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INTRACELLULAR TRAFFICKING OF CANNABINOID

RECEPTOR 1

A THOROUGH CHARACTERISATION AND INVESTIGATION

INTO THE ROLE OF THE INTRACELLULAR POOL

NATASHA LILLIA GRIMSEY

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ABSTRACT

Cannabinoid Receptor 1 (CB₁), an abundant G-protein coupled receptor (GPCR) in the central nervous system, is currently of significant interest as a therapeutic target. The cellular control of receptor trafficking is intimately linked with drug effects, however in comparison with other GPCRs, the study of CB₁ trafficking is in its infancy. Although the existing literature suggests CB₁ should be classified as a "dual-fate" receptor, some conflicting evidence exists as to the conditions under which CB₁ recycles or degrades. Of particular interest is the widely noted intracellular pool which has been speculated to form part of a constitutive internalisation and recycling pathway.

This study performs a detailed quantification of CB₁ trafficking in four cell lines, one of which expresses CB₁ endogenously. A novel high-throughput immunocytochemistry-based approach is applied to quantitatively measure receptor trafficking. An important advance on previous studies is the use of a proteolytic method to directly quantitate intracellular receptors. Contrary to previous reports, the data suggests that CB₁ does not recycle following constitutive or agonist-induced internalisation but instead exhibits a primarily degradative phenotype. Evidence is obtained through antibody "live-feeding" protocols and the effects of protein synthesis inhibitors, among other approaches. In addition, the data suggests that the intracellular pool does not traffic to the cell surface and therefore does not contribute to CB₁ signalling via classical paradigms. The effects of Rab GTPase dominantly-acting positive and negative mutants on basal CB₁ localisation corroborate these results.

The findings of this thesis have significant implications for the interpretation of CB_1 biochemical studies and call for a revision of the currently held theories of CB_1 intracellular trafficking. The study provides a foundation for further mechanistic studies and may impact the design and application of cannabinoid therapeutics.

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ABBREVIATIONS

ANOVA, analysis of variance	min, minutes
ATCC, American Type Culture Collection	M, mol/L (molar)
$\beta_2 AR$, β_2 -adrenergic receptor	MFR, mean fluorescence ratio
BSA, bovine serum albumin	NA, not applicable
cAMP, cyclic adenosine monophosphate	NFM, non-fat milk
CB ₁ , Cannabinoid receptor 1	PCR, polymerase chain reaction
CB ₂ , Cannabinoid receptor 2	PBS, phosphate-buffered saline
cDNA, complementary DNA	PBS-T, PBS with 0.2% Triton X-100
CHX, cycloheximide	PFA, paraformaldehyde
ConA, Concanavalin A	p, p-value
D ₁ , Dopamine receptor 1	pg., page
DMEM, Dulbecco's modified eagle's medium	PNGase F, peptide-N-glycosidase F
EC ₅₀ , half maximal effective concentration	Rab, Ras-like from brain
EGFP, enhanced green fluorescent protein	RT, room temperature
ER, endoplasmic reticulum	RM, repeated measures
FBS, fetal bovine serum	sec, seconds
FSM, full-serum media	SFM, serum-free media
g, grams	SR, SR 141716A
G-protein, GTP binding protein	t½, half-life
GASP, GPCR-associated sorting protein	TBS-T, Tris Buffered Saline with 0.05%
GPCR, G-protein coupled receptor	Tween
h, hour	TIS, trypsin inhibitor from soybean
HA, haemagglutinin	TGVC, total grey value per cell
HEK, human embryonic kidney-293	WIN, WIN 55212-2
HU, HU 210	wt, wild-type
kDa, kilodaltons	xg, times gravity