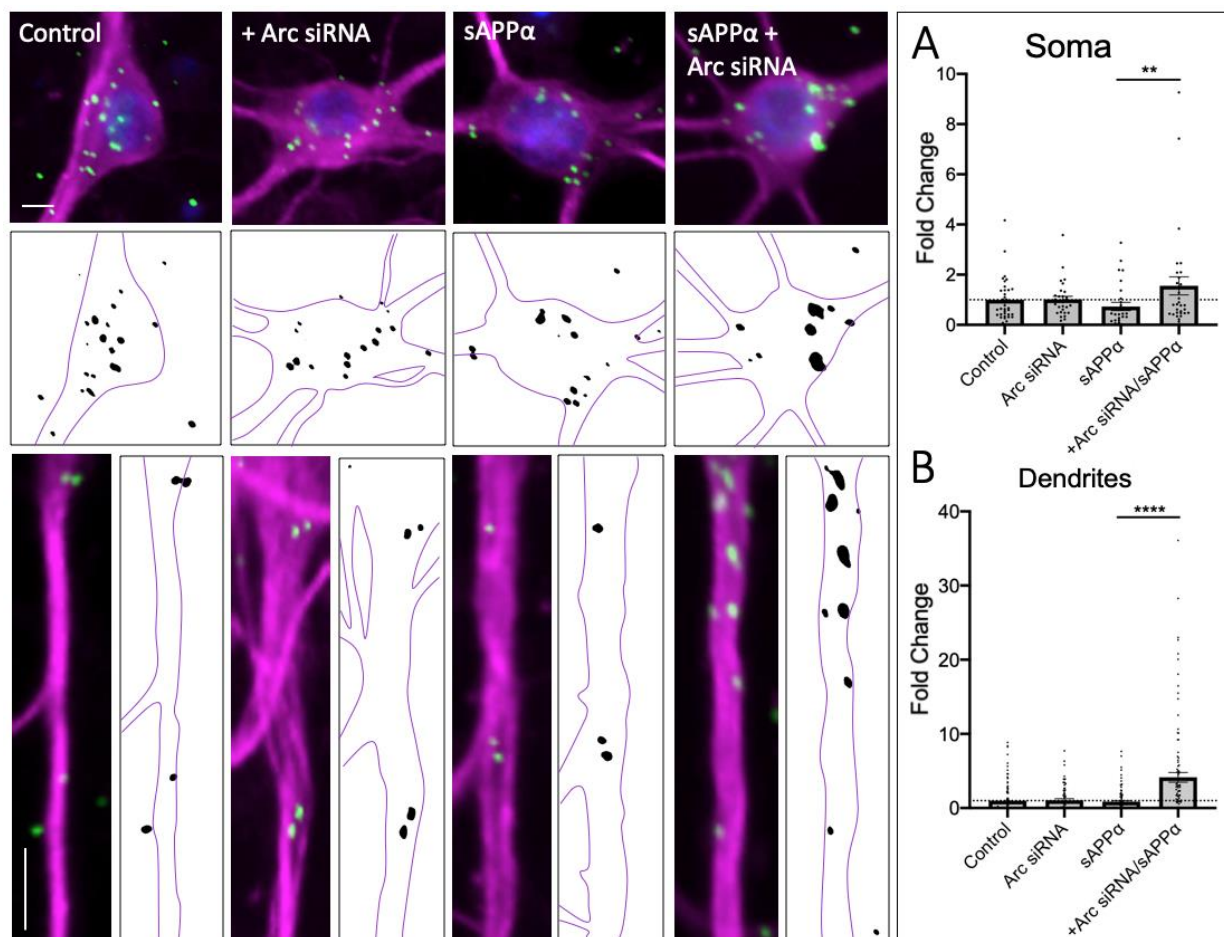


Figure 6-6 | sAPP α -induced *de novo* GluA1 persist at the cell surface following siRNA-mediated knockdown of Arc protein. Representative images of somatic (upper panels) and dendritic (lower panels) of control and sAPP α -treated conditions \pm treatment with the Arc siRNA. A) Average data showing treatment with sAPP α (1 nM, 120 min) and Arc siRNA (1 μ M, pre-treatment: 60 min, co-treatment 120 min) promotes an increase in somatic ($n = 28$ -35 cells) and dendritic ($n = 79$ -132 dendrites) *de novo* cell surface GluA1. Outliers were removed from each experiment prior to amalgamation using Grubb's tests, and normality was detected by D'Agostino and Pearson omnibus normality tests. All data are expressed relative to control. Data assessing the effect of siRNA are expressed as mean ratio of sAPP α + Arc siRNA/Arc siRNA alone \pm SEM from 3 experiments. Significance between control and treatment was assessed by student's t-test, significance between sAPP α -treated and siRNA-treated was assessed by Mann-Whitney two-tailed u-test, ** $p \leq 0.001$, **** $p \leq 0.0001$. Representative images show neuronal soma (upper panels) and dendrites (lower panels; MAP2; \blacksquare , GluA1; \blacksquare , DAPI; \blacksquare). Scale bars = 10 μ m.

6.1.6. *Non-Targeting siRNA has no Significant Effect on de novo Cell Surface GluA1*

In order to assess the specificity of the effects observed following treatment of cultures with Arc siRNA, cultures were similarly treated with the non-targeting (NT) siRNA and processed for FUNCAT-PLA (preincubation: 1 μ M, 120 min, followed by coincubation with or without sAPP α : 1 nM, 120 min), in order to examine non-specific effects due to the addition of small nucleotides.

Treatment of cultures with the NT siRNA alone had no observable effect on the levels of *de novo* cell surface GluA1 at the soma (0.94 ± 0.72 , $p = 0.7247$; Figure 6-7A), or dendrites (1.083 ± 2.069 , $p = 0.7050$; Figure 6-7B). While past experiments have shown a small, non-significant reduction in *de novo* GluA1 at the somatic cell surface following sAPP α treatments (1 nM, 120 min; see section 6.1.2. *sAPP α Promotes the Rapid and Transient Trafficking of de novo GluA1-Containing AMPAR to the Somatic and Dendritic Cell Surface*), here, co-incubation of sAPP α with the NT siRNA showed a small but significant decrease in somatic *de novo* GluA1 soma (0.69 ± 0.50 , $p = 0.0224$; Figure 6-7A), however dendritic levels remained unchanged (1.63 ± 2.84 , $p = 0.2844$; Figure 6-7B) relative to control conditions. Therefore, the observed effects on cell surface *de novo* GluA1 following Arc siRNA treatment were specific to the addition of Arc siRNA and subsequent knockdown of Arc protein expression, and not as a result of non-specific siRNA-mediated effects.

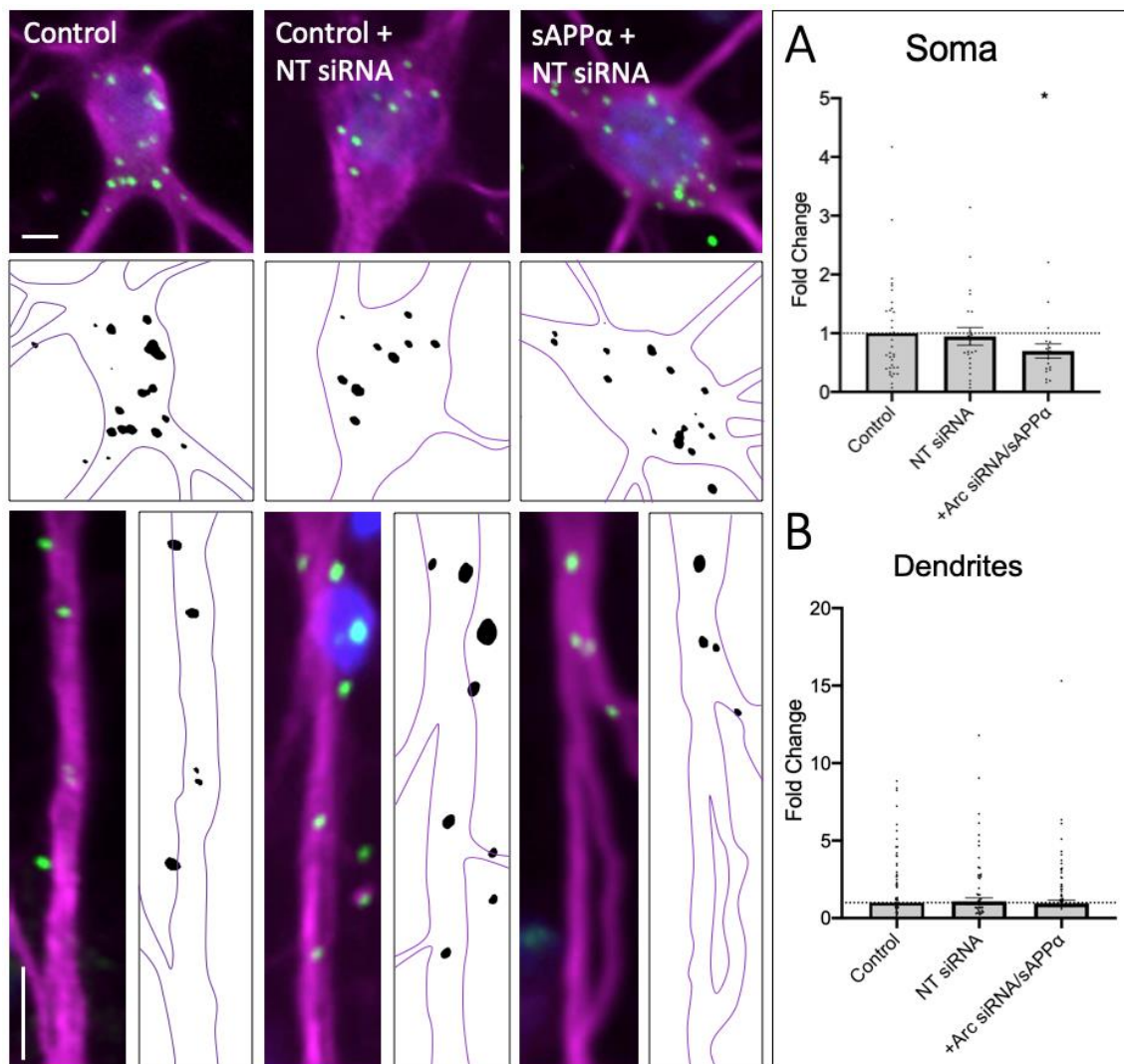


Figure 6-7 | Non-targeting siRNA does not affect *de novo* cell surface GluA1. Representative images show cell surface *de novo* GluA1 in the soma (upper panels) and dendrites (lower panels) following treatment with NT siRNA in the presence or absence of sAPP α . Application of NT siRNA alone did not significantly affect expression of cell surface *de novo* GluA1, while NT siRNA in the presence of sAPP α resulted in a small but significant decrease in the A) soma ($n = 23-24$ cells) but not B) dendrites ($n = 89-98$ dendrites) cell surface GluA1. All data are expressed relative to the experimental control from 3 experiments. Data assessing the effect of siRNA are expressed as mean ratio of sAPP α + NT siRNA/NT siRNA alone \pm SEM. Normality was detected by D'Agostino and Pearson omnibus normality tests and significance was calculated using by student's t-test, $*p = 0.0224$. Representative images show neuronal soma, dendrites (MAP2; magenta), Arc protein (green), nuclei (DAPI; blue). Scale bars = 10 μ m.

6.1.7. *sAPP α Promotes the Delayed Expression of Cell Surface GluA1/2-Containing AMPAR*

While previous research examining acute (30 min) sAPP α treatments (Mockett et al., 2019), as well as the current work described above, has found no evidence for an increase in *de novo* GluA2 synthesis in response to sAPP α , this does not exclude the possibility that sAPP α additionally promotes the trafficking of pre-existing GluA2 subunits to the cell surface. Indeed, in response to synaptic activity (Bagal et al., 2005; Kopec et al., 2006; Guire, et al., 2008; Tanaka and Hirano, 2012; Park et al., 2016; Pandya et al., 2018), behavioural learning (Whitlock et al., 2006; Fachim et al., 2016), and neuromodulators (Leonoudakis et al., 2008; Jourdi and Kabbaj, 2013), cell surface or synaptic accumulation of GluA2-containing AMPAR has been shown to occur. The insertion of these receptors typically follows the incorporation of GluA1-containing homomers. For example, GluA1/2-containing AMPAR have been shown to replace homomeric AMPAR in order to consolidate synaptic potentiation and long-term memories (Shi et al., 2001; Guire et al., 2008; Hong et al., 2013; Park et al., 2016). Therefore, we extended our analysis to examine cell surface populations of GluA1- and GluA2-containing (GluA1/2) AMPAR within somatic and dendritic compartments.

Here we utilized PLA to detect the coincident proximity and expression of GluA1 and GluA2 AMPAR at the cell surface (refer section 2.3.6. *Detection of Cell Surface Receptor Subunit Dimers (PLA)*). Using this technique, we found no significant increase in GluA1/2-containing AMPAR at the cell surface following 30 minute sAPP α treatment, in the soma (0.81 ± 0.58 ; $p = 0.709$; Figure 6-8A), nor dendrites (1.056 ± 0.92 ; $p = 0.54$; Figure 6-8B) of cultures primary neurons. However, the cell surface expression of GluA1/2-containing AMPAR significantly increased in both the soma (2.15 ± 1.65 ; $p = 0.0013$; Figure 6-8A), and dendrites (2.28 ± 1.56 ; $p \leq 0.0001$; Figure 6-8B) by 120 minutes. These results indicate that GluA1/2-containing AMPAR are expressed at the cell surface following prolonged sAPP α treatment in a manner which adds to, or replaces cell surface GluA1-containing homomers.

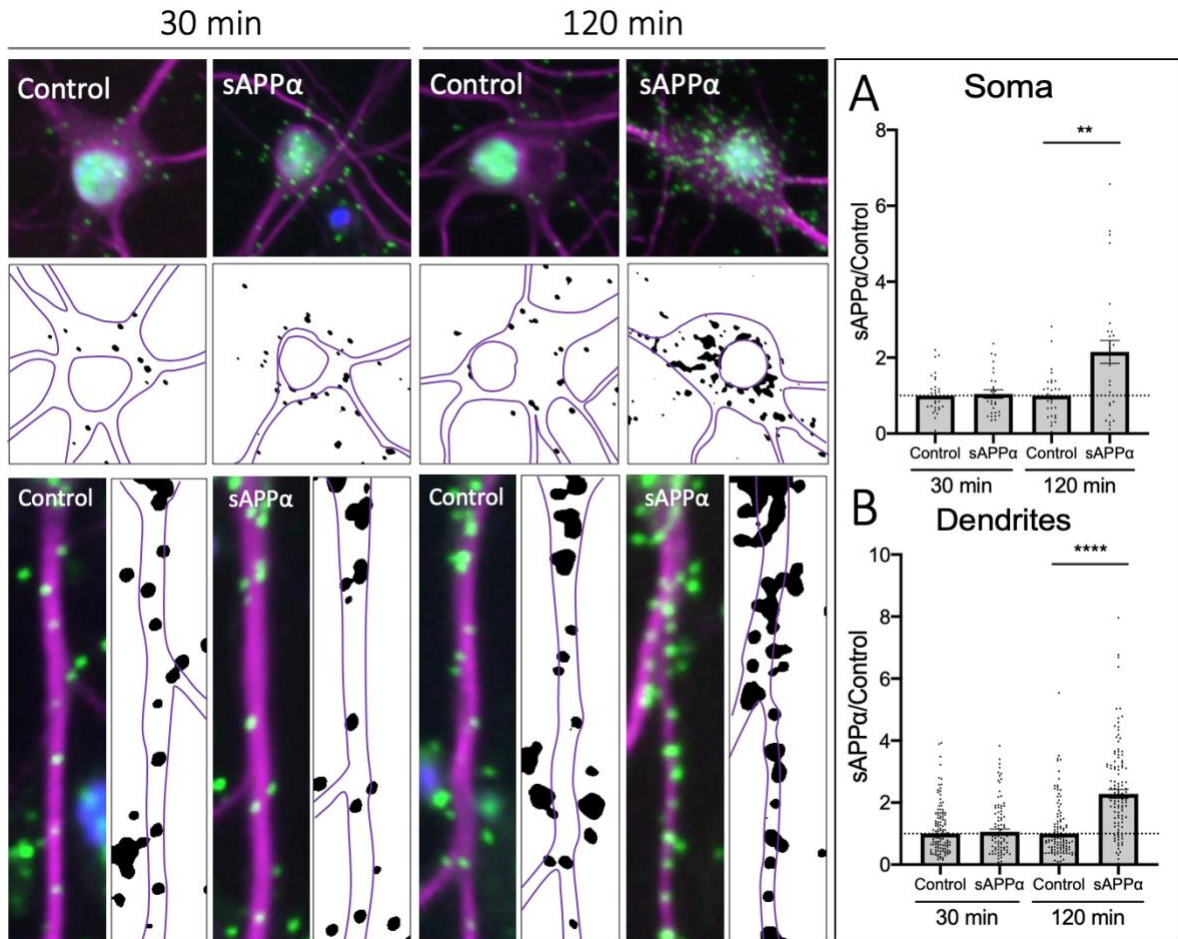


Figure 6-8 | sAPP α enhances cell surface GluA1/2-containing AMPAR following prolonged treatment. Representative images showing cell surface GluA1/2 levels in the soma (top panels) and dendrites (lower panels) from 30 minute (left) and 120 minute (right) controls and sAPP α treated conditions. A) Average data showing 1 nM sAPP α promotes an increase in the A) soma ($n = 28-31$ cells) and B) dendrites ($n = 98-142$ dendrites) following 120- but not 30-minute treatment. All data are expressed relative to control, as mean \pm SEM from 3 experiments. Normality was detected by D'Agostino and Pearson omnibus normality tests and significance was assessed by student's t-test, $**p \leq 0.001$, $****p \leq 0.0001$. Representative images show neuronal soma (upper panels) and dendrites (lower panels; MAP2; \blacktriangle , GluA1/2; \blacktriangle , DAPI; \blacktriangle). Scale bars = 10 μ m.

6.1.8. *sAPP α Promotes the Rapid and Sustained Internalization of GluA2/3-Containing AMPAR*

Following the above findings that sAPP α (1 nM) is able to promote the cell surface expression of heteromeric GluA1/2-containing AMPAR, we sought to further examine cell surface populations of GluA2- and GluA3-containing (GluA2/3) AMPAR; those which comprise the second largest majority of hippocampal AMPAR. The presence of GluA2/3 AMPAR is thought to denote synaptic maturity, with expression increasing throughout development and acting to replace GluA1/2 AMPAR at the synapse via constituent recycling (Zhu et al., 2000; Shinohara and Hirase, 2009). Interestingly, past research has shown that GluA3-containing AMPAR are regulated by *in vivo* synaptic potentiation (Williams et al., 2007), *ex vivo* synaptic depression (Holman et al., 2007), and following *in vitro* growth factor treatment (Narisawa-Saito et al., 1999). Curiously, GluA3-containing AMPAR do not appear to directly regulate the expression of LTP or context fear memory formation (Meng et al., 2003; Humeau et al., 2007), but their removal from the synapse may be an essential step required for LTD (Holman et al., 2007). Regardless, their synaptic expression is considered essential for basal synaptic transmission (Meng et al., 2003).

Using PLA to label cell surface GluA2/3-containing AMPAR, we showed that sAPP α (1 nM) significantly decreases the cell surface expression of GluA2/3-containing AMPAR within the dendrites of cultured neurons (Figure 6-9A,B). Within 30 minutes, sAPP α (1 nM) significantly decreased cell surface GluA2/3 AMPAR expression in the dendrites (0.63 ± 1.28 , $p = 0.0033$; Figure 6-9B), which remained decreased by 2 hours (0.57 ± 1.18 , $p = 0.0002$). Interestingly, somatic levels of GluA2/3 AMPAR remained unaffected following both 30-minute (0.72 ± 1.30 , $p = 0.255$; Figure 6-9A), and 120-minute (1.19 ± 1.81 , $p = 0.557$) treatments. These results may indicate that GluA3-containing AMPAR are removed from the dendritic cell surface to permit the insertion of GluA1- and GluA2-containing AMPAR (Shi et al., 2001; Diering et al., 2017). Alternatively, the removal of GluA3-containing AMPAR may reflect homeostatic processes, maintaining synaptic activity within a physiological range (Rial Verde et al., 2006; Diering et al., 2014; Tan et al., 2015).

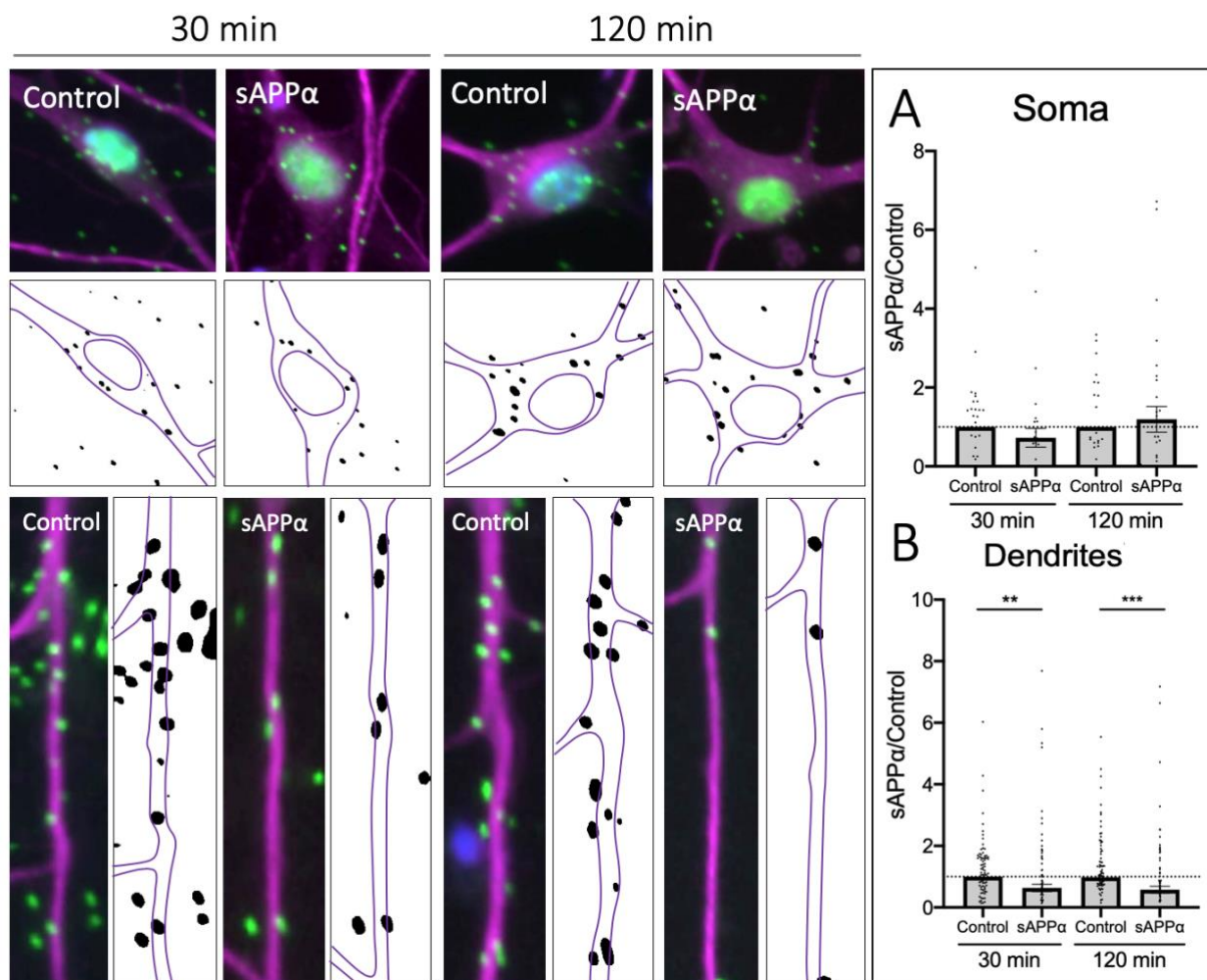


Figure 6-9 | sAPP α decreases cell surface GluA2/3-containing AMPAR expression. Representative images showing cell surface GluA2/3 levels in the soma (top panels) and dendrites (lower panels) from 30 minute (left) and 120 minute (right) controls and sAPP α treated conditions. A) Average data showing sAPP α (1 nM) does not affect somatic GluA2/3 following 30- and 120-minute treatment ($n = 30$ -32 cells). B) Average data showing sAPP α (1 nM; 30, 120 min) promotes a decrease in the dendrites ($n = 109$ -111 dendrites). All data are expressed relative to control, as mean \pm SEM from 3 experiments. Normality was detected by D'Agostino and Pearson omnibus normality tests and significance was assessed by student's t-test, ** $p = 0.0033$, *** $p = 0.0002$. Representative images show neuronal soma (upper panels) and dendrites (lower panels; MAP2; Mg , GluA1/2; G , DAPI; B). Scale bars = 10 μm .

6.2. Summary

The work described in this chapter aimed to further examine the trafficking dynamics, and cell surface expression of GluA1-, GluA2-, and GluA3-containing AMPAR. Further, we aimed to examine the specific expression characteristics of *de novo* cell surface GluA1- and GluA2-containing AMPAR, with the hopes of identifying the possible AMPAR composition of newly-synthesised cell surface receptors. Interestingly, we found that sAPP α (1 nM) increased total cell surface GluA1 protein following 30-minute and 2-hour treatments. As well as this, we found a rapid increase in *de novo* GluA1-containing AMPAR within 30 minutes, at extrasynaptic but not synaptic sites. These AMPAR were found to be decreased within 2 hours, possibly indicating a preferential targeting of *de novo* AMPAR over existing AMPAR for endocytosis. In fact, the endocytosis of *de novo* GluA1 was found to be dependent on the synthesis of Arc protein, as incubation of hippocampal cultures with Accell™ siRNA targeting *Arc* mRNA inhibited Arc protein expression, and promoted the persistence of *de novo* GluA1 following prolonged sAPP α treatment. Importantly, while *de novo* GluA1 increased in a time-dependent manner, *de novo* GluA2 did not, supporting the hypothesis that sAPP α promotes the rapid synthesis and trafficking of homomeric GluA1-containing CP-AMPAR to the cell surface. In addition to this we aimed to examine cell surface populations of GluA1/2- and GluA2/3-containing AMPAR. Here we found a delayed increase in GluA1/2 AMPAR at the dendritic cell surface, but a rapid and persistent decrease in GluA2/3 AMPAR. These results may indicate a removal of GluA2/3 AMPAR from the synapse in order to incorporate firstly GluA1-containing CP-AMPAR, and secondly GluA1/2-containing AMPAR.

Chapter 7: Discussion

7.1. *Aims and Objectives*

Dynamic changes in AMPA receptor expression govern changes in neuronal synaptic efficacy, and promote synaptic plasticity. In turn, these changes are thought to underlie information coding and storage in learning and memory processes (Anggono and Huganir, 2012). Of importance, is the regulated synthesis and trafficking of AMPAR to and from the synapse, under strict, activity-regulated guidance (Rumpel et al., 2005). Importantly, many of the mechanisms which govern these processes are negatively affected in neuropsychiatric and neurodegenerative disorders including schizophrenia (Hammond et al., 2010; Corti et al., 2011), major depressive disorder (Maeng et al., 2008; Autry et al., 2011; Sossin et al., 2019), stress and anxiety (Kiselycznyk et al., 2013; Kabir et al., 2017), Parkinson's disease (Chartier-Harlin et al., 2011; Cortese et al., 2016; Zhu et al., 2018), and AD (Langstrom et al., 1989; Ding et al., 2005; Chang et al., 2006; Garcia-Esparcia et al., 2017; Guntupalli et al., 2017; Li et al., 2019). Therefore, much research has been undertaken in order to understand the role of synthesis and trafficking of AMPAR in both health and disease.

This thesis aimed to understand the mechanisms through which sAPP α may regulate LTP and memory, by investigating cell surface AMPAR expression and Arc protein expression within cultured hippocampal neurons, and acute hippocampal tissue. Previously, sAPP α has been shown to enhance LTP (Taylor et al., 2008; Hick et al., 2015), increase cell surface GluA1 (Mockett et al., 2011), upregulate synaptodendritic protein synthesis (Claasen et al., 2009), enhance gene expression (Ryan et al., 2013), and protect against A β -related impairments in learning and memory (Seabrook et al., 1999; Xiong et al., 2017; Tan et al., 2018; Morrissey et al., 2019a). Based on these findings, we hypothesised that sAPP α would regulate the enhancement of LTP, in part through the insertion of newly synthesised GluA1-containing CP-AMPAR to the cell surface. Moreover, it was hypothesised that the expression of these AMPAR would be regulated by the expression and function of the IEG Arc. Using a combination of electrophysiology, immunohistochemistry, and FUNCAT-PLA and BioPLAY techniques, we have shown that the enhancement of LTP by sAPP α occurs primarily through the insertion of cell surface and synaptic CP-AMPAR. Further, we have shown that sAPP α enhances the early expression of extrasynaptic *de novo* GluA1- but not GluA2-containing AMPAR at the cell surface, and that their expression is regulated by Arc. Simultaneously, cell surface GluA1/2-containing AMPAR were found to increase at the cell surface within 2 hours, while GluA2/3-containing AMPAR showed a rapid and persistent decrease in response to treatment. Through this, sAPP α appears to utilize the expression and regulation of Arc and AMPAR similar to that of canonical NMDAR- or mGluR-driven LTP, as well as the strengthening of synapses by previously identified growth factors and

neuromodulators, such as BDNF (Caldeira et al., 2007; Kuipers et al., 2016) and dopamine (Sgambato-Faure et al., 2005; Bellone and Lüscher, 2006), however likely through distinct signalling cascades and mechanisms of action. The results discussed within this thesis provide possible explanations and describe critical mechanisms through which sAPP α regulates protein synthesis, Arc expression and AMPAR expression in unique concert to enhance synaptic plasticity within hippocampal neurons.

7.2. *sAPP α Mediates LTP Through the Expression of Ca²⁺-Permeable AMPA Receptors*

Experience-dependent learning and memory require multiple forms of plasticity at hippocampal synapses (Edelmann et al., 2017). While both NMDAR- (Lüscher and Malenka, 2012) and mGluR-dependent (Bortolotto et al., 1999) LTP comprise much of the our understanding of synaptic plasticity, emerging evidence indicates that GluA1-containing CP-AMPA may contribute significantly to the expression of certain forms of LTP (Man, 2011).

Here, we sought to examine the contribution of CP-AMPA to the enhancement of LTP by sAPP α , following the induction of a weak LTP protocol in hippocampal area CA1 of Sprague Dawley rats. Through these experiments, we validated previous research finding that sAPP α enhanced both the induction and persistence of LTP following a mild TBS protocol (Mockett et al., 2019). Importantly, the enhancement of LTP induction following sAPP α treatment was found to be dependent on the synaptic expression of CP-AMPA (refer section 5.1.3. *CP-AMPA Contribute to the Initial Enhancement of sAPP α -LTP*). Washout-of IEM-1460 showed a recovery of enhancement indicating that the persistence of potentiation may also be dependent on CP-AMPA. Interestingly, the induction of LTP following mild TBS alone was found to not comprise a significant CP-AMPA dependent component (refer section 5.1.2. *CP-AMPA do not Contribute to LTP Following a Mild Theta-Burst Stimulation Protocol*). These results support the hypothesis that sAPP α mediates the enhancement of LTP induction through the incorporation of CP-AMPA at the synapse within area CA1 of the adult rat hippocampus.

Although much research has shown an involvement of CP-AMPA recruitment during LTP (Table 7-1), significant controversy still exists from evidence to the contrary. Importantly, with mounting experimental evidence, it has become apparent that the contribution of CP-AMPA to LTP is influenced by a number of variables, including most prominently the age (Jensen et al., 2003; Lu et al., 2007b), and species (Gray et al., 2007) of the animals, the recording methods (Plant et al., 2006; Adesnik and Nicoll, 2007), and the induction protocol used (Guire et al., 2008). Previously, CP-AMPA

dependent LTP has been shown following spaced, but not compressed TBS-induced stimulation (Park et al., 2016) as well as patch-clamp, pre- and post-synaptic pairing protocol (Plant et al., 2006). Notably, both groups found a dependence on CP-AMPA specific to the induction of LTP, such that application of CP-AMPA antagonists during spaced tetanisation (Park et al., 2016), or the initial 10 minutes of LTP induction (Plant et al., 2006) impaired both the induction and persistence of LTP. Conversely, application of CP-AMPA antagonists 20- or 60-minutes post LTP induction did not affect the maintenance of established LTP, indicating that the role of CP-AMPA in these paradigms is transient, yet necessary for LTP induction.

Contrasting this, additional groups have provided evidence that CP-AMPA are not involved in the induction of LTP. Both Adesnik and Nicoll, (2007) and Gray et al., (2007) have used patch clamp electrophysiology in area CA1 of Sprague Dawley and C57BL/6 mice, respectively, finding an insensitivity to CP-AMPA antagonists, and no alteration in the rectification index. Importantly, Gray et al., (2007) have shown that the same patch clamp pairing protocol used by Plant et al., (2006) in rats, does not induce a CP-AMPA dependent LTP in C57BL/6 mice. These results may be explained by anatomical and electrophysiological differences between species, affecting the expression of LTP (Routh et al., 2009; Cao and Harris, 2014). However, these differences are also further influenced by the age of each species. The expression of CP-AMPA dependent LTP has been linked to mechanisms which enhance the activity of PKA (Park et al., 2016) and CaMKII (Derkach et al., 1999; Terashima et al., 2004). In rodents, PKA dominates early in development (≤ 2 weeks; Yasuda et al., 2003), while a CaMKII-dependent component develops beyond 2 weeks (Wikström et al., 2003). Conversely PKA-dependent LTP may predominate in older, not younger mice (Lu et al., 2007b). Together, these results indicate that the expression of CP-AMPA is highly regulated, with expression characteristics depending on stimulation type, frequency and pattern, as well as animal model, and thus may reflect the observations from our experiments, such that application of mild TBS alone was not sufficient to induce an IEM-1460-sensitive component of LTP.

Importantly, it is possible that regulation of CP-AMPA during plasticity events may also require input from other systems (i.e. hormones, neurotrophins, neuromodulators) in some instances. In fact, CP-AMPA dependent potentiation has been further observed following manipulations *in vivo* including HFS (Williams et al., 2007), brief restraint stress (Whitehead et al., 2017), single-whisker stimulation (Clem and Barth, 2006; Clem et al., 2008; Wen and Barth, 2012), high-fat diet exposure (Suyama et al., 2017), food restriction (Ouyang et al., 2017), irritable bowel syndrome (Liu et al., 2015a), chronic itch (Zhang et al., 2016b), addiction (Conrad et al., 2008), auditory and context fear conditioning (Clem and Huganir, 2010; Hong et al., 2013; Takemoto et al., 2017), as well as some aspects of spatial

memory (Torquatto et al., 2019). In line with this, many molecules that have been investigated have shown diverse roles in regulating AMPAR expression, with the primary aim of enhancing CP-AMPAR expression. These include serotonin (Jitsuki et al., 2011), nicotine (Tang et al., 2015), dopamine (Bellone and Lüscher, 2006; Gao et al., 2006), norepinephrine (Clem and Huganir, 2013), estrogen (Tada et al., 2013; Tada et al., 2015), tumour necrosis factor- α (TNF- α ; Leonoudakis et al., 2008), glycine (Jaafari et al., 2012), BDNF (Caldeira et al., 2007; Nakata and Nakamura, 2007; Li and Wolf, 2011; Fortin et al., 2012), as well as drugs such as cocaine (Lee et al., 2013; Ma et al., 2014b; Ma et al., 2016; Wright et al., 2020), methamphetamine (Scheyer et al., 2016) and Δ (9)-tetrahydrocannabinol (THC; Good and Lupica, 2010). The presence of these many regulatory systems governing CP-AMPAR expression may indicate endogenous control of CP-AMPAR by neurotrophic support. Therefore, the application of sAPP α in the current experiments is one of importance. Here, we establish sAPP α as a likewise neurotrophic molecule, capable of modulating synaptic activity through the incorporation of CP-AMPAR.

Following the observation that sAPP α involves a CP-AMPAR dependent component of LTP, an important distinction to be made is the comparison between the mechanism harnessed by sAPP α with those of canonical CP-AMPAR dependent LTP. Past research has shown that the insertion of CP-AMPAR at the cell surface is PKA-dependent (Lu et al., 2007b; Park et al., 2016), while translocation of these AMPAR from the perisynaptic membrane to the synapse is PKC-dependent (Yang et al., 2010). Further, CAMKI has been shown to regulate the trafficking of CP-AMPAR (Guire et al., 2008), while CaMKII governs phosphorylation of GluA1 AMPAR subunits at s831 to enhance Ca²⁺-permeability or trafficking of CP-AMPAR to the cell surface (Derkach et al., 1999; Terashima et al., 2004).

With relevance to our current observations, previous work has shown that sAPP α enhances LTP through a trafficking-dependent mechanism. The induction of sAPP α -primed LTP is reduced, but not fully eliminated by inhibition of endoplasmic reticulum–Golgi transport, while the maintenance of LTP and expression of cell surface GluA1 is fully eliminated (Mockett et al., 2019). Further, washout of endoplasmic reticulum–Golgi transport inhibitor, BFA, before the application of TBS restored the induction of LTP, indicating that some trafficking was able to occur following sAPP α treatment and before TBS. Additionally, inhibition of endoplasmic reticulum–Golgi transport, *de novo* translation, as well as CaMKII and PKG significantly impair the cell surface expression of GluA1, while inhibition of both CaMKII and endoplasmic reticulum–Golgi transport also significantly reduced the sAPP α -induced increase in s831. Conversely, sAPP α treatment did not affect s845 phosphorylation at the cell surface.

Phosphorylation of s831 has been previously linked to enhancements in single channel conductance (Derkach et al., 1999), likely through the addition of higher conductance CP-AMPAR (Kim

and Ziff, 2014; Yang et al., 2018; Park et al., 2019b; Summers et al., 2019), primarily by CaMKII-mediated signalling. On the other hand, s845 phosphorylation has been associated with increased single-channel open probability as well as promoting GluA1 targeting or retention of AMPAR at the cell surface (Oh et al., 2006; Man et al., 2007; Diering and Huganir, 2018). Interestingly, a PKG-dependent increase in s831 phosphorylation has been found necessary for cocaine-induced increases in locomotor activity (Yang et al., 2018), while cGMP-dependent s831 phosphorylation has been shown to mediate GluA1- but not GluA2 cell surface expression (Cabrera-Pastor et al., 2017). Therefore, these results may imply a mechanism of CaMKII- or PKG-mediated trafficking of s831-phosphorylated CP-AMPA to the cell surface. Compared to s845, phosphorylation of s831 is enriched in the postsynaptic density (PSD), suggesting that s831 may play a role in targeting to the PSD or stabilization within the PSD (Diering et al., 2017). Together, these results indicate that the priming of LTP by sAPP α is fully dependent on the trafficking of AMPAR to the cell surface and partly dependent on the synthesis of new proteins, while the maintenance of sAPP α -primed LTP is dependent on both mechanisms. Importantly, in both the results observed by (Mockett et al., 2019) and those presented within this thesis, application of sAPP α alone or in conjunction with IEM-1460 did not significantly alter baseline recordings. These observations indicate that sAPP α does not enhance the direct synaptic incorporation of CP-AMPA but instead increase the extra- or perisynaptic population of AMPAR to be translocated to the synapse following TBS.

With this in mind, observations from (Park et al., 2019a) have described a similar two-step model for the induction of LTP by CP-AMPA. Here, it is proposed that initial TBS stimulation activates NMDARs and drives CP-AMPA from extrasynaptic sites into the synapse to induce the induction of LTP. Simultaneously, NMDAR activation also activates PKA to promote further trafficking of internal CP-AMPA to the extrasynaptic membrane. Subsequent synaptic activity then drives these AMPAR into the synapse where basal synaptic transmission is able to trigger protein synthesis through the increased influx of Ca²⁺ (Asrar et al., 2009). It has been further proposed that these AMPAR lower the threshold for plasticity at independent, heterosynaptic pathways by promoting the translocation of CP-AMPA, and local synthesis through PI3K and MAPK activation, ultimately priming synapses for further plasticity.

These results indicate two possibilities; firstly, sAPP α may promote the early synthesis and trafficking of CP-AMPA to the cell surface. Following TBS stimulation these AMPAR may translocate to the synapse to potentiate the induction of LTP. Alternatively, sAPP α may enhance the trafficking of pre-existing CP-AMPA from extrasynaptic sites towards the synapse to promote the induction of LTP. Activity at these AMPAR may directly potentiate postsynaptic currents as well as promote activation of downstream Ca²⁺-sensitive processes including protein synthesis, which may include the trafficking

of *de novo* CP-AMPA to repopulate extrasynaptic sites. Indeed, it is possible that sAPP α may induce both the trafficking of CP-AMPA to the cell surface as well as simultaneous movements from perisynaptic sites to synaptic sites to enhance the induction of LTP. Further, while we have shown that sAPP α enhances LTP in a manner dependent on the activation of CP-AMPA, as discussed above these AMPAR have been shown to regulate a protein synthesis-dependent component of LTP (Park et al., 2018). Therefore, in order to fully understand the role of CP-AMPA in sAPP α -mediated LTP, future experiments should aim to examine the link between CP-AMPA and protein synthesis following sAPP α treatment.

Table 7-1 | Summary of literature examining CP-AMPA in LTP and behavioural paradigms

Author	Animal Species	Age (weeks)	Stimulation protocol						CP-AMPA Antagonist	CP-AMPA dependent?
			Trains	Bursts	Interburst (Hz)	Pulse Count	Pulse (Hz)			
Park et al., (2016)	Sprague Dawley	3–12	cTBS	3 (1/10s)	5	20	5	0.01	IEM1460 (30 μ m), NSAPM (30 μ m), PhTx433 (5–10 μ m)	X
			sTBS	3 (1/10min)	5	20	5	0.01		✓
Guire, et al., (2008)	Rats	4-6	HFS	3		5	1	100	IEM1460 (30 μ M)	X
			TBS	5		5	4	100		✓
Sanderson et al., (2016)	C57BL6 mice	2	LTD	1	1	100	100	IEM1460 (70 μ M)	✓	
		3							X	
Adesnik et al., (2007)	Sprague Dawley	2–3		4	5	100	100	20	PhTx433 (10uM)	X
Lu et al., (2007)	C57BL6 mice	2, 8		2	1		1	100	PhTx-433 (2.5 μ M), NSAPM (20 μ M)	✓
		3-4								✓
		2, 8		1	1		1	100		X
		3-4								X
Asrar et al., (2009)	CD1 GluR2 ^{+/+}	12–24		4	5	100		100	IEM1460 (100uM)	X
	CD1 GluR2 ^{-/-}									✓

Yang et al., (2010)	Sprague Dawley	2-3	2	5	5	5	100	PhTx433 (10 μ M), IEM-1460 (50 μ M)	✓
			+ postsynaptic depolarisation						
Gray et al., (2007)	C57BL6 mice	8-12	2	1	10	100	100	IEM1460 (100-200 μ M)	X
		2-3, 3-4,	Pairing Protocol					IEM1460 (100 μ M)	X
			Membrane potential	Pulses		Hz			
			-10 mV	100	2				
Plant et al., (2006)	Sprague Dawley	3-4	-10-0 mV		50-100	0.5-2 Hz		PhTx 433 (10 μ M)	✓
Yamanaka et al., (2017)	C57BL6 mice	6-14	+ 30 mV		80	2 Hz		NASPM (50 μ M)	✓
Purkey et al., (2018)	C57BL6 mice	2-8	0 mV		2	100		NASPM (20 μ M)	X
			0mV		270	3			✓
Cepeda-Prado et al., (2019)	C57BL6 mice	4	Pairing Protocol					NASPM (100 μ M)	✓
			Repeats	Action Potential Count	Hz				
				6	1, 4	0.5			
<i>In vivo</i> Behavioural Paradigms									
Clem and Barth, (2006)	C57BL6 mice	1-2	Single-whisker stimulation protocol					Joro spider toxin (10-20 μ M)	✓
Clem et al., (2008)	C57BL6 mice	1-2	Single-whisker stimulation protocol					Assessed by rectification	✓
Wen and Barth, (2012)	C57BL6 mice	2	Single-whisker stimulation protocol					NASPM (50 μ M), PhTx (10 μ M)	✓
Clem and Haganir, (2010)	C57BL6 mice	4-7	Context fear conditioning					NASPM (50 μ M)	✓
Whitehead et al.,	Wistar rats	4-5	Brief restraint stress					Spermine (100 mM), IEM: 100 mM	✓

(2017)					
Suyama et al., (2017)	C57BL6 mice	3–5	High-fat diet exposure	IEM 1460 (100 μ M)	✓
Ouyang et al., (2017)	Sprague Dawley rats		Food restriction	NASPM (200 μ M)	✓
Zhang et al., (2016)	Sprague Dawley rats	3–5	Chronic itch	Assessed by rectification	✓
Conrad et al., (2008)	Sprague Dawley rats	Unknown	Cocaine addiction	NASPM (100-200 μ M)	✓
Takemoto et al., (2017)	C57BL6 mice	4	Context fear conditioning	Assessed by rectification	✓
		8			✓
Hong et al., (2013)	Sprague Dawley rats	4-5	Auditory fear condition	NASPM (50 μ M)	✓
Torquatto et al., (2019)	Wistar rats	2-3	Auditory fear condition	NASPM (0.4 μ M, 4 μ M, 40 μ M)	✓
			Contextual fear memory	NASPM (0.4 μ M)	✓
			Object location task	NASPM (0.4 μ M)	✗
			Spatial memory test	NASPM (0.4 μ M)	✓

7.3. *sAPP α regulates the Trafficking of Existing and Newly-Synthesized AMPAR Receptors*

7.3.1. *GluA1-containing AMPA Receptors*

As discussed previously, past research has shown that sAPP α (1 nM, 30 min) enhances cell surface GluA1 expression in a protein synthesis-dependent manner, in acute hippocampal slices (Mockett et al., 2019). Throughout this thesis, we have further described the requirement of CP-AMPA at the synapse for the induction of sAPP α -primed LTP (refer section 5.1.3. *CP-AMPA Contribute to the Initial Enhancement of sAPP α -Mediated LTP*). This evidence suggests either a dependence on the synthesis of GluA1 proteins directly, or synthesis of chaperone or scaffolding proteins to aid the trafficking and anchoring of pre-existing, GluA1-containing AMPAR to the cell surface. Alternatively, the protein synthesis component of this may indeed require aspects of both. To address this, we first sought to determine whether sAPP α (1 nM) enhances cell surface GluA1 in our primary hippocampal neurons.

Using BioPLAy, we found that GluA1 expression at the cell surface was enhanced following sAPP α treatment for both 30 minute and 2-hour incubations (refer section 6.1.1. *sAPP α Promotes the Rapid and Persistent Expression of Cell Surface GluA1 in the Soma and Dendrites of Primary Hippocampal Neurons*). Data from these experiments indicates an early enhancement of GluA1 at the somatic surface, followed by a later increase in the dendrites. While this may indicate distinct mechanisms of somatic and dendritic exocytosis of GluA1-containing AMPAR, it may also result from lateral diffusion from somatic to dendritic compartments (Cognet et al., 2006; Earnshaw and Bressloff, 2008). Of interest, work from Adesnik et al., (2005) has made comparisons between the recycling rates of somatic and dendritic recycling pools, finding that intracellular dendritic AMPAR cycle to the synapse on the scale of hours, while trafficking from internal stores to extrasynaptic somatic sites occurs on the scale of minutes. These newly inserted AMPAR are then capable of lateral travel along dendrites to reside at synapse. Given a coefficient of Brownian diffusion of 0.01–0.5 $\mu\text{m}^2/\text{s}$ (Tardin et al., 2003), an AMPAR at the cell body could take up to 1.5 hours to travel 50 μm , placing it in the timescale of our experiments. Of consideration is the saturating nature of the mean square displacement, such that with time roughly 25% of freely diffusing extrasynaptic receptors display spatially restricted diffusion within a domain size of ~ 300 nm, or the equivalent of a PSD (Kusumi et al., 1993; Tardin et al., 2003). Thus, diffusion from the soma follows an exponential fit as laterally diffusing AMPAR track towards and are captured by, or reside within, perisynaptic and synaptic spaces. Regardless of the mechanism of action, we can conclude that *in vitro* treatments of

sAPP α increase the cell surface population of GluA1-containing AMPAR in a manner similar to previous *ex vivo* experiments (Mockett et al., 2019).

Similarly, using FUNCAT-PLA we have also shown that cell surface populations of *de novo* GluA1 are dynamically regulated following sAPP α treatment (refer section 6.1.2. *sAPP α Promotes the Rapid and Transient Trafficking of de novo GluA1-Containing AMPAR to the Somatic and Dendritic cell surface*). Here, we found that short (30 minute) but not long (2 hour) treatments of sAPP α significantly increased newly synthesised GluA1-containing AMPAR at both the somatic and dendritic cell surface. Interestingly, *de novo* GluA1 at 2 hours was significantly reduced in both compartments returning to control levels. These results may be explained through a few different possibilities. While direct exocytosis of *de novo* GluA1 may occur at the somatic cell surface (Yudowski et al., 2007), we cannot rule out 3 possible routes for the expression of *de novo* GluA1 at the dendritic cell surface. Firstly, as previously mentioned, somatic *de novo* GluA1 may diffuse along the plasma membrane. However, given the time constraints of AMPAR present within 50 μm of proximal dendrites within 30 minutes, it is unlikely. Secondly, *de novo* dendritic GluA1 may be translated and packaged into vesicles within the somatic Golgi apparatus and trafficked anterogradely along the dendrites at a previously identified mean speed of 1.5 $\mu\text{m}/\text{s}^{-1}$ (Hangen et al., 2018). This active transport is ten-fold faster than Brownian diffusion at the cell surface, placing the trafficking of *de novo* GluA1 in the dendrites, and the delivery to the cell surface, within our time constraints. Thirdly, while we have not directly assessed the role of local dendritic synthesis in the formation and trafficking of these AMPAR, previous evidence has shown that sAPP α is able to stimulate synaptodendritic protein synthesis (Claasen et al., 2009), and APP has been shown to directly bind the RNA binding protein cytoplasmic polyadenylation element binding protein (CPEB) at the cytoplasmic surface (Cao et al., 2005; Savtchouk et al., 2016). Activation of CPEB has been shown to be important for the local synthesis of GluA1 and GluA2 AMPAR subunits (Si et al., 2003; Pavlopoulos et al., 2011), and the stabilization and persistence of LTP and long-term memory (Fioriti et al., 2015). Therefore, it may be possible that these AMPAR are synthesised locally and inserted directly.

Interestingly, in the current experiments cell surface *de novo* GluA1-containing AMPAR were found to be expressed primarily at extrasynaptic sites (refer section 6.1.2.1. *sAPP α Enhances the Extrasynaptic, but not Synaptic Population of de novo Cell Surface GluA1*). GluA1-containing AMPAR are essential for the formation of extrasynaptic pools of AMPAR, such that GluA1^{-/-} mice show little to no extrasynaptic AMPAR populations (Andrásfalvy et al., 2003; Lisman and Raghavachari, 2006), and the expression of extrasynaptic AMPAR has been deemed necessary for the induction of LTP (Oh et al., 2006; Penn et al., 2017), while increasing the proportion of extrasynaptic AMPAR primes synapses

for LTP (Oh et al., 2006). These results may further support the role of sAPP α in the priming of LTP, through the expression of *de novo* GluA1-containing AMPAR at extrasynaptic domains.

These results are further corroborated by observations of similar neurotransmitters and neuromodulators, including glutamate, dopamine, BDNF, and the mGluR agonist DHPG, all of which have been shown to stimulate local protein synthesis (Kacharina et al., 2000; Ju et al., 2004; Smith et al., 2005; Claasen et al., 2009; Leal et al., 2014). Of interest, glutamate, dopamine and BDNF have been found to promote the local synthesis and trafficking of GluA1, but not GluA2-containing AMPAR and their trafficking to the cell surface within 30 minutes (Smith et al., 2005; Sutton et al., 2006; Caldeira et al., 2007; Mameli et al., 2007; Li and Wolf, 2011; Fortin et al., 2012). Interestingly, in response to dopamine, GluA1-containing AMPAR have been shown to traffic directly to the synapse of AMPA-silent synapses in DIV 14-21 cultured hippocampal neurons (Smith et al., 2005), as well as enhance the extrasynaptic population of GluA1-containing AMPAR in DIV 14-21 cortical neurons (Gao et al., 2006). In the latter of these experiments, subsequent NMDAR activation was found to promote the trafficking of these extrasynaptic AMPAR to the synapse. Importantly, application of both BDNF (Akaneya et al., 1997; Ying et al., 2002; Ji et al., 2010) and dopamine (Shetty et al., 2017) to acute hippocampal slices potentiates the EPSP in the absence of tetanic stimulation. Interestingly, subsequent induction of LTP is impaired following BDNF-induced enhancement of baseline synaptic transmission, indicating that these AMPAR are susceptible to removal by depotentiation-like mechanisms, or saturation of AMPAR responses. These observations distinguish both BDNF and dopamine from sAPP α , such that application of sAPP α to acute hippocampal slices has no effect on baseline synaptic transmission (refer section 5.1.1. *CP-AMPA Contribute a Small Fraction of Basal Synaptic Transmission*; Richter et al., 2018; Mockett et al., 2019), indicating that the trafficking of these AMPAR occurs at primarily extrasynaptic sites, and requires the induction of LTP to promote their synaptic localization. Therefore, while sAPP α appears to employ distinct mechanisms to that of BDNF and dopamine, the induction of protein synthesis and CP-AMPA trafficking may be a common underlying factor of these neuromodulators

7.3.1.1. *Regulation of de novo GluA2-containing AMPA Receptors*

Following the observation that *de novo* GluA1-containing AMPAR increased at the cell surface and that CP-AMPA provide a significant contribution to sAPP α -enhanced LTP, we further sought to determine the identity of these AMPAR by likewise examination of *de novo* cell surface GluA2. Here, we found no significant increase in cell surface *de novo* GluA2 following 30 minute or 2-hour incubations with sAPP α , indicating these AMPAR are GluA1 homomers. In fact, we found a small but significant decrease in *de novo* GluA2 at the dendritic cell surface, within 30 minutes of treatment.

These results support earlier observations from our lab that *de novo* GluA2 is decreased in the dendrites following 2-hour treatments (Elder et al., 2019). This may indicate one of two possible mechanisms. Firstly, GluA2 synthesis may be directly inhibited during this time. As previously mentioned, CPEB has been shown to bind APP and regulate the local synthesis of GluA1 and GluA2, however, CPEB3 has been shown to bind and inhibit translation of *GluA2* mRNA (Huang et al., 2006). Additionally, sAPP α (1 nM, 15 min) has been previously shown to upregulate miR-30 (Ryan et al., 2013), a miRNA which has been linked to the downregulation of GluA2 in the hippocampus (Song et al., 2019). Of note, the upregulation of miR-30 is transient, and was not found to be significantly upregulated following 2 hours of sAPP α treatment (Ryan et al., 2013), reflecting the transient decrease in GluA2 in the current experiments. This observation adds an additional possible level of control over the synthesis and formation of AMPAR following sAPP α treatment. Alternatively, active processes may govern the restriction of GluA2 proteins from trafficking to the cell surface. Under basal conditions N-ethylmaleimide-sensitive factor (NSF) inhibits PICK1-mediated intracellular GluA2 retention (Hanley et al., 2002; Hanley, 2007; Makuch et al., 2011), permitting the constitutive cycling of GluA2-containing AMPARs. However, following glycine-induced LTP, increased PICK1-GluA2 interaction within the endosomal compartment inhibits forward trafficking of GluA2, permitting the expression of primarily GluA1-containing CP-AMPA at the cell surface (Terashima et al., 2004; Bellone and Luscher, 2006; Jaafari et al., 2012). Together, it is possible that either the dendritic translation of GluA2 or the export of *de novo* GluA2 from the soma may be regulated as such to favour export of GluA1-containing AMPAR to the cell surface. Therefore, we can conclude that the rapid synthesis of GluA1-containing AMPAR likely involves the formation of Ca²⁺-permeable GluA1 homomers.

7.3.2. *GluA1/2-containing AMPA Receptors*

The expression of GluA1/2-containing AMPAR is closely related to the expression and persistence of LTP (Isaac et al., 2007; Díaz-Alonso et al., 2017; Penn et al., 2017; Zhou et al., 2018), and found to be crucial for the maintenance of hippocampal LTP (Penn et al., 2017). Therefore, we have utilized PLA for coincident detection of GluA1 and GluA2 protein at the cell surface of cultured hippocampal neurons, finding a delayed increase in the proportion of GluA1/2-containing AMPAR following 2 hours of sAPP α treatment, at both the somatic and dendritic cell surface. Importantly, GluA2-containing AMPAR have previously been thought to contribute to the switch of GluA1-containing CP-AMPA to GluA2-containing Ca²⁺-impermeable (CI)-AMPA (Shi et al., 2001; Bellone and Lüscher, 2005b; Sutton et al., 2006; Mameli et al., 2007). As previously mentioned, many electrophysiology experiments have described a sensitivity of LTP to CP-AMPA antagonists during early but not late potentiation (Guire et

al., 2008; Park et al., 2016), likely implicating a switch from CP-dependent to CP-independent potentiation, indicating that early activity at CP-AMPA is necessary for the expression of later potentiation (Park et al., 2016). This process appears to require interactions between GluA2 and NSF, GRIP, or PICK1, as inhibition of these interactions results in prolonged expression of cell surface CP-AMPA and LTP governed solely by CP-AMPA (Clem and Huganir, 2010; Yang et al., 2010).

During memory formation, the incorporation of CP-AMPA at synapses is thought to place the synapse into a less stable, and more 'labile' state (Hong et al., 2013). Activity at these AMPAR has been found to be required for the reconsolidation of memories, and promote the later exchange for GluA2-containing CI-AMPA. Interestingly, the initial insertion of synaptic CP-AMPA may also be dependent on the initial removal of existing CI-AMPA from the cell surface, as inhibition of CI-AMPA endocytosis blocked the initial exchange for CP-AMPA. This may support the idea that synaptic domains contain limited spaces, or 'slots,' for the addition of AMPAR (MacDougall and Fine, 2013).

Interestingly, impairing Arc protein degradation and increasing Arc protein expression in hippocampal cultures results in a dramatic decrease in GluA1-containing AMPAR at the cell surface and a small but significant increase in GluA2-containing AMPAR (Wall et al., 2018), following activation of mGluR. Here, the authors discuss the possibility that mGluR activation promotes the removal and replacement of CP-AMPA with GluA1/2-containing AMPAR in an Arc-dependent manner. In the current experiments, it is possible that the Arc-dependent removal of *de novo* GluA1-containing AMPAR also permits the trafficking of GluA1/2-containing AMPAR to the cell surface. Such observations warrant further experiments to clarify Arc's role in this mechanism.

7.3.3. *GluA3-containing AMPA Receptors*

GluA2/3-containing AMPAR are the next major heteromer within the hippocampus (Wenthold et al., 1996), and PSD (Pandya et al., 2017). While under certain conditions these AMPAR contribute to LTP (Renner et al., 2017), for the most part GluA3-containing AMPAR exist in low-conductance states, contributing solely to basal transmission (Meng et al., 2003). Due to this, we extended our experiments to cover the quantification of GluA2/3 levels at the cell surface following sAPP α treatment. Unexpectedly, we found an early and prolonged reduction in GluA2/3-containing AMPAR in the dendrites, while somatic GluA2/3 remained unchanged.

As mentioned above, past research has indicated a necessity of GluA2-containing CI-AMPA internalization before the addition of GluA1-containing CP-AMPA (Bellone and Lüscher, 2005; Bellone and Luscher, 2006; Hong et al., 2013). Here, it is thought that the number of receptors in a given synapse may be limited by 'slots,' determined by the number of available anchoring proteins of

the PSD (MacDougall and Fine, 2013). Preventing the removal of GluA2-containing AMPAR by inhibiting the GluA2-PICK1 interaction prevents cocaine-induced expression of CP-AMPA and transition of the synapse into a labile state (Bellone and Luscher, 2006). Importantly, the GluA2-PICK1 interaction is necessary for the endocytosis and lysosomal targeting of GluA2/3-containing AMPAR (Koszegi et al., 2017). Live cell imaging studies reflect these observations, however on shorter time-scales. Total internal reflection fluorescence (TIRF) live-cell microscopy has shown that while GluA1-containing AMPAR increase at the cell surface within 5–15 minutes post LTP induction, GluA2/3-containing AMPAR show a marked decrease within 5 minutes and a gradual recovery upon 15 minutes (Tanaka and Hirano, 2012). While these timescales perhaps do not reflect the results presented here, this may be due to differences in the mechanisms involved between electrical field stimulation and treatment with exogenous neurotrophins, including sAPP α . Similarly, *in vivo* research has shown that HFS stimulation upregulates GluA1 and GluA3 at the cell surface within 20 minutes of stimulation, of which GluA1, but not GluA3 is likewise upregulated in the synapse. Within 20 minutes GluA3 is decreased at the cell surface, persisting until at least 4 hours post-tetanus (Williams et al., 2007). These results may indicate a shift in receptor subunit composition following synaptic activity, such that synaptic priority is given to GluA1-containing AMPAR.

Previously, we have shown that the trafficking of GluA1-containing AMPAR, synaptic protein synthesis, and expression of Arc protein is dependent on the activity of PKG and MAPK (Claasen et al., 2009; Mockett et al., 2011; Livingstone et al., 2019), and may involve cGMP (Ishida et al., 1997). Interestingly, the NO-cGMP-PKG and MAPK pathways have been found to be involved in the declustering of GluA2/3-containing AMPAR (Endo and Launey, 2003), an event which is typically associated with subsequent internalization of receptors (Matsuda et al., 2000), indicating that these processes may be linked through a similar mechanism. Additionally, while sAPP α treatment has been shown to reliably protect against A β -induced impairments in LTP (Morrissey et al., 2019b), spine morphology (Tackenberg and Nitsch, 2019), and memory (Tan et al., 2018), these impairments appear to be mediated through the removal of cell surface GluA3-containing AMPAR at the synapse (Reinders et al., 2016), and transgenic APP/PS1 mice lacking GluA3 do not show increased mortality or memory deficit, like APP/PS1 mice. Here, the authors note that chronic downregulation of GluA3-containing AMPAR, without compensatory or activity-dependent increases in GluA1- or GluA2-containing AMPAR permit the disintegration of the synapse, ultimately leading to impairments in LTP and memory. This may suggest that sAPP α acts in one manner to protect neurons through the rapid and persistent internalization of GluA3-containing AMPAR and filling of these available slots with AMPAR that promote synaptic strengthening.

Importantly, it has been shown that the endocytosis of GluA2/3-containing AMPAR is Arc-dependent in cultured hippocampal slices (Rial Verde et al., 2006), and during conditioned morphine withdrawal (Liu et al., 2012). We have previously shown that the endocytosis of *de novo* GluA1-containing AMPAR is dependent on the synthesis of Arc protein (refer section 6.1.5. *Internalization of de novo GluA1 is Dependent on Arc Expression*), therefore it may also be possible that Arc has dual roles in targeting both GluA1- and GluA2/3-containing AMPAR. While we have provided evidence that Arc mRNA levels remained unchanged at 15- and 30-minute treatments, it is possible the early endocytosis of GluA2/3-containing AMPAR is mediated by the synthesis of Arc protein from local mRNA pools, independent of *de novo* transcription (Steward et al., 2015). Alternatively, endocytosis of GluA2/3-containing AMPAR may be under the influence of other endocytosis-related proteins, such as candidate plasticity gene 2 (CPG2), found to regulate both constitutive and LTD-dependent removal of GluA2-containing AMPAR from the cell surface (Loeblich et al., 2013; Cottrell et al., 2004).

7.4. *A Role for Arc Expression and Function*

Within the past 10 years, the immediate early gene Arc has been well characterised as a reliable and easily detectable marker of plasticity in both *in vitro* and *in vivo* applications (Link et al., 1995; Lyford et al., 1995; Minatohara et al., 2016). Arc expression is highly regulated, showing high signal-to-noise expression in both somatic and dendritic compartments following synaptic activity (Huang et al., 2007; Chawla et al., 2018; Janz et al., 2018). Here, we have shown that sAPP α treatment promotes the expression Arc mRNA and protein, in the soma and dendrites of cultured primary neurons. Notably, Arc expression was dependent on CaMKII, MAPK, and PKG activity, which is consistent with previous reports of signalling pathways which promote Arc expression during synaptic activity. Further these kinases have been shown to be essential for sAPP α 's facilitation of local protein synthesis in hippocampal synaptoneuroosomes and AMPAR trafficking in acute hippocampal slices (Claasen et al., 2009; Mockett et al., 2011). Additionally, we have identified a crucial relationship between NMDA and α 7nACh receptors in triggering this effect. These findings provide evidence of a coordinated and overlapping set of signalling mechanisms through which sAPP α regulates the expression of plasticity-related proteins, including Arc, and thus regulates synaptic plasticity.

The regulation of Arc transcription and translation has been shown to be highly regulated, such that it has been hypothesized that there may exist separate pools of translating and non-translating Arc mRNA (Steward et al., 2014). Arc mRNA may be located and translated within the soma and serve to regulate gene transcription (Korb et al., 2013), while separate, translationally repressed pool is

trafficked throughout the dendrites, to be translated at synapses locally (Link et al., 1995). A third pool may govern rapid transcription-independent translation of *Arc* mRNA already associated with polyribosomes throughout the dendrites (Bagni et al., 2000; Na et al., 2016).

Early experiments provided evidence that nanomolar amounts of sAPP α promote the expression of *Arc* and *Zif268* mRNA in a time-dependent manner (refer section 4.1.1. *sAPP α Facilitates an Increase in Arc and Zif268 mRNA Expression*). Importantly, this was corroborated through observations that sAPP α increases Arc protein expression in a concentration-dependent manner, such that both 0.1 nM and 1 nM treatments of sAPP α for 2 hours significantly increased Arc protein expression in the dendrites, however only 1 nM treatment of sAPP α significantly enhanced somatic Arc protein (refer section 4.1.2. *sAPP α Facilitates an Increase in Arc Protein Expression*). This may be explained by the relative abundance of receptors necessary for sAPP α 's activity. As described in section 4.1.6. *Dendritic Arc Protein Expression is Dependent on Activation of NMDA- and α 7nACh Receptors*, we have shown that the full complement of dendritic Arc protein expression is dependent on the dual activity of NMDAR and α 7nAChR. While both α 7nAChR (Klein and Yakel, 2006; Fayuk and Yakel, 2007; Pidoplichko et al., 2013) and NMDAR (Dodt et al., 1998; Köhr, 2006) have been shown to be expressed at both somatic and dendritic membranes, it has been shown that α 7nAChR-dependent Ca²⁺ signals are significantly larger in the dendrites than in the soma (Fayuk and Yakel, 2007), while the density of NMDAR is much greater in dendritic spines than in dendritic shaft and somatic membrane (Köhr, 2006). Therefore, the required signals for Arc expression may be reduced in response to 0.1 nM sAPP α within the soma.

Importantly, both the somatic and dendritic expression of Arc protein was found to be dependent on both transcription and translation (refer section 4.1.4. *Arc Protein Expression is Transcription- and Translation-Dependent*), further validating the observed increase in *Arc* mRNA, and likewise an increase in *Zif268* mRNA. Together these data provide evidence to suggest that sAPP α enhances the *de novo* transcription, synthesis and dendritic localization of Arc.

Of note, the concentration-dependent effects appeared to be specific to the treatment of sAPP α , as the closely related APP metabolite sAPP β did not show similar effects. While previous reports indicate that sAPP α is able to rescue morphological and plasticity-related deficits observed in APP and APP-like protein 2 (APPL2) knockout mice (Ring et al., 2007; Fol et al., 2016) and conditional APP/APPL2 NexCre knockdown mice (Li et al., 2010; Hick et al., 2015), sAPP β is unable to ameliorate these deficits. sAPP β differs from sAPP α by a 16 amino-acid truncation at the C-terminus (CT α 16). Due to this sAPP β adopts a completely different structure to sAPP α (Peters-Libeu et al., 2015). Interestingly, application of CT α 16 alone has been found to enhance LTP to a similar degree as sAPP α , in a manner

dependent on protein synthesis and activation of $\alpha 7nAChRs$ (Morrissey et al., 2019b). The preservation of these amino acids in the sAPP α protein, and the common mechanisms employed by sAPP α and CT $\alpha 16$ stress a unique ability of these amino acids in mediating these effects. Therefore, the physiological differences between sAPP α and sAPP β may underlie a divergence in each molecule's ability to bind appropriate receptors, initiating different signalling cascades between the two sAPP metabolites, further distinguishing their distinct biological functions. Interestingly, treatment of cultures with 1 nM sAPP β significantly reduced basal Arc protein in the soma but remained unaffected in the dendrites. Both sAPP α and sAPP β have been found to bind GABA $_B$ receptors at high concentrations (250 nM; Rice et al., 2019) and enhanced GABA $_B$ activity has been tied to a reduction of Arc protein (Terunuma et al., 2014). Thus, sAPP β may negatively modulate the expression of Arc protein by activation or modulation of GABA $_B$ receptors.

While previous work has described a multitude of signalling pathways mediating sAPP α -induced neuroprotection and plasticity, of particular interest is sAPP α 's ability to increase cGMP and MAPK activity (Furukawa et al., 1996; Gakhar-Koppole et al., 2008). Interestingly, in previous studies using isolated synapses, sAPP α has been shown to enhance *de novo* protein synthesis in a manner partially dependent on CaMKII and MAPK, and fully dependent on PKG (Claasen et al., 2009). Likewise, trafficking of GluA1-containing AMPA receptors to the cell surface requires CaMKII and PKG, as well as protein synthesis (Mockett et al., 2011). In the present experiments, inhibition of CaMKII significantly impaired both somatic and dendritic Arc expression, while inhibition of MAPK and PKG significantly reduced Arc expression in the dendrites alone (refer section 4.1.5. *Arc Protein Expression is Dependent on CaMKII/MAPK/PKG Signalling*). Thus CaMKII, MAPK, and PKG may mediate distinct aspects of sAPP α -induced functions throughout each neuronal compartment.

Indeed, evidence suggests that PKG may act to facilitate trafficking of Rab11-positive vesicles. Rab11 is a protein primarily associated with recycling endosomes, and can mediate anterograde trafficking from the trans-Golgi network and perinuclear endosome (Chen et al., 1998; Takahashi et al., 2003; Ang et al., 2004; Lock and Stow, 2005). This trafficking is achieved through close association with the Ca $^{2+}$ -sensitive motor protein myosin Vb (Wang et al., 2008). Interestingly, PKG has been linked to the nitric oxide (NO)-dependent stimulation of anterograde trafficking of Rab11A-positive recycling endosomes (Zhai et al., 2017) and has been shown to directly bind Rab11B (Reger et al., 2014). Both Arc protein and mRNA colocalize with Rab11 (Wu et al., 2011) and inhibition of Rab11 activity impairs postsynaptic expression of Arc protein in *Drosophila* motor neurons (Ashley et al., 2018). Thus, PKG may play an important role in the activity-dependent transport of Arc-containing vesicles throughout the dendrites. Additionally, PKG has been previously shown to be necessary for

the induction and persistence of protein synthesis-dependent LTP (Son et al., 1998; Kleppisch et al., 2003; Liu et al., 2003; Paul et al., 2008). Specifically, Liu et al., (2003) have shown that application of the PKG inhibitor Rp-8-Cl-cAMPS 5 minutes prior to, and 5 minutes following the induction of LTP by TBS, significantly attenuated the induction of LTP and fully eliminated its persistence. This may be explained through the PKG-dependent trafficking of GluA1 and the incorporation of CP-AMPA at the synapse (Incontro et al., 2013) and the induction of IEGs, including Arc (Ota et al., 2010; Gallo and Iadecola, 2011). Therefore, it may be possible that PKG signals both the early insertion of CP-AMPA as well as the trafficking of Arc protein, necessary for the conversion of early- to late-phase LTP (Plath et al., 2006).

The role of CaMKII and the regulation of Arc is intriguing. Arc protein is expressed in glutamatergic CaMKII-positive neurons and interacts with both CaMKII α and CaMKII β to varying degrees. The interaction between CaMKII α has been shown to be weaker than that of CaMKII β , however is able to regulate neurite extension (Donai et al., 2003). Interestingly, Arc protein shows stronger correlations with the inactive form of CaMKII β at inactive synapses following BDNF application *in vitro* or in the primary visual cortex *in vivo* (Okuno et al., 2012). While BDNF treatment alone was found to increase cell surface GluA1 expression, following BDNF treatment with the synapse specific application of the sodium channel blocker tetrodotoxin resulted in a downscaling of AMPAR at inactive synapses specifically (Okuno et al., 2012). These results indicate that while Arc is upregulated strongly with synaptic activity, and appears to localise to active synapses, preferential targeting to inactive synapses may govern control of Arc actions. In this sense, Arc may elicit non-Hebbian 'inverse synaptic-tagging' to maintain differences between synaptic weights during Hebbian plasticity. Interestingly, single synapse inactivation, as utilized by Okuno et al., (2012), has also been shown to promote synapse specific upscaling of CP-AMPA in a manner dependent on the expression of Arc protein, however on a much longer timescale of hours to days (Béïque et al., 2011). Therefore, it may be possible that Arc acts as an inverse tag during synaptic activity at inactive sites in order to produce a reserve pool of GluA1-containing AMPAR to be utilized during synaptic upscaling following longer periods of activity.

Our results show that inhibition of CaMKII inhibits both dendritic as well as somatic Arc protein expression. In many cases, the expression of Arc is under control of CREB expression (Ying et al., 2002; Lv et al., 2015; Chen et al., 2017). In the current studies, we have shown that sAPP α enhances Arc protein expression in area CA1 of acute hippocampal tissue and within the dendrites of cultured hippocampal neurons, in a manner dependent on NMDAR and α 7nAChR activation. Importantly, this increase occurs subsequent to an increase in pCREB (refer 4.2. *sAPP α Increases CREB Phosphorylation and Arc Protein in Acute Hippocampal Slices*). The Arc gene contains a binding site for

CREB protein located within a unique cluster of synaptic activity-responsive elements (SARE; Kawashima et al., 2009). Importantly, PKG (Gudi et al., 1999; Chen et al., 2003) and CaMKII have been shown to regulate CREB-dependent transcription or *Arc* mRNA transcripts (Sheng et al., 1991; Wheeler et al., 2008; Wheeler et al., 2012; Yan et al., 2016), with CaMKII likely mediating CREB phosphorylation via a mechanism which requires retrograde synapse to nucleus signalling (Ma et al., 2014a). Alternatively, once present at the synapse, PKG, in concert with MAPK (Huang et al., 2007; Bramham et al., 2010) and CaMKII may also regulate protein synthesis of synaptic proteins including *Arc* (Kleppisch et al., 2003; Claasen et al., 2009; Mockett et al., 2011), in a manner which may include direct phosphorylation of p38 MAPK (Browning et al., 2000; Michel et al., 2011) or CPEB (Atkins et al., 2004).

A crucial, yet outstanding question in the literature is the identity of the sAPP α receptor or receptors through which sAPP α may act to promote these downstream mechanisms. Previous evidence has described a role of GABA $_B$ (Rice et al., 2017; Rice et al., 2019), Na $^+$ /K $^+$ ATPase (Dorard et al., 2018), α 7nACh (Richter et al., 2018) and NMDA receptors (Gakhar-Koppole et al., 2008; Mockett et al., 2019) in mediating sAPP α 's neurotrophic and plasticity-enhancing effects. To understand the receptors contributing to the facilitated *Arc* expression, we investigated the possible contributions of these and other candidate receptors, including mGluRI/II and TrkB, due to their similar neuromodulatory or plasticity-promoting properties (Raymond et al., 2000; Mockett et al., 2011). Of note, is the observed lack of dependence of TrkB, the receptor responsible for mediating the plasticity-enhancing effects of BDNF (Minichiello et al., 1999), indicating that the enhancement of *Arc* protein by sAPP α is distinct from that of BDNF.

Importantly, our data suggest a synergistic effect between activation of NMDARs and α 7nAChRs (refer section 4.1.6. *Dendritic Arc Protein Expression is Dependent on Activation of NMDA- and α 7nACh Receptors*). Sole inhibition of either receptor alone led to a partial impairment in the sAPP α -mediated expression of *Arc* protein, whereas simultaneous inhibition of both receptors fully eliminated the enhancement of *Arc* protein expression in the dendrites. Further, we have extended our studies to the more complex biological system of acute hippocampal slices (refer section 4.2. *sAPP α Increases CREB Phosphorylation and Arc Protein in Acute Hippocampal Slices*). Here, our findings closely reflected that of the primary hippocampal culture work, as sAPP α significantly enhanced *Arc* protein expression in area CA1 of the hippocampus in a manner dependent on activation of NMDA and α 7nACh receptors. This finding was corroborated by an increase in pCREB expression. Interestingly, this effect was specific to area CA1, as likewise analysis of area CA3 showed

no significant change in Arc protein expression, while a small but non-significant increase in both pCREB and Arc protein was observed in the dentate gyrus.

NMDA and $\alpha 7$ nACh receptors show somatic and dendritic distribution throughout hippocampal pyramidal neurons (Dominguez del Toro et al., 1994; Rao and Craig, 1997), and in some cases form $\alpha 7$ nAChR-NMDAR complexes (Li et al., 2012; Li et al., 2013). Importantly, the activation of $\alpha 7$ nAChR has been shown to enhance the activation of NMDAR (Aramakis and Metherate, 1998; Aramakis et al., 2000), specifically at synapses lacking functional AMPAR expression, likely through greater permeability to Ca^{2+} than that of NMDAR (McGehee, 1999; Levy and Aoki, 2002). Such $\alpha 7$ nAChR-enriched, AMPAR-lacking synapses may depend on $\alpha 7$ nAChR to provide voltage dependent activation of NMDAR. Importantly, both NMDAR and $\alpha 7$ nAChR promote the activation of the NO-cGMP-PKG pathway (Contestabile, 2000; Serulle et al., 2007; Ota et al., 2010; Khan et al., 2016; Gulisano et al., 2019; Kusuda et al., 2020), as well as MAPK (Haddad, 2005; Gubbins et al., 2010; Yang et al., 2014; Ma et al., 2018) and CaMKII (Cammarota et al., 2000; Thalhammer et al., 2006; Gubbins et al., 2010), leading to the phosphorylation of CREB (Xia et al., 1996; Gubbins et al., 2010). Therefore, in order to transduce these signalling cascades, sAPP α may directly bind to these receptors. APP has been shown to co-immunoprecipitate with NMDAR subunits (Cousins et al., 2009; Innocent et al., 2012) and is found present at synapses expressing $\alpha 7$ nAChR (Li et al., 2010), while sAPP α itself has been proven to act as a high-affinity, allosteric potentiator of $\alpha 7$ nAChR (Forest et al., 2018; Richter et al., 2018). Importantly, Richter et al., (2018) have shown that application of the $\alpha 7$ nAChR antagonist α -bungarotoxin (α BGT) following the application of sAPP α does not significantly affect the expression of sAPP α -enhanced LTP. However, co-application of sAPP α and α BGT before the induction of LTP significantly inhibits LTP expression. Importantly, these results indicate that sAPP α requires $\alpha 7$ nAChR during the priming phase before the induction of LTP as $\alpha 7$ nAChR do not appear to contribute directly to the induction or maintenance of LTP, likely indicating that $\alpha 7$ nAChR activate downstream cascades and mechanisms which subsequently enhance LTP following TBS.

Many of the reports describing sAPP α 's ability to enhance LTP have been shown in area CA1, including the dependence on NMDA (Mockett et al., 2019) and $\alpha 7$ nACh receptors (Richter et al., 2018). Previous work has also shown that sAPP α enhances LTP within the dentate gyrus *in vivo*, however only occurring at concentrations no lower than 11 nM (Taylor et al., 2008), indicating that concentrations used in the current experiments may not be sufficient to drive the full complement of Arc expression. The dependence on NMDAR and $\alpha 7$ nAChR in our primary hippocampal cultures, but the observed lack of effect within the dentate gyrus (refer section 4.2.1. *Trend in CREB Phosphorylation and Arc Protein Expression in the Dentate Gyrus of Acute Hippocampal Slices*) may in

fact be explained by the heterogeneity of our cultured neuron populations. While excitatory pyramidal neurons contain both NMDAR and $\alpha 7$ nAChR (Perouansky and Yaari, 1993; Chung et al., 2016), excitatory granule cells appear to only express NMDARs (Bernabeu, 2000; Dalby and Mody, 2003; Wright and Jackson, 2014), and lack functional $\alpha 7$ nACh receptors (Frazier et al., 2003; John et al., 2015). Interestingly, diverse populations of inhibitory neurons in CA1 and dentate gyrus subregions of the hippocampus contain both functional NMDAR and $\alpha 7$ nAChR (McQuiston and Madison, 1999; Son and Winzer-Serhan, 2008; Carlén et al., 2012). In response to activity, Arc mRNA and protein expression has been noted within inhibitory neurons of both the hippocampus and cortex (Vazdarjanova et al., 2006; Wang et al., 2016). Therefore, within the mixed population of neurons analysed in our data set, it is possible that inhibition of NMDAR and $\alpha 7$ nAChR during sAPP α treatment differentially targets distinct, but likely overlapping populations of dentate gyrus and CA-derived excitatory and inhibitory neurons expressing NMDAR, $\alpha 7$ nAChR, or both. This interpretation may also be applied to acute hippocampal slices, such that sAPP α treatment may enhance Arc expression in both excitatory and inhibitory cells within area CA1, yet only affect interneurons within the dentate gyrus. Future experiments should aim to incorporate markers of inhibitory and excitatory neurons to aid analysis and further clarify the possible cell-type specific effects of sAPP α .

Alternatively, additional receptors may be required for the full complement of Arc protein expression throughout the hippocampus. Previously, sAPP α has been shown to enhance the expression and activity of Na⁺/K⁺ ATPase (Dorard et al., 2018). Na⁺/K⁺ ATPase is a membrane-bound enzyme responsible for generating and maintaining the Na⁺ and K⁺ electrochemical gradients across the cell membrane. Importantly, Na⁺/K⁺ ATPase is found throughout the hippocampus, including in CA pyramidal and interneuron cells (Richards et al., 2007), as well as excitatory and inhibitory cells of the dentate gyrus (Ross and Soltes, 2000). While research has yet to provide a link between Na⁺/K⁺ ATPase activity and Arc protein expression, the activation of NMDAR-dependent cGMP-NO-PKG signalling has been previously linked to the regulation of Na⁺/K⁺ ATPase (Munhoz et al., 2005), and the activation and expression of Na⁺/K⁺ ATPase regulates MAPK and CaMK activity, CREB phosphorylation, and may regulate aspects of LTP persistence (Gloor, 1997; Glushchenko and Izvarina, 1997; Desfrere et al., 2009). Interestingly, Na⁺/K⁺ ATPase has been found to associate with GluA1- and GluA2/3-containing AMPAR, and inhibition of Na⁺/K⁺ ATPase suppresses EPSPs and downregulates cell surface GluA1 and GluA2/3, possibly implicating this surface-bound enzyme in the regulation of AMPAR trafficking or sequestering at the cell surface (Zhang et al., 2009).

Regardless, these results indicate that concerted activity between NMDARs and $\alpha 7$ nAChRs may act to promote sAPP α -mediated Arc expression through the synergistic activation of downstream

cascades involving CaMKII, PKG and MAPK. This activation of Arc protein may further regulate gene expression, expression of synaptic AMPAR, or modification of the actin cytoskeleton.

7.4.1. *Arc regulates de novo GluA1 expression*

Unexpectedly, short (30 min) but not long (120 min) treatments of sAPP α increased cell surface *de novo* GluA1, with expression of these AMPAR showed a return of *de novo* GluA1 to basal levels, at both the somatic and dendritic cell surface. Given past observations that surface internalisation under basal conditions is low (Passafaro et al., 2001), it is unlikely this is governed by a mechanism of passive endocytosis. Interestingly, clathrin-mediated endocytosis has been found capable of internalizing roughly 58.9% of AMPAR within 1-hour following acute insulin treatment (Man et al., 2000), placing a similar mechanism within our treatment window. Therefore, we further hypothesised that this decrease of *de novo* GluA1-containing AMPAR may be due to processes of active endocytosis. To examine this, we employed Acell™ siRNA-mediated inhibition of *de novo* Arc synthesis and protein expression (refer section 6.1.4. *Accell™ Arc siRNA Inhibits Somatic and Dendritic sAPP α -Dependent, but not Basal, Arc Expression*). Here, we found an accumulation and persistence of *de novo* GluA1-containing AMPAR following 2-hour co-incubation of siRNA with sAPP α (refer section 6.1.5. *Internalization of de novo GluA1 is Dependent on Arc Expression*), indicating that these AMPAR are internalised by Arc within the 2-hour treatment window, and inhibition of Arc expression prevents the observed reduction in these early expressed GluA1.

Previous work has provided evidence that Arc expression may govern regulation of GluA1-containing AMPAR. Knockout of Arc protein in primary hippocampal cultures has been shown to increase cell surface GluA1- but not GluA2-containing AMPAR, and occlude activity-dependent homeostatic scaling (Shepherd et al., 2006). Knockout of Arc expression *in vivo* shows a largely enhanced fEPSP during the initial 60 minutes following tetanisation, perhaps indicating an unregulated increase in CP-AMPA at the synapse (Plath et al., 2006). Interestingly, this group found no increase in rectification during baseline stimulation, however this may be due to the activity-dependent nature of CP-AMPA insertion and thus may have only been uncovered had rectification been measured post-tetanisation or at extrasynaptic sites. Interestingly, knockout of Arc in the visual cortex further upregulates s831 phosphorylation on the GluA1 AMPAR subunit (Gao et al., 2010), a phosphorylation site likely involved in the regulation of CP-AMPA (Kim and Ziff, 2014; Yang et al., 2018; Park et al., 2019b; Summers et al., 2019). While these animals did not show enhanced cell surface GluA1 or GluA2 protein from total PSD homogenate, they did show enhanced mEPSC amplitude and impaired experience-dependent homeostatic plasticity. While enhancements in s831

phosphorylation did not alter rectification, this may indicate that absence of Arc protein leads to increased persistence of CP-AMPA at the perisynaptic or extrasynaptic cell surface, and that this persistence occludes experience-dependent scaling. Further, in response to mGluR-mediated LTD, application of the mGluR agonist DHPG results in a decrease in rectification, alongside a decrease in cell surface GluA1 but not GluA2 protein. Given mGluR-LTD requires an increase in Arc protein synthesis (Waung et al., 2008) and removal of cell surface CP-AMPA (Lanté et al., 2011; Scheyer et al., 2018), it is possible that this mechanism is governed through the actions of Arc. Conversely, overexpression of Arc protein has been previously shown to significantly increase the decrease in rectification in neurons, in a manner effect dependent on Arc's ability to bind the clathrin-associated protein AP2 (DaSilva et al., 2016). These observations likely support a role for Arc-dependent endocytosis in the regulation of *de novo* CP-AMPA in the current experiments. The Arc-dependent removal of these AMPAR may thus facilitate the exchange for GluA1/2-containing AMPAR by increasing the availability of synaptic slots (McCormack et al., 2006).

Additionally, we have shown that the *de novo* GluA1-containing AMPAR are primarily extrasynaptic (refer section 6.1.2.1. *sAPP α Enhances the Extrasynaptic, but not the Synaptic Population of *de novo* Cell Surface GluA1*). This domain contains proteins necessary for the formation of the endocytic zone and clathrin-coated pits (Lu et al., 2007a). Therefore, this may indicate that *de novo* AMPAR present at extrasynaptic domains are primed to be removed from the cell surface following treatment of cultures with sAPP α for 30 minutes. Previously, it has been shown that extrasynaptic AMPAR are removed rapidly from the cell surface following NMDAR activation, and preceded the removal of synaptic AMPAR (Ashby et al., 2004; Sanderson et al., 2011). In these experiments, extrasynaptic sites showed a recovery of AMPAR following NMDAR washout, indicating that extrasynaptic sites are repopulated with either synaptic AMPAR from adjacent regions of the plasma membrane, or rapid trafficking of AMPAR from internal recycling pools. This may indicate that extrasynaptic AMPAR are initially internalized to facilitate the removal of synaptic AMPAR, possibly through the formation of extrasynaptic 'slots' within the endocytic zone (Haucke et al., 2011). This likely promotes the return of AMPAR to an internal recycling pool to be utilized in subsequent plasticity events. Interestingly, past evidence has shown that application of NMDA to cortical cultures transiently increases the phosphorylation of GluA1 at s831, followed by the dephosphorylation of s845 and removal of cell surface GluA1. This was found to increase the endosomal pool of GluA1-containing AMPAR and facilitate their reinsertion at the cell surface and later accumulation at synapses following both basal- and activity-dependent activity in primary cultures (Ehlers, 2000). Interestingly, BDNF has been shown to likewise regulate the expression of cell surface GluA1-containing AMPAR, such that short-term (30 minute) BDNF treatments enhance cell surface AMPAR in

nucleus accumbens medium spiny neurons, while long-term (24 hour) treatments decrease cell surface AMPAR beyond control levels. These results indicate that homeostatic processes may govern the regulation of AMPAR expression following both BDNF and sAPP α treatments. The current experiments may reflect similar mechanisms, such that treatment of hippocampal neurons with sAPP α may transiently enhance the cell surface expression of CP-AMPAR and s831 phosphorylation, while Arc-dependent internalization of these AMPAR may act to increase the endosomal recycling pool. The current experiment did not detect a decrease in total cell surface GluA1, as assessed by BioPLAy, however, examining the *de novo* population of GluA1-containing AMPAR with FUNCAT-PLA provided evidence for this.

7.5. Mechanism of Action

So far, this chapter has aimed to assess the role of sAPP α in regards to existing literature, encompassing aspects of LTP and synapse strengthening by previously identified neurotrophins. In an attempt to further clarify how this literature has influenced how sAPP α regulates the synthesis, expression, and function of AMPAR and Arc, two likely mechanisms are posited.

Firstly, the activation of NMDA and α 7nACh receptors by sAPP α may promote NO, and cGMP signalling via Ca²⁺ influx, further promoting the activation of CaMKII, MAPK and PKG (Figure 7-1). These signalling cascades signal CREB phosphorylation and begin to enhance transcription of IEGs Arc and *Zif268*, and further upregulate miR-30 expression. During this time CAMKII, possibly in concert with PKG may promote the trafficking of pre-existing internal reserve pools of GluA1-containing CP-AMPAR to the cell surface, and likely stimulate lateral movement of AMPAR from extrasynaptic to perisynaptic sites. Simultaneously, NMDAR and α 7nACh signalling may promote both the removal of GluA2/3-containing AMPAR by endocytosis, increasing the number of available synaptic slots. These AMPAR may then be targeted towards either the lysosome for degradation or recycling endosomes. These signalling cascades further promote the synthesis of GluA1 subunits either locally or via trafficking from somatic ER, the formation of CP-AMPAR, and refilling of internal recycling endosome pools. Parallel to this, *de novo* GluA2 subunits may be restricted from ER exit via associations with PICK1. Alternatively, miR-30 expression may downregulate GluA2 expression by inhibiting synthesis or promoting mRNA degradation. Regardless of the mechanism, a reduction in GluA2 forward trafficking promotes the formation of GluA1 homomeric CP-AMPAR. Following TBS, perisynaptic CP-AMPAR are inserted into the synapse to potentiate the EPSP, while extrasynaptic CP-AMPAR translocate to perisynaptic domains. During this time, *de novo* AMPAR likely traffic to the cell surface to expand the extrasynaptic pool, possibly governed via signals from synaptic CP-AMPAR. By 2 hours, synaptic CP-AMPAR may then diffuse back to the extrasynaptic membrane, and alongside *de novo* GluA1-

containing AMPAR, are removed from the cell surface, possibly by an Arc-dependent mechanism. Internalization of CP-AMPAR may permit the trafficking and replacement with GluA1/2-containing AMPAR at synaptic or extrasynaptic sites.

Alternatively, in addition to promoting the lateral trafficking of pre-existing cell surface CP-AMPAR, activation of NMDAR and $\alpha 7$ nAChR may signal the rapid synthesis and exocytosis of *de novo* CP-AMPAR (Figure 7-2). Simultaneously, sAPP α promotes the removal of GluA2/3-containing AMPAR, increasing the number of available synaptic slots. Following TBS stimulation in slices, these AMPAR may traffic to the synapse to enhance the EPSP and promote downstream signalling, returning to extrasynaptic sites to be removed during the maintenance of LTP. In culture, basal synaptic transmission may be sufficient to drive these AMPAR to the surface but not to the synapse (Oh et al., 2006), thus these AMPAR may reside at extrasynaptic sites. Regardless of whether *de novo* GluA1-containing AMPAR reach the synapse both pre-existing and *de novo* AMPAR return to, or reside at extrasynaptic sites, where Arc-dependent clathrin-mediated endocytosis occurs (Blanpied et al., 2002; Ashby et al., 2004; Tao-Cheng et al., 2011). The removal of these AMPAR likely permits the replacement of CP-AMPAR by GluA1/2-containing AMPAR.

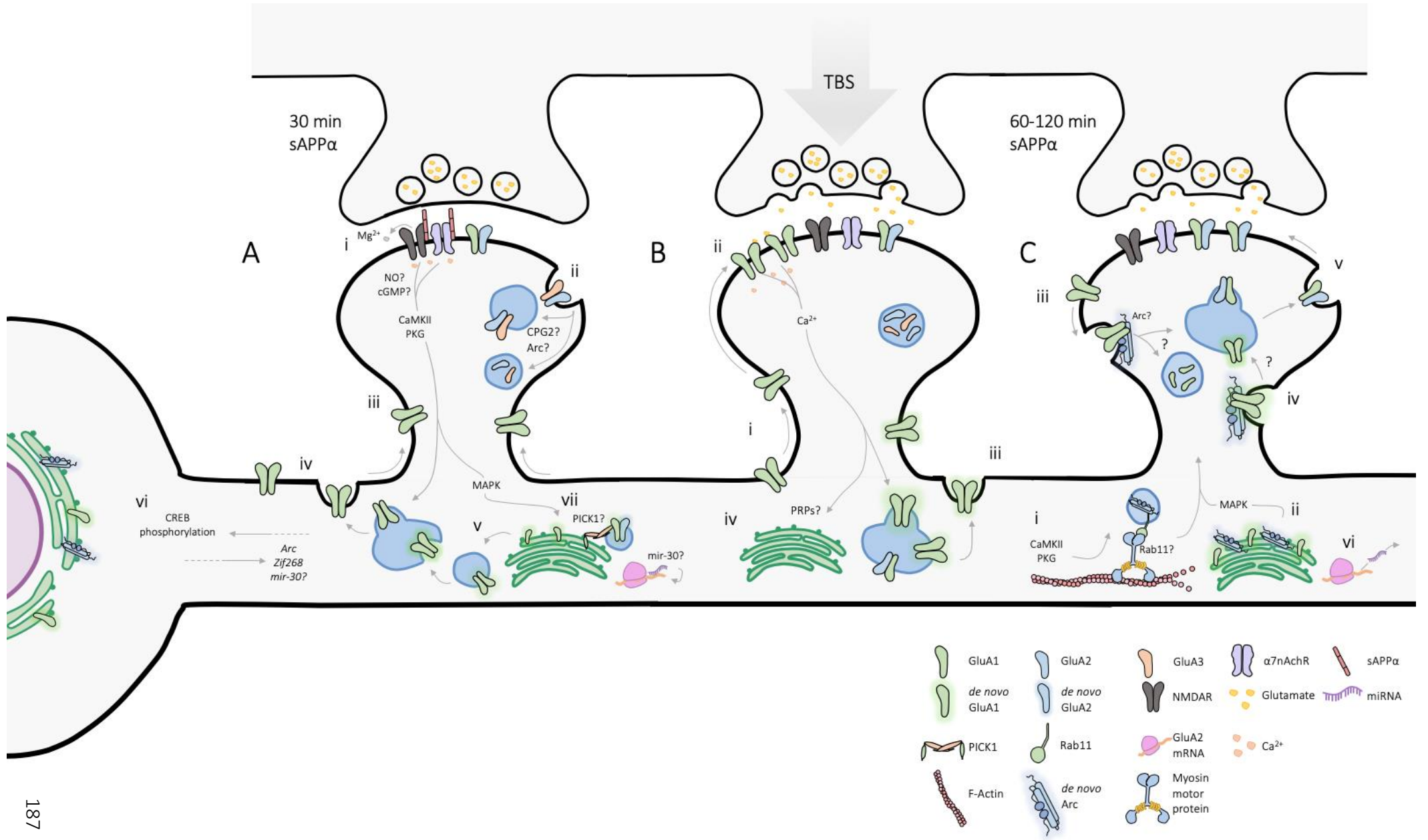


Figure 7-1 | Regulation of cell surface AMPAR – Extrasynaptic Exocytosis model. A) Application of sAPP α promotes the i) activation of NMDAR and $\alpha 7nAChR$, allowing the influx of Ca^{2+} , possible activation of NO and cGMP, and activation of CaMKII, MAPK, and PKG. Following this ii) GluA2/3-containing AMPAR are removed from the cell surface, possibly in a manner dependent on Arc or CPG2. These AMPAR are then targeted towards either the lysosome for degradation or recycling endosomes. During this time, iii) CP-AMPA are trafficked towards the synapse by lateral diffusion. In addition to this, iv) CP-AMPA are trafficked from existing internal stores to refill extrasynaptic domains. Downstream signalling may further v) enhance the early synthesis of GluA1 subunits for formation of *de novo* CP-AMPA and refilling of recycling pools. Signalling from NMDAR and $\alpha 7nAChR$ vi) also promotes CREB phosphorylation and induction of *Arc*, *Zif268*, and possibly miR-30 transcripts. vii) sAPP α may further promote reductions in cell surface *de novo* GluA2 expression through associations with PICK1 or by suppression of translation by miR-30. B) Following synaptic activity, i) perisynaptic CP-AMPA are incorporated at the synapse, while extrasynaptic CP-AMPA translocate to perisynaptic domains, and ii) synaptic activity at synaptic CP-AMPA may promote the iii) trafficking of *de novo* CP-AMPA to extrasynaptic sites. iv) Additionally, activity through CP-AMPA has been shown to promote the protein-synthesis component of LTP (Park, 2018; Park et al., 2018), and thus may provide the necessary signals for the synthesis of additional plasticity related proteins (PRPs). C) Within 2 hours of sAPP α treatment CREB signalling promotes the transcription of *Arc* mRNA and subsequent protein. i) *Arc* mRNA or protein is thus trafficked throughout the dendrites in a manner dependent on CaMKII, MAPK, and PKG. Alternatively, ii) *Arc* protein may be synthesised locally. iii) Synaptic CP-AMPA, as well as extrasynaptic *de novo* CP-AMPA are removed from the cell surface via *Arc*, and are either iv) directed towards the lysosome for degradation or more likely refill the recycling pool of AMPAR. The removal of these AMPAR likely permit v) the exocytosis of GluA1/2-containing AMPAR from internal stores. vi) Previous restrictions of cell surface *de novo* GluA2 by PICK1 or miR-30 may be relieved by this time.

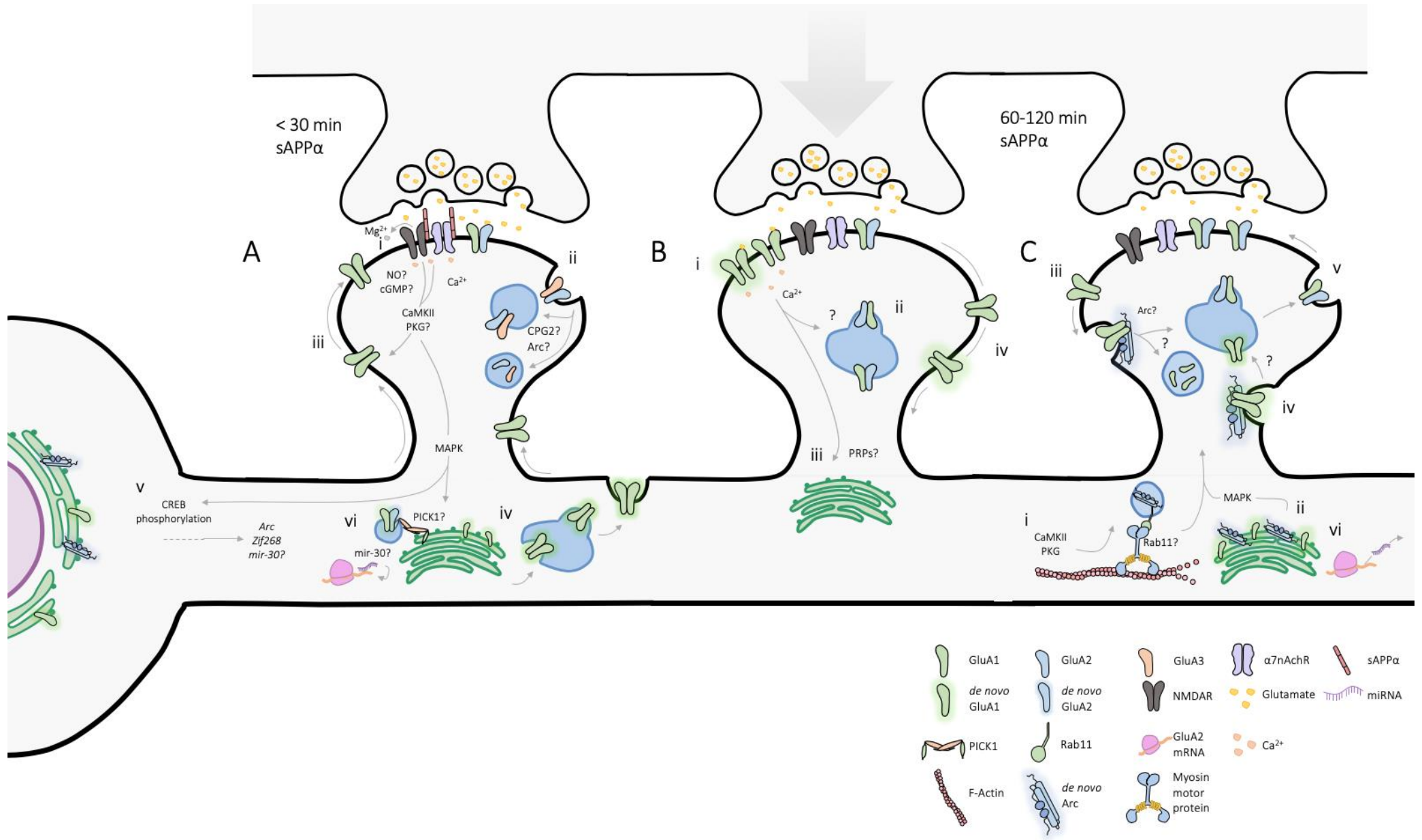


Figure 7-2 | Regulation of cell surface AMPAR – Extrasynaptic Endocytosis model. Application of sAPP α promotes the i) activation of NMDAR and α 7nAChR, allowing the influx of Ca²⁺, possible activation of NO and cGMP, and activation of CaMKII, MAPK, and PKG. Following this ii) GluA2/3-containing AMPAR are removed from the cell surface, possibly in a manner dependent on Arc or CPG2. These AMPAR are then targeted towards either the lysosome for degradation or recycling endosomes. During this time, iii) CP-AMPA are trafficked towards perisynaptic domains synapse by lateral diffusion. Downstream signalling may further enhance iv) the early synthesis of GluA1 subunits for formation of *de novo* CP-AMPA and trafficking to the cell surface to refill extrasynaptic domains. Signalling from NMDAR and α 7nAChR v) also promotes CREB phosphorylation and induction of *Arc*, *Zif268*, and possibly miR-30 transcripts. vi) sAPP α may further promote reductions in cell surface *de novo* GluA2 expression through associations with PICK1 or by suppression of translation by miR-30. B) Following synaptic activity, i) perisynaptic CP-AMPA are incorporated at the synapse and ii) synaptic activity at CP-AMPA may promote the iii) trafficking of *de novo* CP-AMPA to synaptic sites. iv) Activity through CP-AMPA has been shown to promote the protein-synthesis component of LTP (Park et al., 2018), and thus may provide the necessary signals for the synthesis of additional plasticity related proteins (PRPs), or the formation of existing GluA1/2 endosomal pools. Following this, CP-AMPA including both pre-existing and *de novo* AMPAR may iv) return to extrasynaptic sites for endocytosis. C) Following 2 hours of sAPP α treatment CREB signalling promotes the transcription of *Arc* mRNA and subsequent protein. i) *Arc* mRNA or protein is thus trafficked throughout the dendrites in a manner dependent on CaMKII, MAPK, and PKG. Alternatively, ii) *Arc* protein may be synthesised locally. iii) Extrasynaptic pre-existing CP-AMPA, as well as iv) extrasynaptic *de novo* CP-AMPA are removed from the cell surface via *Arc*, and are either directed towards the lysosome for degradation, or more likely to refill the recycling pool of AMPAR. The removal of these AMPAR likely permits v) the exocytosis of GluA1/2-containing AMPAR from internal stores. vi) Previous restrictions of cell surface *de novo* GluA2 by PICK1 or miR-30 may be relieved by this time.

7.6. A Possible Role for Silent Synapses

In early postnatal development, the expression of NMDAR precedes that of AMPAR at glutamatergic synapses, acquiring AMPAR throughout later development (Petralia et al., 1999). These early AMPAR-lacking synapses are termed 'AMPA-silent' or 'silent' synapses, and have been proposed as a likely mechanism underlying synaptogenesis during both development and learning-induced plasticity. The presence of NMDAR permits NMDAR-dependent LTP, assuming the voltage-dependent Mg^{2+} block of NMDAR is relieved either by direct depolarisation of the postsynaptic membrane (Isaac et al., 1995), or activation of non-AMPA receptors (Smith et al., 2005; Lozada et al., 2012). Many mechanisms have been put forward as a means to determine how silenced synapses become 'unsilenced,' or active. The existence of silent synapses has previously been explained through both presynaptic and postsynaptic mechanisms, with presynaptic mechanisms describing a handicap of neurotransmitter release in response to action potentials, with LTP enhancing both the probability of release (Gasparini et al., 2000) or increases in neurotransmitter quanta (Kullmann and Nicoll, 1992). Alternatively, postsynaptic changes, including AMPAR trafficking have been proposed (Liao et al., 2001; Xiao et al., 2004; Abrahamsson et al., 2007; Busetto et al., 2008; Huupponen et al., 2016).

Importantly, many of these postsynaptic trafficking mechanisms implicate CP-AMPA in mitigating the formation of intermediate 'AMPA-labile' synapses. Upon synapse awakening, these AMPARs are thought to be inserted at previously AMPA-silent synapses and promote the further insertion of CI-AMPA. Conversely, this period of lability also means recently awakened synapses are susceptible to re-silencing through low frequency baseline stimulation or LTD (Xiao et al., 2004; Morita et al., 2014). The initial formation of AMPA-silent synapses appears to be under the guidance of CaMKIV and CREB, while the insertion of CP-AMPA to AMPA-labile synapses has been shown to be dependent on s831 phosphorylation, CaMKII and PKA (Liao et al., 2001; Poncer et al., 2002; Zheng and Keifer, 2009). In the adult brain, few silent synapses exist at basal (Petralia et al., 1999), however, silent synapses have been found to exist within DIV 21-28 primary cell cultures (Liao et al., 1999; Xu et al., 2020). Notably, while synapses present on spines were primarily occupied by both AMPAR and NMDAR by DIV 11, many dendritic shaft synapses were AMPAR-lacking even at DIV 23. Importantly, following cLTP, many of these AMPAR-lacking synapses gained greater proportions of GluA1 than synapses present in spines, and thus were deemed more "potentiable" (Xu et al., 2020).

In vivo, many mechanisms have been shown which enhance both the formation of AMPA-silent and AMPA-labile synapses, as well as their conversion into mature synapses. Of note, cocaine-induced drug addiction behaviour has been shown to enhance the proportion of silent synapses in adult rats (Brown et al., 2011), initially through the synthesis and insertion of GluN2B-containing NMDAR receptors (Huang et al., 2009), followed by insertion of CP-AMPA (Lee et al., 2013; Ma et al.,

2016; Wright et al., 2020), possibly in a manner involving dopamine- or BDNF-dependent local protein synthesis (Itami et al., 2003; Smith et al., 2005). Following the generation of silent synapses, withdrawal of cocaine or application of an enriched environment induces LTP-like mechanisms to enhance both the synthesis (Churchill et al., 1999) and synaptic expression (Boudreau and Wolf, 2005) of GluA1-containing AMPAR, in a manner which occludes additional LTP (Goto and Grace, 2005; Moussawi et al., 2009; Ma et al., 2016). Interestingly, application of the mGluR5 agonist DHPG during the CP-AMPA mediated AMPA-labile period also induces a removal of CP-AMPA and replacement of CI-AMPA (McCutcheon et al., 2011), while application of NMDAR-dependent LTD re-silences synapses by the removal of CP-AMPA without replacement (Ma et al., 2016). Many systems which regulate local protein synthesis and trafficking of CP-AMPA also regulate the expression and development of silent synapses, including both dopamine and BDNF (Smith et al., 2005; Caldeira et al., 2007; Li and Wolf, 2011; Fortin et al., 2012; Leal et al., 2014). Specifically, BDNF has been shown to play an important role in the maturation of silent synapses (Itami et al., 2003). Knockout of BDNF shows an increase in the proportion of silent synapses and an inability to convert these synapses following an LTP pairing protocol. Application of exogenous BDNF restores the ability to convert silent synapses to mature synapses, requiring rapid GluA1-dependent trafficking, followed by a GluA2-dependent trafficking.

With relevance to the current studies, we posit that one of the possible mechanisms through sAPP α may regulate synaptic plasticity is, in part, through the formation or maturation of silent synapses. Previously in this chapter, we have provided evidence that sAPP α may modulate synaptic plasticity at mature synapses, however these mechanisms may not be mutually exclusive (Figure 7-3). sAPP α has been shown to enhance the expression (Hoe et al., 2009; Mockett et al., 2011) and activation (Xiong et al., 2004) of NR1- and NR2B- containing AMPAR, a necessary step in the induction of AMPA-silent synapses (Nakayama et al., 2005; Xia et al., 2017). In addition to this, we have shown that sAPP α enhances the early expression of *de novo* GluA1-containing CP-AMPA (refer section 5.1.3. *CP-AMPA Contribute to the Initial Enhancement of sAPP α -LTP* and 6.1.2. *sAPP α Promotes the Rapid and Transient Trafficking of de novo GluA1-containing AMPAR to the Somatic and Dendritic Cell Surface*), likely exchanging these with GluA2-containing AMPAR (refer section 6.1.7. *sAPP α Promotes the Delayed Expression of Cell Surface GluA1/2-Containing AMPAR*). In further support of this, we have also shown that Arc protein synthesis is, in part, regulated by α 7nAChR as well as NMDAR (refer section 4.1.6. *Dendritic Arc Protein Expression is Dependent on Activation of NMDA- and α 7nACh Receptors*), while others have shown that α 7nAChR are necessary for sAPP α 's enhancement of LTP (Richter et al., 2018). Importantly, α 7nAChR are found to be present at both AMPAR-positive and

AMPA-negative synapses (Levy and Aoki, 2002), but also couple to (Li et al., 2012; Zhang et al., 2016a) and regulate NMDAR (Delibas et al., 2005; Shen et al., 2016; Tang et al., 2018). It has been recently shown that nicotinic activation of $\alpha 7$ nAChR enhances the frequency of postsynaptic AMPA-mediated mEPSCs, typically associated with a decrease in the proportion of AMPA-silent synapses, and an increase in AMPAR-responses (Isaac et al., 1995; Tang et al., 2015). This effect was found to be dependent on the trafficking of CP-AMPAR, as well as phosphorylation mediated by CaMKII, PKC, and PKA (Tang et al., 2015). These results possibly implicate $\alpha 7$ nAChRs in mediating an enhancement of AMPA-labile synapses and therefore may play a role in enhancing synaptic plasticity in response to sAPP α treatment by a similar means.

Morphologically, the structural correlates of silent synapses are relatively unknown. Observations from cell culture indicate that AMPA-silent synapses exist primarily on the dendritic shaft (Xu et al., 2020), with NR2B-containing NMDAR appear to predominate in young spines, and an increasing contribution of GluA1 as the synapse matures (Oray et al., 2005). Cocaine- and alcohol-dependent addiction behaviour studies further indicate that the formation of silent synapses may occur through the generation of new spines, finding that the number of spines increases by increasing the proportion of new immature thin and filopodia spines, with no change in the number of mature mushroom spines (Graziane et al., 2016; Beroun et al., 2018). Conversely, silent synapses have also been observed to occur at mushroom spines (Busetto et al., 2008), concluding that the morphology of silent synapses does not always predict the AMPAR content. Additionally, this may indicate that rejuvenation or elimination of existing synaptic contacts also occurs by mechanisms governing the trafficking of AMPAR and the silencing and unsilencing of these synapses (Dong, 2016).

We have further shown that the proportion of *de novo* cell surface GluA1-containing AMPAR are expressed within extrasynaptic domains (refer section 6.1.2.1. *sAPP α Enhances the Extrasynaptic, but not Synaptic Population of de novo Cell Surface GluA1*). Interestingly, it has been previously shown that extrasynaptic CP-AMPAR permit the formation of new synapses, by providing the necessary NMDAR voltage-dependent relief (Schmidt-Salzman et al., 2014). These synapses appear capable of transducing presynaptic activity and integrating into the neural circuit (Kwon and Sabatini, 2011). Further, CP-AMPAR have been shown to be essential for the formation of synapses following repetitive LTP in culture (Tominaga-Yoshino et al., 2020), a stimulation paradigm which enhances synaptogenesis, increasing the proportion of immature synapses and the frequency of miniature EPSCs (Urakubo et al., 2006; Tominaga-Yoshino et al., 2008). Therefore, the presence of extrasynaptic CP-AMPAR following sAPP α treatment may not be a passive mechanism, and may instead contribute significantly to the formation of new spines and synapses.

Lastly, APP, and specifically sAPP α have been implicated in the formation and maturation of synapses (Wang et al., 2009; Southam et al., 2019). Knockout of APP reduces spine density (Tyan et al., 2012), in a manner which is restored with viral expression of sAPP α , but not sAPP β (Richter et al., 2018). This knockout of APP preferentially increases the number of stubby spines, with a relative decrease in mushroom spines, while knock-in of sAPP α restores the proportion of mushroom spines, with relative decreases in stubby spines (Weyer et al., 2014). These results indicate that chronic expression of sAPP α may promote the conversion of young, possibly AMPA-silent, spines into mature, functional spines. Conversely, the A β domain of APP has been found necessary for activity-induced synaptic depression (Kamenetz et al., 2003), and the reduction of synaptic GluA1, s831 phosphorylation, and CaMKII *in vitro*, further decreasing mEPSC frequency *ex vivo* (Gu et al., 2009). These characteristics were found to impair the conversion of silent synapses into functional synapses and correlated to impaired induction of LTP and performance on a spatial memory task (Bie et al., 2018). Together, this evidence suggests that sAPP α and A β may play opposing roles in the generation and maintenance of silent synapses.

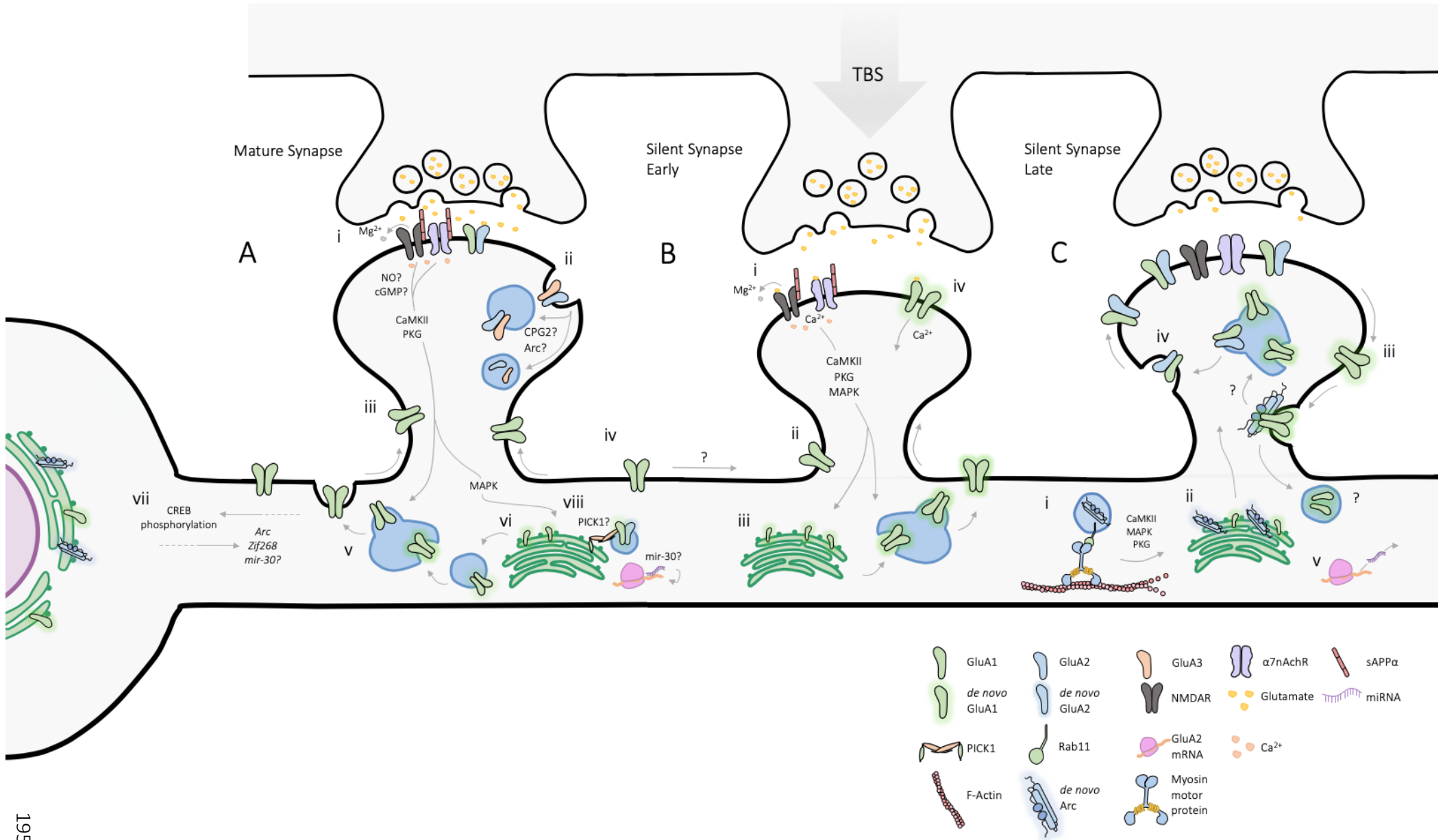


Figure 7-3 | Regulation of cell surface AMPAR at silent synapses. A) Application of sAPP α promotes the i) activation of NMDAR and α 7nAChR, allowing the influx of Ca²⁺, possible activation of NO and cGMP, and activation of CaMKII and PKG. Following this, ii) GluA2/3-containing AMPAR are removed from the cell surface, possibly in a manner dependent on Arc or CPG2. These AMPAR are then targeted towards either the lysosome for degradation or recycling endosomes. During this time, iii) CP-AMPAR are trafficked towards the synapse by lateral diffusion (Ehlers et al., 2007). iv) This lateral diffusion may also supply the CP-AMPAR at silent synapses by diffusional trapping (Harrison et al., 1991; Ehlers et al., 2007). Alternatively, v) a pool of CP-AMPAR are trafficked to the cell surface by exocytosis. vi) MAPK signalling may then promote the rapid synthesis and refilling of these AMPAR at recycling pools. Signalling from NMDAR and α 7nAChR vii) also promotes CREB phosphorylation and induction of *Arc*, *Zif268*, and possibly miR-30 transcripts. viii) sAPP α may further promote reductions in cell surface *de novo* GluA2 expression through associations with PICK1 or by suppression of translation by miR-30. B) At immature, AMPA-silent synapses, i) activation of NMDAR and α 7nAChR promotes the activation of CaMKII, PKG, and MAPK signalling permitting the ii) trapping of cell surface AMPAR, supplied by neighbouring mature synapses, or iii) the synthesis and trafficking of *de novo* CP-AMPAR to the synapse, effectively converting a previously AMPA-silent synapses into a labile, awakened synapse. While it is possible that exocytosis of existing CP-AMPAR from recycling endosomes also occurs at silent synapses, this would likely only occur at synapses which had previously been unsilenced and have formed a local pool of endosomal AMPAR following silencing (Xiao et al., 2004). Alternatively, silent synapses may share endosomal compartments with neighbouring mature synapses, however, this appears rare (Cooney et al., 2002; English et al., 2015). Following synaptic activity these AMPAR may then integrate into the synapse and iv) further promote the influx of Ca²⁺ and downstream signalling cascades, as well as contribute to the EPSP. C) Within 2 hours of sAPP α treatment, CREB signalling promotes the transcription of *Arc* mRNA and subsequent protein. i) *Arc* mRNA or protein is thus trafficked throughout the dendrites in a manner dependent on CaMKII, MAPK, and PKG. Alternatively, ii) *Arc* protein may be synthesised locally. iii) Synaptic CP-AMPAR may be removed from the cell surface via *Arc*, and permit iv) the exocytosis of GluA1/2-containing AMPAR from internal stores. v) Previous restrictions of cell surface *de novo* GluA2 by PICK1 or miR-30 may be relieved by this time.

7.7. *A Promising Role for sAPP α in Synaptic Disorders*

Many molecules and pathways are involved in the expression of both basal synaptic transmission, the induction of synaptic plasticity, and the maintenance of synaptic strength. These processes are controlled through concerted actions of transcription factors (Alberini, 2009; Liu et al., 2011), the synthesis, degradation, and synaptic distribution of Arc and AMPA receptors (Cajigas et al., 2010; Korb and Finkbeiner, 2011; Park, 2018; Pandey et al., 2020), the actions of secreted factors, including neurotrophins, cytokines, hormones, and growth factors (Sastray et al., 1988; Kelly et al., 1998; Moulton and Harvey, 2008; Wang et al., 2012), and the activation of signalling cascades by Ca²⁺-sensitive kinases such as PKA, PKC, PKG, and CaMKII (Huang and Kandel, 1994; Wu et al., 2006; Giese and Mizuno, 2013).

Through this, research has aimed to target the modulation of these systems as a means towards manufacturing a therapeutic for neurodegenerative disorders including AD. Past research has focused on the delivery of neurotrophins and growth factors as a means to enhance downstream neuroprotective and neurotrophic signalling pathways (Aloe et al., 2012). However, the direct application of these molecules in clinical therapeutic use is limited, due to the insurmountable hurdles of unfavourable pharmacokinetic properties (plasma half-life <10 min; Wu, 2005), poor blood–brain barrier (BBB) permeability (Pardridge, 2002), and severe adverse effects (von Bartheld et al., 1994), including hyperinnervation of blood vessels (Isaacson et al., 1990), hypophagia (Williams, 1991), increased hyperexcitability and the susceptibility to seizures (Xu et al., 2004), and off-target effects (Zhao et al., 2017). Through this, alternative means of enhancing the endogenous production of neurotrophins and growth factors have arisen, including small-molecule mimetics (Kazim and Iqbal, 2016; Gupta and Sharma, 2017), botanicals (Sangiovanni et al., 2017), exercise (Rasmussen et al., 2009; Griffin et al., 2011; Coelho et al., 2014), dietary supplementation (Martin et al., 2017), and caloric restriction (Maswood et al., 2004). A facet of these treatments is the application of molecules which directly and positively modulate AMPAR function and kinetics directly. Research into these drugs, labelled AMPAkinetics, stems from the growing realization that abnormalities in synaptic plasticity contribute to a wide range of neurological and cognitive disorders, most notably AD, but extending to autism, bipolar disorder, schizophrenia, addiction, multiple sclerosis, Parkinson's disease and chronic pain (Bliss et al., 2013). AMPAkinetics include agonists (Black, 2005), positive allosteric modulators (Chappell and Witte, 2004), and treatments targeting signalling pathways regulating protein synthesis (Liu et al., 2015b), to facilitate AMPAR-mediated depolarization and mimic AMPAR insertion in LTP, increase depolarization-induced NMDAR Mg²⁺ relief, or enhance the induction of downstream neurotrophic factors to augment further signalling pathways. While some AMPAkinetics have shown promising results in clinical phase 2 studies in AD, Major Depressive Disorder (Bretin et

al., 2017), and Schizophrenia (Noorbala et al., 1999), they do so in the presence of side effects (Wezenberg et al., 2007; Urban and Gao, 2014). Due to this, research has begun to investigate alternative delivery methods of neurotrophins and growth factors into the CNS through means such as encapsulated cell bio-delivery devices (Eyjolfsson et al., 2016), viral vectors (Tuszynski et al., 2005), receptor-mediated BBB transcytosis (Pardridge et al., 1994), and biodegradable microspheres (Aubert-Pouëssel et al., 2004). Most recently, small (40-100 nm) lipid-membrane bound extracellular vesicles (EVs) have been studied as a means of targeted drug delivery (Ha et al., 2016; Akuma et al., 2019). These EVs, or exosomes, have the potential to package proteins of interest, as well as mRNA, cDNA, and miRNA (Statello et al., 2018), and are able to be delivered intranasally or intravenously (Haney et al., 2015), cross the BBB (Saint-Pol et al., 2020), and contain the specific expression of tetraspanins, which preferentially interact with ligands in a tissue- and cell- specific manner (Rana et al., 2012; Luan et al., 2017), thus decreasing off-target effects.

The neurotrophic, neuroprotective, and memory enhancing effects of sAPP α cannot go understated. Indirect modulators of α -secretase activity, including the GABAR modulator Etazolate (Marcade et al., 2008), the 5-HT₄ agonist PRX-03140 (Sabbagh, 2009), the green tea extract epigallocatechin-gallate (Obregon et al., 2006), or the cholinesterase inhibitor Rivastigmine (Maccacchini et al., 2012) have shown promising alleviation of pathology-related symptoms. However, in order to prevent off-target side effects, cell- and tissue-targeted viral- or EV-mediated application of sAPP α , or equally effective peptides derived from sAPP α , should be considered the gold standard method of delivery, and warrant future research.

7.8. *Future Directions*

While the results described within this thesis support a novel role of sAPP α in the synthesis, trafficking, and expression of both the IEG Arc, as well as cell surface AMPA receptors, questions remain regarding the nature of these changes. Firstly, we have shown that sAPP α enhances the cell surface expression of *de novo* GluA1-containing AMPAR at extrasynaptic domains and their internalization parallels the expression of cell surface GluA1/2-containing AMPAR. In order to clarify the role of these AMPAR in sAPP α -mediated plasticity, experiments should aim to determine GluA1/2-containing AMPAR are synaptic, or likewise populate extrasynaptic sites. Additionally, due to sAPP α 's ability to enhance local protein synthesis, further experiments should aim to address this with relevance to the synthesis of AMPAR or Arc protein. Microfluidic local perfusion chambers are a readily available alternative to MatTek culture dishes and allow for the compartmentalization of dendrites from the soma, as well as the ability to apply treatments to discrete populations of

synapses (Taylor et al., 2010). Further, recent advances allow for the photo-uncaging of puromycin, capable of labelling newly synthesised proteins with a higher degree of spatiotemporal resolution (Elamri et al., 2018). The use of these techniques would increase the spatial resolution of observed protein synthesis, as well as allow for much finer temporal quantification of protein synthesis occurring locally at synapses. Further, part of the hypothesis that sAPP α regulates cell surface AMPAR trafficking relies on the assumption that pre-existing or *de novo* cell surface AMPAR translocate towards the synapse by lateral diffusion (see Figure 7-1, Figure 7-2). In order to examine this, previous research has employed the cell surface labelling of AMPAR by nanosized fluorophores called quantum dots, for the examination of AMPAR lateral diffusion (Howarth et al., 2005). In addition to this, examining the contribution of AMPAR lateral diffusion in the enhancement of sAPP α -mediated LTP has been made possible through the cross-linking and immobilisation of cell surface AMPAR during the induction of LTP (Penn et al., 2017). These techniques used separately or combined would further enhance our understanding of the role of AMPAR trafficking and mobility in LTP following sAPP α treatment.

Secondly, throughout this thesis I have made comparisons to the neurotrophic protein BDNF and the neuromodulator dopamine, on the basis of observations from supporting literature. Like sAPP α , BDNF and dopamine enhance cell surface GluA1 (Bellone and Lüscher, 2006; Gao et al., 2006; Caldeira et al., 2007), and strengthen synaptic transmission (Ying et al., 2002; Shetty et al., 2017), however in a manner distinct from sAPP α . Therefore, in order to understand the full complement of sAPP α 's neurotrophic support, and how these plasticity-enhancing proteins mediate the strengthening of synapses and formation of memories, biochemical and electrophysiological experiments should be made in order to compare the relative regulation of synaptic and cell surface AMPAR, contribution to LTP, and disparate or overlapping mechanisms of action.

Thirdly, as part of this thesis, we have proposed that sAPP α may act to strengthen synapses through the formation and awakening of AMPA-silent synapses. To further clarify this, examining the proportion of AMPAR-positive synapses by electron microscopy (Petralia et al., 1999) or the frequency of postsynaptic AMPA-mediated mEPSCs using *in vitro* by the use of multielectrode arrays (Arnold et al., 2005) or *ex vivo* field electrophysiology (Wasling et al., 2012), in the presence or absence of sAPP α , would be a worthy avenue to examine.

Finally, in order for sAPP α to express any relevant clinical applicability, the observations made within this thesis, as well as those previously described, including neuroprotection (Furukawa et al., 1996; Ryan et al., 2013; Tackenberg and Nitsch, 2019), neurogenesis (Demars et al., 2011), and morphological- and synaptic plasticity (Clarris et al., 1994; Taylor et al., 2008; Mockett et al., 2011), should be made through the use of cultured transgenic APP/PS1 mouse cultures as well as cultured

human neurons. As shown previously, the culturing of adult mouse neurons expressing mutations in APP/PS1 genes is possible (refer section 3.2. *Observations from the Culturing of Adult Cortical Mouse Neurons*). In addition this, recent research has established both induced pluripotent stem cell (iPSC) cultures (Konagaya et al., 2015), as well as the direct culturing of patient derived neural tissue (Lee et al., 2020), for the incomparable advantage of a direct representation of human neurons in culture. Ideally, these systems would be used in conjunction with delivery methods such as the incorporation of sAPP α into exosomes or viruses for the justification of these delivery methods *in vivo*, and allowing for the analysis of cell-specific effects, justifying any future clinical applicability.

Many of the experiments and hypotheses described within this thesis examine the expression of AMPAR in primary hippocampal cultures. This system benefits from an increased spatial resolution to that of more complex biological systems, however limitations exist due to possible genetic (Bowling et al., 2016) and physiological (Szczot et al., 2010) differences between cultured neurons and acute hippocampal slices. It has recently been shown that FUNCAT-PLA is possible in *ex vivo* preparations (Evans et al., 2019), thus in combination with cell surface biotin-labelling techniques (Mockett et al., 2019), it is possible that total *de novo* AMPAR as well as cell surface *de novo* AMPAR could be targeted for analysis by immunohistochemistry and western blot, respectively. This would add strength to the conclusions drawn from cultured neurons by examining AMPAR expression in intact tissue.

7.9. *Concluding Remarks*

This research aimed to examine the role of Arc protein expression and AMPAR trafficking in hippocampal neurons. The experiments in this thesis support previous work indicating that sAPP α enhances protein synthesis and AMPA receptor trafficking. Here, we have shown that sAPP α enhances LTP in a manner dependent on the synaptic expression of Ca²⁺-permeable GluA1-containing homomeric AMPAR. Further, we have shown that sAPP α enhances the expression of both pre-existing and newly synthesised GluA1 at the cell surface. Curiously, while an increase in GluA1 protein was found at the neuronal surface following both short-term and long-term treatments, the cell surface expression of *de novo* GluA1-containing AMPAR was short-lived, and found to be internalized from the cell surface in an Arc-dependent manner. Complementary to this, we have described a role for GluA1/2- and GluA2/3-containing AMPAR, finding a rapid and persistent decrease in cell surface GluA2/3-containing AMPAR specific to the dendrites, possibly as a means to increase available synaptic slots. Conversely, GluA1/2-containing AMPAR show a pattern of delayed cell surface expression and may act to replace homomeric GluA1-containing AMPAR.

The research described in this thesis describes a novel role of sAPP α in the regulation of key plasticity-related proteins, in line with similar neurotrophins, and describes sAPP α as a significant modulator of plasticity in hippocampal neurons. These observations further our understanding of synaptic plasticity in both health and disease and set a strong precedent for subsequent experiments regarding the functions and mechanisms of sAPP α .

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Appendix

1. Image analysis

1.1. Quantifying Arc Protein Expression in Primary Hippocampal Neurons

To quantify Arc protein expression throughout somatic and dendritic compartments of cultured hippocampal neurons (refer section 4.1. *Examining Arc Expression in Response to sAPP α*), individual MAP2 and Arc channel images are first imported into ImageJ as .tif files. Here, neurons of interest are manually outlined and regions of interest (ROIs) are determined for measurements of neuronal area and integrated density (Figure A-1,2). These measurements are then accounted for by average measurements of mean gray value from close-by selections.

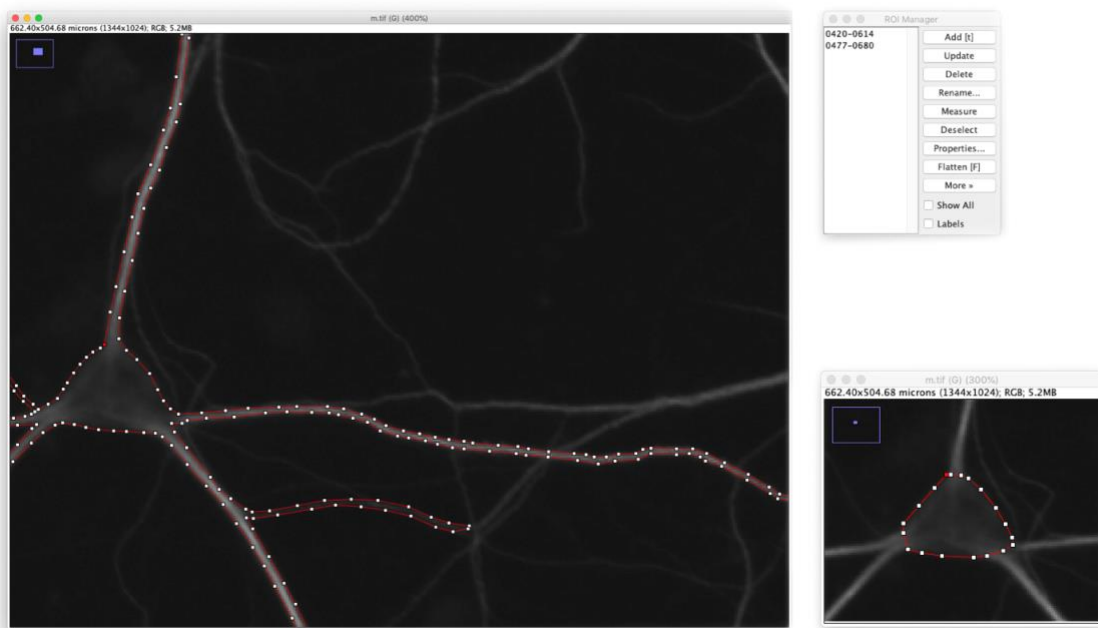


Figure A-1 | Setting of MAP2 mask. Using the MAP2 channel as a guide, an identified neuron and individual soma is traced using the polygon selection tool (○), and is saved as regions of interest (ROIs). Representative image shows magnified (400%) window of a neuron of interest (left), and somatic compartment (300% magnification, right) with selected ROIs.

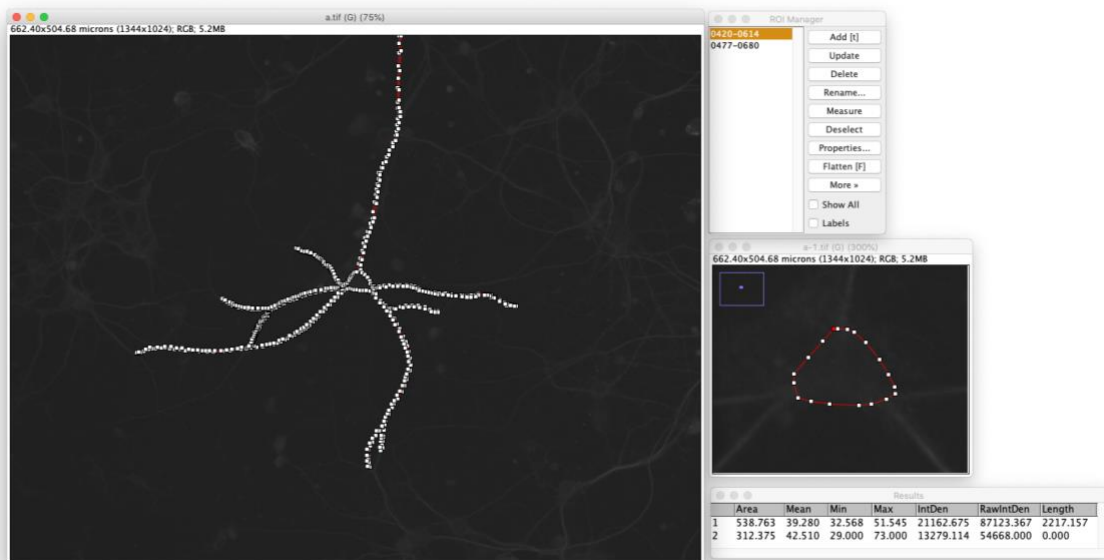


Figure A-2 | Measuring integrated density. Using the masks generated above, measurements including neuron area and integrated density (IntDen) are taken for both whole cell and somatic masks. Representative images show whole cell (75% magnification, left) and somatic (300% magnification, right).

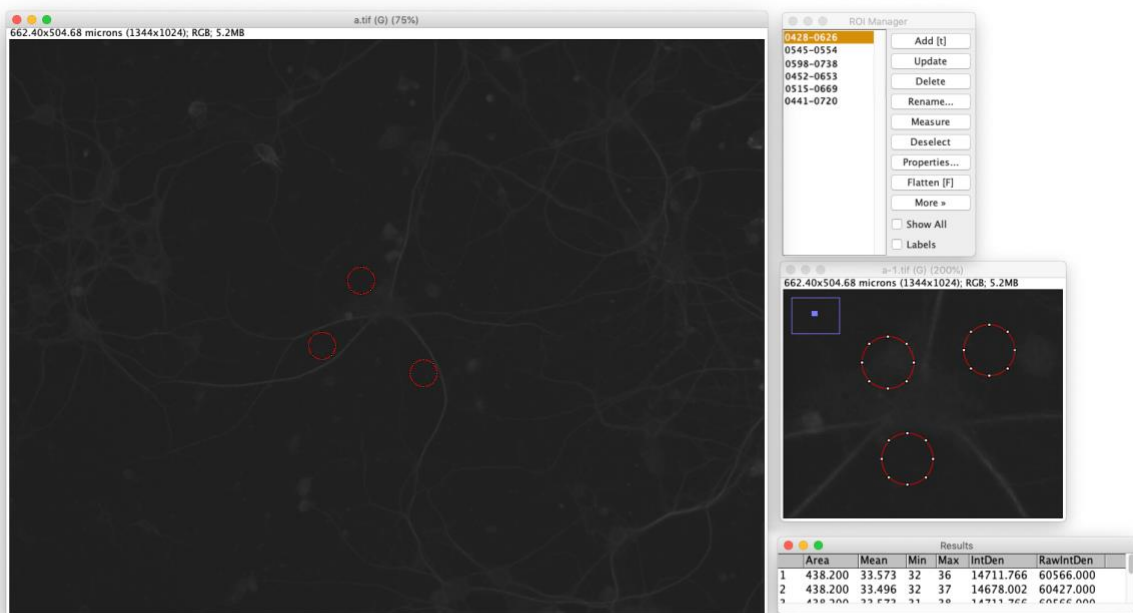


Figure A-3 | Accounting for background fluorescence. Following measurements of integrated density, in order to determine background fluorescence, three circular selections (○) of equal size are obtained adjacent to both dendritic and somatic compartments, from which the mean gray value is obtained. These values were averaged for each compartment, multiplied by neuron or soma area and subtracted from respective integrated density values for corrected total cell fluorescence (CTCF).

1.2. Quantifying pCREB Protein in Primary Hippocampal Slices

To quantify pCREB expression in hippocampal slices (refer section 4.2. *sAPP α Increases CREB Phosphorylation and Arc Protein in Acute Hippocampal Slices*), a threshold image of the DAPI channel was generated and used to define a ROI within the CA1 area, specific to the cell body layer (Figure A-4). This ROI was then used to define the area to be measured using the integrated density of pCREB

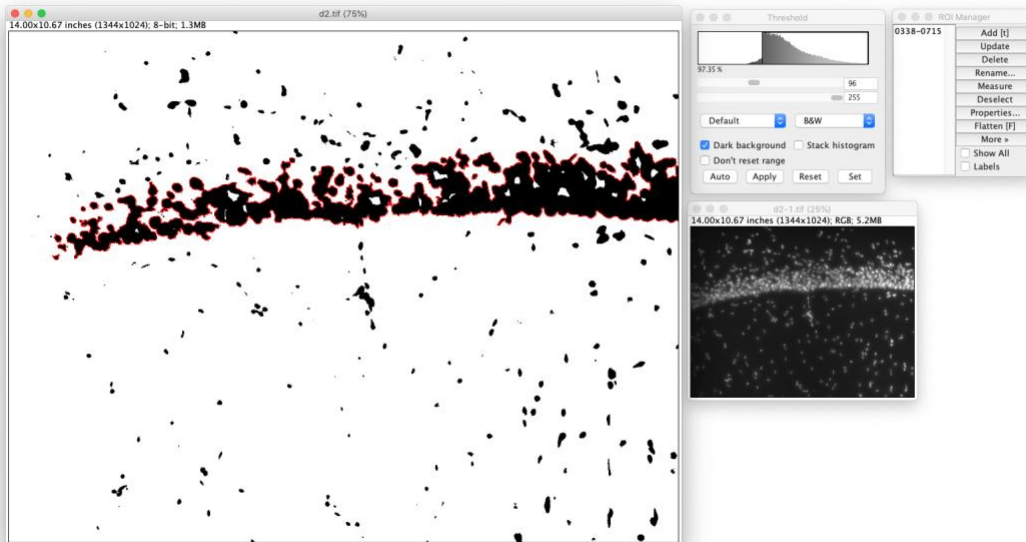


Figure A-4 | Setting the ROI of the cell body layer. The cell body layer of area CA1 is used to define the ROI (Figure A-5). The Threshold tool in ImageJ.

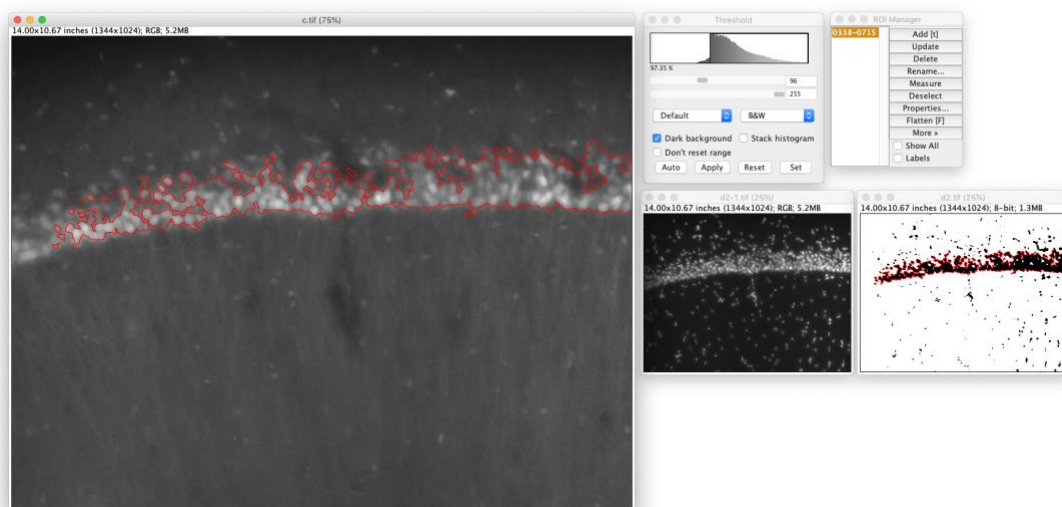


Figure A-5 | Measuring integrated density of the cell body layer. Representative image of pCREB fluorescence, measured using the defined ROI.

1.2.1. Quantifying Arc Protein Signal in Hippocampal Slices

To quantify Arc protein expression, a region of interest was set which encompassed area CA1, CA3 or the DG of all slices quantified. This ROI was used to measure the integrated density of Arc protein fluorescence (Figure A-6).

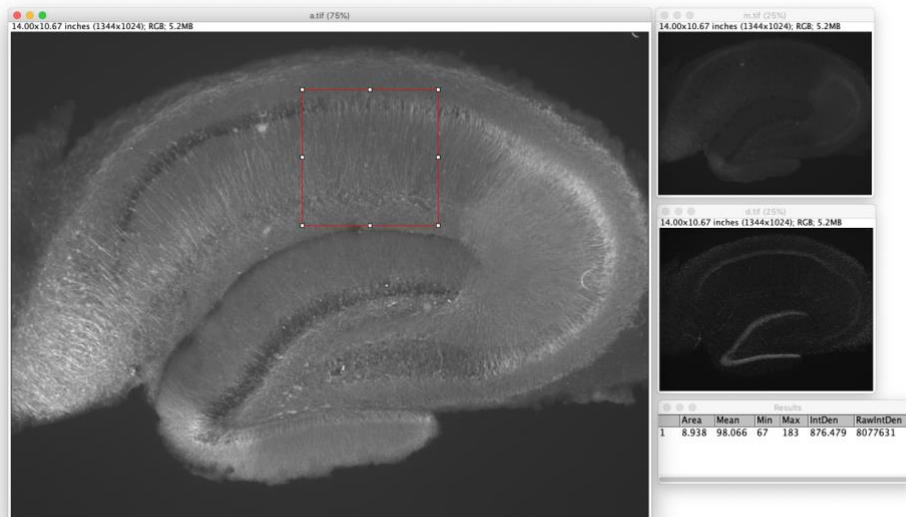


Figure A-6 | Measuring the fluorescence of the CA1 ROI. Representative image of Arc protein fluorescence, measured using the defined ROI

1.3. Quantifying PLA Signal in Primary Hippocampal Neurons

To quantify PLA signal in cultured hippocampal neurons (refer section 6.1. *sAPP α Regulates the Dynamic Control of AMPA Receptors at the Cell Surface*), a custom-made ImageJ macro (Maximilian Heumüller, Schuman Laboratory, Max Planck Institute for Brain Research, as used in (tom Dieck et al., 2015) was used. Using this, a MAP2 mask is generated to determine the area of PLA signal within a neuron of interest. In order to achieve this, the MAP2 mask generated is dilated by 1 pixel to ensure the inclusion of signal in dendritic spines (Figure A-7). RGB .tif files are composed from corresponding MAP2, PLA, and DAPI channels, and MAP2 and PLA signals are assigned as mask and signal channels, respectively (Figure A-7). Manually, a threshold for the PLA signal is defined by the average of all images and applied across conditions (Figure A-7). These parameters are thus used throughout the course of the macro in order to determine PLA signal per neuron of interest.

Henceforth, the PLA macro is used to define a MAP2 mask (Figure A-8), isolate the neuron of interest from surrounding neurons (Figure A-9,10), and detection of PLA signal within the defined MAP2 mask (Figure A-10). This allows for quantification of PLA signal per neuron, normalized to the area of the neuron of interest. For the quantification of PLA within somatic and dendritic compartments, individual soma were isolated from dendrites and analysed. Similarly, the proximal 50 μm of dendrites were isolated and straightened using the ImageJ 'straighten' function. Dendrites were then analysed using the PLA quantification macro.

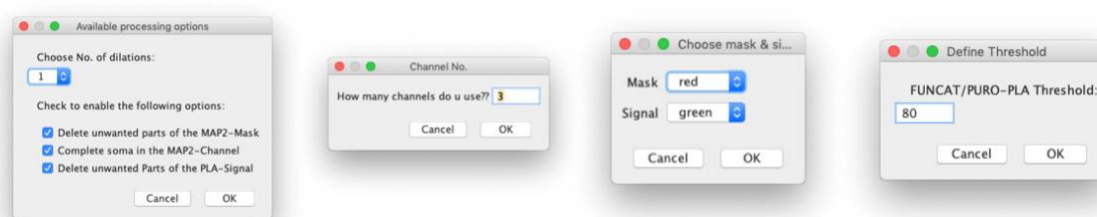


Figure A-7 | Running the PLA quantification macro. Before images are imported, parameters are set including (from left to right); mask signal dilations and appropriate optional steps, the number of channels comprising the RGB image, mask and signal channel assignment, and the previously determined PLA threshold value.

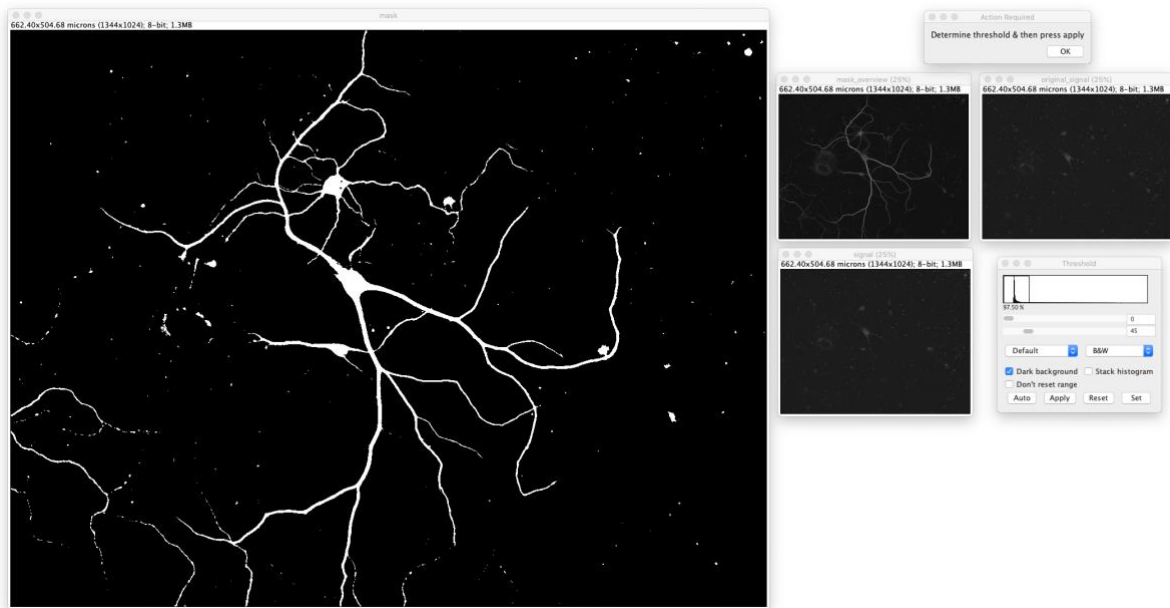


Figure A-8 | Defining the MAP2 threshold and mask. The MAP2 signal threshold was manually defined to create a mask of the neuronal somato-dendritic compartments (■). The threshold signal is pictured on the left, the raw MAP2 and PLA signal channels are shown on the right. Representative images show the MAP2 mask (left), raw MAP2 signal (top right), and raw PLA signal (top right, bottom right)

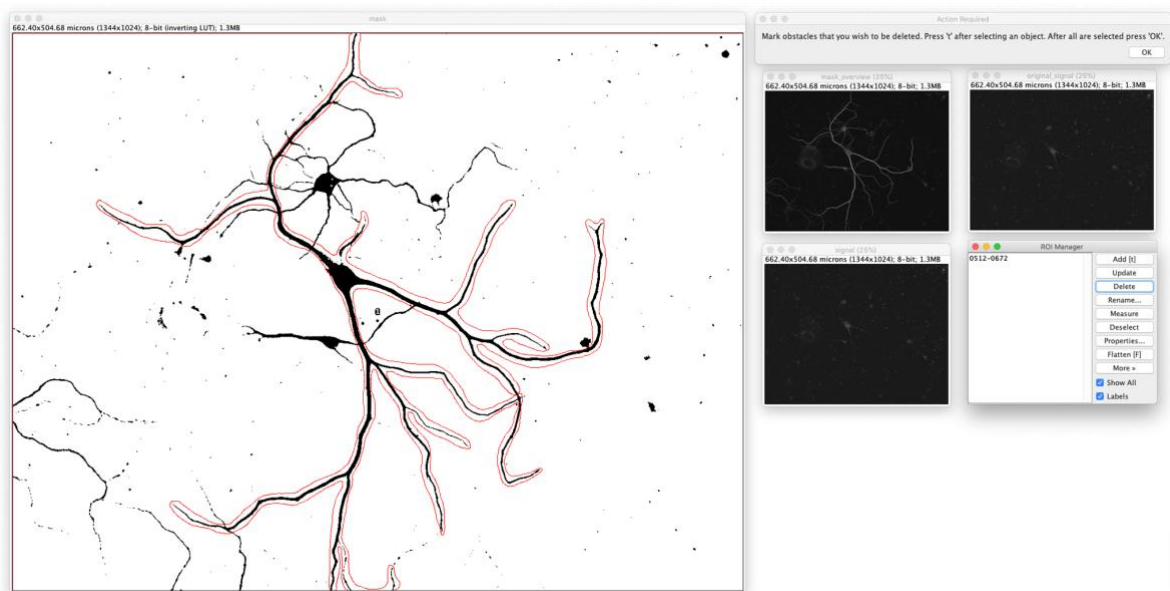


Figure A-9 | Isolation of the cell of interest from surrounding cells. Using the MAP2 mask, the processes and cell body belonging to the target cell are outlined (○) using the freehand selection tool. Following this, the selection was inverted to select surrounding non-target signal. This is saved as an ROI to be removed by the macro.

Due to the low level of MAP2 in the somatic compartment, some neurons require the soma to be manually defined to create a solid mask, permitting measurement of PLA signal within the soma (Figure A-10,11).

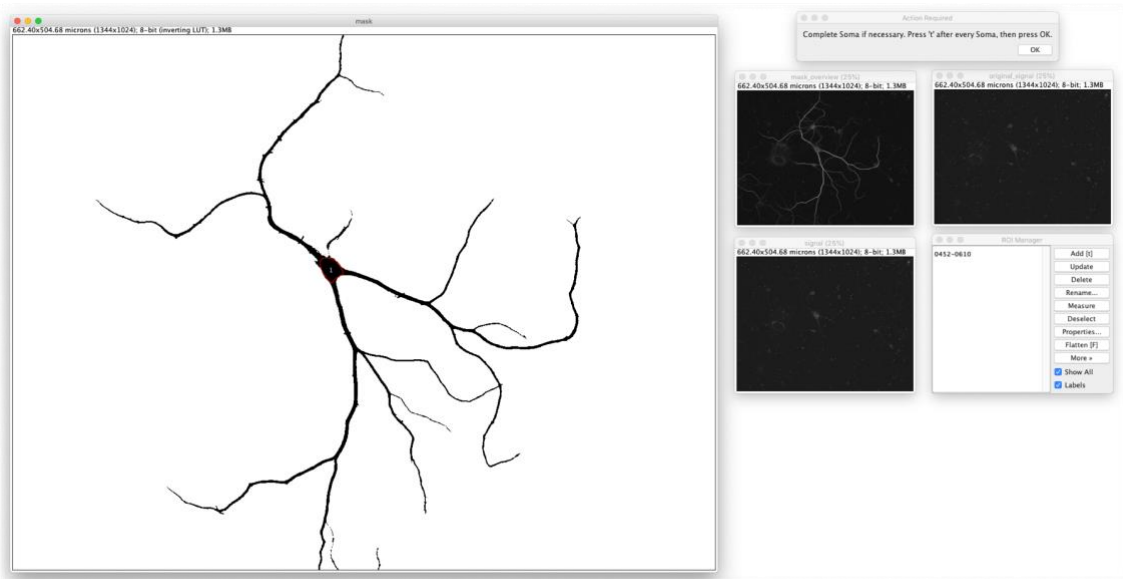


Figure A-10 | Isolated target neuron. Following isolation of the target neuron from all surrounding cells, the constraints of the somatic compartment are defined, where necessary as a ROI, using the raw MAP2 signal as a guide

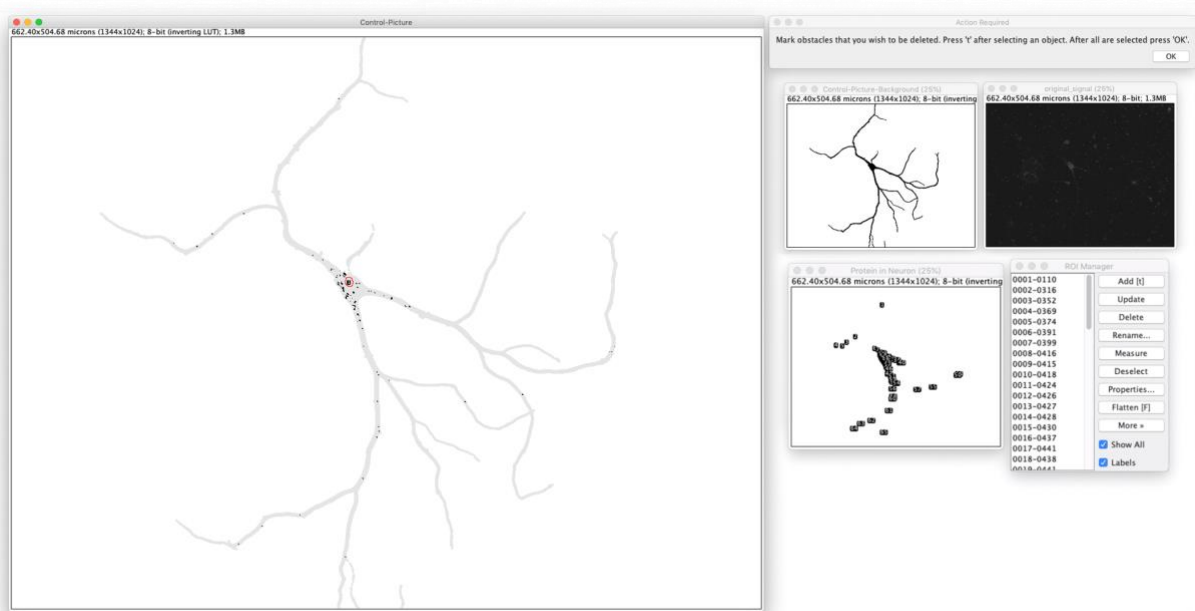


Figure A-11 | Detection and quantification of PLA signal. The final step includes verification of the PLA signal, and an option to delete any signal deemed as either noise or non-neuronal. Following this, the macro calculates the PLA signal area within the MAP2-defined mask, and is divided by the non-dilated MAP2 area. Representative images show the MAP2 mask (left, ■), PLA signal (■), and removed PLA puncta (○), defined MAP2 mask (top right), raw PLA signal (far right), PLA signal mapped by ROI (bottom left), and ROI manager of identified PLA signal (bottom right).

1.4. Quantifying Colocalization of PLA Signal Within Synapses

In order to quantify the PLA signal within synapses the ImageJ plugin 'Just Another Colocalization Plugin' (JACoP) was used (Figure A-12). Before analysis within ImageJ, the threshold value of both PLA and Synapsin-1 signal is generated to be using during JACoP analysis. As shown by Figure A-13, threshold values are entered into JaCoP and a Mander's overlap coefficient is calculated, generating a value proportional to the level of B (PLA) overlapping A (synapsin-1). Following JACoP analysis, the centre of the PLA was determined as the brightest pixel and used to measure distance to the nearest synapsin-1 centre of mass (Figure A-14).

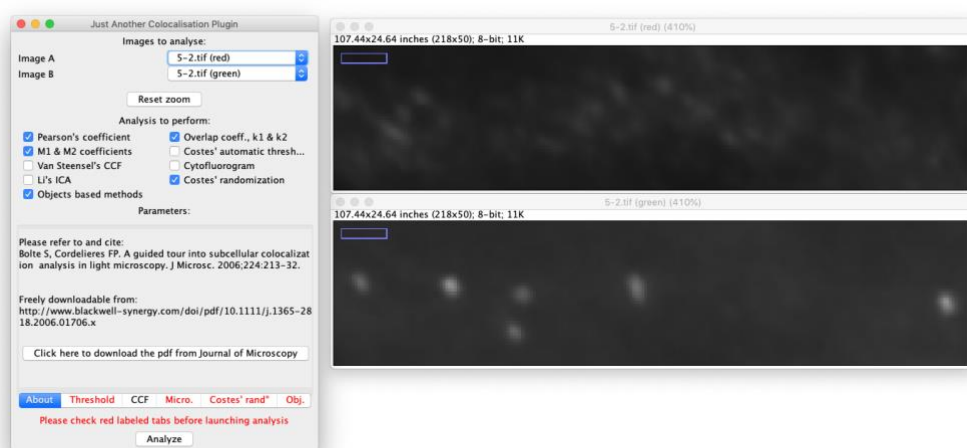


Figure A-12 | Running JACoP. Synapsin-1 (upper panel) and PLA (lower panel) signal channels are split and JACoP is run with the settings pictured above (left panel).

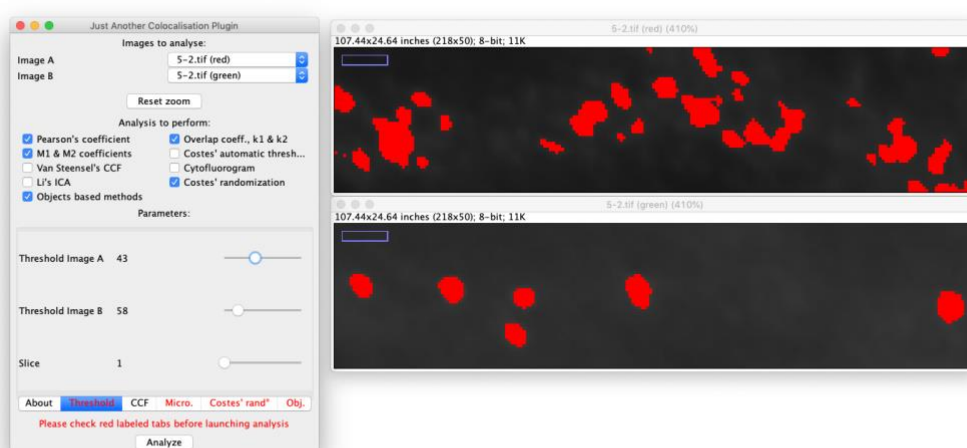


Figure A-13 | Setting of the threshold values. Previously determined threshold values were input into JACoP to generate a mask (■) for both PLA and synapsin-1 signal.

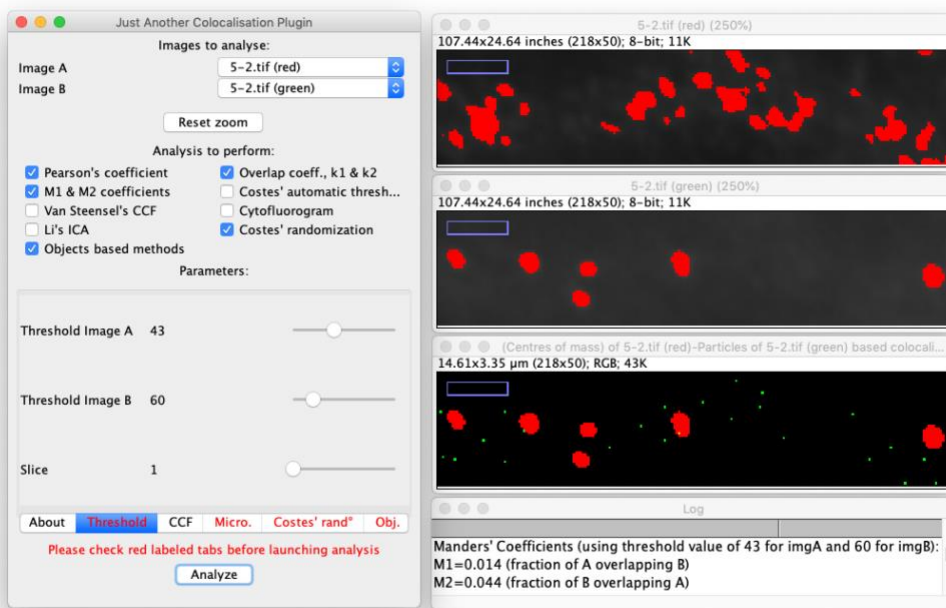


Figure A-14 | Measuring distance to synapse centre. JACoP generates a Mander's Coefficient (fraction of B (PLA) overlapping A (synapsin-1; lower panel) and representative image of center of mass of Synapsin-1 and PLA signal (third panel).

2. Cell Health

As described in section 3.1.3. *Cellular Populations Within Primary Hippocampal Cell Cultures*, the health of cells in culture can be determined by observation of MAP2 immunoreactivity. In response to insult, cultured neurons generate increased free radicals, which in turn promotes lipid peroxidation (Catlin et al., 2016). This presents as characteristic neuritic blebbing, fragmented dendrites, and swollen cell bodies as indicated in Figure A-15.

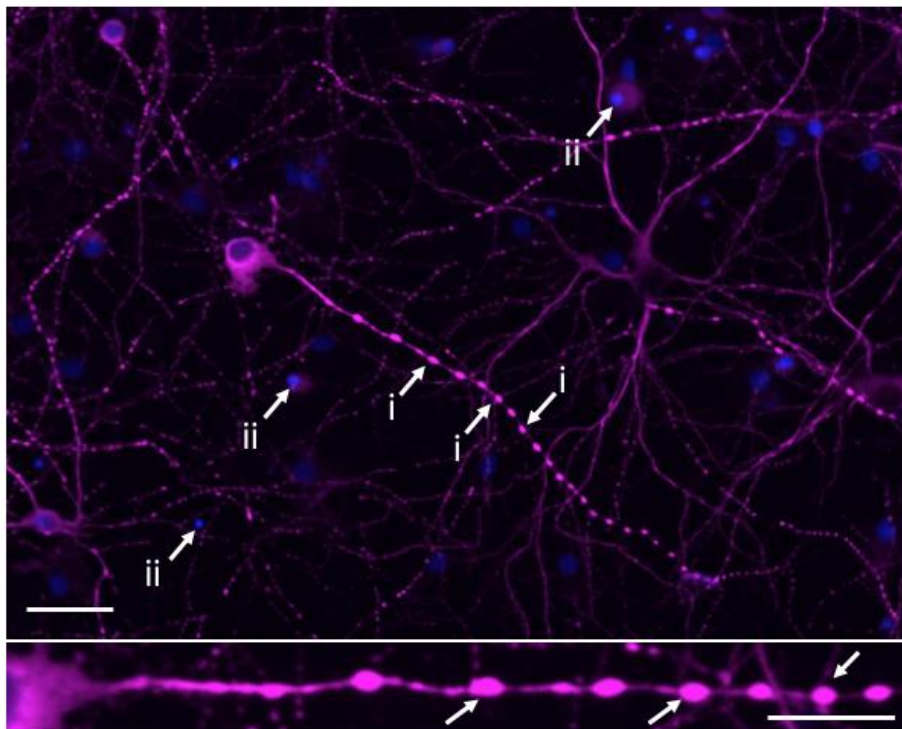


Figure A-15 | Representative image of an unhealthy hippocampal neuron. Image shows MAP2 (■), and DAPI (■). Arrows (i) indicate sites of serious membrane fragmentation (blebbing) in the absence of strong continuous MAP2-positive staining, (ii) shows populations of condensed nuclei. Inset image shows magnified proximal dendritic segment, arrows indicate sites of blebbing. Scale bar = 50 μm (A), inset image = 10 μm .

3. Accell™ siRNA Specificity

Within the last ten years, gene silencing by small interfering RNAs (siRNAs) has emerged as a promising method for inhibiting the expression of target genes and proteins (Akhtar and Benter, 2007; de Fougerolles et al., 2007). Alternative to complete gene knockout animals (Bevan, 2010), siRNAs serve as an effective, inexpensive method for inhibiting gene expression both *in vitro* and *in vivo* (Mocellin and Provenzano, 2004). Unfortunately, naked siRNAs are relatively unstable due to the presence of endo- and exonucleases (Bartlett and Davis, 2007). Therefore, various delivery systems have been developed to circumvent this problem, including liposomes (Pulford et al., 2010), viruses (Dreyer, 2010), chemical modifications (Walton et al., 2010), electroporation (Zhao et al., 2005), exosomes (Alvarez-Erviti et al., 2011), and conjugation to lipid based reagents (i.e. Lipofectamine 2000)(Chen et al., 2009). Recently, Thermo Scientific Dharmacon have developed Accell™ siRNA, a chemically modified siRNA which allows for passive delivery of antisense oligonucleotides in the absence of viral- or lipid-based transfection agents, increasing functionality and stability of the interfering RNA.

Endogenous siRNA, and synthetic Accell™ siRNA both consist initially of a double stranded RNA oligonucleotide bearing both a 5' phosphate (on the antisense strand) and 3' double uracil (3'-UU) overhang. When incorporated exogenously into the cell of interest, double-stranded siRNA is separated and the 5' antisense single-stranded RNA binds the multiprotein component complex RISC (RNA-induced silencing complex). Here, the antisense RNA guides and aligns the RISC complex on the target mRNA to allow for cleavage and degradation of the target mRNA (Bartel, 2009; Kim et al., 2009; Ketting, 2011; Horizon Discovery, 2014; Dana et al., 2017).

In order to first assess the efficacy of Accell™ siRNA in our hippocampal cell cultures (refer sections 6.1.4. *Accell™ Arc siRNA Inhibits Somatic and Dendritic sAPP α -Dependent, but not Basal, Arc Expression*, 6.1.5. *Internalization of de novo GluA1 is Dependent on Arc Expression* and 6.1.6. *Non-Targeting siRNA has no Significant Effect on de novo Cell Surface GluA1*), we utilized fluorescent Accell™ red non-targeting control siRNA for visualization of siRNA expression by conventional epifluorescence microscopy. As shown by Figure A-16, treatment of cultures with the fluorescent Accell™ siRNA across an equivalent treatment duration of our experimental conditions, resulted in clear expression within MAP2-positive neurons in both the soma and dendrites. Interestingly, cells present in culture which appeared negative for MAP2 expressed the highest levels of fluorescent Accell™ siRNA. These populations may be indicative of glial cells, such as astrocytes, microglia, or oligodendrocytes.

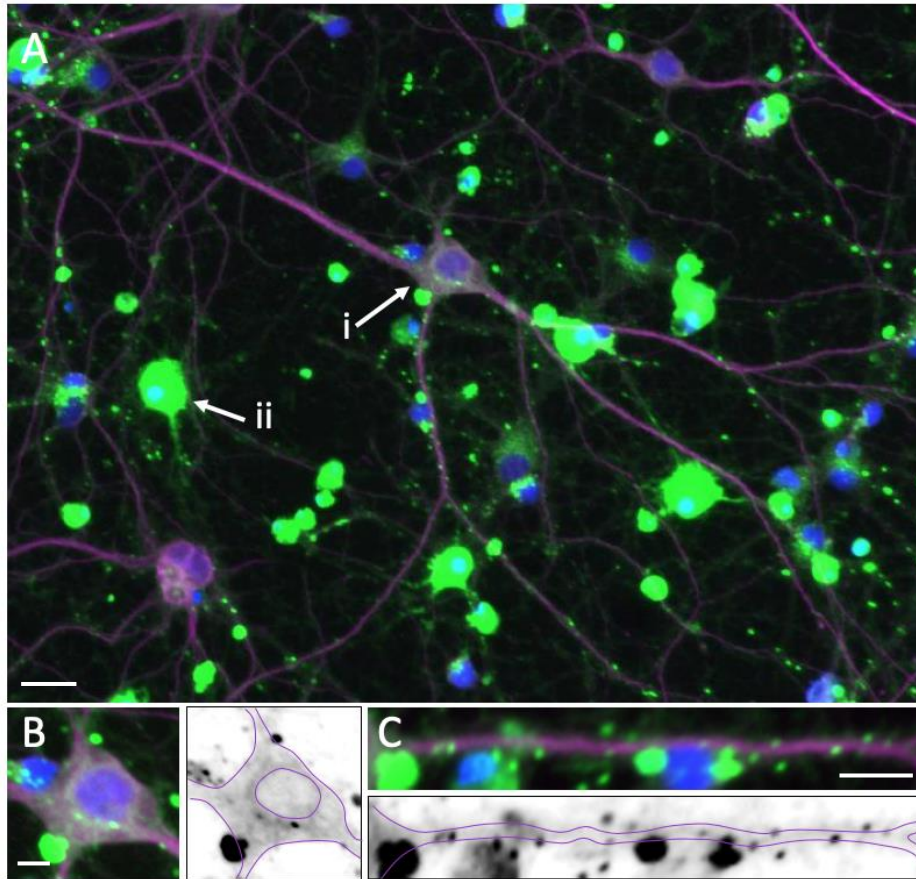


Figure A-16 | Specificity of Accell™ siRNA expression. A) Immunocytochemistry showed populations of i) neurons (MAP2-positive, ■) expressing fluorescent Accell™ siRNA (■). ii) cells negative for MAP2 but positive for DAPI (■) also appear to express Accell™ siRNA. Lower panels (B & C) show magnified somatic and dendritic compartments, respectively, and corresponding black & white Accell™ siRNA signal. Scale bars = 50 μm (A), 10 μm (B & C).

4. *Antibody Specificity*

Here we have utilized western blotting as a method to validate the specificity and reactivity of the antibodies used in a majority of the experiments described. Protein was extracted from primary cortical cultures and processed for western blot as described in section 2.4.3. *Western Blot*. The highly abundant protein α Tubulin (55 kDa) was used as a loading control. We then probed for the proteins Arc (55 kDa), and GluA1 (100 kDa) using antibodies targeted towards both C- and N-terminal epitopes (Figure A-17).

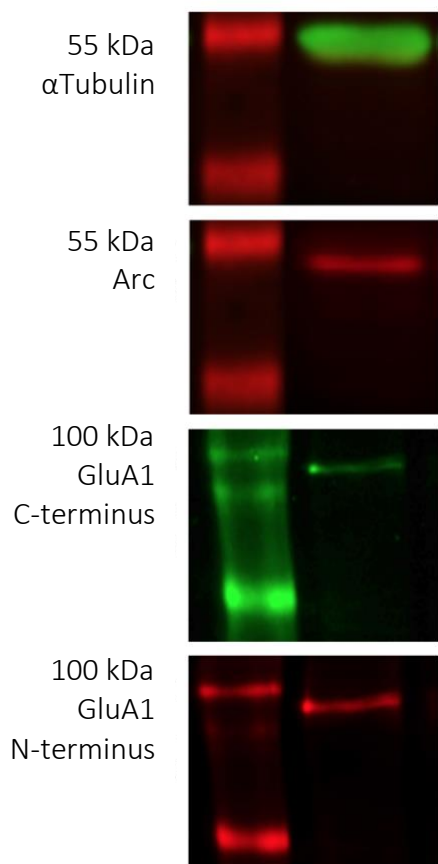


Figure A-17 | Specificity of Primary Antibodies. Representative image of western blots showing immunoreactivity for the loading control anti- α Tubulin (upper panel; 50 kDa; IRDye800, ■), anti-Arc (second panel, 45 kDa; IRDye680, ■), GluA1 detected using a C-terminal antibody (third panel 100 kDa; IRDye800, ■), and GluA1 detected using an N-terminal antibody (lower panel, 100 kDa; IRDye680, ■).

Tubulin and Arc western blots were provided by Honours student Maya Barrett. GluA1 western blots provided by Honours student Courtney Westlake.