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**CANNABINOID RECEPTORS IN THE 3D RECONSTRUCTED MOUSE BRAIN:
FUNCTION AND REGULATION**

A dissertation submitted in partial fulfillment of the requirements for the degree of Doctor of
Philosophy at Virginia Commonwealth University

By
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Abbreviations:**2-AG:** 2-arachidonoylglycerol**AEA:** Arachidonylethanolamide (anandamide)**ANOVA:** Analysis of variance **β -Arr1:** Beta-arrestin type 1 **β -Arr2:** Beta-arrestin type 2**B_{max}:** Maximal specific binding site**BSA:** Bovine serum albumin**CB₁:** Cannabinoid receptor type 1**CB₂:** Cannabinoid receptor type 2**CP:** CP55,940 ((-)-*cis*-3-[2-hydroxy-4-(1,1-dimethylheptyl)phenyl]-*trans*-4-(3-hydroxypropyl)cyclohexanol)**dH₂O:** Deionized water**EC₅₀:** Concentration at half maximal effect**E_{max}:** Maximal effect**FAAH:** Fatty acid amide hydrolase**GPCR:** G-protein coupled receptor**GRK:** G-protein coupled receptor kinase**GTP:** Guanosine triphosphate**[³⁵S]GTP γ S:** Guanosine 5'-O-[gamma-thio]triphosphate**i.p.:** Intraperitoneal**KO:** Knockout**MAGL:** Monoacylglyceride lipase

ROI: Region of interest

THC: Δ^9 -tetrahydrocannabinol

SPM: Statistical Parametric Mapping

SR1: SR141716A (N-piperidino-5-(4-chlorophenyl)-1-(2,4-dichlorophenyl)-4-methyl-3-pyrazole-carboxamide), Rimonabant

SR2: SR144528 (N-[(1S)-endo-1,3,3-trimethyl bicyclo [2.2.1] heptan-2-yl]-5-(4-chloro-3-methylphenyl)-1-(4-methylbenzyl)-pyrazole-3-carboxamide)

THC: Δ^9 -tetrahydrocannabinol

WIN: WIN55,212-2 (R-(+)-[2,3-Dihydro-5-methyl-3-[(morpholinyl)methyl]pyrrolo[1,2,3-de]-1,4-benzoxazinyl]-(1-naphthalenyl)methanone mesylate)

WT: Wild-type

Neuroanatomical abbreviations

AMYG: Amygdala

A/V: Auditory/Visual

CBLM: Cerebellum

CG: Cingulate

CPu: Caudate Putamen

CTX: Cortex

GP: Globus Pallidus

HIPP: Hippocampus

HYPO: Hypothalamus

LC: Locus Coeruleus

LEnt: Lateral Entorhinal

NAc: Nucleus Accumbens

PAG: Periaqueductal gray

PIR: Piriform

SN: Substantia Nigra

SS: Somatosensory

THAL: Thalamus

Abstract

CANNABINOID RECEPTORS IN THE 3D RECONSTRUCTED MOUSE BRAIN: FUNCTION AND REGULATION

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A dissertation submitted in partial fulfillment of the requirements for the degree of Doctor of
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Virginia Commonwealth University, 2010

Director: Dr. Laura Sim-Selley, Ph.D.
Associate Professor
Department of Pharmacology and Toxicology

CB₁ receptors (CB₁R) mediate the psychoactive and therapeutic effects of cannabinoids including Δ^9 -tetrahydrocannabinol (THC), the main psychoactive constituent in marijuana. However, therapeutic use is limited by side effects and tolerance and dependence with chronic administration. Tolerance to cannabinoid-mediated effects is associated with CB₁R adaptations, including desensitization (receptor-G-protein uncoupling) and downregulation (receptor degradation). The objectives of this thesis are to investigate the regional-specificity in CB₁R function and regulation. Previous studies have investigated CB₁Rs in a subset of regions involved in cannabinoid effects, but an inclusive regional comparison of the relative efficacies of different classes of cannabinoids to activate G-proteins has not been conducted. A novel unbiased whole-brain analysis was developed based on Statistical Parametric Mapping (SPM)

for 3D-reconstructed mouse brain images derived from agonist-stimulated [35 S]GTP γ S autoradiography, which has not been described before. SPM demonstrated regional differences in the relative efficacies of cannabinoid agonists methanandamide (M-AEA), CP55,940 (CP), and WIN55,212-2 (WIN) in mouse brains. To assess potential contribution of novel sites, CB $_1$ R knockout (KO) mice were used. SPM analysis revealed that WIN, but not CP or M-AEA, stimulated [35 S]GTP γ S binding in regions that partially overlapped with the expression of CB $_1$ Rs. We then examined the role of the regulatory protein Beta-arrestin-2 (β arr2) in CB $_1$ R adaptations to chronic THC treatment. Deletion of β arr2 reduced CB $_1$ R desensitization/downregulation in the cerebellum, caudal periaqueductal gray (PAG), and spinal cord. However in hippocampus, amygdala and rostral PAG, similar desensitization was present in both genotypes. Interestingly, enhanced desensitization was found in the hypothalamus and cortex in β arr2 KO animals. Intra-regional differences in the magnitude of desensitization were noted in the caudal hippocampus, where β arr2 KO animals exhibited greater desensitization compared to WT. Regional differences in β arr2-mediated CB $_1$ R adaptation were associated with differential effects on tolerance, where THC-mediated antinociception, but not catalepsy or hypothermia, was attenuated in β arr2 KO mice. Overall, studies using SPM revealed intra- and inter-regional specificity in the function and regulation of CB $_1$ Rs and underscores an advantage of using a whole-brain unbiased approach. Understanding the regulation of CB $_1$ R signaling within different anatomical contexts represents an important fundamental prerequisite in the therapeutic exploitation of the cannabinoid system.

I. Introduction

A. Cannabis use: past and present

Marijuana, also known as cannabis, is perhaps one of the oldest psychoactive plants known to civilization. Its cultivation and utility as an industrial fiber (hemp fiber) has been approximated by modern historians to have started 10,000 years ago, roughly around pottery making and before metal working (Herer, 2000). Americans began using hemp for the production of rope, sails, and clothing in the 17th century. In the 1920s, Mexican immigrants introduced the recreational use of marijuana leaves, which sparked the early anti-marijuana campaigns and initiated an era of 'Reefer Madness' or national propaganda efforts to campaign against the "dangerous weed" (Herer, 2000). This eventually led Congress to pass the Marijuana Tax Act in 1937, which essentially criminalized marijuana and restricted its possession for authorized medical and industrial uses. Despite the enactment of stricter sentencing laws in the mid 1950s, marijuana usage surged in the 1960s following a shifting political and cultural climate. In 1996, the medical use of marijuana was first legalized in the state of California under the successful passing of proposition 215, allowing for the sale and medicinal use of marijuana for patients with debilitating conditions such as AIDS and cancer (Herer, 2000). Presently, 14 states have legalized the medical use of marijuana and two states have passed laws that, although favorable towards medicinal usage of marijuana, does not legalize its use (www.ProCon.org, 2010).

Currently marijuana, including various other tetrahydrocannabinol constituents of the plant (i.e. Δ^9 -tetrahydrocannabinol (THC), Δ^8 -tetrahydrocannabinol, etc.), is classified as a

Schedule I drug, along with other drugs of abuse such as heroin, lysergic acid diethylamide (LSD), and psilocybin (constituent of "Magic Mushrooms") (www.justice.gov, 2010). THC is also the primary psychoactive constituent in marijuana. Under the Controlled Substances Act for the United States, Schedule I drugs or substances are classified by the DEA to have a high potential for abuse, have no currently accepted medical indication, and lack safe standards of use under medical supervision. However, the FDA has approved two cannabinoids for use as medical therapies. For example, Dronabinol (Marinol) or synthetic THC is currently used to treat nausea and vomiting associated with cancer chemotherapy and to treat anorexia associated with AIDS-related weight loss. In addition, Nabilone, a synthetic cannabinoid that mimics the effects of THC, is used as a last resort to treat nausea related to cancer chemotherapy for patients not responsive to other existing anti-emetics. More recently in March 2010, encouraging results from a large scale U.S. phase IIb trial reported better pain scores (indicative of pain management) comparing Sativex (an oromucosal spray containing THC and cannabidiol) versus placebo in patients with advanced stages of cancer. Plans are now underway to commence Phase III trials for Sativex in managing cancer pain.

B. The Endocannabinoid System

Pharmacological evidence of a cannabinoid receptor in brain was first suggested by Howlett and Fleming in their work demonstrating the inhibition of adenylate cyclase by cannabimimetic drugs (Howlett and Fleming, 1984). This work eventually led to the elucidation and characterization of a cannabinoid agonist binding site (Devane et al., 1988), and shortly thereafter, the CB₁ receptor was cloned from rat cerebral cortex cDNA library (Matsuda et al., 1990). A second cannabinoid receptor (CB₂) with 44% structural homology to CB₁, has also

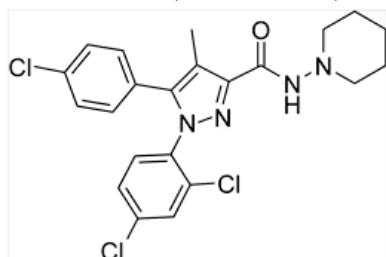
been cloned from cDNA prepared from the human promyelocytic leukaemic line HL60 (Munro et al., 1993). Molecular characterization and identification of these receptors stimulated a search for their endogenous ligands. Several lipid-based compounds have since been isolated from brain and identified as endogenous ligands to the cannabinoid receptor. Of these, arachidonylethanolamide (also known as anandamide; AEA) (Devane et al., 1992) and 2-arachidonoylglycerol (2-AG) (Mechoulam et al., 1995; Sugiura et al., 1995) are best characterized. Unlike classical neurotransmitters, endocannabinoids are not stored in vesicles, but are synthesized on demand via membrane phospholipid precursors. Synthesis of AEA was previously thought to occur from the enzymatic hydrolysis of *N*-acyl-phosphatidylethanolamines (NAPE) by a NAPE selective phospholipase D (Schmid et al., 1990). However, studies using NAPE-PLD knockout mice demonstrated equivalent levels of AEA as in wild-type animals (Leung et al., 2006), suggesting existence of other biosynthetic pathways. Alternative NAPE-PLD independent pathways thought to contribute to the synthesis of AEA include for example the double-deacylation of NAPE by α/β -hydrolase 4 (ABH4) followed by phosphodiesterase-mediated cleavage by GDE1 (Simon and Cravatt, 2006). In addition, phospholipase C-catalyzed cleavage of NAPE and its subsequent dephosphorylation (Liu et al., 2006) represents another potential biosynthetic pathway. Interestingly, a recent report found unaltered levels of AEA in GDE1 knockout mice, as well as only partial disruption of *N*-acyl ethanolamine biosynthesis in GDE1/NAPE double knockout mice (Simon and Cravatt, 2010). Collectively, these reports suggest multiple biosynthetic pathways for AEA, which may be brain region-dependent. As for 2-AG, the biosynthetic substrates are the *sn*-1-acyl-2-arachidonoylglycerols (DAGs) and requires DAG lipase (DAGL) (Bisogno et al., 2003). Recent studies using mice lacking either DAGL isotype (DAGL α or DAGL β) suggest that DAGL α is the primary biosynthetic enzyme for 2-AG

in the CNS as well as an important mediator of retrograde signaling (Gao et al., 2010; Tanimura et al., 2010).

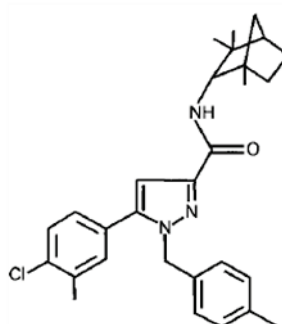
The actions of endocannabinoids are relatively short lived and endocannabinoid tone is regulated by metabolic enzymes that are codistributed in most cannabinoid containing brain regions. Fatty acid amide hydrolase (FAAH) is primarily responsible for the metabolism of AEA (Cravatt et al., 1996) and other fatty acid amides, whereas monoacylglyceride lipase (MAGL) is the major metabolic enzyme of 2-AG (Dinh et al., 2002). The regional differences in the distribution of these two enzymes and their intricate cellular compartmentalization within the CNS (Dinh et al., 2002; Gulyas et al., 2004; Thomas et al., 1997), creates an elaborate metabolic machinery to modulate endocannabinoid signaling. Together, the cannabinoid receptors, endogenous ligands that bind these receptors, and degradative and synthetic enzymes, comprise the endogenous cannabinoid system.

A

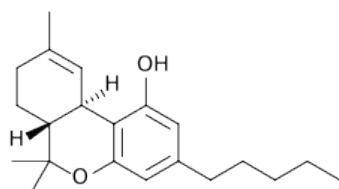
CB₁ receptor antagonist
SR141716A (Rimonabant)



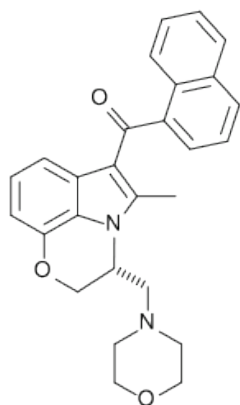
CB₂ receptor antagonist
SR144528

**B**

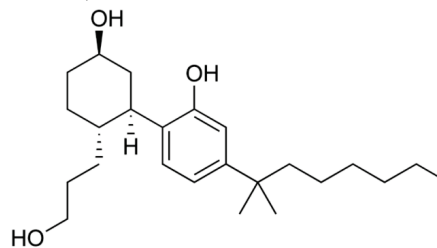
Phytocannabinoid
 Δ^9 -tetrahydrocannabinol



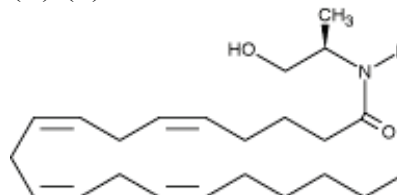
Aminoalkylindole
WIN 55,212-2



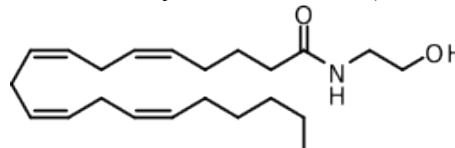
Non-classical
CP 55,940



Eicosanoid
(R)-(+)-Methanandamide



Arachidonylethanolamide (Anandamide)



2-Arachidonoylglycerol (2-AG)

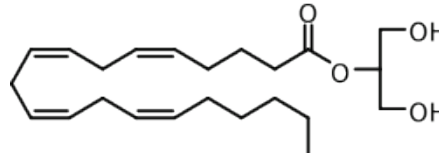


Figure 0.1. Chemical structures of CB₁ and CB₂ receptor selective antagonists (A) and different classes of cannabinoid receptor agonists (B).

C. Cannabinoid Pharmacology

The cannabis plant, *Cannabis sativa*, contains a mixture of cannabinoids (Elsohly and Slade, 2005) including Δ^9 -tetrahydrocannabinol (THC), the primary psychoactive constituent of marijuana. The structural elucidation of THC by Gaoni and Mechoulam in 1964 (Gaoni and Mechoulam, 1964) led to the development of more potent synthetic cannabinoid agonists, such as CP55,940 and WIN55,212-2 (Fig. 0.1), which has advanced our understanding of the cannabinoid system (Melvin and Johnson, 1987). CP55,940 ((-)-*cis*-3-[2-hydroxy-4-(1,1-dimethylheptyl)phenyl]-*trans*-4-(3-hydroxypropyl)cyclohexanol), a bicyclic analog of THC, belongs to the class of nonclassical cannabinoids. It is a high efficacy partial agonist at the CB₁ receptor and is a full agonist at the CB₂ receptor, with similar binding affinities to both CB₁ and CB₂ receptors (Howlett et al., 2002). CP55,940 is one of the most widely used radiolabeled cannabinoid ligands and has historical significance, as it was first used to demonstrate a specific cannabinoid binding site (Devane et al., 1988) and to anatomically map the distribution of cannabinoid receptors in rat brain tissue (Herkenham et al., 1991). WIN55,212-2 (R-(+)-[2,3-Dihydro-5-methyl-3-[(morpholinyl)methyl]pyrrolo[1,2,3-de]-1,4-benzoxazinyl]-(1-naphthalenyl)methanone mesylate) is a full agonist at CB₁ receptors, and the prototype of the aminoalkylindole family (Howlett et al., 2002). Synthesis of a CB₁ selective antagonist SR141716A (N-piperidino-5-(4-chlorophenyl)-1-(2,4-dichlorophenyl)-4-methyl-3-pyrazole-carboxamide) helped establish the specificity of CB₁ receptor-mediated effects, and demonstrate that most *in vivo* effects of cannabinoids are mediated by the CB₁ receptor (Rinaldi-Carmona et al., 1994). SR141716A is a highly potent CB₁ antagonist that effectively inhibits and reverses CB₁-mediated effects both for *in vitro* and *in vivo* assays (Howlett et al., 2002). SR141716A has also been shown to act as an inverse agonist by reducing the constitutive activity (functional

coupling to effector mechanisms in the absence of an agonist) of CB₁ receptors, although concentrations significantly greater than the normal dose range to antagonize CB₁-mediated effects may be required in brain (Bouaboula et al., 1997; Landsman et al., 1997; Pertwee, 2005a; Sim-Selley et al., 2001).

The eicosanoid class of cannabinoids include the endocannabinoids AEA and 2-AG, which are derivatives of arachidonic acid and are the prototypic and most investigated members of this group. Although AEA and 2-AG have similar binding affinities, 2-AG exhibits higher efficacy than AEA at both CB₁ and CB₂ receptors (Pertwee, 2005b). Because AEA is highly susceptible to metabolism, synthetic derivatives such as (R)-(+)-Methanandamide have been developed, which exhibit greater metabolic stability, affinity, and CB₁ selectivity (Di Marzo et al., 2001; Lin et al., 1998).

D. Cannabinoid receptor neuroanatomy

Cannabinoid receptors are among the most abundant G-protein coupled receptors (GPCR) in the brain. CB₁ receptors represent the predominant subtype in the CNS, whereas CB₂ receptor expression is restricted mainly to the immune system with limited expression in the CNS (Onaivi et al., 2006; Van Sickle et al., 2005). CB₁ receptors are highly expressed in brain areas, including the cortex, basal ganglia, hippocampus, amygdala, and cerebellum (Herkenham et al., 1991; Jansen et al., 1992; Tsou et al., 1998). This neuroanatomical distribution is consistent with *in vivo* effects of cannabinoids, including antinociception, cognitive and memory disruption, catalepsy, decreased motor activity, and hypothermia (Dewey, 1986; Hollister, 1998). Studies utilizing CB₁ receptor knockout mice (Zimmer et al., 1999) and CB₁ receptor selective antagonists (Rinaldi-Carmona et al., 1994) have also indicated that most of the *in vivo* effects of

THC and other cannabinoids are primarily mediated via the CB₁ receptor. Development of agonist-stimulated [³⁵S]GTPγS autoradiography in our laboratory (Sim et al., 1995) allowed for the initial demonstration of regional differences in desensitization (see *Receptor Desensitization* below) of cannabinoid-receptor mediated G-protein activity following chronic administration of THC (Sim-Selley and Martin, 2002; Sim et al., 1996a). Agonist-stimulated [³⁵S]GTPγS autoradiography provides not only a measurement of receptor-mediated G-protein activation, but also its neuroanatomical distribution. Figure 0.2 illustrates the first 3D image reconstruction of cannabinoid-stimulated G-protein activity produced by the full CB₁ receptor agonist WIN55,212-2 and was derived from the average of multiple naive mouse brain (n = 7) images (image reconstruction is described in *Chapter 1*). CB₁ receptor-mediated G-protein activity was found highest in regions including the amygdala and basal ganglia output nuclei, such as the substantia nigra and globus pallidus. Moderate levels of agonist-stimulated [³⁵S]GTPγS binding was noted in the hippocampus, deeper layers of cortex, and the cerebellum. In medullary nuclei important for mediating respiration, CB₁ receptors are low in abundance and therefore have low probability of lethality from overdose.

Studies on the subcellular localization of CB₁ receptors revealed that they are highly expressed on axon terminals and preterminal segments (Hajos et al., 2000; Katona et al., 2001). Double-label immunostaining experiments in the forebrain have also indicated that CB₁ receptors are primarily found on GABAergic interneurons (Tsou et al., 1999). Cannabinoid receptor modulation of other neurotransmitters have also been demonstrated. Interestingly, the synthetic cannabinoid WIN inhibited glutamatergic neurotransmission in the hippocampus of both CB₁ receptor wild-type and knockout mice (Hajos et al., 2001), a brain area that has previously been reported to contain putative non-CB₁ sites and exhibiting WIN-stimulated G-

protein activity ((Breivogel et al., 2001; Nguyen et al., 2010) and see *Chapter 2*). As opposed to inhibition, systemic administration of WIN has been shown to result in the efflux of norepinephrine in the rat frontal cortex, which appears to be modulated by the presynaptic localization of CB₁ receptors on noradrenergic axon terminals (Oropeza et al., 2007; Oropeza et al., 2005; Reyes et al., 2009). The spatial localization of CB₁ receptors thus suggests that the cannabinoid system plays an important neuromodulatory role in the CNS.

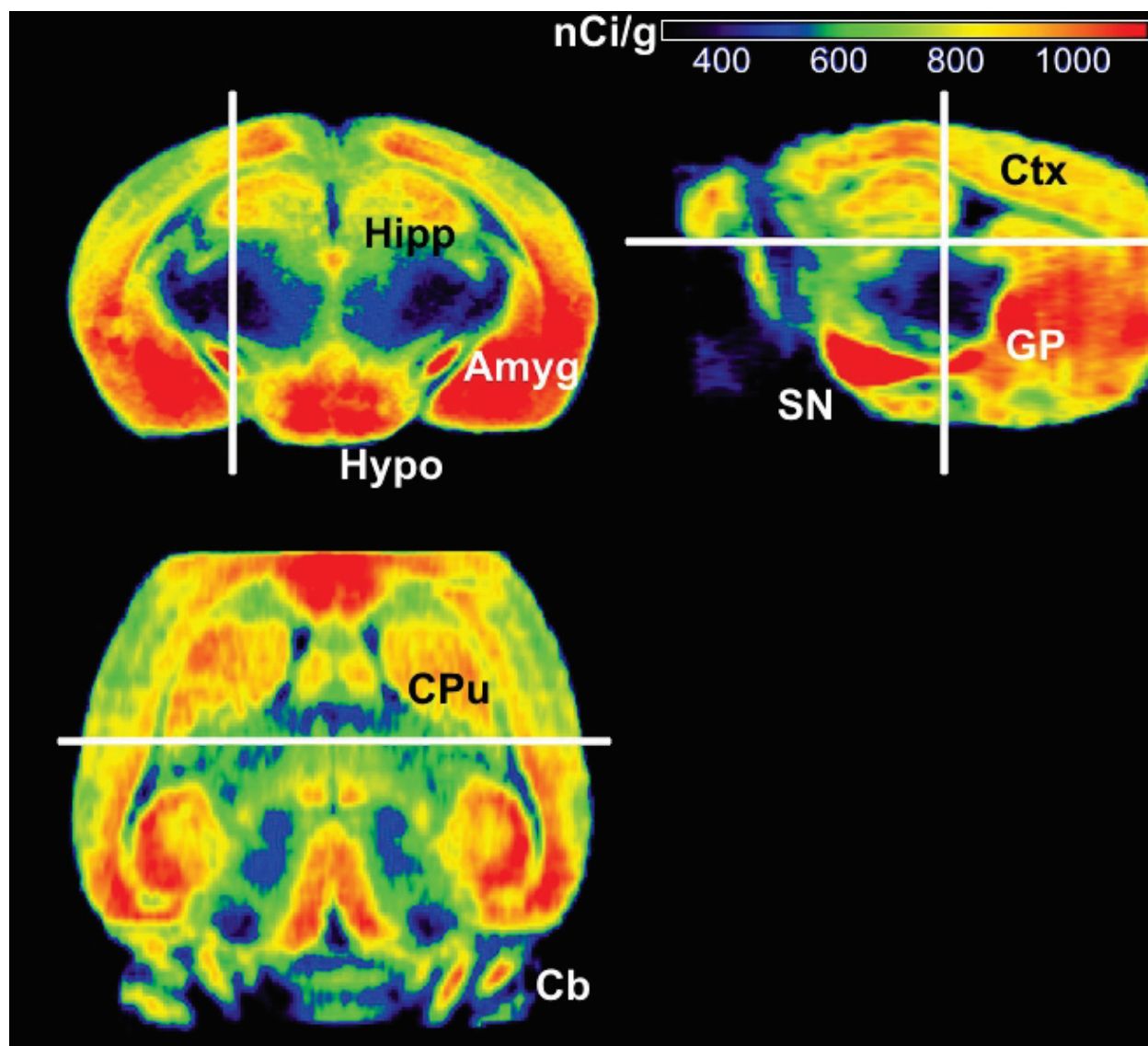


Figure 0.2. Image average ($N = 7$) of WIN55,212-2-stimulated [^{35}S]GTP γ S binding in the 3D reconstructed mouse brain produced by a maximally effective concentration of the full CB $_1$ receptor agonist WIN55,212-2 (10 μM). A coronal, sagittal, and transverse section are shown in the upper left, upper right, and bottom left corners, respectively. Stimulated [^{35}S]GTP γ S binding values (nCi/g) are shown in pseudocolor, demonstrating highest and lowest magnitudes of stimulated G-protein activation in red/orange and blue/black, respectively. White lines represent the level of each respective anatomical plane as shown in the figure. Highest WIN-stimulated G-protein activity are shown in the basal ganglia output nuclei (substantia nigra (SN), globus pallidus (GP)), amygdala (Amyg), cerebellum (Cb), hypothalamus (Hypo), hippocampus (Hipp), caudate-putamen (CPu), and cortex (Ctx). Details of 3D image reconstruction is described in *Chapter 1*

E. CB₁ receptor signal transduction pathways

Cannabinoid receptors belong to the superfamily of seven-transmembrane spanning G-protein coupled receptors (Fig. 0.3). CB₁ receptors are predominantly expressed presynaptically and inhibit neurotransmitter release (Ishac et al., 1996; Kathmann et al., 1999; Nakazi et al., 2000; Shen et al., 1996; Szabo et al., 1999). Agonist binding activates the receptor, which promotes interaction with its cognate heterotrimeric G-protein. This facilitates exchange of GDP for GTP, which binds and activates the α subunit. The activated α subunit then dissociates from the $[\beta\gamma]$ complex, and each can activate intracellular effectors (Hall et al., 1999; Wickman and Clapham, 1995). The α subunit inactivates via an intrinsic GTPase, thus increasing the affinity of α for $\beta\gamma$, and association of the subunits. G-protein activation is catalytic because each receptor can activate multiple G-proteins (Gierschik et al., 1991; Sim et al., 1996c). CB₁ receptors primarily activate the pertussis toxin-sensitive G_i/G_o family of G-proteins that inhibit adenylyl cyclase (Howlett et al., 1986; Pacheco et al., 1991). CB₁ receptors inhibit several types of voltage gated calcium channels, such as N-type and Q-type currents, and activate G-protein-coupled inwardly rectifying potassium channels 1 and 2 (Howlett et al., 2002). In addition, CB₁ receptor activation has been shown to regulate ceramide metabolism and activate various intracellular kinases such as mitogen-activated protein (MAP) kinases, phosphatidylinositol-3-kinase, focal adhesion kinase, protein kinase B/Akt, and c-Jun N-terminal kinase (JNK1 and JNK2) (Howlett et al., 2002).

The production and release of endocannabinoids is thought to occur through a number of mechanisms and has been recently reviewed (Mackie, 2008). Wilson, Nicoll, and colleagues were the first to report feedback mechanisms involving endogenous cannabinoids by which a depolarized post-synaptic neuron can modulate the pre-synaptic release of an inhibitory or

excitatory neurotransmitter (Wilson et al., 2001; Wilson and Nicoll, 2001, 2002). This retrograde modulation by endocannabinoids is also referred to as depolarization-induced suppression of inhibition (DSI) or excitation (DSE). The underlying mechanism is now understood to involve postsynaptic intracellular increases in calcium followed by retrograde inhibition of presynaptic terminals, which was first noted by Llano et al. (Llano et al., 1991). Further, a recent report found a loss of retrograde endocannabinoid signaling in mice lacking DAGL α , the biosynthetic enzyme of 2-AG, suggesting an important role for the endocannabinoid 2-AG in retrograde synaptic plasticity (Gao et al., 2010). Depolarization-induced release of endocannabinoids has also been demonstrated to occur through a G_{q/11}-dependent mechanism involving the activation of postsynaptic group I metabotropic glutamate receptors (Varma et al., 2001) or M1 and M3 muscarinic receptors (Ohno-Shosaku et al., 2003). The actual underlying mechanism by which cannabinoid receptors modulate neurotransmitter release is unclear, however some evidence point to involvement of various ion channels, including K⁺ channels (Kreitzer et al., 2002), or N or P/Q type Ca²⁺ channels (Guo and Ikeda, 2004).

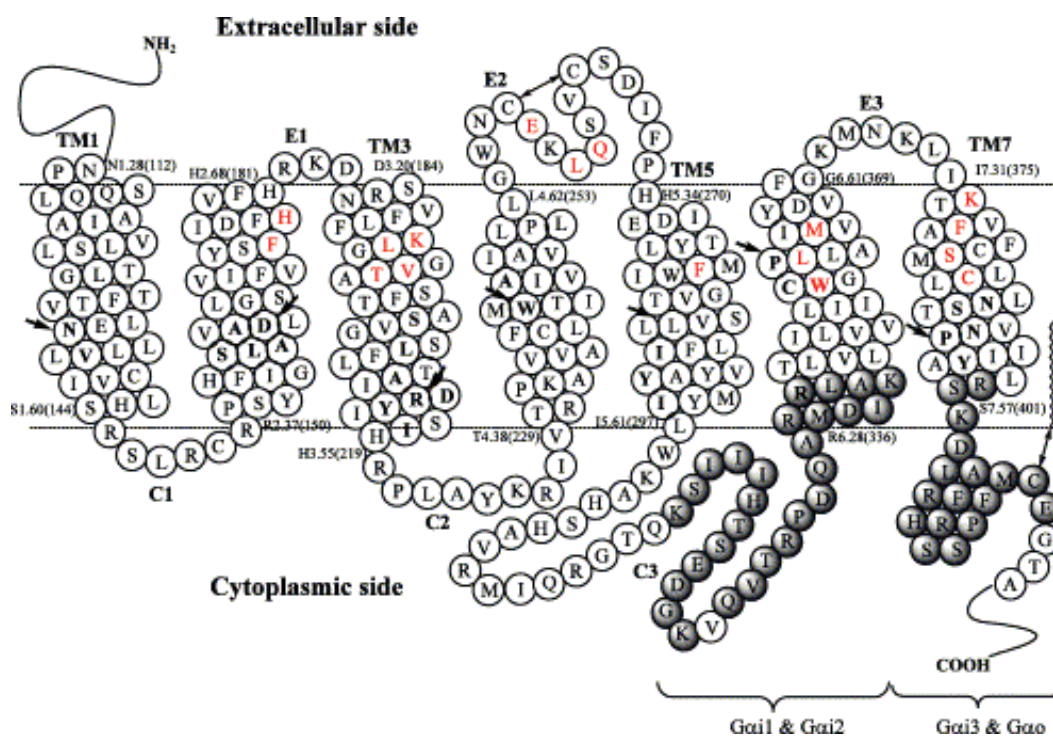


Figure 0.3. Two-dimensional structure of the human CB₁ receptor. Three extracellular (E1-3) and three intracellular (C1-3) regions are represented along with highly conserved key residues shown in bold. Sequences in the third intracellular domain (C3) important for G_{ai1} and G_{ai2} and C-terminal residues important for G_{ao} and G_{ai3} interactions are represented by shaded circles. Red colored amino acid letters illustrate proposed binding site residues within 2.5 Å of the bound non-classical cannabinoid CP55,940 (figure and caption adapted from Mukhopadhyay et al., *Chem Phys Lipids* 2002)

F. Acute effects of cannabinoids

At present, there is no evidence for structural changes in the brain following either acute or chronic use of marijuana. Using magnetic resonance imaging (MRI), frequent marijuana users showed no evidence of cerebral atrophy or gross reductions in brain volume (Block et al., 2000). The *in vivo* effects of THC and other cannabinoids are well characterized. The most established behavioral model used to assess a wide array of cannabinoid-mediated effects in laboratory animals is the classical tetrad model, developed by Martin and colleagues (Compton et al., 1993). Acute administration of THC consistently produces hypothermia, catalepsy, antinociception, and decreased spontaneous motor activity. Porrino and colleagues (Freedland et al., 2002) have investigated the changes in cerebral metabolism using quantitative 2- ^{14}C deoxyglucose (2-DG) autoradiography following THC administration. When assessed 15 minutes after drug administration, the acute effects of THC dose-dependently decreased regional brain metabolism, as measured by the rate of local cerebral glucose utilization. Other prominent central effects of cannabinoids include memory and cognitive impairment, which has been demonstrated in a number of memory paradigms showing the disruptive effect of cannabinoids on memory related tasks (Ferrari et al., 1999; Varvel et al., 2001). Interestingly, endocannabinoids have been implicated in the extinction of aversive memories (Marsicano et al., 2002). In this study, elevated levels of endocannabinoids were found in the basolateral amygdala following tone presentation during extinction trials. In addition, the authors found that both CB₁ knockout mice and CB₁ wild-type mice treated with the CB₁ receptor antagonist SR141716A had impaired extinction of fear-conditioned tests.

Previous reports have demonstrated the effects of cannabinoids on synaptic plasticity, particularly long-term potentiation (LTP). Nowicky and colleagues first demonstrated the effects

of THC on modulating the duration of LTP of the CA1 evoked field potential in rat hippocampal slices (Nowicky et al., 1987), thus providing insight into the role of endocannabinoids in synaptic plasticity. Inhibition of long-term depression (LTD) by cannabinoids has also been demonstrated in the hippocampal CA1 field, induced by lower frequency stimulation (Misner and Sullivan, 1999).

One other notable effect of cannabinoids include its orexogenic effect. Hyperphagia generally follows THC administration (Williams et al., 1998), whereas CB₁ receptor blockade results in a reduction in food intake (McLaughlin et al., 2003).

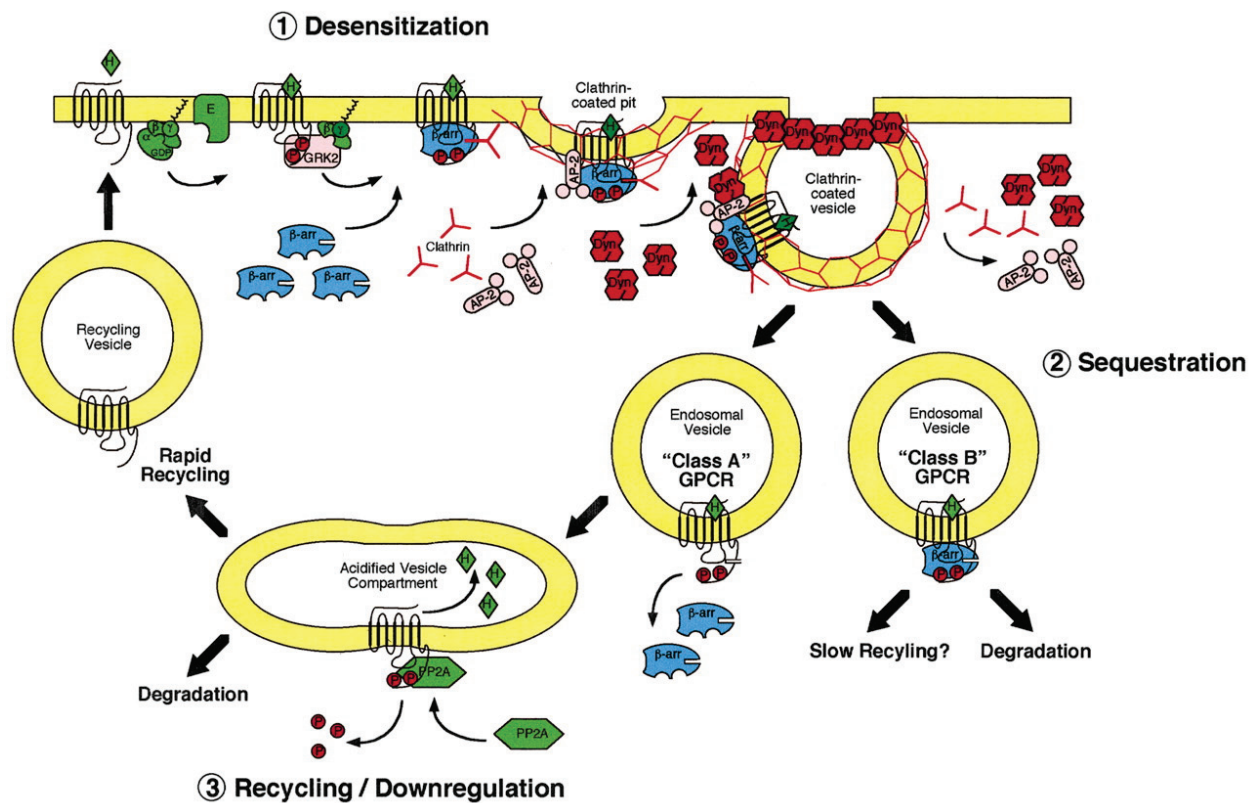


Figure 0.4. Regulatory mechanisms of G-protein coupled receptors. Following prolonged exposure to an agonist, GPCR signaling is attenuated through receptor desensitization (1), internalization (2), or downregulation where it is targeted for degradation (3). Resensitization or recycling of the receptor may also occur following internalization (from Luttrell et al, 2002).

G. Regulation of cannabinoid receptors: mechanisms of cannabinoid tolerance

Tolerance occurs when there is a reduction in the magnitude of a drug effect following chronic administration at a constant drug dose. Chronic administration of THC and other synthetic cannabinoid agonists produce tolerance to the behavioral effects of cannabinoids, which have been well characterized in laboratory animals. These include, for example, tolerance to cannabinoid-mediated antinociception, hypothermia, catalepsy, and reduction in spontaneous motor activity (Carlini, 1968; Gonzalez et al., 2005; Pertwee et al., 1993). Interestingly, tolerance to the memory impairment effects of cannabinoids does not appear to develop following prolonged administration (Barna et al., 2007; Boucher et al., 2009; Ferraro and Grilly, 1973). Studies in humans have been limited, however tolerance to the cardiovascular (Benowitz and Jones, 1975) and memory/cognitive impairment (D'Souza et al., 2008) effects of cannabinoids have been demonstrated. At the molecular level, chronic cannabinoid exposure results in the functional uncoupling of CB₁ receptors from G-proteins (desensitization) (Sim et al., 1996a) and agonist-promoted internalization (Jin et al., 1999); followed by either receptor degradation in lysosomes (downregulation) or recycling to the cell membrane (resensitization) (Sim-Selley et al., 2006; Tappe-Theodor et al., 2007). These receptor adaptations are thought to contribute to the development of cannabinoid tolerance.

Receptor downregulation

Adaptation to chronic administration of cannabinoids does not appear to be pharmacokinetic (Dewey et al., 1973; Martin et al., 1976), but rather pharmacodynamic in nature. It is also likely that these neuroadaptive changes are reversible. For example, chronically administering THC for 90 days in rats resulted in no changes in CB₁ receptor levels in the

striatum, cerebral cortex, cerebellum, hippocampus, and brainstem/spinal cord, following a 60 day recovery period (Westlake et al., 1991). However, studying CB₁ receptor properties at earlier time points after chronic treatment can resolve characteristic CNS adaptations that have been implicated to contribute towards cannabinoid tolerance.

Agonist-activated GPCRs are rapidly phosphorylated by G protein-coupled receptor kinases (GRKs) and subsequently bound by arrestin proteins, which facilitate receptor uncoupling from G-proteins (see Fig. 0.4 and next section, *Receptor Desensitization*) and receptor internalization (Claing et al., 2002; Lefkowitz et al., 1990). These molecular events have been well characterized for the β_2 -adrenergic receptor (β_2 AR). Like the β_2 AR, CB₁ receptors are internalized through clathrin-coated pits into early endosomes and this process requires the extreme carboxy tail of the receptor (Hsieh et al., 1999). Internalization occurs rapidly, and its rate correlates well with the relative efficacy of cannabinoid agonists to activate G-proteins. Recycling of internalized CB₁ receptors back to the cell membrane also occurs rapidly following brief incubations with agonist. However, longer agonist incubation times (60 minutes) may result in irreversible internalization and receptor degradation (downregulation) via lysosomes. The targeting of CB₁ receptors toward lysosomal degradation appears to require G-protein-associated sorting protein 1 (GASP1), a protein that has been shown to interact with CB₁ receptors and was required for agonist-induced downregulation of CB₁ receptors in spinal neurons (Tappe-Theodor et al., 2007). A recent report also demonstrated that GASP1 and CB₁ receptors were colocalized in both GABAergic and glutamatergic cells of the thalamus (Martini et al., 2010). The authors of this study also found a loss in downregulation in both the spinal cord and cerebellum, as well as a lack of tolerance development to antinociception, motor incoordination, and locomotor hypoactivity, but not hypothermia, in GASP1 knockout mice treated chronically with WIN. In

other studies, prolonged agonist exposure times required new protein synthesis in order to normalize receptor levels (Hsieh et al., 1999). In fact, CB₁ receptor protein levels, but not CB₁ receptor mRNA, matched the downregulation of CB₁ receptors as well as its recovery after cessation of THC treatment, suggesting that regulation of CB₁ receptors primarily occurs at the level of the protein (Sim-Selley et al., 2006).

Downregulation of CB₁ receptors was first suggested by Oviedo et al. as one of the underlying receptor-mediated mechanisms of cannabinoid tolerance using quantitative [³H]CP55,940 binding autoradiography in rat forebrain sections (Oviedo et al., 1993). In that study, animals were injected once daily with intraperitoneal (i.p.) of THC (10 mg/kg), CP55,940 (1, 3, or 10 mg/kg), or vehicle for 14 days. Behavioral assessment of a separate group of rats under the same drug paradigm demonstrated tolerance to the inhibitory effects of THC and CP55,940 on spontaneous motor activity. Tolerance to the motor effects of THC and CP55,940 was associated with a reduction in [³H]CP55,940 binding (indicative of receptor levels) in THC treated compared to vehicle control rats in all brain areas examined including: olfactory tubercle, septum, caudate-putamen, and nucleus accumbens. These changes in receptor density also followed a dose-response relationship, with greatest reduction in the higher dose group (70-80% decrease) and lowest reduction in the lower dose group (40-50% decrease). Another study also found a positive association with the magnitude of CB₁ receptor downregulation and dose of THC administration (McKinney et al., 2008). Interestingly, as depicted in Figure 0.5, the magnitude of receptor downregulation in that study appeared to vary not only as a function of dose, but brain region as well.

The degree of cannabinoid tolerance appears to vary based on the specific behavior assessed. Martin and colleagues found a high degree of tolerance to the pharmacological effects

of CP55,940 when dosing mice chronically (2 mg/kg) twice a day for 6.5 days (Fan et al., 1996). The ability of CP55,940 to decrease motor activity, produce hypothermia, and induce catalepsy was reduced by 163-, 97-, and 19-fold, respectively. One implication from this study is that the magnitude of tolerance does not develop proportionally for various cannabimimetic effects. Thus, differential tolerance may reflect the relative adaptability of different regions to chronic cannabinoids. The regional specificity in CB₁ receptor downregulation has further been demonstrated by Sim-Selley and Martin (Sim-Selley and Martin, 2002) using [³H]SR141716A binding autoradiography to localize changes in CB₁ receptor levels. In this study, mice were treated with escalating doses of THC, WIN-55,212-2, or vehicle subcutaneously (s.c.) twice daily for 15 days. Densitometry showed that downregulation occurred in all CB₁ receptor-containing brain regions, albeit at varying magnitudes of reduction. High levels of downregulation (55-70%) were found in prefrontal cortex, nucleus accumbens, hippocampus, amygdala, hypothalamus, thalamus, and entorhinal cortex, and intermediate levels (45-50%) in cerebral cortex, caudate-putamen, periaqueductal gray (PAG), and cerebellum. The lowest levels (10-25%) were found in basal ganglia output nuclei: globus pallidus, entopeduncular nucleus, and substantia nigra. These three regions are also highly dense in CB₁ receptor levels; however it is unclear if this is related to the relative lower magnitudes of downregulation observed in these brain areas.

Receptor desensitization

Different families of regulatory molecules are known to participate in desensitization of GPCRs: second messenger-dependent kinases (i.e. PKA, PKC, etc.), GPCR kinases (GRKs), and the arrestins (visual and non-visual) (Gainetdinov et al., 2004; Lefkowitz, 1998). GRKs

(Gainetdinov et al., 2004) selectively phosphorylate agonist-activated receptors, which leads to the recruitment and binding of an arrestin protein (Lefkowitz, 1993, 1998). The binding of arrestin sterically hinders and disrupts the ability of the receptor to initiate signal transduction by functionally uncoupling the receptor and G-protein, a process called homologous desensitization as only the activated receptor is affected (Gainetdinov et al., 2004). In the brain, the major isoforms are arrestins 2 (β arr1) and 3 (β arr2), each having its unique distribution pattern in the CNS (Gurevich et al., 2002). β -arrestin is also involved in receptor internalization through its interactions with key proteins, including clathrin and adaptor protein-2 (Moore et al., 2007). There are seven known mammalian GRK isotypes. GRK2 and GRK3, also known as β -adrenergic receptor kinase 1 and 2, respectively, are the predominant CNS isotypes and are widely distributed throughout synapses in the brain (Arriza et al., 1992).

The role of GRK and β -arrestin in mediating CB₁ receptor desensitization has been demonstrated in the *Xenopus* oocyte expression system (Jin et al., 1999). Anatomically, the brain distribution of β arr2 is ubiquitous and partially overlaps with CB₁ receptors, suggesting that these two proteins may be co-distributed in similar neuronal populations (Attramadal et al., 1992). However, the regional abundance of β arr2 varies; with highest levels in cortex, hypothalamus, amygdala, and hippocampus, and lower levels in striatum and cerebellum (Attramadal et al., 1992; Gurevich et al., 2002). Chronic THC treatment also increases the expression of specific isoforms of GRKs and β -arrestins at different extents by brain region; with GRK2, GRK4, and β arr1 predominantly in striatum, GRK4 and β arr2 in cerebellum, and GRK2 and β arr2 in hippocampus (Rubino et al., 2006). This regional specificity suggests differential regulation between neuronal populations, which could account for the differences in the

regulation of CB₁ receptors in distinct brain regions (Breivogel et al., 1997; Sim-Selley, 2003; Sim et al., 1996a).

The development of functional binding assays such as cannabinoid-stimulated [³⁵S]GTPγS binding in homogenized membrane preparations (Selley et al., 1996) and brain tissue sections (Sim et al., 1995) offered the ability to quantitate CB₁ receptor-mediated G-protein activation. Sim et al. (Sim et al., 1996a) first demonstrated desensitization of CB₁ receptors in brain tissue sections from rats chronically treated with THC (10 mg/kg for 21 days). In this paradigm, almost all sampled brain regions exhibited a profound decrease in WIN-stimulated [³⁵S]GTPγS binding. Large decreases (>50%) in receptor-mediated G-protein activation were found in hippocampus, cortex, caudate-putamen, and cerebellum. However, a number of regions exhibited lesser desensitization (20-30%), such as PAG, septum, globus pallidus, and substantia nigra. Further intra-regional differences in the magnitude of desensitization occurred within brain areas. For example, greater desensitization was found in the ventral aspects (60%) compared to dorsal aspects (34%) of entorhinal cortex. Other reports have found desensitization of CB₁ receptor-mediated G-protein activation in similar brain regions chronically administering other cannabinoid agonists including THC (Breivogel et al., 1999; McKinney et al., 2008; Sim-Selley and Martin, 2002; Sim-Selley et al., 2006), CP55,940 (Rubino et al., 1997), and WIN55,212-2 (Sim-Selley and Martin, 2002; Sim-Selley et al., 2006). In most of these reports, the cortex, hypothalamus, and hippocampus, exhibited the largest magnitude in desensitization (ranging 50-70%), while others were moderate, such as cerebellum, thalamus, and PAG (ranging 40-50%). Regions dense with CB₁ receptors, such as globus pallidus, entopeduncular nucleus, and substantia nigra, tend to be least sensitive to desensitization.

Sim-Selley and Martin explored the possible ligand-specific differences in receptor adaptation in mice that were chronically treated with equally active and escalating doses of either THC or WIN55,212-2 for 15 days (Sim-Selley and Martin, 2002). In this report, desensitization had an inverse association with agonist efficacy, as the low efficacy partial agonist THC produced greater desensitization than the full CB₁ agonist WIN55,212-2 in most brain regions examined. No differences however were detected between the two agonists in the magnitude of CB₁ receptor downregulation. When comparing the regional differences in the magnitude of desensitization between the two agonists, THC produced approximately 2-fold greater desensitization than WIN55,212-2 in striatum, hippocampus, hypothalamus, PAG and amygdala. This finding is in agreement with a different study using the same treatment paradigm (Sim-Selley et al., 2006). Further, the regional desensitization profile was: hypothalamus > cortex > hippocampus > striatum > PAG > thalamus > globus pallidus > substantia nigra > entopeduncular nucleus (Sim-Selley and Martin, 2002). Interestingly, the degree of tolerance that developed in this paradigm differed by the type of behavior assessed and also by the agonist used. THC demonstrated a tolerance profile of antinociception (119 fold) > hypothermia (53 fold) > decreased spontaneous motor activity (6.3 fold). These data indicate that differential tolerance can occur during chronic THC treatment.

McKinney et al. (McKinney et al., 2008) explored the regional differences in CB₁ receptor adaptation after administration of varying doses of THC and assessed tolerance produced by this chronic paradigm. Mice were treated twice daily for 6.5 days with either vehicle, or varying doses of THC: Low = 10 mg/kg, Medium = ramping dose of 10 to 20 to 30 mg/kg, High = ramping dose of 10 to 30 to 60 mg/kg. This paradigm demonstrated differential tolerance to THC-mediated effects and regionally-specific CB₁ receptor adaptations as a function

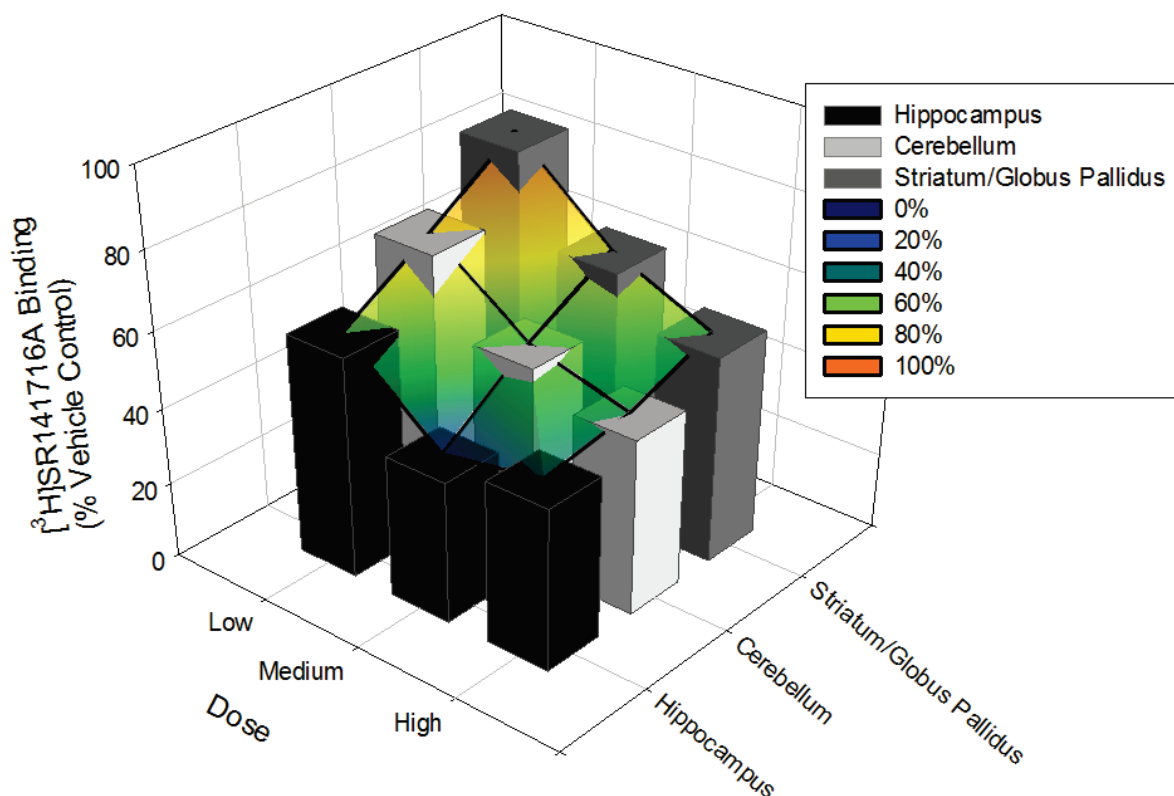
of THC dose (Fig. 0.6). For example, desensitization of the striatum and globus pallidus occurred only after medium and high doses of THC administration, whereas CB₁ receptor downregulation occurred after the high dose, with an insignificant trend following the medium dose. This dose-dependent trend was also observed for measures of motor function that may be related to these brain regions. Here, tolerance to THC-mediated decrease in spontaneous motor activity and catalepsy was detected only in medium and high doses of THC treatment. In contrast, tolerance to THC-mediated hypothermia and antinociception (associated with desensitization in PAG) was evident beginning with the low dose group. The regional specificity in CB₁ receptor desensitization may have implications in the development of tolerance to various cannabinoid-mediated behaviors, and suggests that different mechanisms may exist in regulating CB₁ receptor function.

Recently, studies in mice lacking FAAH, the enzyme primarily responsible for the degradation of AEA, showed that repeated administration of AEA produced less adaptive changes at the CB₁ receptor than THC (Falenski et al., 2010). Conversely, sustained elevation of the endocannabinoid 2-AG produced by chronic administration of JZL184 (Long et al., 2009), an inhibitor of MAGL (the enzyme primarily responsible for the degradation of 2-AG), resulted in region-specific desensitization of CB₁ receptor-mediated G-protein activity (Appendix Fig. A1, Schlosberg et al., *in press*). Results from these studies suggest that FAAH inhibition may be a better therapeutic target versus inhibition of MAGL or chronic treatment with synthetic cannabinoids, which produce greater tolerance to their own effects.

Data on CB₁ receptor localization, interaction with various proteins, and signal transduction pathways, are providing important insight into the physiological role of the endogenous cannabinoid system. However, a growing challenge is the translation of knowledge

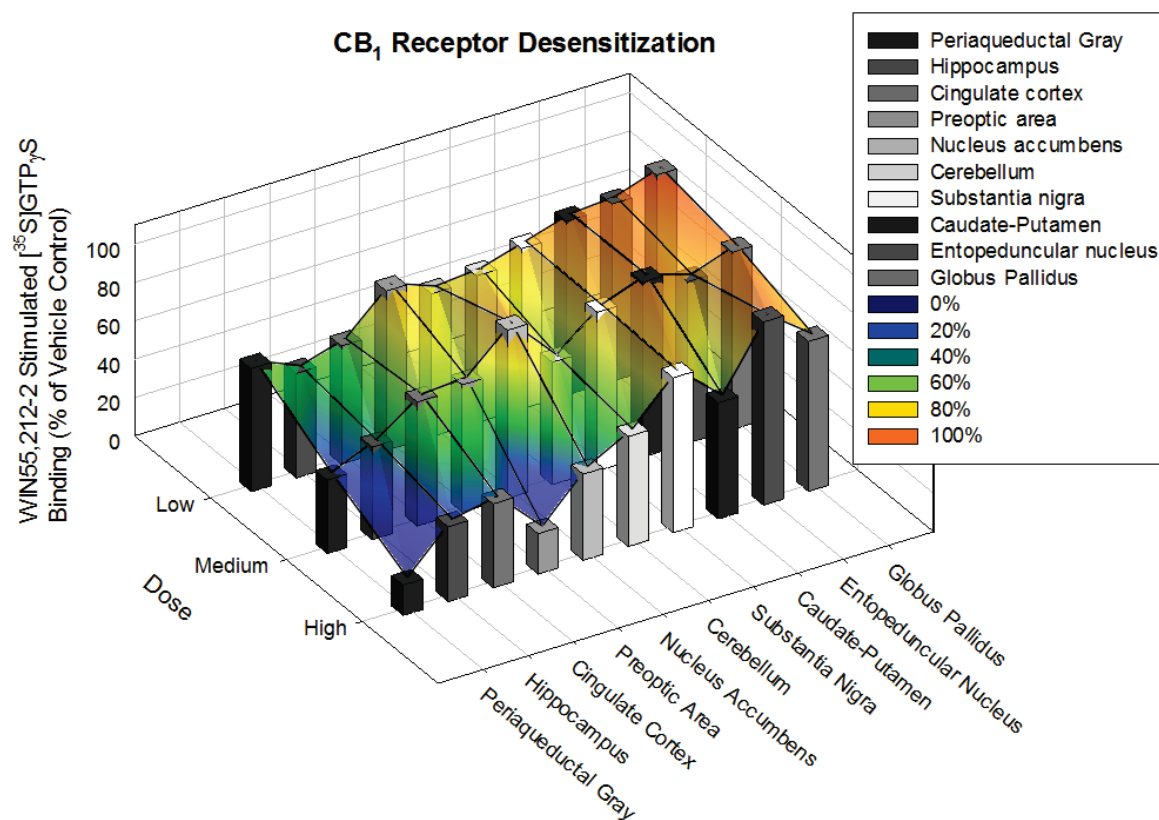
gained from mechanistic studies in cellular systems into native anatomical contexts. An important matter is understanding how the signaling and regulation of CB₁ receptors may vary in different neuronal populations, and how this contributes to the *in vivo* effects of cannabinoids. Studies in this dissertation will address these questions, and introduce novel approaches for the study of CB₁ receptor function and regulation in the CNS.

CB₁ Receptor Downregulation



| Brain Region | Dose (% Vehicle Control) | | |
|--------------------------|--------------------------|--------|-------|
| | Low | Medium | High |
| Hippocampus | 58.06 | 37.33 | 42.62 |
| Cerebellum | 72.12 | 53.54 | 46.24 |
| Striatum/Globus Pallidus | 87.39 | 65.98 | 54.54 |

Figure 0.5. CB₁ receptor downregulation following chronic THC administration as a function of THC dose and brain region. B_{max} values were determined through [³H]SR141716A saturation binding in membrane preparations from various brain regions, and is represented as %Vehicle Control. A low (10 mg/kg), medium (escalating from 10 to 20 to 30 mg/kg), or high (escalating from 10 to 30 to 60 mg/kg) dose of THC was administered twice daily for 6.5 days. A 3D pseudocolored gradient is shown to highlight differences in the magnitude of CB₁ receptor downregulation as a function of dose and region (adapted from McKinney et. al., 2008)



| Brain Region | Dose (%Vehicle Control) | | |
|------------------------|-------------------------|--------|-------|
| | Low | Medium | High |
| Hippocampus | 54.59 | 48.35 | 39.05 |
| Cingulate cortex | 61.64 | 64.82 | 43.79 |
| Preoptic area | 83.13 | 66.46 | 21.06 |
| Nucleus accumbens | 74.53 | 87.76 | 45.08 |
| Cerebellum | 76.66 | 63.84 | 57.40 |
| Substantia nigra | 83.64 | 82.75 | 80.85 |
| Caudate-putamen | 90.65 | 91.18 | 60.64 |
| Entopeduncular nucleus | 92.55 | 84.29 | 95.51 |
| Globus Pallidus | 100.52 | 92.51 | 78.18 |

Figure 0.6. CB₁ receptor desensitization following chronic THC administration as a function of THC dose and brain region. A low (10 mg/kg), medium (escalating from 10 to 20 to 30 mg/kg), or high (escalating from 10 to 30 to 60 mg/kg) dose of THC was administered twice daily for 6.5 days. WIN-stimulated [³⁵S]GTP_γS binding is represented as %Vehicle Control. A 3D pseudocolored gradient is shown to highlight differences in magnitude of CB₁ receptor desensitization as a function of dose and region (adapted from McKinney et. al., 2008)

II. Rationale and Hypotheses

CB₁ cannabinoid receptors belong to the superfamily of G-protein coupled receptors (GPCR) and are widespread throughout the CNS, with greatest abundance in the basal ganglia, hippocampus, and cerebellum. CB₁ receptors also mediate the psychoactive and therapeutic effects of Δ^9 -tetrahydrocannabinol (THC), the primary psychoactive constituent of marijuana. Interestingly, the acute and chronic cellular actions of CB₁ receptors vary by brain region, suggesting that specificity in CB₁ receptor signaling may contribute to differential therapeutic versus side effects of cannabinoids as well as its chronic effects, including tolerance and physical dependence. Our laboratory and others have found regional differences in the regulation of CB₁ receptors by examining a subset of CB₁ receptor containing regions that are likely to mediate various robust cannabimimetic effects, including memory disruption, antinociception, catalepsy, hypothermia, and reduction in spontaneous motor activity. However, the endocannabinoid system is implicated in diverse physiological functions, highlighting the importance of conducting an anatomically inclusive analysis. Yet, it has been difficult to conduct a comprehensive and thorough anatomical study of CB₁ receptors due to limitations in autoradiographic analytical approaches and inherent challenges in defining anatomical boundaries for sampling pre-defined regions of interest; especially when the distribution of differences are not known a priori.

In the following studies in this thesis, we propose that the acute and chronic signaling and regulation of CB₁ receptors occur in a region-specific manner. Furthermore, development of an unbiased whole-brain based approach will facilitate answering questions at the receptor level among anatomically distinct systems. This will be accomplished by using a novel voxel-based

image analysis approach, based on Statistical Parametric Mapping (SPM), to systematically investigate CB₁ receptor signaling throughout the brain, which has previously not been described. In the first chapter, we establish an approach to reconstruct mouse brain images derived from agonist-stimulated [³⁵S]GTPγS binding autoradiographic data into 3D volumetric images. In addition, various image processing techniques are implemented and assessed. This process lead to the development of a novel analytic approach for assessing autoradiographic data based on SPM that was subsequently applied in the following studies.

Ligand-dependent regulation of CB₁ receptors has been demonstrated in cellular systems examining various adaptations such as receptor desensitization, internalization, and downregulation. CB₁ receptors have also been shown to exhibit domain selectivity for coupling to various subtypes of Gα_{i/o}, and in various brain regions, activate different subtypes of G-proteins with varying efficacy and potency following agonist stimulation. Few studies however have directly compared the relative efficacy of different classes of cannabinoids in relation to receptor-mediated G-protein activation as a function of region. In the second chapter, we hypothesize that cannabinoid-receptor mediated G-protein activity will differ by cannabinoid ligand and that relative efficacy of these ligands will vary by brain region. Regional differences in the relative efficacy of cannabinoid agonists may highlight unique signaling properties of the CB₁ receptor, or suggest the existence of non-CB₁ sites. In addition, these findings may have implications regarding the regulation of CB₁ receptors following chronic administration of THC. For example, regional differences in the signaling of CB₁ receptors may invoke different downstream regulatory pathways in a region-specific manner, which may contribute to differential tolerance to various cannabinoid-mediated effects.

The regulation of cannabinoid receptors may potentially have important implications in regard to cannabinoid tolerance. Understanding the underlying mechanisms leading to cannabinoid tolerance not only is important from a therapeutic standpoint, but may also give insight into physical dependence or addiction to cannabinoids through potentially convergent regulatory pathways. This also has direct clinical relevance because THC and its synthetic derivatives are currently approved in the U.S. and indicated for treatment of adverse symptoms related to cancer chemotherapy and the anorexic effect of AIDS-related wasting syndrome. In addition, some states have permitted the medicinal use of marijuana. However, THC is the primary psychoactive constituent of marijuana, which is still the most commonly abused illicit drug in the U.S. Previously our laboratory demonstrated region-specific differences in the magnitude of CB₁ receptor desensitization and downregulation following chronic THC treatment. Other reports have demonstrated the importance of various regulatory proteins, such as β -arrestin-2 (β arr2), and kinases, such as GPCR kinase, in the regulation of CB₁ receptors in cellular systems. However, the *in vivo* physiological role of β arr2 in relation to the regulation of CB₁ receptor function is unclear. The final chapter will test the hypothesis that β arr2 plays a role in the regulation of CB₁ receptor desensitization and downregulation following chronic administration of THC. We predict that mice lacking β arr2 will exhibit a region-specific attenuation in the desensitization and downregulation of CB₁ receptors to chronic THC treatment, for example, in particular CB₁ receptor brain regions with high abundance of β arr2. Further, we propose that regional differences in β arr2-mediated regulation of CB₁ receptors will impact the development of tolerance to THC-mediated effects. Specifically, region-specific regulation of CB₁ receptor adaptation will result in a differential profile of tolerance to THC-mediated effects in associated anatomical systems.

Overall, we hypothesize that regional-differences in the acute and chronic signaling of CB₁ receptors reflect differences in its regional regulation, and that this specificity will be revealed using a novel whole-brain unbiased approach. This will be important in understanding not only the differences in the regulation of CB₁ receptors within various anatomical brain regions, but may also provide insight as to how this regional-specificity may contribute or play a role in the development of tolerance to various cannabinoid-mediated effects. As this novel approach is not restricted to predefined anatomical boundaries, we predict that it will extend our understanding of the function and regulation of the cannabinoid system with unprecedented anatomical precision.

III. Methods

Subjects

Mice were generally housed four to six per cage and maintained on a 12-hr light/dark cycle in a temperature controlled environment (20-22°C), with free access to food and water. All experiments were performed with the approval of the Institutional Animal Care and Use Committee at Virginia Commonwealth University in accordance with the *Guide for Care and Use of Laboratory Animals* (National Research Council, 1996).

Drug treatment and Behavioral Evaluation

Specific drug treatments are described within individual chapters.

Antinociception. Antinociception is assessed using the tail warm water withdrawal assay at 52°C. The intensity of the warm water stimulus is fixed to yield control latencies of 3-4 sec, and an automatic 8 sec cutoff is used to prevent tissue damage. Tail-flick response latencies are expressed as the percentage of the maximum possible effect (%MPE) calculated by: $\%MPE = [(test\ latency - control\ latency)/(cut-off\ time/control\ latency)] \times 100\%$

Rectal Temperature. Core temperature to the nearest 1°C is measured by inserting a rectal probe connected to a Telethermometer (Yellow Springs Industries, Inc.) to a depth of 4.5 cm. Data are expressed as the difference in post- and pre-injection values from each animal expressed in units of °C.

Catalepsy. The effect of chronic cannabinoid injection on catalepsy were assessed using the ring immobility test. Each mouse was placed on a ring (5.5 cm in diameter) that is elevated 16 cm

above the tabletop for a 5 min session. The amount of time the mouse remains motionless will be recorded to the nearest second. Latencies of 100 sec or more will be considered cataleptic.

Drugs and chemicals

Guanosine 5'-O-[gamma-thio]triphosphate ($[^{35}\text{S}]\text{GTP}\gamma\text{S}$, 1250 Ci/mmol) and $[^3\text{H}]\text{SR141716A}$ (SA: 44.0 Ci/mmol) were purchased from PerkinElmer Life Sciences (Boston, MA). CP55,940, SR141716A, $\Delta^9\text{-THC}$ and $[^3\text{H}]\text{CP55,940}$ (88.3 Ci/mmol) were provided by the Drug Supply Program of the National Institute on Drug Abuse (Rockville, MD). Bovine serum albumin (BSA), GDP, $\text{GTP}\gamma\text{S}$, and WIN55,212-2, WIN55,212-3 were purchased from Sigma-Aldrich (St. Louis, MO) and methanandamide (R-1) was purchased from Cayman Chemicals. All other chemicals were obtained from Sigma-Aldrich or Fisher Scientific.

Agonist-Stimulated $[^{35}\text{S}]\text{GTP}\gamma\text{S}$ Autoradiography

Mice were sacrificed by rapid decapitation, and brains were removed and immediately frozen in isopentane at -30°C and stored at -80°C . Autoradiographic assays were conducted as previously published from our laboratory (Sim et al., 1995). Briefly, coronal sections ($20\ \mu\text{m}$) were cut on a cryostat maintained at -20°C , thaw-mounted onto gelatin-subbed slides, and stored desiccated at 4°C overnight. Slides were then stored desiccated at -80°C until use. To minimize variation in assay conditions, slides from each experimental condition within a single animal were processed concurrently. This allowed for identical assay conditions for basal and agonist incubated sections from each animal. For the $[^{35}\text{S}]\text{GTP}\gamma\text{S}$ autoradiography assay, slides were brought to room temperature ($\sim 22^\circ\text{C}$) for 40 min, then equilibrated in 50 mM Tris-HCl buffer (pH 7.4) with 3 mM MgCl_2 , 0.2 mM EGTA, and 100 mM NaCl (Assay Buffer) for 10 min at

25°C. Next, slides were transferred to Assay Buffer + 0.5% BSA, with 2 mM GDP and 10 mU/ml adenosine deaminase for 20 min at 25°C. Slides were then incubated in Assay Buffer + 0.5% BSA containing 0.04 nM [³⁵S]GTPγS in the presence or absence (basal) of appropriate drug(s) and/or vehicle for 2 hrs at 25°C. After final incubation, slides were rinsed twice in 50 mM Tris buffer (pH 7.4) at 4°C, then in deionized water. Slides from each condition were then dried and loaded together in the same cassette with a [¹⁴C] standard, and exposed to Kodak BioMax MR film for 24-36 hrs. Films were digitized at 8-bits per pixel with a Sony XC-77 video camera. [³⁵S]GTPγS binding data from autoradiography was generally expressed as Net Stimulation (nCi/g), which was calculated as: (agonist - basal).

[³H]CP55,940 receptor binding autoradiography

[³H]CP55,940 receptor binding autoradiography was conducted as previously described (Herkenham et al., 1991; Moise et al., 2008), with slight modifications. Brain tissue sections were initially thawed to room temperature for 40 mins and incubated for 3 hrs in assay buffer containing 50 mM Tris-HCl (pH 7.4), 5% BSA, and 3 nM [³H]CP55,940 (88.3 Ci/mmol). Slides were then rinsed twice in wash buffer (50 mM Tris-HCl (pH 7.4), 1% BSA) maintained at 4°C for 2 hrs each. Sections were then briefly fixed in a solution containing 0.5% formalin in 50 mM Tris-HCl (pH 7.4) for 1 min and dried under a cool stream of air. Non-specific binding was assessed in the presence of 10 μM CP55,940. Slides from each subject (Total or Non-Specific) were loaded together in the same cassette with a [³H] standard, and exposed to Kodak BioMax MS film for 18 weeks. Films were digitized at 8-bits per pixel with a Sony XC-77 video camera. [³H]CP55,940 receptor binding data from autoradiography was generally expressed as Specific-binding (nCi/mg), which was calculated as: (Total binding - Non-specific binding).

Agonist-Stimulated [³⁵S]GTPγS binding for membrane homogenates

Membrane agonist-stimulated [³⁵S]GTPγS binding experiments were conducted as previously published (Sim-Selley et al., 2006). Briefly, mice were sacrificed by decapitation and the whole spinal cord and brain were extracted, and individual brain regions dissected. Tissue was immediately frozen on dry ice and stored at -80°C until use. On the day of assay, tissue samples were homogenized in 5 ml of cold Assay Buffer (*see Agonist-Stimulated [³⁵S]GTPγS Autoradiography section above*) and centrifuged at 50,000g at 4°C for 10 min. Supernatant was then discarded and tissue sample resuspended in 5 ml of Assay Buffer. Sample protein concentrations were determined by the Bradford method (Bradford, 1976). Tissue homogenates were then incubated with adenosine deaminase (3 mU/ml) in Assay Buffer for 15 min at 30°C. To generate concentration-effect curves, membrane protein (8 μg for whole brain, 10 μg for cerebellum or whole spinal cord) was incubated in Assay Buffer (0.5 mL total volume) containing 0.1 nM [³⁵S]GTPγS, 0.125% BSA, 30 μM GDP, and varying concentrations of drug(s) for 2 hrs at 30°C. Non-specific binding was assessed in the presence of 20 μM unlabeled GTPγS. The reaction was terminated by vacuum filtration through Whatman GF/B glass fiber filters, and rinsed three times with cold Tris Buffer (50mM Tris-HCl, pH 7.4) at 4°C. Bound radioactivity was determined by liquid scintillation spectrophotometry following 15 hr extraction in Econo-Safe scintillation fluid. [³⁵S]GTPγS binding data from membranes was generally expressed as %Net Stimulation, which was calculated as: [(agonist - basal)/basal] x 100%.

[³H]SR141716A receptor binding for membrane homogenates

Membrane and protein preparations were conducted as described above. Whole spinal cord membrane protein (30 μg) was incubated in buffer (pH 7.4) containing 50 mM Tris-HCl, 0.2 mM EGTA, 3 mM MgCl_2 , 100 mM NaCl, 0.5% BSA and varying concentrations of [^3H]SR141716A (0.1 - 2.5 nM) for 1.5 hrs at 30°C. Non-specific binding was assessed in the presence of 5 μM unlabeled [^3H]SR141716A. The reaction was terminated by vacuum filtration through Whatman GF/B glass fiber filter paper soaked in Tris buffer (50mM Tris-HCl, pH 7.4) containing 0.5% BSA, and then rinsed three times with cold Tris buffer + 0.5 BSA at 4°C. Filtered samples were then placed in scintillation vials containing Econo-Safe scintillation fluid, shaken for 1 hr, and bound radioactivity was determined by liquid scintillation spectrophotometry. [^3H]SR141716A receptor binding data from membranes was generally expressed as Specific-binding (pmol/mg), which was calculated as: (Total binding - Non-specific binding).

[^3H]CP55,940 receptor binding for membrane homogenates

Membrane and protein preparations were conducted as described above. Whole cerebellar membrane protein (8 μg) was incubated in sodium-free buffer (pH 7.4) containing 50 mM Tris-HCl, 0.2 mM EGTA, 3 mM MgCl_2 , 0.5% BSA and varying concentrations of [^3H]CP55,940 (0.03 - 8.5 nM) for 1.5 hrs at 30°C. Non-specific binding was assessed in the presence of 10 μM unlabeled [^3H]CP55,940. The reaction was terminated by vacuum filtration through Whatman GF/B glass fiber filter paper soaked in Tris buffer (50mM Tris-HCl, pH 7.4) containing 0.5% BSA, and then rinsed three times with cold Tris buffer + 0.5 BSA at 4°C. Filtered samples were then placed in scintillation vials containing Econo-Safe scintillation fluid, shaken for 1 hr, and bound radioactivity was determined by liquid scintillation

spectrophotometry. [³H]CP55,940 receptor binding data from membranes was generally expressed as Specific-binding (pmol/mg), which was calculated as: (Total binding - Non-specific binding).

Thionin (Nissl) Staining

Unfixed brain tissue sections were initially placed in a 95% ethanol solution for 15 min and then hydrated in solutions of 70% ethanol, 50% ethanol, and then dH₂O water each for 1 min. Sections were then transferred to thionin working solution containing 93% buffer (7g Na-acetate, 2 mL glacial acetic acid, 1 L dH₂O) and 7% thionin stock (1 g thionin per 100 mL hot dH₂O) for 2 min (sections requiring lighter or darker staining were left in solution shorter or longer, respectively). Sections were next dehydrated stepwise in the following solutions for 1 min each: dH₂O, 50% ethanol, 70% ethanol, 95% ethanol, 100% ethanol. Sections were finally rinsed twice in Xylene for 1 min and preserved with permount and cover slipped.

3D image reconstruction and Statistical Parametric Mapping (SPM) analysis

Please see next chapter for complete methodology and assessment

Region of Interest (ROI) analysis

To validate and compare regions found to be significant with SPM analyses, separate ROI analyses were performed. ROI measurements were conducted on the original unprocessed images, averaged bilaterally across hemispheres, and analyzed with GraphPad Prism Version 5 using appropriate statistical tests and Tukey's post-hoc analysis for ANOVA designs. ROI anatomical boundaries were defined by a mouse brain atlas (Franklin and Paxinos, 2008). The

following brain nuclei were included within each regional ROI measurement: amygdala (basomedial, basolateral, & medial, lateral, central nuclei), auditory cortex (primary, secondary), cerebellum (molecular layer), cingulate cortex (primary, secondary), hippocampus (CA1-3, dentate gyrus), hypothalamus (medial), motor cortex (primary, secondary), somatosensory cortex (primary, secondary), thalamus (central, ventral posteromedial & posterolateral, ventromedial, and ventrolateral thalamic nuclei), and visual cortex (primary, secondary). All other brain regions (i.e. caudate-putamen, globus-pallidus, periaqueductal gray, substantia nigra) were measured in entirety based on anatomical boundaries defined by a mouse atlas (Franklin and Paxinos, 2008).

IV. Chapter 1: Statistical Parametric Mapping (SPM) analysis of cannabinoid-mediated G-protein activation in the 3D reconstructed mouse brain

1.1 General overview of SPM analysis for reconstructed data sets

Previously our laboratory developed agonist-stimulated [^{35}S]GTP γ S autoradiography for the examination of receptor-activated G-proteins in brain tissue sections (Sim et al., 1995). This technique allows for both anatomical- and pharmacological-specific assessment of cannabinoid-stimulated G-protein activity (Figures 1.1-1.2) in a quantitative manner. Analysis of these datasets generally involves manual measurements of pre-defined regions of interest (ROI). ROI-based approaches therefore are limited by a priori selection of regions and subject to inter-rater bias. To avoid limitations in ROI-based approaches and investigate CB $_1$ receptor signaling in an anatomically inclusive way, we adapted a novel whole-brain unbiased approach based on Statistical Parametric Mapping (SPM) to study CB $_1$ receptor signaling in the 3D reconstructed mouse brain. The volumetric reconstruction of images derived from agonist-stimulated [^{35}S]GTP γ S autoradiography and procedure for SPM analysis is outlined in Figure 1.3. Briefly, coronal brain sections are collected throughout the neuroaxis, processed for agonist-stimulated [^{35}S]GTP γ S autoradiography, and digitized. Digitized images are then realigned to reestablish spatial consistency and stacked into a volumetric image array. SPM software is then used for further image manipulation and processing, including spatial normalization and image smoothing, which are required before implementation of voxel-based statistical analysis of data. Application of these methods are detailed in this chapter and further demonstrated with [^3H]ligand autoradiographic data in Chapter 3, and Appendix Figure A3. The reference to “SPM” throughout this dissertation will refer to both the Statistical Parametric Maps generated

from SPM analysis as well as the collection of tools packaged with the SPM software, which is available in the public domain (<http://www.fil.ion.ucl.ac.uk/spm/>). All image processing, analyses, and display of data were done on a Windows-based 32-bit architecture PC, having 4 gigabytes of RAM, a 3.2 Ghz Intel Pentium 4 processor, and a 256 MB 3D video card.

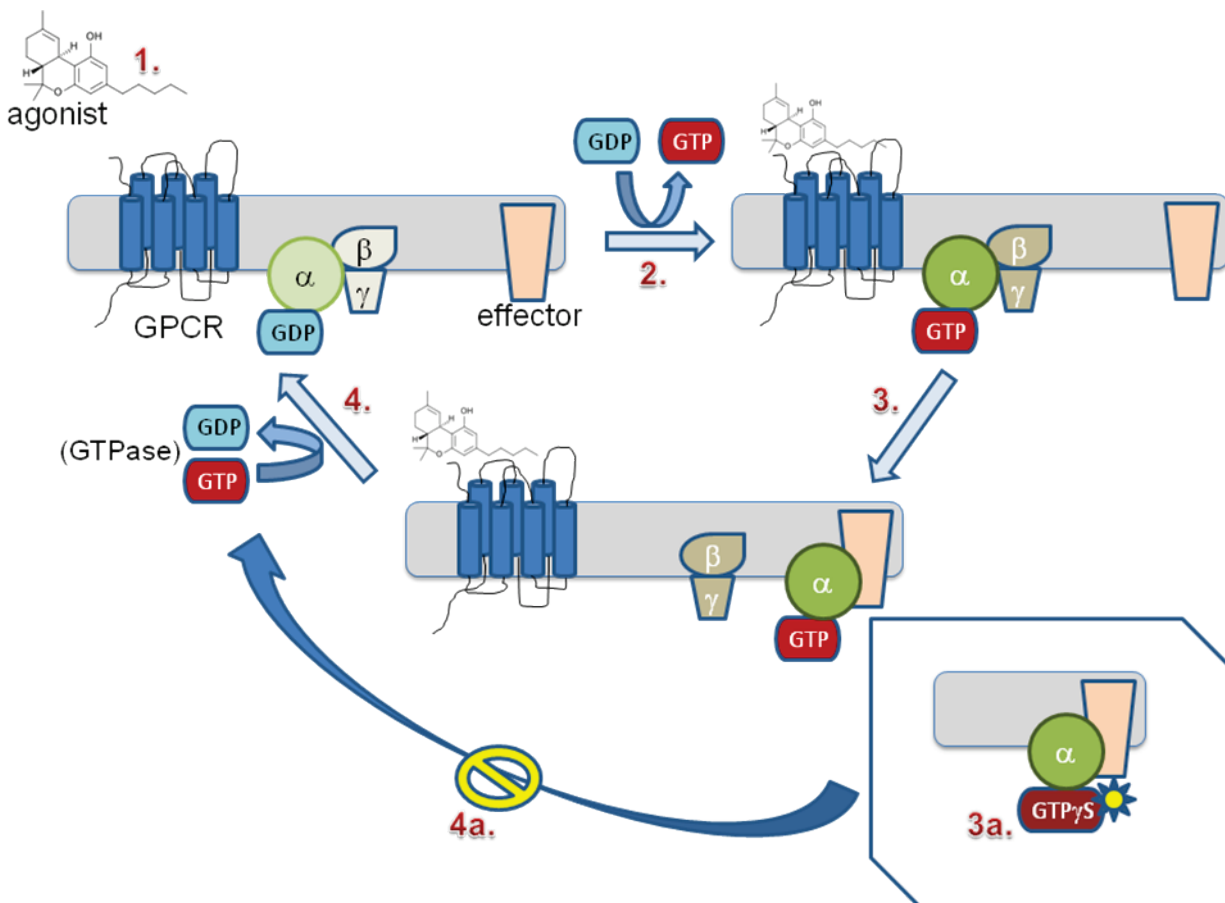


Figure 1.1. Overview of agonist-stimulated $[^{35}\text{S}]\text{GTP}\gamma\text{S}$ binding assay. Binding of an agonist (1) to a G-protein coupled receptor (GPCR) results in a guanine nucleotide exchange reaction of GDP to GTP (2) and subsequent activation of the G-protein. Activation leads to the dissociation of the G-protein into both $\beta\gamma$ and α subunits, which interact with specific effectors (3). Termination of signal transduction occurs via an intrinsic GTPase (4), hydrolyzing GTP back to GDP. A non-hydrolyzable radiolabeled GTP analogue, $[^{35}\text{S}]\text{GTP}\gamma\text{S}$ (shown in bottom right, 3a), is used for quantification of receptor-mediated G-protein activity. This prevents the hydrolysis step and therefore leads to the accumulation of agonist-stimulated $[^{35}\text{S}]\text{GTP}\gamma\text{S}$ binding (4a).

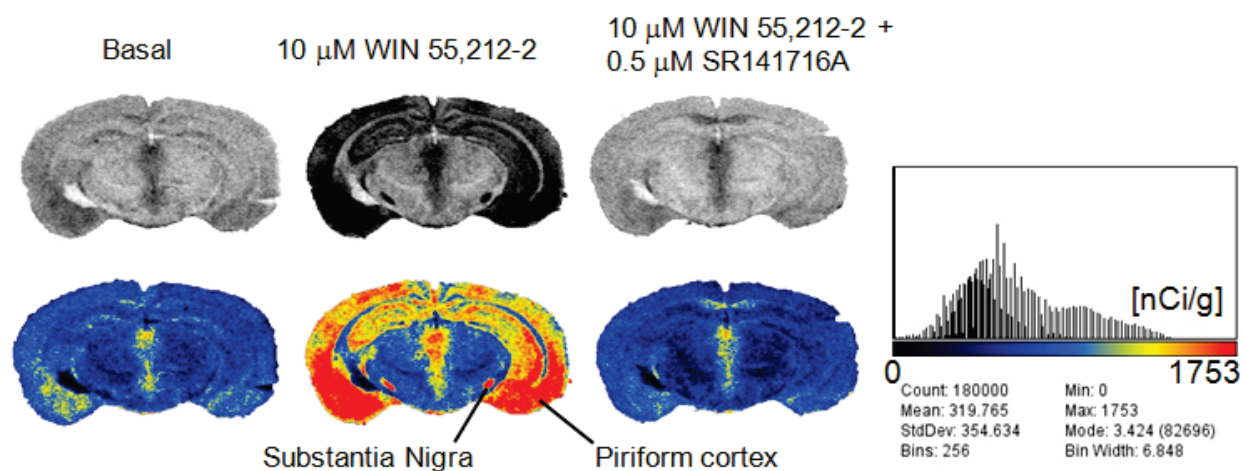


Figure 1.2. Cannabinoid-stimulated $[^{35}\text{S}]\text{GTP}\gamma\text{S}$ autoradiography. Agonist-stimulated $[^{35}\text{S}]\text{GTP}\gamma\text{S}$ autoradiography was performed as described in *Methods*. Autoradiographs are shown in grayscale (top row) and pseudocolor (bottom row), where black or red/yellow pixels represent areas with the lowest and highest levels of stimulated $[^{35}\text{S}]\text{GTP}\gamma\text{S}$ binding, respectively. Stimulated $[^{35}\text{S}]\text{GTP}\gamma\text{S}$ binding is shown for the basal (no agonist, left column) condition, and after incubation with the full CB_1 receptor agonist WIN55,212-2 alone (middle column) or in the presence of the CB_1 receptor antagonist SR141716A. A histogram shows the distribution of CB_1 receptor stimulated $[^{35}\text{S}]\text{GTP}\gamma\text{S}$ binding by WIN55,212-2 alone.

1.2 Preparation of brain tissue sections and image pre-processing

Brain image reconstruction of autoradiographic data was conducted based on previously published methods (Holschneider et al., 2006; Nguyen et al., 2004), with modifications. For each study in this dissertation, reconstructed brain images from each condition (i.e. agonist or basal (absence of agonist)) were created from coronal sections collected throughout the neuroaxis from bregma 2.34 mm to -6.84 mm (Franklin and Paxinos, 2008) with an inter-slice distance of 200 μm (Fig. 1.4). Volumetric reconstructions derived from coronal tissue sections produced the best results qualitatively compared to reconstructions from transverse sections (Fig. 1.5). Using an inter-slicing distance of 200 μm for transverse sections resulted in suboptimal slice realignment, likely due to rapid changes in anatomical structures as well as larger changes in overall surface area in this plane (see section *1.3 Slice registration and 3D image reconstruction*). The larger perimeter in transverse versus coronal sections also presents a greater challenge in minimizing edge distortion that results from tears and folding of tissue during collection. Larger surface areas in transverse sections in addition increase the risk for trapping debris, condensed water droplets on the surface of the blade, or pockets of air, which can create bumps or bubbles in the mounted tissue section. Furthermore, the asymmetrical surface with respect to the cutting direction in transverse (shaped like an irregular ellipsoid) versus coronal (shaped like a regular ellipsoid) sections may lead to non-uniform adhesion of biological tissue onto the glass slide, which can be further perturbed by other environmental variables such as humidity or static electricity. Significant edge distortions can lead to uneven and serrated edges, which can best be visualized in the reconstructed coronal plane (Fig. 1.5A).

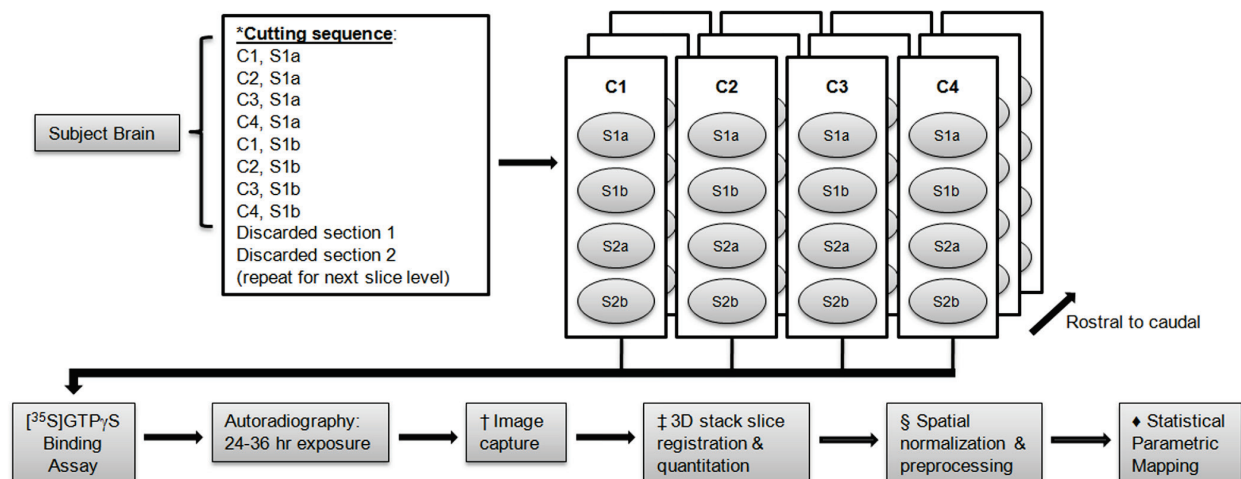


Figure 1.3. Flow chart of tissue preparation for autoradiography, 3D image reconstruction and SPM analysis (from *Nguyen et al., NeuroImage 2010*).

* 20 μm coronal sections are cut in a cryostat maintained at -20°C . C = condition; S = slice level; a & b = set 1 & 2 of duplicate sections

† The section free from artifact (i.e. S1a or S1b) at each slice level is digitized at 8-bits per pixel and saved in TIFF format

‡ Image reconstruction and slice registration described in *Nguyen et al., NeuroImage 2004*. Registered image stacks are quantitated and saved as 16-bit images in Analyze image format.

§ Individual image reconstructions are spatially normalized to a study-specific brain template as described in *Nguyen et al., NeuroImage 2004*. Spatially normalized images are then smoothed with a Gaussian kernel (Full Width Half-Max = 3X the voxel value)

◆ Statistical Parametric Mapping (SPM) software was used to setup experimental design and analysis of imaging data.

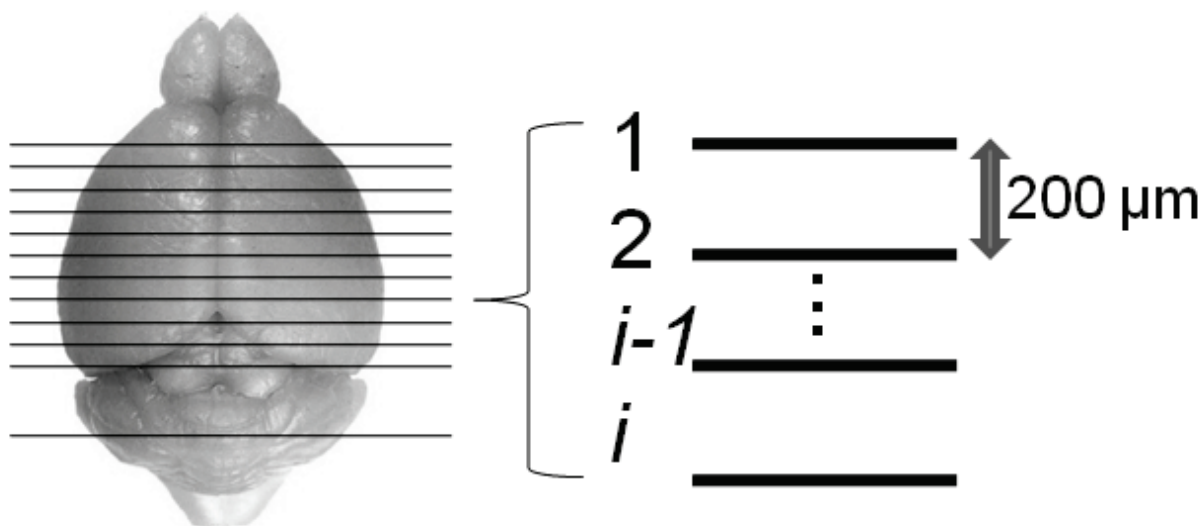


Figure 1.4. Brain sectioning strategy for 3D reconstruction. Volumetric reconstructions were derived from coronal sections (20 μm thick) collected throughout the neuroaxis from bregma 2.34 mm to -6.84 mm (Franklin and Paxinos, 2008) with an inter-slice distance of 200 μm . ($i-1$) = second to last slice; i = last slice

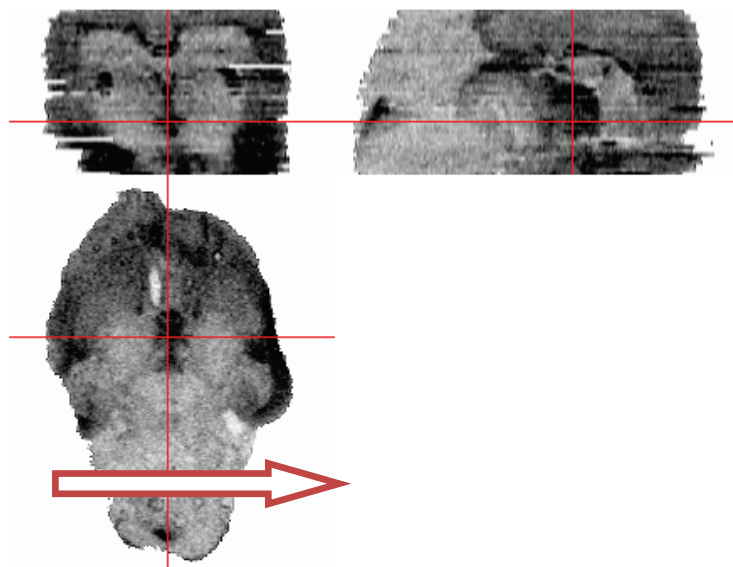
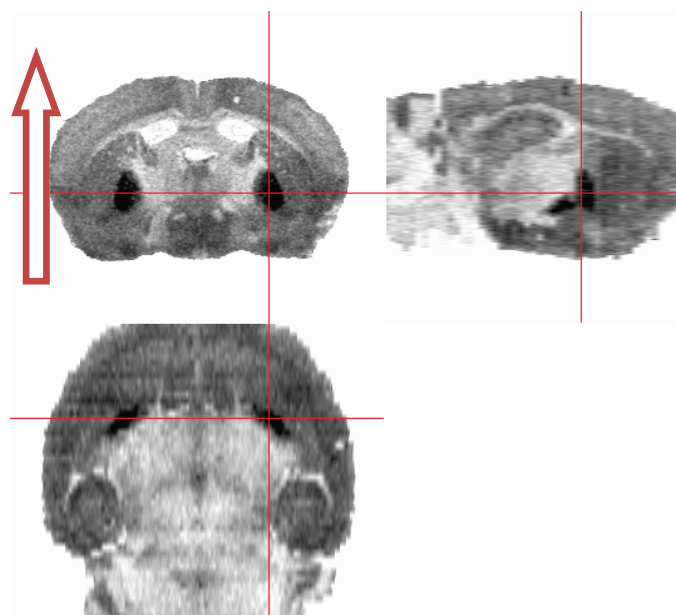
A**B**

Figure 1.5. Image reconstructions derived from coronal or transverse sectioning. Volumetric reconstructions of 10 μM DAMGO- (A) and 10 μM WIN55,212-2- (B) stimulated [^{35}S]GTP γ S binding autoradiographs in wild-type naive mice. Image reconstructions were derived from 200 μm spaced transverse and coronal sections for DAMGO and WIN55,212-2 images, respectively. Crosshairs highlight the medial thalamus (A) and globus pallidus (B) in three orthogonal planes. Arrows represent the direction of sectioning in the cryostat with respect to the cutting plane. Agonist-stimulated [^{35}S]GTP γ S autoradiography was performed as described in *Methods*.

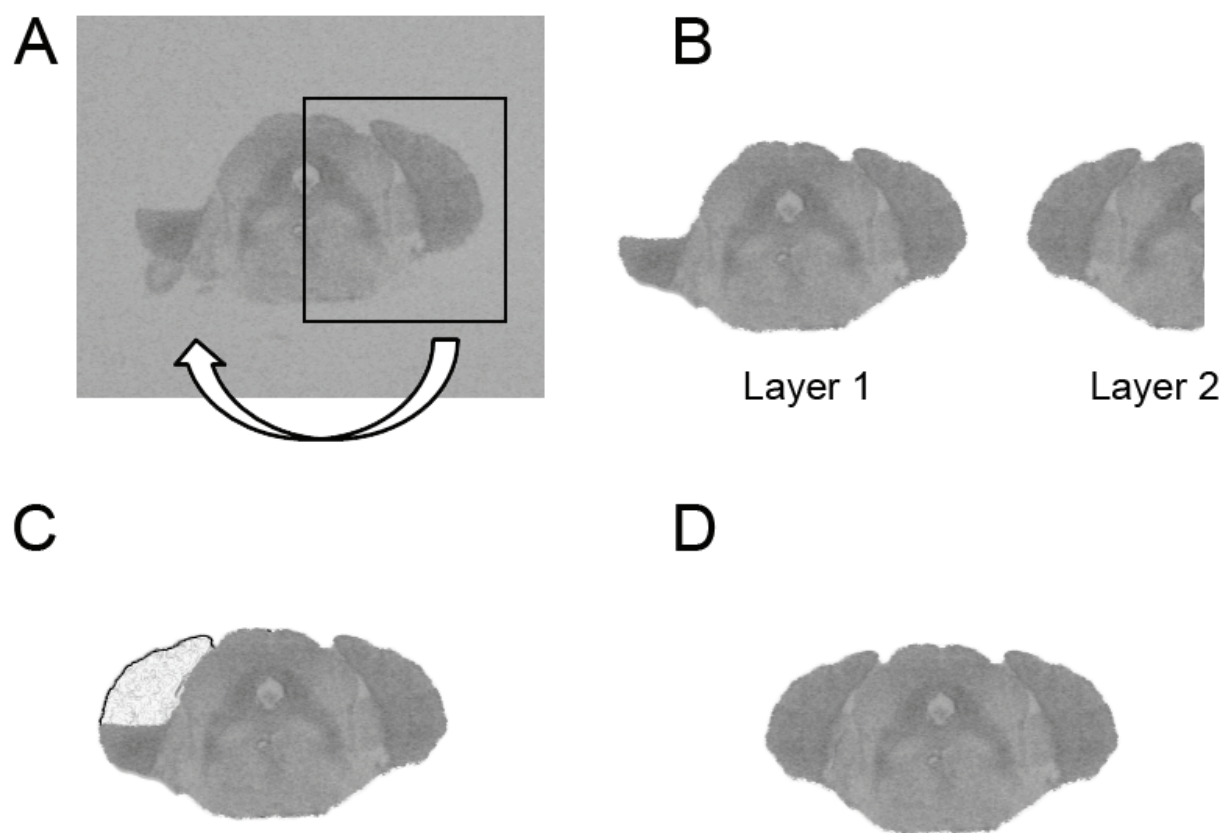
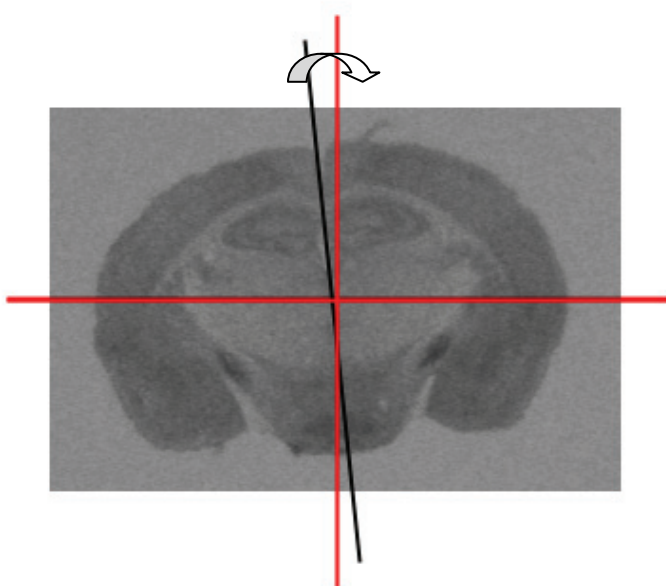
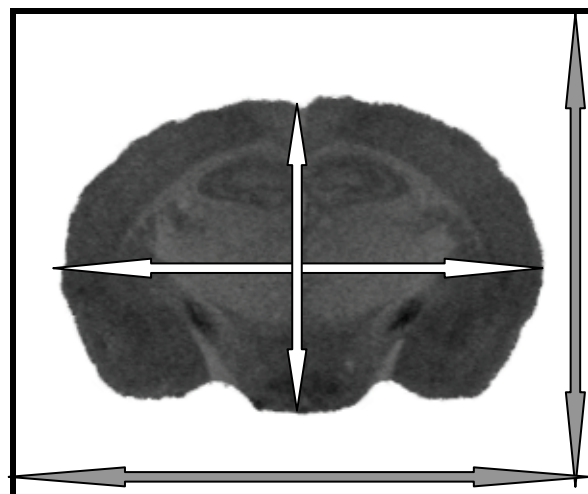


Figure 1.6. Image editing strategy for digitized autoradiographs having substantial artifact in one hemisphere. Missing tissue in one hemisphere is replaced by duplicating the missing tissue from the opposite intact hemisphere (A). The intact hemisphere is initially selected or image-masked, flipped horizontally, and duplicated as a new layer (B). The duplicated layer (layer 2 above) is placed behind the original layer (layer 1 above) and the two layers are manually aligned for spatial consistency. Replacement of the missing tissue area by the duplicated opposite hemisphere is represented as a shaded outline in the figure above (C). Both layers are then combined as a single layer or flattened image (D).

Serial adjacent sections from a single brain were collected for different assay conditions in duplicate sets. This scheme allowed for duplicate sets of at most 4 different conditions (reconstructions) from a single mouse brain as outlined in Figure 1.3. For sections with extensive artifact(s) or missing tissue in one hemisphere, the intact opposite side was duplicated and reflected (flipped horizontally) either behind or over the damaged hemisphere in order to preserve original imaging data (Fig. 1.6). For severely damaged sections that made this strategy impossible, the other duplicate section was utilized. In these special cases, the true inter-slice distance varied between 100 to 260 μm .

Tissue sections free from artifact related to extraction of the brain, tissue sectioning, etc., were selected for image reconstruction. A mask was next created for each selected digitized autoradiographic section. Most standard mask creation tools select connected pixels whose data values are within a defined tolerance of neighboring reference pixels. The Quick Selection Tool in Adobe Photoshop CS3 (Version 10) was used in these studies as it is suitable for both agonist-stimulated [^{35}S]GTP γ S binding and [^3H]ligand binding autoradiographic data. Masked sections were then copied and pasted onto a new 8-bit grayscale image with a white background at 100 dpi and size of 300 x 250 pixels (width x height), and saved in TIFF format. Pixel size was calculated by measuring the width of a brain section on film by a ruler (units in mm) and dividing by the captured image width (units in pixels). For example from studies in this dissertation, the average width of a mouse section at bregma -1.8 mm (Franklin and Paxinos, 2008) is 10.6 mm and has an average corresponding pixel length of 266 pixels. This equates to a pixel dimension of about 40 $\mu\text{m}/\text{pixel}$. Thus for mouse brain sections captured at pixel dimensions of 40 x 40 μm^2 , a white background of image size 300 x 250 pixels allowed adequate space for rigid-body transformations during slice realignment (see next section). In addition,

masked sections were centered and rotated manually so that midline was approximately parallel to the vertical reference axis of the white background image (Fig. 1.7). This initial prealignment provided a good starting estimate for slice registration.

A**B**

Section dimension: 250x165 pixels

White image dimension: 300x250 pixels

Figure 1.7. Slice image editing of digitized autoradiographs. Raw mouse brain images are initially outlined with a selection mask, pasted onto a new image with a white background and rotated manually if the midline axis of the raw image is not parallel to the vertical axis of the new image. (A) An arrow shows the manual rotation used for prealignment. The raw image is then centered vertically and horizontally to complete section prealignment. (B) Section and total image dimensions (*width x height*) in pixels are shown with white and gray arrows, respectively.

1.3 Slice registration and 3D image reconstruction

Image reconstructions were generated in ImageJ (version 1.42q, <http://rsb.info.nih.gov/ij/>) by importing coronal sections that were preprocessed as outlined in the previous section, and saving them as an image stack in Analyze format. The Analyze format (<http://www.mayo.edu/bir/>) is a common multidimensional biomedical imaging format that includes both a header (*.hdr) and data (*.img) file associated with each 3D image. The header file contains information such as voxel sizes, which must be defined prior to viewing and further processing within the SPM software. To make brain reconstructions spatially consistent in 3D, a section-to-section registration technique was used. Briefly, a section in the middle of the brain was chosen as the initial target to align adjacent sections in a stepwise fashion. Each registered section was then used as a new target to register the next adjacent section in either the anterior or posterior direction. A section in the middle of the brain was selected as the starting point to 1) allow for independent registration of slices in the anterior and posterior directions and 2) minimize the propagation of misregistration error that may occur in early slices if a section in the anterior-most pole was selected as the reference image. This registration algorithm utilizes the intensity of all image pixels for a section and searches for the transformation that maximizes a measure of intensity similarity between corresponding pixels of an adjacent section (Thévenaz et al., 1998). In other words the transformation is computed to minimize the mean-square difference between the target and source images. The registration algorithm is available as a plugin within the ImageJ environment called TurboReg (<http://bigwww.epfl.ch/thevenaz/turboreg/>). An auxiliary plugin, StackReg (<http://bigwww.epfl.ch/thevenaz/stackreg/>), was used for the recursive alignment of reconstructed image stacks in this dissertation. In order to preserve the original shape of tissue

sections, a non-warping rigid-body transformation was selected that consisted of only rotations and translations. It is important to note that the alignment algorithm performs optimally when the source and target images are comparable in size and have similar starting points (Nguyen, unpublished observations). Therefore, if the centers of two images are far apart, it is important to remove the translational offset manually (i.e. centering images) before proceeding with finer registration. StackReg offers an automatic and manual mode. In manual alignment, associated landmarks are defined on a source and target image to establish initial correspondence between them. All image registration in this dissertation used the automatic mode to minimize inter-rater variability.

Header files of registered image stacks were opened and edited using MRIcro software, which is available in the public domain (<http://www.cabiatl.com/mricro/mricro/index.html>) from the Center for Advanced Brain Imaging, Atlanta, GA. Voxel sizes of mouse brain images in this dissertation were scaled up 10X their true size ($40 \times 40 \times 200 \mu\text{m}^3$) and saved in the header files. This allowed for proper viewing within the SPM environment, which is originally designed for human brain imaging data having dimension sizes on the order of millimeters (Nguyen et al., 2004). Gray level intensities of the raw image stack were then quantitated to activity values (nCi/g of tissue) as previously described (Sim et al., 1996b). Briefly, [^{35}S] was incorporated into sections of frozen brain paste and sections were then weighed to obtain nCi/g of tissue. Radioactivity in each section was determined by liquid scintillation spectrophotometry. [^{14}C] microscale standards and [^{35}S] sections were then exposed to film and correction factors were calculated to convert [^{14}C] values to [^{35}S]. Raw optical density values (OD) are quantitated to radioactivity values (Y) using the following linear equation, where m is the slope and b is the intercept, as calculated from [^{14}C] standards:

$$Y = m \bullet OD + b$$

Reconstructed stacks were quantitated using a macro created within ImageJ and its complete code is shown in Figure 1.8. This fully automated macro script opens a registered image stack and prompts the user to enter the slope (m) and intercept (b) coefficients, as calculated from standards, in order to globally quantitate raw voxel values to radioactivity units (nCi/g) and then save the image at a bit depth of 16-bits. Saving at a dynamic range of 16-bits allowed for a potential data range from 0 to ($2^{16}-1$), or 65,535 nCi/g. The StackReg utility normally introduces "registration artifact" or black edges to visually show the transformations that were applied to realign sections (see registration results in Figures 1.10-1.12). The above macro also includes functionality to automatically remove registration artifact.

Although not required, volumetric images were reoriented in coordinate space to correspond to the standard viewing axis defined within the SPM software environment. In this standard coordinate space lateral, anterior-posterior, and dorsal-ventral correspond to the X, Y, and Z axes, respectively (Fig. 1.9). An automated macro script was written to reorient images using the `To_AxialTP` function (part of a suite of alignment plugins found at: <http://www.med.harvard.edu/JPNM/ij/plugins/AlignStacks.html>) within the ImageJ environment. The macro code and description is detailed in (Fig. 1.9).

| Line # | ImageJ macro for quantitation of [³⁵ S]GTPγS binding imaging data |
|--------|--|
| 1 | open(); |
| 2 | run("Invert", "stack"); |
| 3 | run("Duplicate...", "title=mask.img duplicate"); |
| 4 | run("Invert", "stack"); |
| 5 | run("Max...", "stack value=1"); |
| 6 | run("Calculator Plus", "i1 i2=mask.img operation=[Multiply: i2 = (i1*i2) x k1 + k2] k1=1 k2=0 create"); |
| 7 | run("Invert", "stack"); |
| 8 | run("32-bit"); |
| 9 | run("Multiply..."); |
| 10 | run("Add..."); |
| 11 | run("Min...", "stack value=0"); |
| 12 | run("16-bit"); |
| 13 | run("Analyze 7.5...", "save"); |
| 14 | close(); |
| 15 | close(); |
| 16 | close(); |

Description of macro code by line number:

- 1: prompts user for selecting image volume (analyze format, *.img)
- 2-3: inverts source image and creates a duplicate of itself
- 4: duplicate image is inverted
- 5: data values >1 are assigned a value of 1. This creates a binary (mask) image, so that areas with registration artifact have a data value of 0 and all else have a value of 1.
- 6: image array multiplication of source image and binary image
- 7: image inversion reverts source image back to original state (without registration artifact)
- 8: image bit depth increased to 32-bit to allow for the image quantitation
- 9: prompts user to enter slope coefficient calculated from ¹⁴C standards using a linear fit
- 10: prompts user to enter the intercept (of abscissa) calculated from ¹⁴C standards
- 11: data values < 0 (i.e. negative numbers) are assigned a data value of 0
- 12: quantitated images are saved at a dynamic range of 16-bit, to encompass the data range of [³⁵S]GTPγS binding imaging data, which typically ranges from 0 to 2,500 nCi/g
- 13: prompts user to save quantitated stack image in analyze format
- 14-16: closes all active windows

Note: This macro removes slice alignment artifact generated from using the StackReg plugin for ImageJ. General requirements: ImageJ ver 1.36b (or later) and calculator plus. **No other images should be open at time of use and "Scale when converting" must be disabled (under edit; options; conversions).**

Figure 1.8. ImageJ macro for removing slice registration artifact and quantitation of raw imaging data to radioactivity units (nCi/g).

| Line # | ImageJ macro for reorienting images to correspond to SPM standard axis |
|--------|--|
| 1 | open(); |
| 2 | run("To AxialTP", "input=[Coronal (anterior-to-posterior)]"); |
| 3 | run("Analyze 7.5...", "save"); |
| 4 | close(); |
| 5 | close(); |

Description of macro code by line number:

- 1: prompts user for selecting image volume (analyze format, *.img)
- 2: reorients image to correspond to the standard SPM axis (see image below)
- 3: prompts user to save image in analyze format
- 4-5: closes all active windows

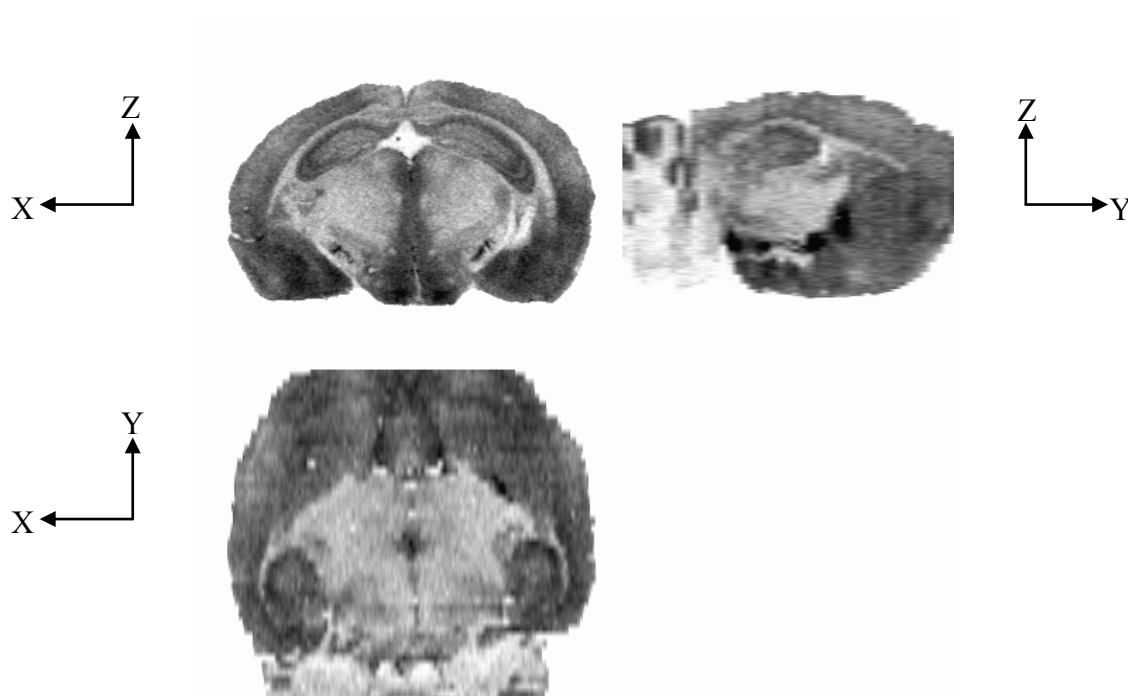
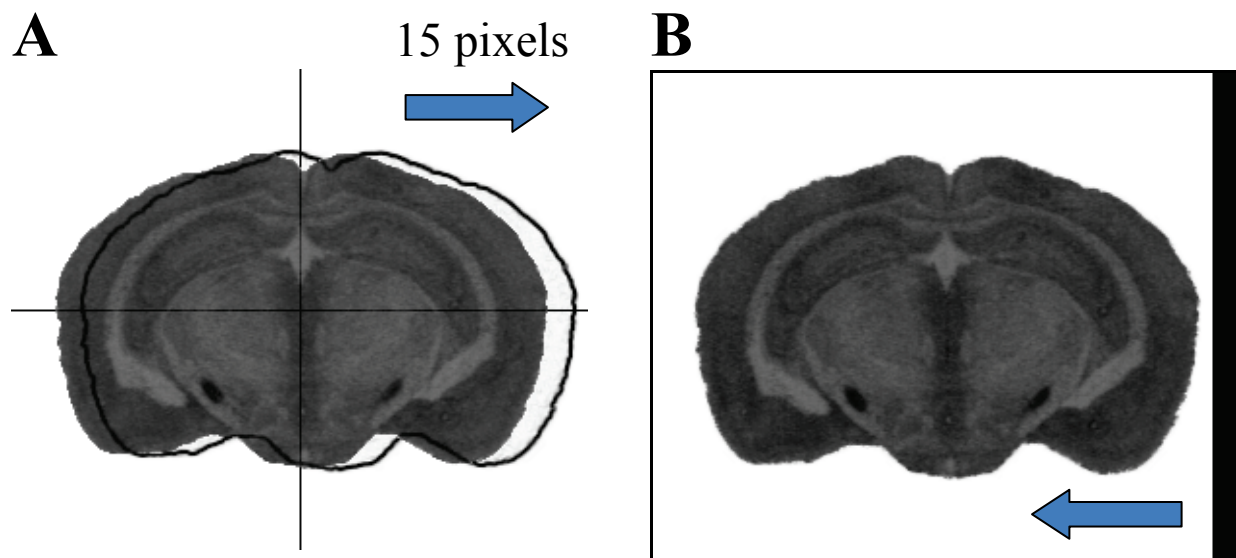
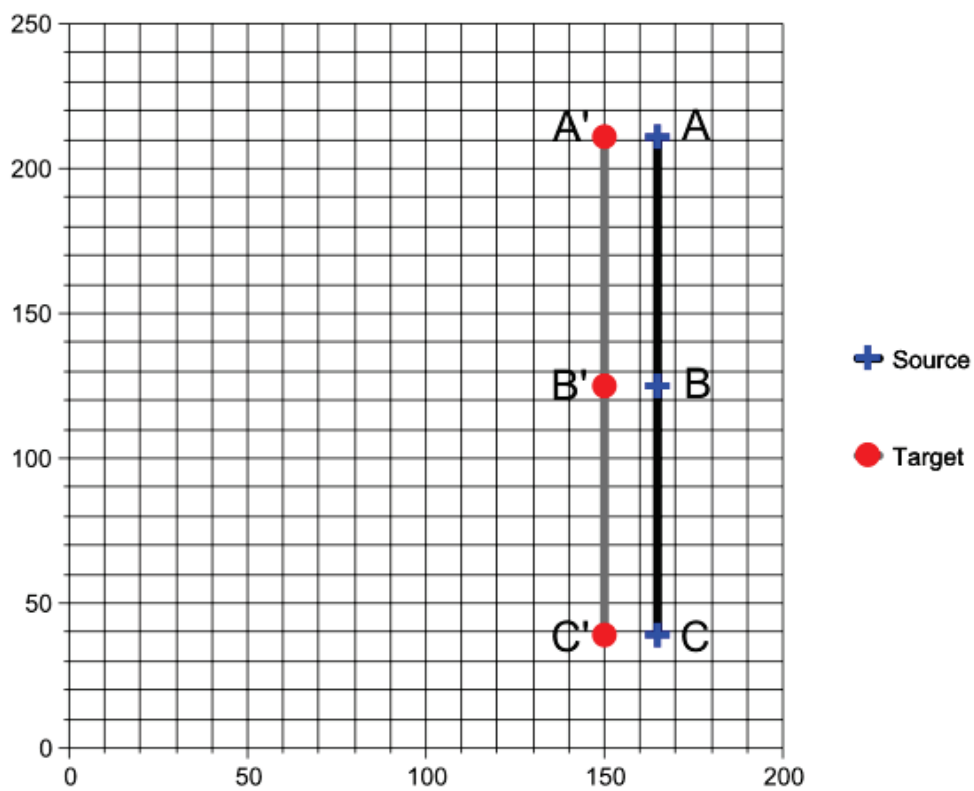


Figure 1.9. ImageJ macro for reorienting image volumes to correspond to the SPM standard axis: lateral left-right, anterior-posterior, and dorsal-ventral are the X, Y, and Z planes, respectively



C

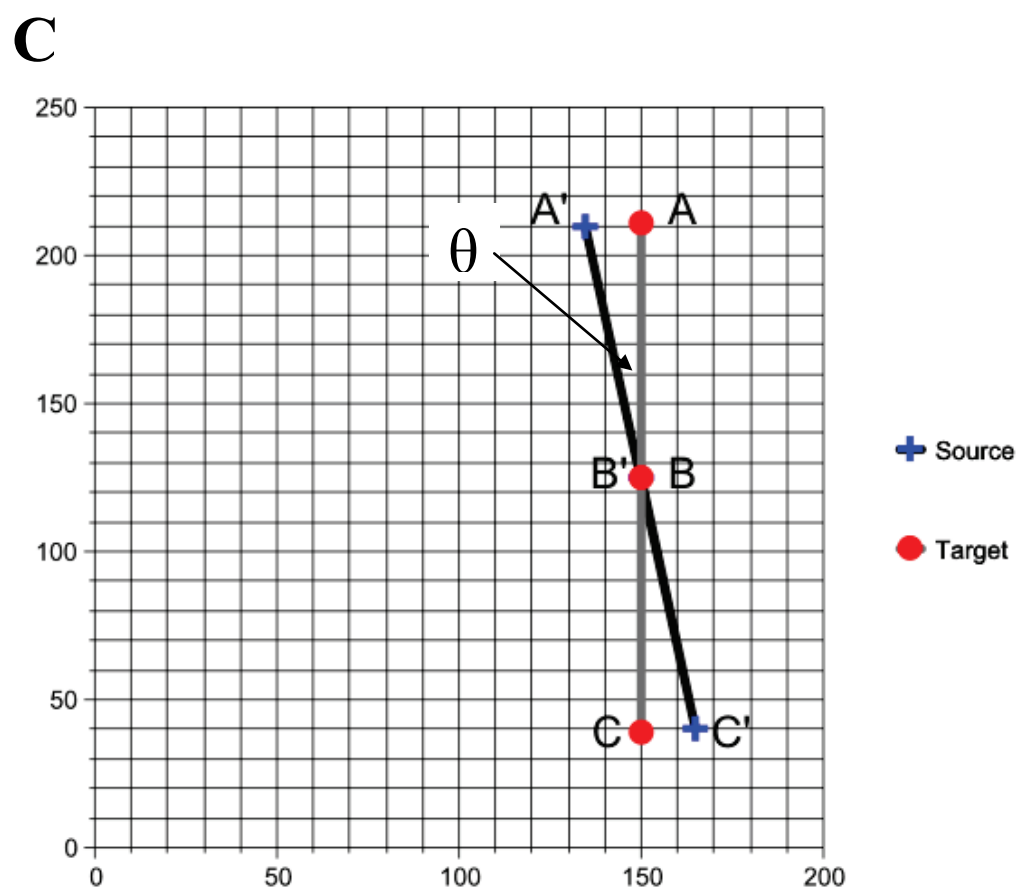
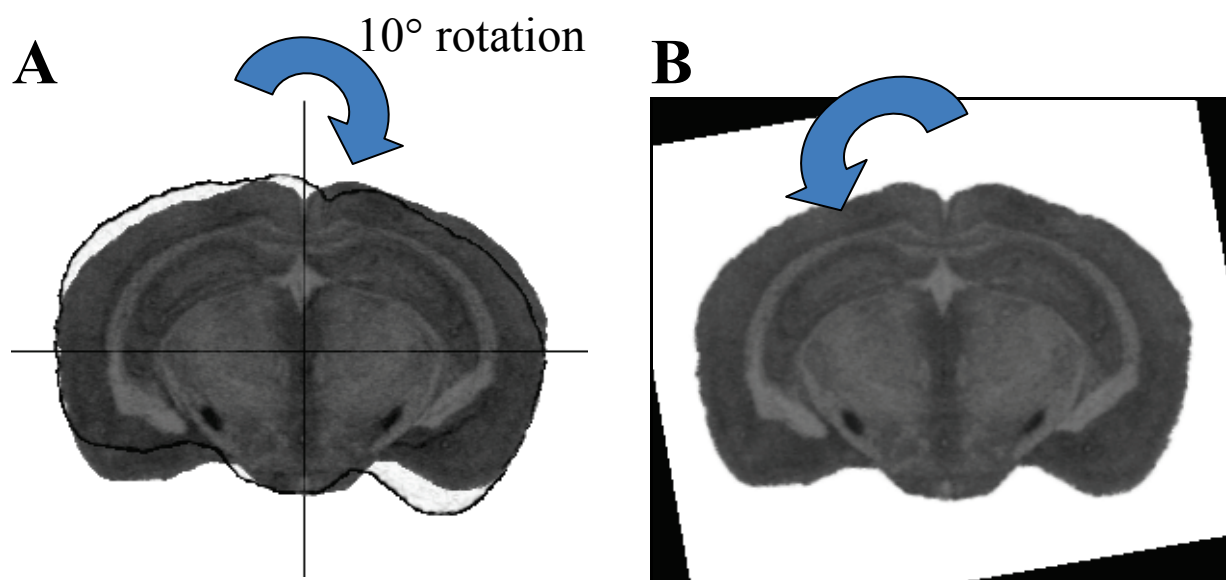


D

| Refined source landmarks (x, y) | Target landmarks (x, y) |
|------------------------------------|----------------------------|
| A (164.99, 210.99) | A' (150, 211) |
| B (164.99, 124.99) | B' (150, 125) |
| C (164.99, 38.99) | C' (150, 39) |

Length of B' to B = $B_x - B'_x = 164.99 - 150 = 14.99$ pixels

Figure 1.10. Image registration: translation simulation. (A) An image was duplicated and translated by 15 pixels. An outline of the translated slice is shown as an overlay on the original image. (B) An arrow and black area illustrates the applied transformation after image registration. (C) StackReg (TurboReg) utilizes landmarks on the target and source image to apply the transformation (D) Calculating the magnitude of translation can be done by vector subtraction of coordinate pairs.



D

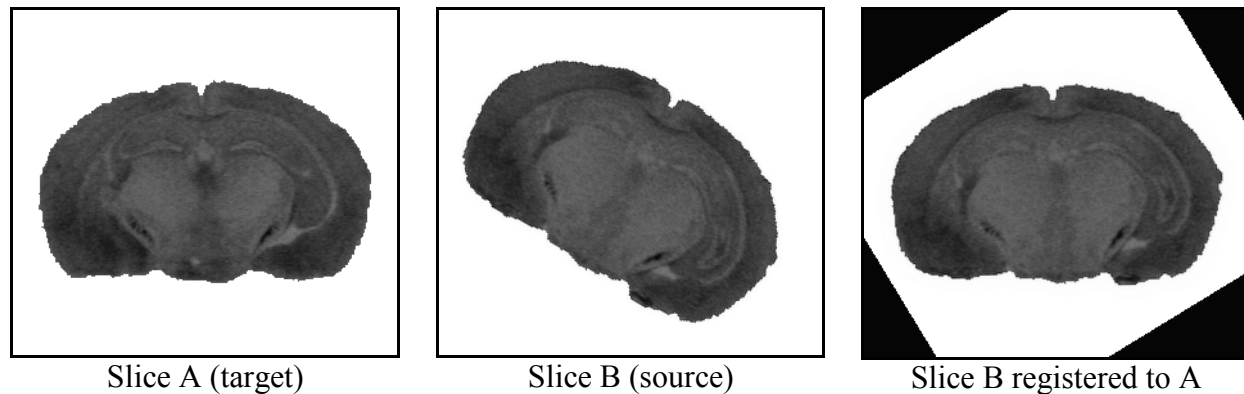
| Refined source landmarks (x, y) | Target landmarks (x, y) |
|------------------------------------|----------------------------|
| A' (134.88, 209.85) | A (150, 211) |
| B' (149.81, 125.16) | B (150, 125) |
| C' (164.75, 40.47) | C (150, 39) |

$$\theta = \tan^{-1}[(\text{length A' to A})/(\text{length A to B})]$$

$$= \tan^{-1} [(A_x - A'_x)/(A_y - B_y)] = \tan^{-1} [(150 - 134.88)/(211 - 125)] = \tan^{-1} (15.12/86) = \mathbf{9.97^\circ}$$

Figure 1.11. Image registration: rotation simulation. (A) An image was duplicated and rotated by 10 degrees. An outline of the rotated slice is shown as an overlay on the original image. (B) An arrow and black area illustrates the applied transformation after image registration. (C) StackReg (TurboReg) utilizes landmarks on the target and source image to apply the transformation. (D) Calculating the degree of rotation (θ) can be done trigonometrically.

A



B

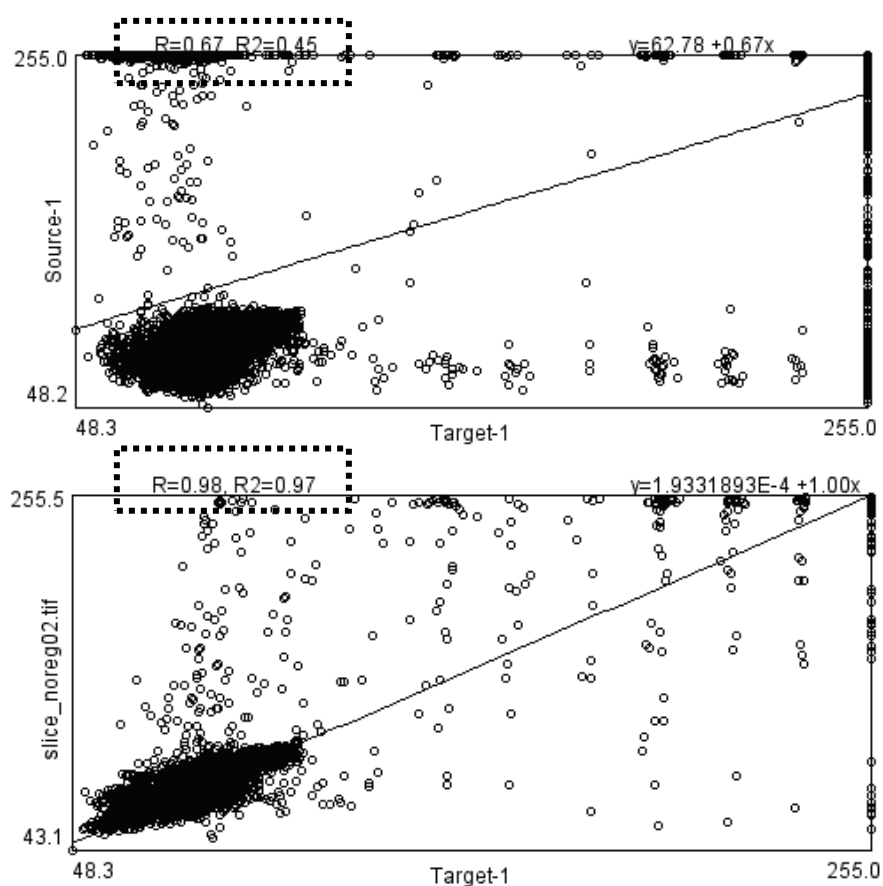


Figure 1.12. Registration of two representative coronal images (A) and image correlation plots before (B, top) and after registration (B, bottom). Slice registration increased the image correlation coefficient (R^2 value) to 0.97 (up from 0.45)

1.4 Assessment of registration algorithm: simulation studies

The quality of brain reconstructions was assessed by visual inspection of internal structures viewed in different orthogonal angles and correspondence of brain areas across reconstructions of different conditions and/or subjects. The SPM software includes a utility, called CheckReg, to load and view multiple images of the same size. Spatial correspondence between images can be assessed by a crosshair or point of reference, which updates each orthogonal frame in all loaded images. To quantitatively assess the accuracy of the registration algorithm used for agonist-stimulated [³⁵S]GTPγS autoradiographic data, simulation studies were done with representative brain tissue sections. A 2D image was registered to its duplicate that was either translated to the right by 15 pixels (Fig. 1.10) or rotated clockwise by 10° (Fig. 1.11). The calculated translation and rotation after applying image registration were 14.99 pixels and 9.97°, respectively. The differences from actual values were 0.01 pixels (misregistration error of 0.067% or about 0.4 μm) in the translation simulation and 0.03° (misregistration error of 0.3% or about 2.61 μm) in the rotation simulation.

To further assess the registration algorithm, an image correlation plot was constructed for two different adjacent sections (spaced at 200 μm) before and after applying image registration (Fig. 1.12). Corresponding pixel values from both images (source and target) at each coordinate were graphed and correlated using a linear fit. The correlation coefficient (R^2 value) was 0.45 before image registration and increased to 0.97 after application of registration, suggesting an improvement in spatial correspondence between the two adjacent sections. These simulation studies thus demonstrate the robustness and viability of using the registration algorithm implemented in StackReg for the recursive alignment of images derived from agonist-stimulated [³⁵S]GTPγS autoradiographic data.

1.5 Voxel-based Analysis using Statistical Parametric Mapping (SPM)

The SPM package exists as a collection of scripts written within the Matlab environment (<http://www.mathworks.com/>), which is a software program designed for numerical computation, creation of user-interfaces, implementation of algorithms, etc. SPM analyses (version SPM5, <http://www.fil.ion.ucl.ac.uk/spm/>) for reconstructed autoradiographs were conducted as previously published (Nguyen et al., 2004), with modifications. Prior to SPM analysis, all images from a study were spatially normalized into the same coordinate space (Ashburner J., 1999; Friston et al., 1995a) as defined by a study-specific brain template. This template was derived from brain reconstructions of the most efficacious agonist, due to its high structural information and contrast of anatomical boundaries, thus optimizing spatial normalization. Initially a subject's reconstructed brain image from the most efficacious agonist was selected based on alignment quality and freedom from artifacts. This image was then smoothed by 3X its voxel size (see below for image smoothing rationale) to serve as the preliminary template. All reconstructions of the most efficacious agonist from different subjects were then spatially normalized to the preliminary template while retaining the original voxel sizes. These spatially normalized images were then averaged, using the SPM image average tool (`spm_avg.m` script in SPM directory), and smoothed by 3X its voxel size to become the study-specific brain template.

Spatial normalization of reconstructions from multiple conditions (agonist(s) and basal) assayed from the same animal was performed by coregistering (using normalized mutual information option in SPM) these images to the most efficacious agonist. The coregistration technique allows within-subject registration of all reconstructions, so that they are aligned within the same coordinate space. This assumes that there are no gross differences among the shapes of

the reconstructed images, which is a reasonable assumption to make for images derived from the same animal. Intra-subject coregistration thus allows one to determine spatial normalization parameters from a single reconstruction (i.e. the most efficacious agonist) and subsequently apply them to all coregistered reconstructions from the same animal. Using this strategy has the dual advantage of reducing the number of spatial normalization routines as well as estimating the spatial normalization parameters from the set of images likely possessing the most structural information. Furthermore, this avoids spatial normalization challenges when basal images (no agonist) that have relatively low structural information/contrast are directly normalized to a template derived from an agonist (Nguyen, unpublished observations).

A total of 16 iterations were used during the SPM spatial normalization routine, where a 3D non-rigid transformation model was used to warp a source image to match the brain template. Image reconstructions of mouse brains may vary in shape and size due to intrinsic inter-subject differences in anatomical boundaries and/or from preparation of tissue. Therefore, the goal of spatial normalization is to warp, or deform, image reconstructions so that a given location in one subject (or reconstruction) corresponds to the same location in another subject's image. It is important to note that the registration approaches for spatial normalization are different from the techniques in the previous section for individual sections, which employed rigid or non-warping transformations. Correspondence of brain regions are shown in Figure 1.13 before and after performing spatial normalization. Spatial normalization of these three images for example improved the spatial correspondence of the globus pallidus as depicted by the crosshair representing the same coordinate location across all subjects. The accuracy of spatial normalization is very important as it allows signal averaging across subjects and thus the possibility to perform univariate statistical tests at each voxel for the creation of a statistical

parametric map. In addition, it allows for creation of subtraction images, such as net-stimulated images derived from subtracting basal from agonist-stimulated images (see Chapter 3). Spatial normalization lastly serves as a diagnostic point to determine whether there are underlying problems with one's dataset. Unsuccessful spatial normalization of an image may infer 1) inadequate slice registration, 2) significant artifact related to preparation of tissue, or 3) insufficient structural information/contrast related to the autoradiographic assay

Image smoothing was referenced above at various processing steps, for example after averaging of images to create a study-specific brain template. Smoothing is also applied to spatially normalized brain images prior to SPM analysis. Image smoothing essentially convolves the data using a defined kernel or function. In other words, each data point in an image is averaged with its neighbors. Specific to studies in this dissertation, data points were smoothed or replaced by a weighted average of its surrounding neighbors in 3D space, where the closest neighboring voxels were given the greatest weights (Gaussian kernel). Image smoothing is illustrated in Figure 1.14A and demonstrates one benefit of smoothing, such as increasing signal to noise. Following the addition of randomly generated noise into an image in Figure 1.14A, smoothing effectively eliminates it, however at a cost of losing spatial resolution (Fig. 1.14A rightmost column). This is noted by the general “blurring of a smoothed image” and loss of discrete borders, such as the separation of hair in the example image. The extent or magnitude of smoothing is defined by the width of the kernel, also referred as the full-width at half maximum (FWHM) of the Gaussian function. By the matched filter theorem, the optimum smoothing kernel corresponds to the size of the effect that one anticipates (Friston et al., 2007). However, this may be difficult to establish a priori especially for data sets studying receptor-mediated

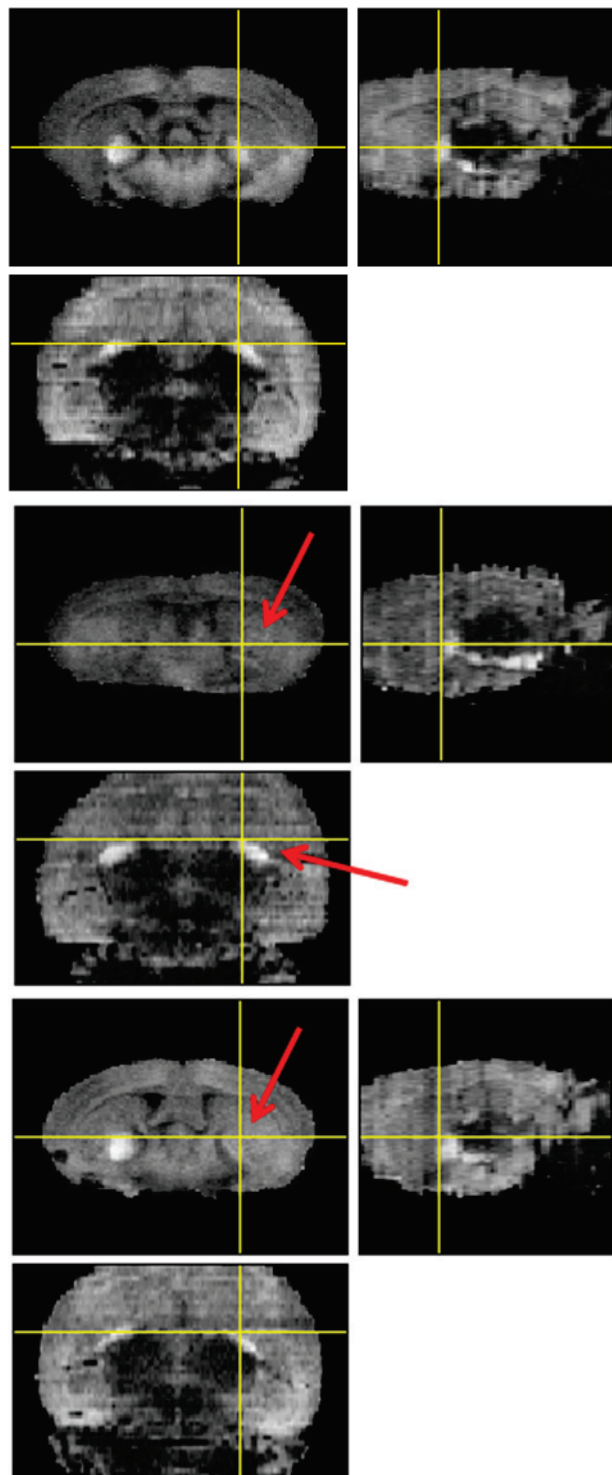
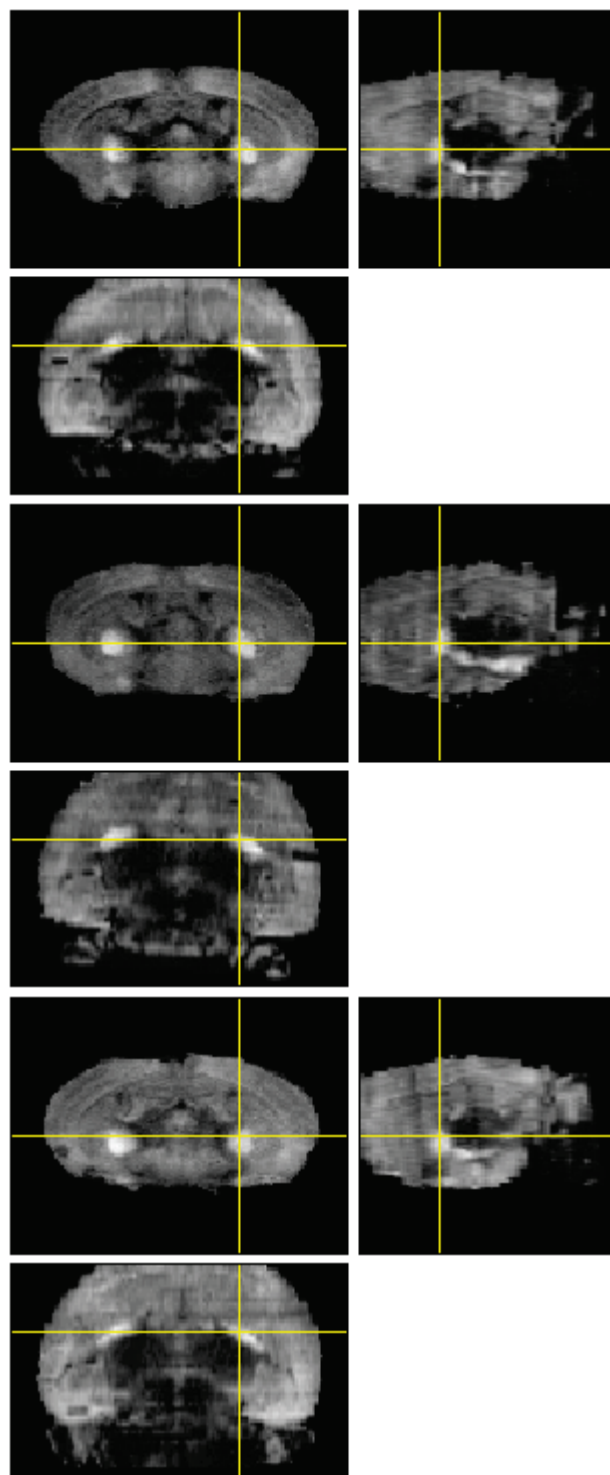
A**B**

Figure 1.13. Spatial normalization of reconstructed brain images. Three representative brain reconstructions are shown before (A) and after (B) application of spatial normalization. Yellow crosshairs in each column represent identical coordinate locations within each subject. Note the poor spatial correspondence of the globus pallidus in images before spatial normalization (red arrows) and its improvement after spatial normalization.

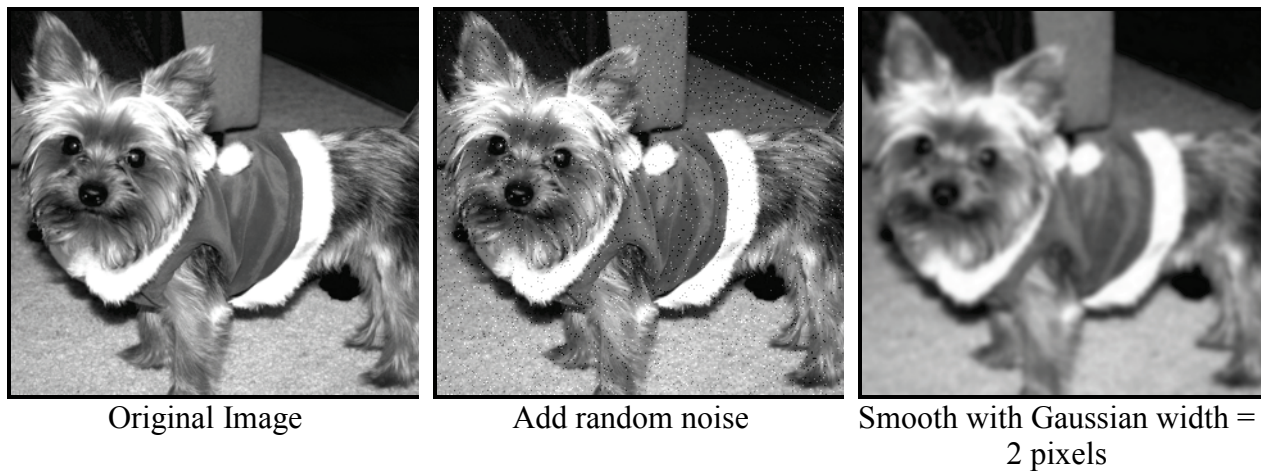
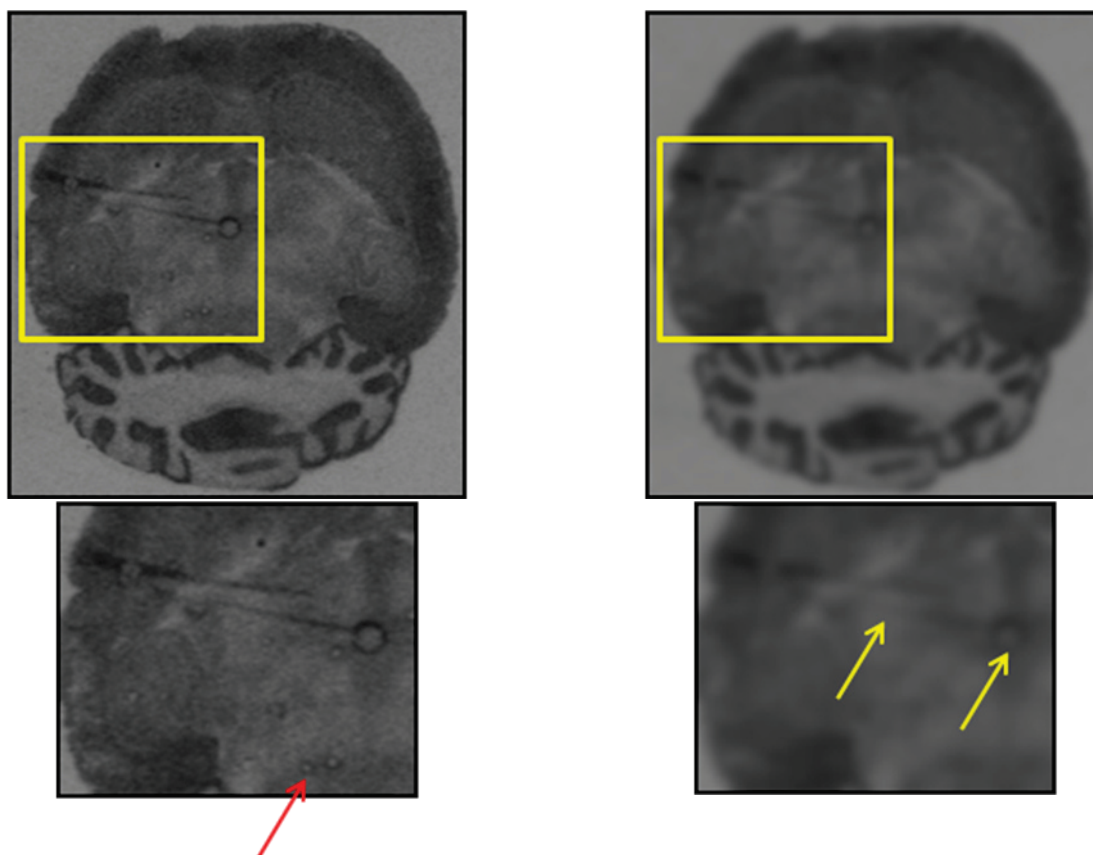
A**B**

Figure 1.14. Image smoothing. (A) Smoothing with a Gaussian width equal to twice the pixel size is applied to a grayscale image after adding random noise (middle column). Note the removal of image noise after smoothing, but at the expense of spatial resolution (right column). (B) Application of image smoothing is shown for agonist-stimulated [³⁵S]GTPγS binding autoradiography. Artifacts such as the smaller air bubbles and folds are removed, but relatively larger ones fail at this given magnitude of spatial smoothing.

G-protein activity, because its magnitude may vary regionally based on the agonists intrinsic efficacy and receptor localization, or the size of the experimental effect may be unknown. Too little smoothing may result in artifactual differences, or “noisy SPMs”, whereas too much smoothing may potentially exclude the detection of smaller differences when signal is “diluted” or averaged out with its neighboring voxels. Therefore, a relatively moderate FWHM equal to 3X the intrinsic voxel size ($\text{FWHM} = 120 \times 120 \times 600 \mu\text{m}^3$) was used whenever smoothing was required, which was generally compatible with our estimate of misregistration error and anatomical variability between our data sets. As mentioned previously, image smoothing helps to increase the signal to noise ratio, but this has its limitations. In Figure 1.14B, smoothing of autoradiographic data can account for relatively minor artifacts related to tissue preparation (i.e. bubbles, folds), but has difficulty with more extensive artifacts such as tearing. Finally, smoothing the data renders the errors more normal in their distribution and ensures the validity of inferences based on statistical parametric tests (Friston et al., 2007).

To ensure that only voxels within the brain were included for SPM analysis, an image threshold was specified to create a mask image using the SPM software. The mask was visually inspected and overlaid onto brain images, and the threshold value was calculated such that voxels less than 10% of the mean voxel value within the brain were not included for SPM analysis. This calculated threshold value of 10% ensured that only voxels in the background and within the ventricles from all brain images (basal and agonist) were excluded. Figure 1.15 shows an image histogram of voxel values from a single reconstructed mouse brain. Note that the global mean has a value of 152.32 nCi/g, which is low due to the inclusion of voxels in the background. After thresholding, the corrected mean voxel value is 496.44 nCi/g and includes about one-third of the total number of voxels in the image.

Because amounts of radiolabeled [³⁵S]GTP γ S for in situ binding assays were kept constant, global normalization (Nguyen et al., 2004) in signal was omitted from SPM analysis. At each voxel, a general linear model was then used to describe the data in terms of experimental and confounding effects, and residual variability (Friston et al., 1995b). A voxel-by-voxel statistical analysis was performed to localize significant differences in receptor-mediated G-protein activation. Because of the extensive number of univariate statistical tests performed by SPM, the multiple comparisons problem was addressed using gaussian random field theory (Worsley et al., 1992). This analysis results in inference based on corrected *p*-values (Friston et al., 1991; Friston et al., 1996; Friston et al., 1994). Each study in this dissertation used an appropriate parametric statistical test at each voxel to test the effect of drug in activating G-proteins, and specific contrasts were evaluated. For all studies, significance ($p < 0.05$) was established at the voxel and/or cluster level (minimum cluster extent of 100 contiguous voxels) after correction for multiple comparisons. Statistical *p*-values were corrected using the false-discovery rate and were adjusted for small search volume for each CB₁ receptor containing region, including cortex, striatum, globus pallidus, substantia nigra, hippocampus, amygdala, hypothalamus, periaqueductal gray, and cerebellum. Small volume corrections used a sphere volume of interest to surround each CB₁ receptor containing region. Significance for novel regions not considered a priori were corrected for multiple comparisons for the whole brain search volume or used an uncorrected threshold of $p < 0.001$ and minimum cluster extent size of 100 contiguous voxels. Nissl staining of brain tissue sections from [³⁵S]GTP γ S autoradiographic studies was also conducted to identify subnuclei and discrete small nuclei in the brainstem. Significant clusters of voxels representing brain regions of interest were also verified to span at least 2-3 adjacent sections. To validate and compare regions found to be significant with SPM

analysis, a separate ROI analysis was performed. ROI measurements were generally conducted on the original unprocessed images, averaged bilaterally across hemispheres, and analyzed with GraphPad Prism Version 5. ROI anatomical boundaries were defined by a mouse brain atlas (Franklin and Paxinos, 2008).

The overall assessment of image registration strategies for both 2D and 3D images derived from agonist-stimulated [^{35}S]GTP γ S autoradiography can be visualized in Figure 1.16, which represents a composite brain image created from the image average ($n = 8$) of WIN-stimulated [^{35}S]GTP γ S binding images from $\text{CB}_1^{-/-}$ mouse brains (dataset from Chapter 3). Spatial normalization resulted in correspondence between brain regions of all animals, therefore allowing successful averaging of voxel values. Success of spatial normalization can further be appreciated by the smooth cortical surface of the rendered composite brain image (Fig. 1.16A). This is further exemplified by the differentiation and contrast of anatomical boundaries of brain structures as illustrated in video sequences (download from <http://catalog.library.vcu.edu>) showing the anterior to posterior progression in the coronal plane, left to right lateral progression in the sagittal plane, and dorsal to ventral progression in the horizontal plane.

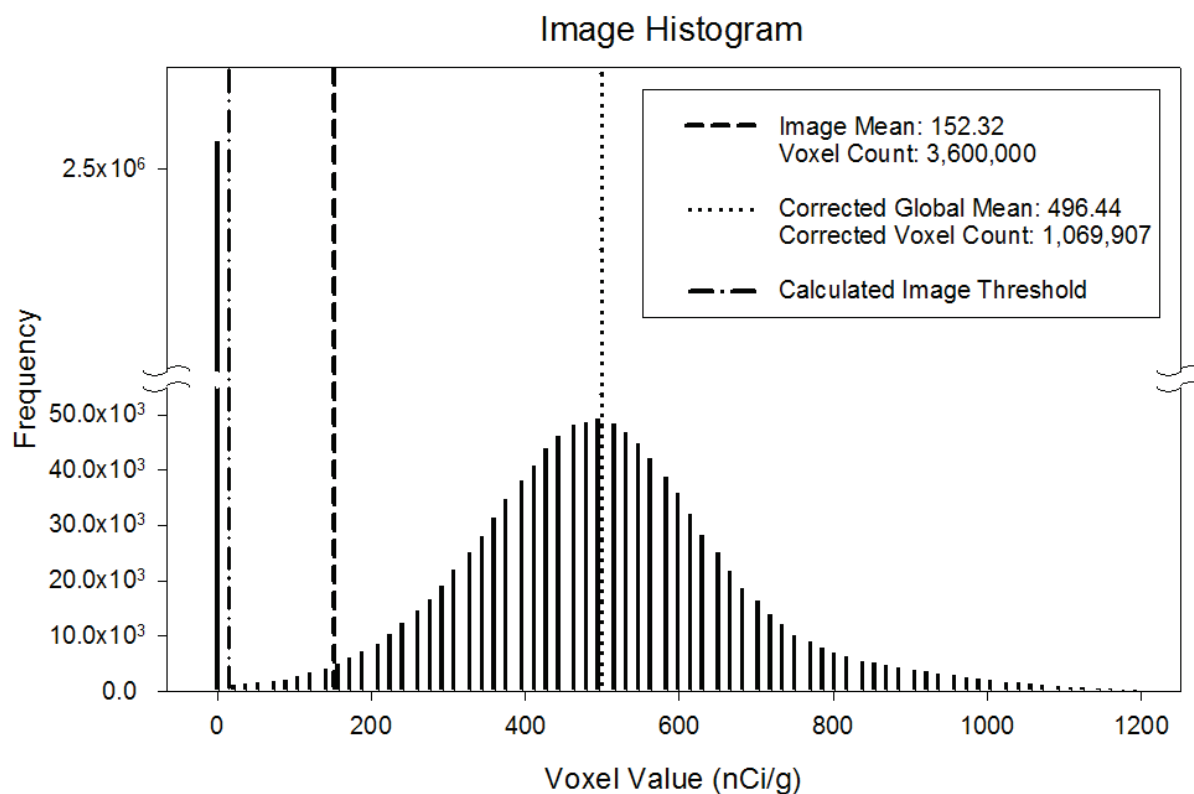


Figure 1.15. Image histogram of voxel values ($[^{35}\text{S}]\text{GTP}\gamma\text{S}$) from a single reconstructed mouse brain under basal (no agonist) conditions. The global image mean (includes background outside the brain) is illustrated by a dashed line and the corrected mean (not including background outside the brain) is shown as a dotted line. Note the closer proximity of the corrected global mean to central tendency after image thresholding.

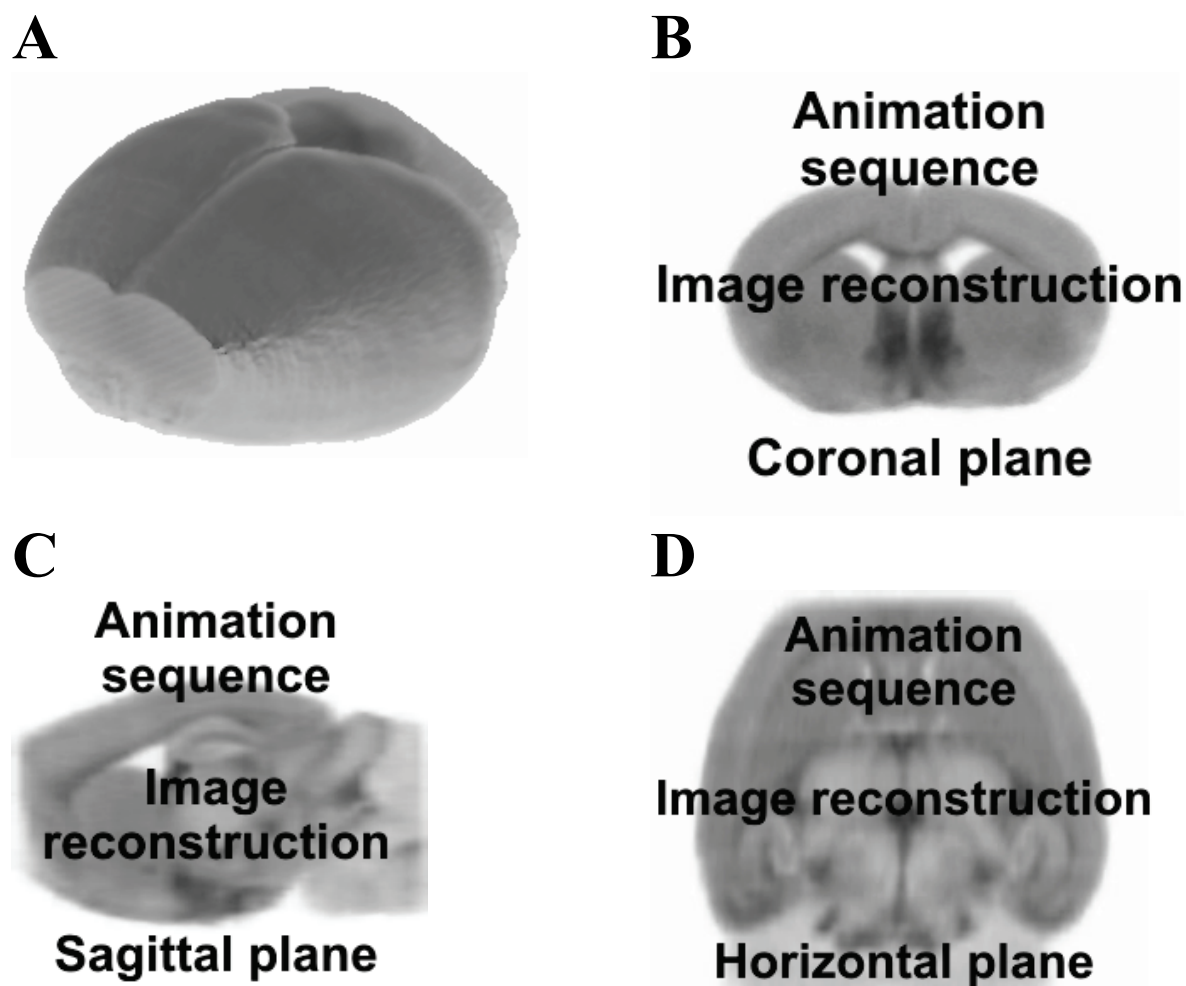


Figure 1.16. Reconstructed brain images derived from agonist-stimulated [35 S]GTP γ S autoradiography provided 3D anatomical visualization in each orthogonal plane. A composite image created from the mean of eight reconstructed WIN-stimulated [35 S]GTP γ S binding images from CB $_1^{-/-}$ mouse brains, was rendered in 3D (A) to demonstrate the result of slice registration and image reconstruction. Video sequences of slices are shown in the coronal (anterior to posterior) (B), sagittal (C), and transverse planes (dorsal to ventral) (D) to illustrate 3D spatial consistency of anatomical regions. The reader is referred to the web version of this dissertation to view/download video sequences in mpg format (search Peter Nguyen in <http://catalog.library.vcu.edu>). Video sequences can also be viewed/downloaded from the supplementary section of: Nguyen PT, Selley DE, Sim-Selley LJ. Statistical Parametric Mapping reveals ligand and region specific activation of G-proteins by CB(1) receptors and non-CB1 sites in the 3D reconstructed mouse brain. 2010. *Neuroimage* 52(4): 1243-1251.

1.6 Discussion: 3D reconstruction and analysis of cannabinoid-mediated G-protein activity

In this chapter we introduced the strategies used for reconstructing imaging data derived from agonist-stimulated [³⁵S]GTPγS autoradiography and methods to analyze these data based on Statistical Parametric Mapping (SPM). The principle behind image reconstruction is similar to creating volumetric images using confocal microscopy. In the case of autoradiography, multiple planes of data are instead collected manually, subsequently assayed and prepared for autoradiography, and digitized. Unlike confocal microscopy where a “Z-stack” contains multiple planes of data that are intrinsically aligned by virtue of the acquisition method, reconstruction of autoradiographic data requires slice realignment or registration. Several registration methods and algorithms have been developed for the alignment of serial images derived from various imaging modality, which differ mainly in the features used to establish a measure of similarity between images and also the extent of required user-input. A review of some image registration approaches for autoradiographic data has previously been published (Hess et al., 1998). We determined that an intensity-based registration algorithm developed by Thévenaz et al. (Thévenaz et al., 1998) was robust for the recursive alignment of brain tissue sections from agonist-stimulated [³⁵S]GTPγS autoradiography. The fully automated ImageJ plugin StackReg, which is based on this registration algorithm, successfully realigned 2D images with greater accuracy versus manual alignment in an unbiased fashion. 3D reconstruction offers the ability to visualize anatomical data in different orthogonal planes, as well as reslicing and visualization of data at virtually any angle. It is interesting to note that the reconstruction techniques in this chapter can possibly be adaptable and used to reconstruct data from different imaging modalities, such as immunohistochemistry or wherever multiple planes of data can be acquired. The application of these methods is extended to [³H]ligand receptor-binding autoradiography in

Chapter 3 and in a study comparing differences in CB₁ receptor levels in the rat pilocarpine model of epilepsy versus controls (Appendix Fig. A3, Table A1). Important internet links for documentation related to analytical software is listed in the Appendix Table A2.

The high abundance and distribution of CB₁ receptors in brain, as well as their neuromodulatory role in synaptic transmission, make them an attractive candidate for whole brain imaging. To date, most *in vivo* based imaging approaches utilize radiotracer compounds and modalities such as positron emission tomography (PET) or single photon emission computed tomography (SPECT) to study, for example, changes in receptor occupancy after chronic drug treatment or during various neurological diseases (Gifford et al., 2002). Most radiotracer compounds are developed using structural templates derived from pre-existing cannabinoid agonists or antagonists (Horti and Van Laere, 2008). However, some of the challenges that limit usage of candidate radiotracer compounds include their affinity and specificity for binding to the receptor, as well as their lipophilicity to penetrate the blood brain barrier (Gifford et al., 2002). These challenges in radiotracer design also influence the technical limitations and resolution of PET images from both human and small animals, which ranges from 2.5 mm to 6 mm and about 1.5 mm, respectively (Cherry, 2006). Although *in vivo* studies offer the ability to study the biodistribution of radiolabeled cannabinoid compounds as a measure of receptor occupancy, it does not however give insight into the functional component of GPCR output at the receptor level.

We present the first attempt to functionally map and localize CB₁ receptor-mediated G-protein activity in 3D reconstructed mouse brains. Reconstructed brain images were analyzed by SPM, which is a well characterized approach for the analysis of human brain imaging data and has been previously adapted for autoradiographic datasets mapping cerebral blood flow (Nguyen

et al., 2004). However, the analysis of reconstructed datasets derived from agonist-stimulated [³⁵S]GTPγS autoradiography has not been described. Data from this chapter demonstrate the feasibility of using SPM to perform various imaging manipulations on reconstructed datasets including coregistration, spatial normalization, and smoothing (Supplemental data using these methods are illustrated in the Appendix Figs. A2-A3, Table A1). The SPM image registration tools were robust and accurate for the spatial normalization of brains, showing satisfactory spatial correspondence of brain areas between subjects. These novel imaging approaches will further be explored in the next two chapters to study ligand- and region-specific activation of CB₁ receptors (Chapter 2) and to determine the role of the protein beta-arrestin 2 in regulating CB₁ receptor function following chronic administration of THC (Chapter 3).

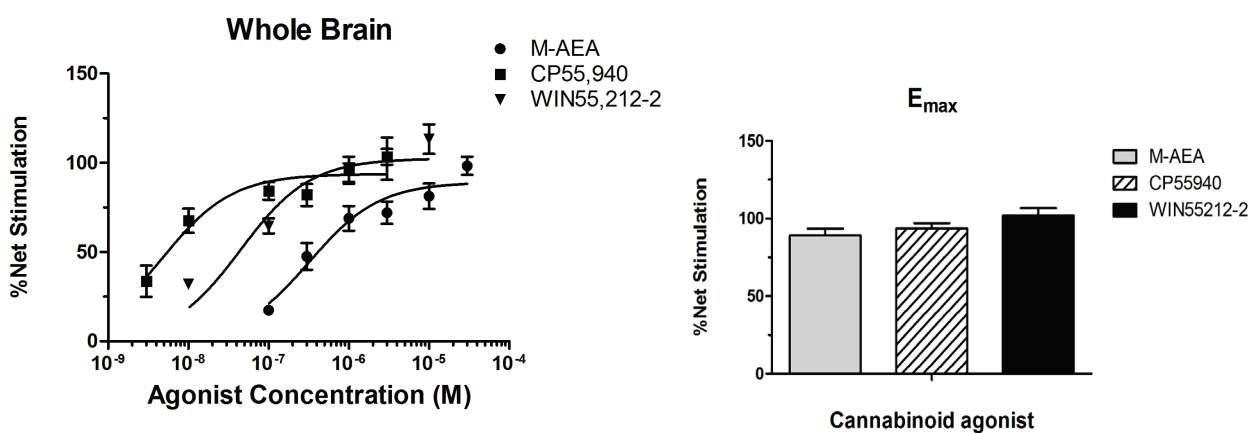
V. Chapter 2: Statistical Parametric Mapping reveals ligand and region specific activation of G-proteins by CB₁ receptors and non-CB₁ sites in the 3D reconstructed mouse brain

The development of selective CB₁ antagonists, such as SR141716A (Rinaldi-Carmona et al., 1994), and CB₁ knockout mice (Valverde et al., 2005; Zimmer et al., 1999) has shown that most effects of THC are primarily mediated by the CB₁ receptor. Our findings have demonstrated that CB₁ receptor signaling varies by brain region, for example when examined following acute activation of CB₁ receptors (Breivogel et al., 1997; Selley et al., 2001). However, the complete regional profile of CB₁ receptor activity has not been elucidated due to limitations of current strategies for design and analysis of autoradiographic studies. In this chapter, we will test the hypothesis that CB₁ receptor-mediated G-protein activity will differ by cannabinoid ligand and that the relative efficacy of these ligands will vary by brain region.

2.1 Cannabinoid-mediated G-protein activation is ligand and region specific

Differences in the efficacy of various cannabinoid agonists to activate G-proteins have previously been studied using agonist-stimulated [³⁵S]GTPγS binding in membranes prepared from various brain regions (Breivogel and Childers, 2000). However it is unclear whether the relative efficacy of cannabinoid agonists to activate G-proteins varies by region as determined autoradiographically in brain tissue sections. SPM was used to determine regional differences in cannabinoid-mediated G-protein activity in reconstructed wild-type C57/Bl6J mouse brains (N=5) using maximally effective concentrations of cannabinoid agonists differing in efficacy and structure, including the aminoalkylindole WIN55,212-2 (WIN), bicyclic CP55,940 (CP), and the metabolically stable endocannabinoid analogue methanandamide (M-AEA). Maximally effective concentrations of agonists were determined in concentration-effect curves, using 0.003-3 μM

CP, 0.01-10 μM WIN, or 0.1-30 μM M-AEA in membrane preparations from mouse whole brain (Fig. 2.1) or cerebellum (data not shown). Membrane agonist-stimulated [^{35}S]GTP γ S binding experiments were conducted as previously published (Sim-Selley et al., 2006). Results from whole brain and cerebellum membranes were similar, and thus concentrations used for agonist-stimulated autoradiographic assays in all studies ($\text{CB}_1^{+/+}$ and $\text{CB}_1^{-/-}$ animal studies) were: CP (3 μM), WIN (10 μM), M-AEA (25 μM). The calculated E_{max} had a net stimulation (agonist-stimulated minus basal [^{35}S]GTP γ S binding) of $89.6 \pm 4.9\%$, $94.2 \pm 3.6\%$, and $110.3 \pm 1.8\%$ over basal for M-AEA, CP, and WIN, respectively. The relative rank order in potency to activate G-proteins was $\text{CP} > \text{WIN} > \text{M-AEA}$, with EC_{50} values of 5.7 nM, 35 nM, and 354 nM, respectively. Volumetric reconstructions of autoradiographic sections provided 3D anatomical visualization and localization of cannabinoid-mediated G-protein activity (Fig. 2.2). The spatial extent of cannabinoid-stimulated G-protein activity as illustrated in Fig. 2.2 is shown in red, and the surface of the brain is rendered in gray for the right hemisphere. All three cannabinoid agonists significantly stimulated greater [^{35}S]GTP γ S binding than basal (no agonist) in all CB_1 receptor containing regions (Fig. 2.3) as determined by SPM analysis. As shown for WIN (Fig. 2.2), cannabinoid-stimulated G-protein activity was widespread in the cortex, densely distributed in the output nuclei of the basal ganglia (globus pallidus, substantia nigra) and seen in bands in the cerebellum that presumably correspond to the molecular layer. To determine the regional relative efficacy, SPM was then used to compare G-protein activity produced by the three cannabinoid agonists. WIN-stimulated G-protein activity was significantly greater than M-AEA



| Agonist | EC ₅₀ (μM) | E _{max} (% Net Stim.) |
|-------------|-----------------------|--------------------------------|
| M-AEA | 0.32 ± 0.08 | 89.2 ± 4.2 |
| CP55,940 | 0.005 ± 0.001 | 93.7 ± 3.4 |
| WIN55,212-2 | 0.04 ± 0.01 | 102.5 ± 4.8 |

Figure 2.1. Concentration-effect curves for cannabinoid agonists in membranes prepared from whole mouse brain. Varying concentrations of drug were incubated in 0.1 nM [³⁵S]GTPγS, 0.125% BSA, 30 μM GDP for 2 hrs at 30°C. No significant differences were found in agonist-stimulated [³⁵S]GTPγS binding produced by M-AEA, CP, and WIN. [³⁵S]GTPγS binding experiments (N=3-4) were performed in triplicate and data are reported as the mean %Net Stimulation [(agonist-basal)/basal x 100%] + S.E.M. Data were fit using Graphpad Prism 5.

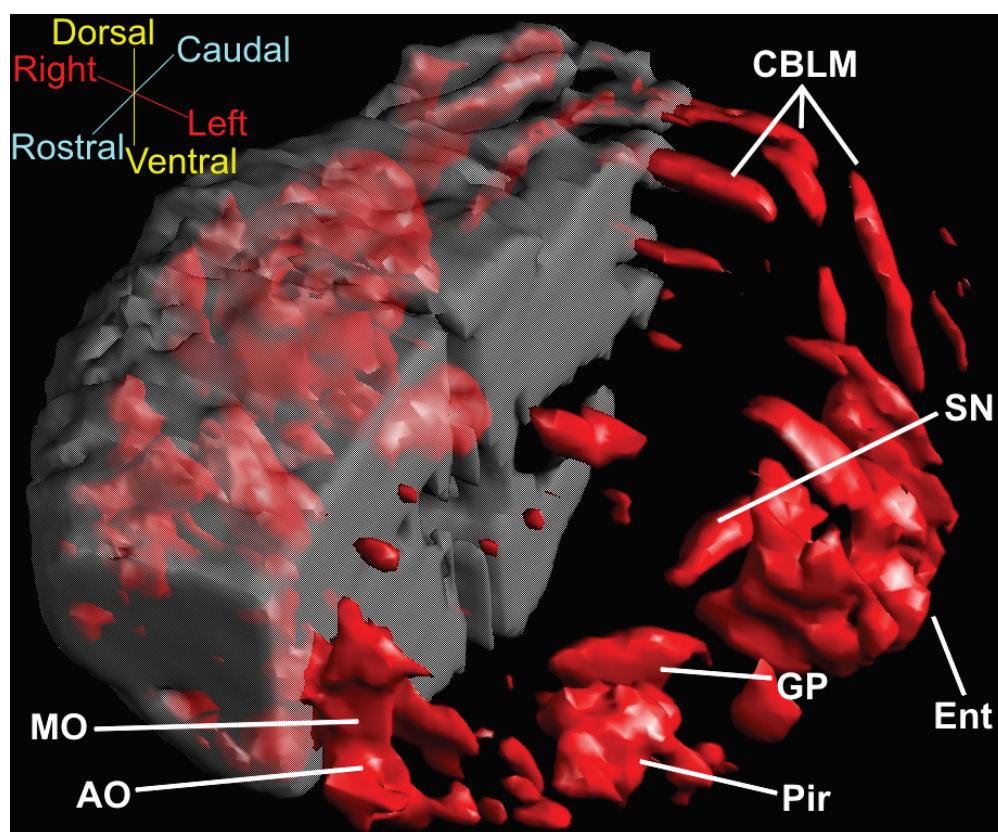


Figure 2.2. 3D image reconstruction and volumetric rendering of average ($N = 3$) cannabinoid-stimulated $[^{35}\text{S}]\text{GTP}\gamma\text{S}$ binding (red) in naïve mouse brain using a maximally effective concentration of the full CB_1 receptor agonist WIN55,212-2 ($10\ \mu\text{M}$). A threshold was applied to show the spatial extent of highest WIN-stimulated G-protein activity in brain regions, including the molecular layer of the cerebellum, cortex, and basal ganglia. AO (Anterior olfactory nucleus), Ent (entorhinal cortex), GP (globus pallidus), MO (medial orbital cortex), Pir (piriform cortex), SN (substantia nigra). Agonist-stimulated $[^{35}\text{S}]\text{GTP}\gamma\text{S}$ binding autoradiography was performed as described in *Methods*

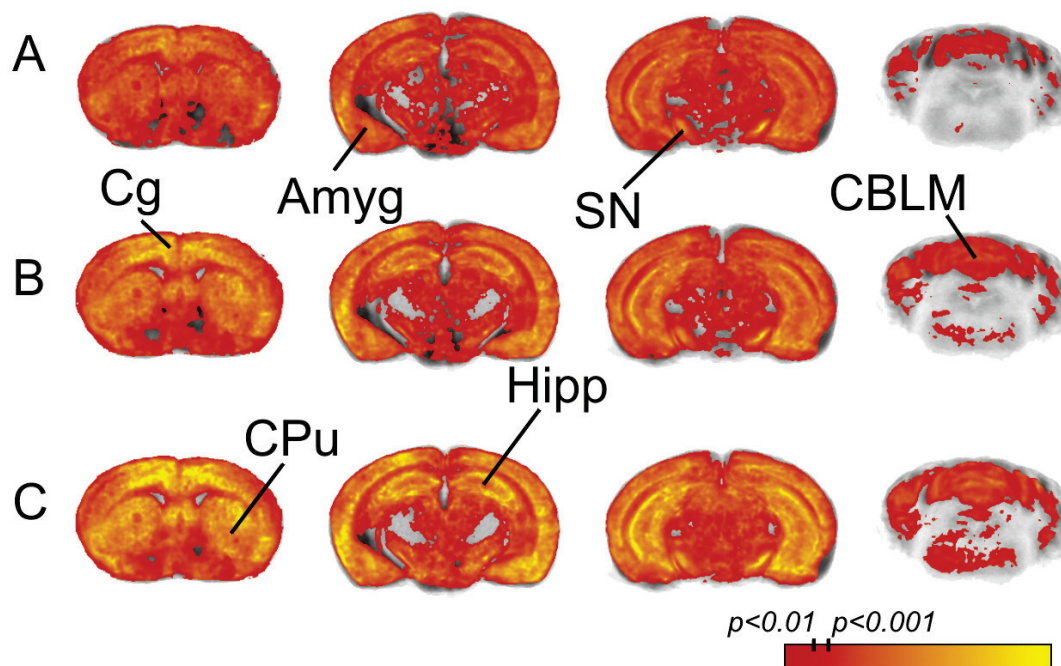


Figure 2.3. SPM analysis showing the regional distribution of significant differences between 25 μM M-AEA- (A), 3 μM CP55,940- (B), or 10 μM WIN55,212-2- (C) versus basal [^{35}S]GTP γ S binding ($p < 0.01$, ANOVA, $N = 5$) in $\text{CB}_1^{+/+}$ reconstructed naive mouse brains. Representative coronal sections with colored overlays (red to yellow) show significant differences corresponding to a p -value scale. Corresponding bregma coordinates from the left- to rightmost column are: 0.26 mm, -2.46 mm, -3.16 mm, -6.12 mm (Paxinos et al., 2008). AMYG (amygdala), CBLM (cerebellum), Cg (cingulate cortex), CPu (caudate-putamen), HIPP (hippocampus), SN (substantia nigra).

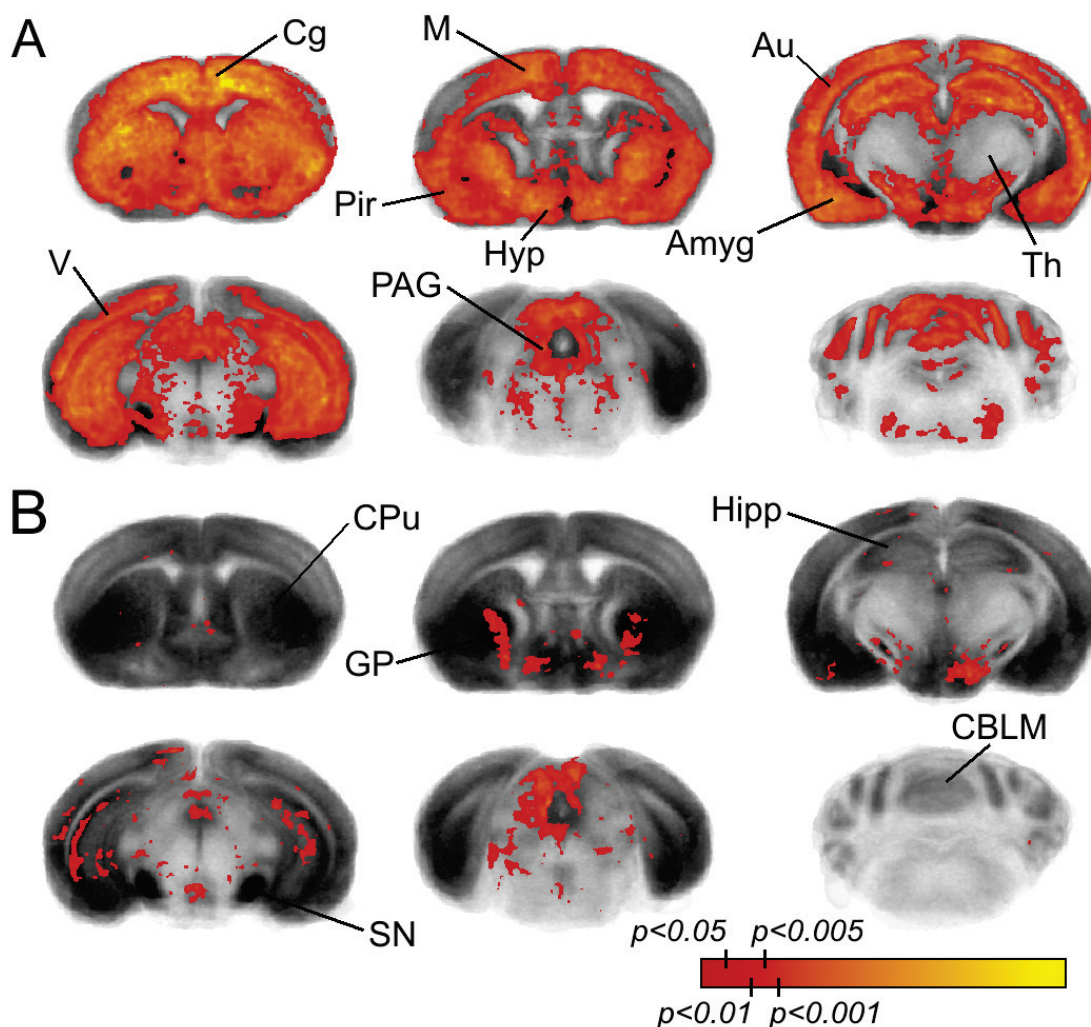


Figure 2.4. Regional comparison of agonist-stimulated [^{35}S]GTP γ S binding produced by the cannabinoid agonists WIN (10 μM), CP (3 μM), and M-AEA (25 μM) in $\text{CB}_1^{+/+}$ reconstructed naive mouse brains. Representative coronal sections illustrate Statistical Parametric Maps ($p < 0.05$, ANOVA, $n=5$) of significant differences in receptor-mediated G-protein activation, between WIN and M-AEA (**A**), or WIN and CP (**B**). WIN stimulated significantly greater G-protein activity than M-AEA in most CB_1 containing regions, with the exception of the thalamus. In addition, WIN-stimulated [^{35}S]GTP γ S binding was greater than CP in globus pallidus, periaqueductal gray, and hypothalamus. Colored overlays (red to orange) correspond to significance level represented by a p -value scale. Corresponding bregma coordinates from the top left anterior-most to bottom right posterior-most slice are: 0.02 mm, -0.7 mm, -1.7 mm, -3.4 mm, -4.16 mm, -6.12 mm (Paxinos et al., 2008). Au (auditory cortex), Hipp (hippocampus), CPU (caudate-putamen), GP (globus pallidus), Hyp (hypothalamus), M (motor cortex), PAG (periaqueductal gray), S (somatosensory cortex), SN (substantia nigra reticular), V (visual cortex), *M-AEA*, methanandamide; *WIN*, WIN55,212-2

in almost all regions examined, with exception of the thalamus (Fig. 2.4A). SPM provided a detailed anatomical comparison, as seen in the cortex (cingulate, somatosensory, and motor cortex) where WIN produced significantly greater G-protein activation than M-AEA in both superficial and deep laminae (Fig. 2.4A). A similar regional activation profile (data not shown) was seen comparing CP and M-AEA, where CP stimulated significantly greater G-protein activity than M-AEA. When comparing WIN and CP however, region-specific differences in the relative stimulation produced by these agonists were identified by SPM. For example, WIN stimulated significantly greater G-protein activity than CP in some CB₁ containing regions including globus pallidus, hypothalamus and periaqueductal gray (Fig. 2.4B). In contrast, WIN- and CP-stimulated G-protein activity were equivalent in the caudate-putamen, hippocampus, amygdala, cerebellum and cortical regions including motor, somatosensory, and cingulate cortices (Fig. 2.4B). Overall, SPM revealed that in some regions, including globus pallidus, hypothalamus, and periaqueductal gray, the activity profile was WIN > CP > M-AEA. In contrast, for most regions including caudate-putamen, hippocampus, amygdala, cerebellum and cortex (motor, somatosensory, and cingulate cortices) the relationship was WIN = CP > M-AEA. Interestingly, a different relative efficacy profile was found in the thalamus compared to all other brain regions. SPM revealed that WIN-, CP-, and M-AEA-stimulated [³⁵S]GTPγS binding did not significantly differ in thalamic nuclei, including ventral posteromedial and posterolateral, ventromedial, and ventrolateral thalamic nuclei. Subsequent ROI analyses substantiated almost all of the SPM findings, except in hypothalamus where WIN and CP did not differ in stimulating [³⁵S]GTPγS binding. In this brain region, ROI analysis revealed similar qualitative differences between WIN and CP as determined using SPM analysis, but failed to reach significance at the $p < 0.05$ level. This could be explained by differences in the analytical technique, where

significance by SPM is based at the individual voxel-level as opposed to a user-defined region of interest, which contains the average of many image pixels or subnuclei.

While the anatomical distribution of agonist-stimulated G-protein activity was similar for each of the three agonists compared to basal (no agonist), the relative magnitude of activity varied by brain region, as determined by an independent ROI analysis of cannabinoid-stimulated [³⁵S]GTP γ S binding for selected brain regions (Table 2.1). The relative efficacies of the three agonists were calculated by expressing net agonist-stimulated [³⁵S]GTP γ S binding produced by CP or M-AEA as percent of [³⁵S]GTP γ S binding stimulated by the full agonist WIN (Table 2.1). For example, the relative efficacy of M-AEA ranged from 32% of WIN in the PAG to 76% of WIN in thalamus. In addition, the relative efficacy of CP ranged from 60% of WIN in periaqueductal gray to 105% in thalamus. Due to the potential contribution of WIN acting at non-CB₁ sites (see next section), [³⁵S]GTP γ S binding data is also reported as %CP (Table 2.2). A similar relative efficacy relationship was revealed when using CP as the standard agonist. The high relative efficacy of WIN in specific brain regions did not correlate with having non-CB₁-mediated activity, indicating that CB₁ receptors contribute to the majority of the signal detected in WIN-stimulated [³⁵S]GTP γ S autoradiography. When normalized to the full CB₁ agonist WIN, there was no significant correlation between the relative efficacies of M-AEA- and CP-stimulated G-protein activation (Fig. 2.5) across the sampled brain regions of interest. In addition, a significant interaction of drug x region ($p < 0.01$) was found when analyzed by a two way repeated measures ANOVA. A significant interaction between the factors drug and region and lack of correlation in the relative efficacy profile, suggests that there may be regional differences in the relative efficacies of M-AEA and CP, which cannot be explained by receptor levels or G-protein abundance. These results thus indicate that the relative G-protein activity

produced by these cannabinoid agonists was region-dependent, as revealed by both SPM and ROI analysis of 3D reconstructed agonist-stimulated [^{35}S]GTP γ S autoradiographic data.

Table 2.1

Regional differences in the relative efficacies of different cannabinoid agonists (25 μ M M-AEA, 3 μ M CP, 10 μ M WIN) were found by both SPM and ROI analysis of agonist-stimulated [35 S]GTP γ S autoradiographic images in CB $_1^{+/+}$ naïve mice.

| Brain Region | Net-stimulated binding (nCi/g) | | | Net stimulation as %WIN | | |
|----------------------|--------------------------------|----------------------------|----------------------------|-------------------------|--------------|--------------|
| | M-AEA | CP | WIN | M-AEA | CP | WIN |
| Motor cortex | 263 \pm 11 ^{Aa} | 470 \pm 14 ^{Bb} | 494 \pm 13 ^{Bb} | 53 \pm 2 | 95 \pm 3 | 100 \pm 3 |
| Somatosensory cortex | 146 \pm 29 ^{Aa} | 272 \pm 44 ^{Bb} | 264 \pm 37 ^{Bb} | 55 \pm 11 | 103 \pm 17 | 100 \pm 14 |
| Cingulate cortex | 273 \pm 17 ^{Aa} | 488 \pm 16 ^{Bb} | 521 \pm 30 ^{Bb} | 52 \pm 3 | 94 \pm 3 | 100 \pm 6 |
| Hippocampus | 170 \pm 34 ^{Aa} | 313 \pm 50 ^{Bb} | 377 \pm 26 ^{Bb} | 45 \pm 9 | 83 \pm 13 | 100 \pm 7 |
| Amygdala | 200 \pm 34 ^{Aa} | 384 \pm 36 ^{Bb} | 457 \pm 28 ^{Bb} | 44 \pm 7 | 84 \pm 8 | 100 \pm 6 |
| Thalamus | 59 \pm 20 ^{Aa} | 81 \pm 24 ^{Aa} | 77 \pm 2 ^{Aa} | 76 \pm 25 | 105 \pm 30 | 100 \pm 27 |
| Hypothalamus | 83 \pm 23 ^{Aa} | 203 \pm 31 ^{Bb} | 235 \pm 16 ^{Cb} | 35 \pm 10 | 86 \pm 13 | 100 \pm 7 |
| Periaqueductal gray | 100 \pm 30 ^{Aa} | 188 \pm 19 ^{Bb} | 313 \pm 23 ^{Cc} | 32 \pm 10 | 60 \pm 6 | 100 \pm 7 |
| Cerebellum | 210 \pm 45 ^{Aa} | 472 \pm 39 ^{Bb} | 456 \pm 37 ^{Bb} | 46 \pm 10 | 103 \pm 8 | 100 \pm 8 |
| Substantia Nigra | 597 \pm 45 ^{Aa} | 801 \pm 28 ^{Bb} | 863 \pm 42 ^{Bb} | 69 \pm 5 | 93 \pm 3 | 100 \pm 5 |
| Globus Pallidus | 480 \pm 28 ^{Aa} | 607 \pm 16 ^{Bb} | 788 \pm 38 ^{Cc} | 61 \pm 4 | 77 \pm 2 | 100 \pm 5 |
| Caudate-Putamen | 189 \pm 9 ^{Aa} | 373 \pm 15 ^{Bb} | 399 \pm 26 ^{Bb} | 47 \pm 2 | 94 \pm 4 | 100 \pm 7 |

A, B, C & a, b, c Net-stimulated binding values labeled with different letters within a brain region are significantly different from each other based on SPM (upper case; $p < 0.05$ corrected, ANOVA, $n=5$) or ROI analysis (lower case; $p < 0.05$, $n=5$, ANOVA, Tukey's post-hoc analysis) as described under *Methods*. Measurements in each column are mean net [35 S]GTP γ S binding values (nCi/g) \pm SEM for M-AEA-, CP-, and WIN-stimulated conditions as determined by ROI analysis. Net values were calculated by subtracting basal from agonist-stimulated [35 S]GTP γ S binding. ROI anatomical boundaries are described in *Section III: Methods*.

Table 2.2

Relative efficacies of different cannabinoid agonists (25 μ M M-AEA, 3 μ M CP, 10 μ M WIN) from ROI analysis of agonist-stimulated [35 S]GTP γ S autoradiographic images in CB $_1^{+/+}$ naïve mice.

| Brain Region | Net stimulation as %CP | | |
|----------------------|------------------------|--------------|--------------|
| | M-AEA | CP | WIN |
| Motor cortex | 56 \pm 2 | 100 \pm 3 | 105 \pm 3 |
| Somatosensory cortex | 54 \pm 11 | 100 \pm 16 | 97 \pm 14 |
| Cingulate cortex | 56 \pm 3 | 100 \pm 3 | 107 \pm 6 |
| Hippocampus | 54 \pm 11 | 100 \pm 16 | 121 \pm 8 |
| Amygdala | 52 \pm 9 | 100 \pm 10 | 119 \pm 7 |
| Thalamus | 72 \pm 24 | 100 \pm 29 | 95 \pm 26 |
| Hypothalamus | 41 \pm 11 | 100 \pm 16 | 116 \pm 8 |
| Periaqueductal gray | 53 \pm 16 | 100 \pm 10 | 167 \pm 13 |
| Cerebellum | 44 \pm 10 | 100 \pm 8 | 97 \pm 8 |
| Substantia Nigra | 75 \pm 6 | 100 \pm 3 | 108 \pm 5 |
| Globus Pallidus | 79 \pm 5 | 100 \pm 3 | 130 \pm 6 |
| Caudate-Putamen | 51 \pm 2 | 100 \pm 4 | 107 \pm 7 |

ROI measurements in each column are mean net [35 S]GTP γ S binding values (nCi/g) \pm SEM for M-AEA-, CP-, and WIN-stimulated conditions expressed as %CP. Net values were calculated by subtracting basal from agonist-stimulated [35 S]GTP γ S binding. ROI anatomical boundaries are described in *Section III: Methods*.

Correlation analysis of regional relative efficacy

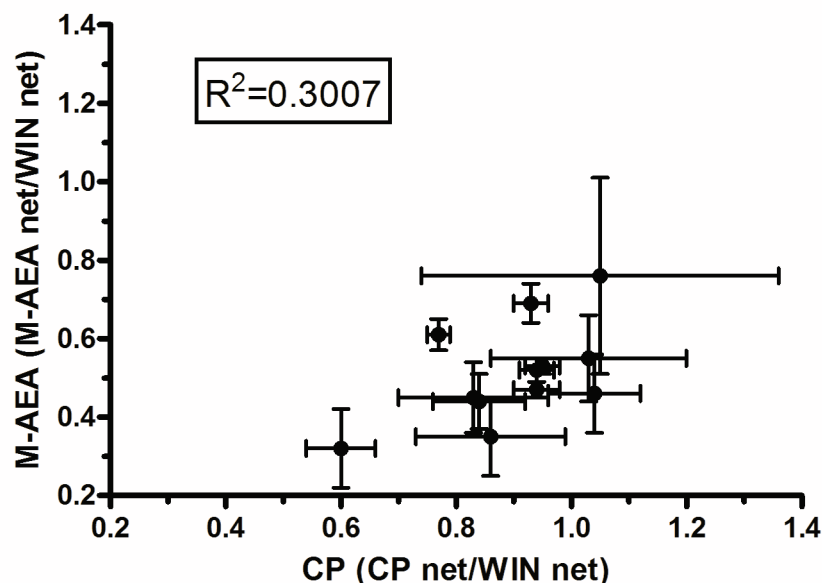


Figure 2.5. Correlation analysis of regional relative efficacy in $CB_1^{+/+}$ naive mice. No significant correlation was found between the relative efficacies of M-AEA (25 μ M) and CP (3 μ M) in sampled brain regions, suggesting regional differences in their relative efficacies. The axes represent the net-stimulated [35 S]GTP γ S binding (basal activity subtracted) value of each agonist (CP or M-AEA) normalized to net-stimulation by WIN (10 μ M). Error bars represent the standard error of the mean and each point represents a sampled brain region, which include: motor cortex, somatosensory cortex, cingulate cortex, hippocampus, amygdala, thalamus, hypothalamus, periaqueductal gray, cerebellum, substantia nigra, globus pallidus, and caudate-putamen. Agonist-stimulated [35 S]GTP γ S binding autoradiography was performed as described in *Methods*.

2.2 WIN55,212-2 stimulates G-protein activity in a subset of brain regions of mice lacking CB₁ receptors

Results in wild-type mice suggested that the relative efficacy of cannabinoid agonists varies by brain region. However, the interpretation of these findings is complicated by the possible contribution of non-CB₁ binding sites to receptor-mediated G-protein activity. This question was addressed using SPM analysis of M-AEA-, CP-, and WIN-stimulated [³⁵S]GTPγS binding in reconstructed CB₁^{-/-} mouse brain (N=8). SPM analysis showed that agonist-stimulated [³⁵S]GTPγS binding produced by CP or M-AEA did not significantly differ from basal activity (in the absence of agonist) in any brain region from CB₁^{-/-} mice (Fig. 2.6). However, WIN-stimulated [³⁵S]GTPγS binding significantly differed from basal binding in a number of areas in CB₁^{-/-} mice as determined by SPM and subsequently confirmed by ROI analyses (Table 2.3, Fig 2.6). As seen in Fig. 2.7, WIN-stimulated [³⁵S]GTPγS binding was significantly greater than basal binding in regions that partially overlapped the distribution of CB₁ receptors. SPM analysis revealed WIN-stimulated [³⁵S]GTPγS binding in visual (V) and auditory cortices (Au) that appeared to be localized to deeper laminae. In the hippocampus, WIN-stimulated [³⁵S]GTPγS binding was noted in the caudal, ventral CA1 and CA3, and to a lesser extent rostral, dorsal CA3. Although ROI analysis of the whole hippocampus showed a similar trend as in the SPM analysis, it failed to reach significance at the $p < 0.05$ criterion, possibly due to the heterogeneity of signal in this brain region as demonstrated in the SPM map (Fig. 2.7). WIN-stimulated [³⁵S]GTPγS binding was widely distributed in the amygdaloid complex, and appeared to be distributed in areas that corresponded to anterior portions of the basomedial and basolateral, and medial, lateral and central nuclei. WIN-stimulated [³⁵S]GTPγS binding was also found in the medial hypothalamus. Interestingly, the greatest magnitude of WIN-stimulated [³⁵S]GTPγS binding in

CB₁^{-/-} mouse brains was found within the brain stem including tegmental nuclei that appeared to correspond to lateral and dorsal tegmentum, and areas adjacent to the fourth ventricle, which corresponds to the locus coeruleus (Table 2.3). Significant WIN-stimulated G-protein activity was also found in the cerebellum that appeared to correspond to the molecular layer. In contrast, no differences between WIN-stimulated G-protein activity and basal binding were detected in basal ganglia (globus pallidus, substantia nigra, caudate-putamen), brain areas that normally contain among the highest levels of CB₁ receptors. It is important to note that the average magnitude of net WIN-stimulated G-protein activation in significant brain areas was approximately 4-5 fold less in CB₁^{-/-} mice compared to wild-type mice (Table 2.1 versus 2.3). For example, net WIN-stimulated G-protein activity (WIN stimulated – basal) in cerebellum was 83 ± 20 nCi/g in CB₁^{-/-}, compared to 456 ± 37 nCi/g in wild-type mice. Thus, data from reconstructed CB₁^{-/-} mouse brains suggest that the aminoalkylindole WIN, but not the endocannabinoid analogue M-AEA or bicyclic CP, activates non-CB₁ sites in a subset of brain areas that only partially overlaps with CB₁ receptor containing regions.

Table 2.3

WIN (10 μ M) stimulated [35 S]GTP γ S binding in CB $_1$ ^{-/-} brains in regions partially overlapping CB $_1$ receptors.

| Brain Region | [35 S]GTP γ S binding (nCi/g) | | | | Sig. SPM | Sig. ROI |
|--------------------------|--|--------------|--------------|-------------|-------------|-------------|
| | Basal | WIN | WIN Net | %Stim | | |
| Auditory cortex | 455 \pm 17 | 533 \pm 18 | 77 \pm 21 | 18 \pm 5 | v,c | * |
| Visual cortex | 434 \pm 20 | 494 \pm 20 | 60 \pm 30 | 16 \pm 7 | v,c | n.s. |
| Amygdala | 763 \pm 20 | 911 \pm 34 | 148 \pm 27 | 19 \pm 3 | v,c | ** |
| Hippocampus | 429 \pm 16 | 478 \pm 18 | 49 \pm 24 | 12 \pm 6 | $p < 0.01$ | n.s. |
| Thalamus | 390 \pm 17 | 397 \pm 8 | 7 \pm 14 | 3 \pm 3 | n.s. | n.s. |
| Hypothalamus | 735 \pm 29 | 863 \pm 35 | 128 \pm 40 | 19 \pm 6 | v | * |
| Dorsal Tegmental complex | 483 \pm 12 | 687 \pm 21 | 205 \pm 19 | 43 \pm 4 | $p < 0.001$ | *** |
| Locus Coeruleus | 523 \pm 23 | 720 \pm 30 | 197 \pm 29 | 39 \pm 6 | $p < 0.001$ | *** |
| Globus Pallidus | 508 \pm 19 | 488 \pm 12 | -19 \pm 14 | -3 \pm 3 | n.s. | n.s. |
| Substantia Nigra | 404 \pm 17 | 419 \pm 13 | 16 \pm 29 | 6 \pm 8 | n.s. | n.s. |
| Caudate-Putamen | 509 \pm 24 | 515 \pm 24 | 6 \pm 20 | 2 \pm 4 | n.s. | n.s. |
| Periaqueductal gray | 758 \pm 27 | 764 \pm 16 | 6 \pm 30 | 2 \pm 4 | n.s. | n.s. |
| Cerebellum | 223 \pm 11 | 306 \pm 20 | 83 \pm 20 | 39 \pm 10 | v,c | ** |

Measurements in columns 1 and 2 are mean [35 S]GTP γ S binding values (nCi/g) \pm SEM for basal- and WIN-stimulated conditions sampled within each brain region by ROI. Net binding equals [WIN stimulated- basal binding]. Percent stimulation (%Stim) for each brain region is calculated as $[(\text{WIN} - \text{basal})/\text{basal}] * 100\%$. Column five shows significance ($p < 0.05$) at the voxel (v) or cluster (c) level (corrected for multiple comparisons, as described in *Section III: Methods*, ANOVA, $n=8$) or uncorrected p -value for each brain region as determined by SPM analysis. Column six shows results obtained by ROI measurement with subsequent analysis using repeated measures ANOVA, followed by Tukey's post-hoc comparison. *, $p < 0.05$, **, $p < 0.01$, ***, $p < 0.001$. ROI anatomical boundaries are described in *Methods*. WIN, WIN55,212-2; n.s. = not significant

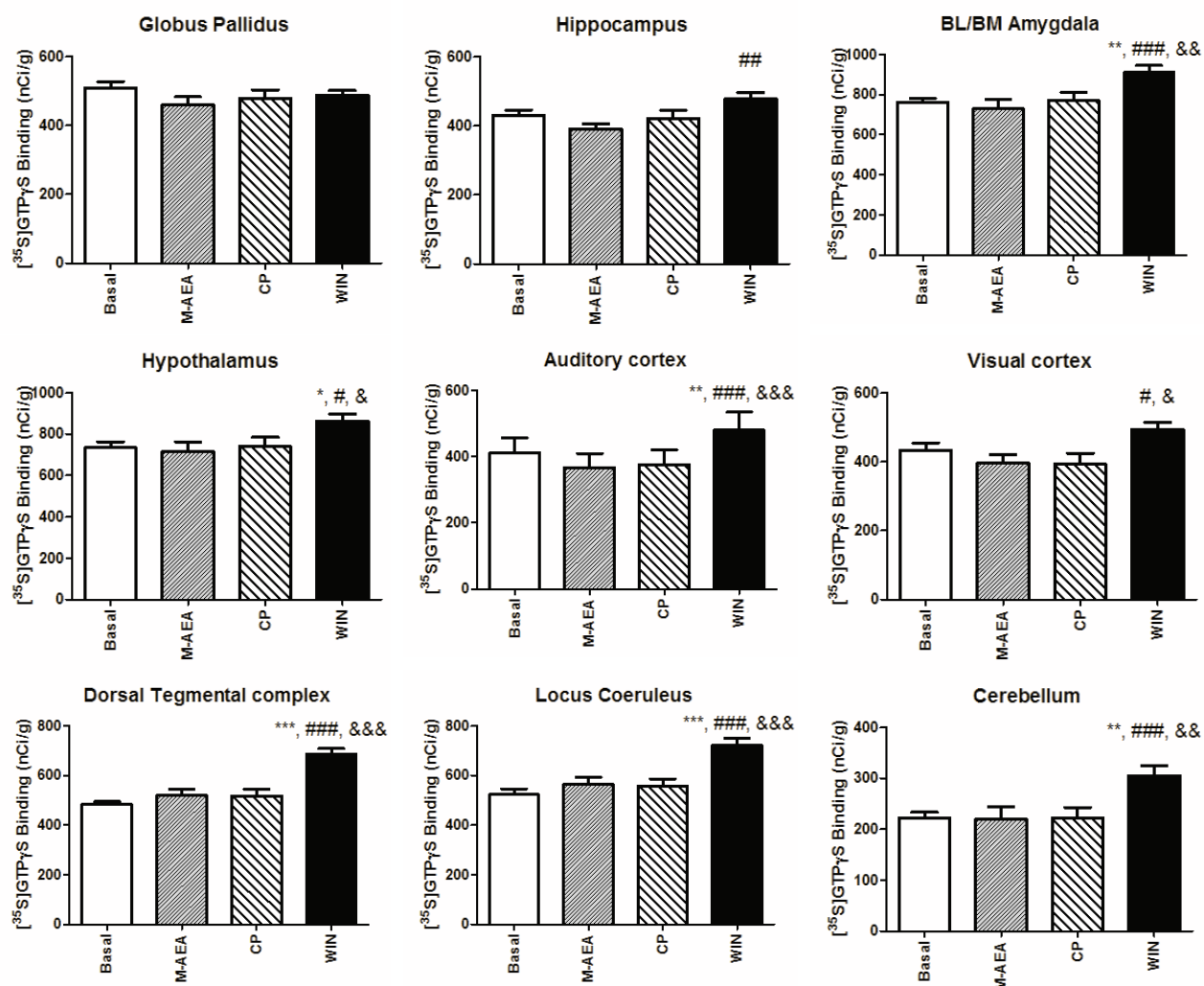


Figure 2.6. Agonist-stimulated [^{35}S]GTP γ S binding values measured and analyzed using regions of interest (ROI) from a subset of brain areas from naive CB $_1^{-/-}$ mice (N = 8) using different cannabinoid agonists (25 μM M-AEA, 3 μM CP, 10 μM WIN). * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$ compared to basal; # $p < 0.05$, ## $p < 0.01$, ### $p < 0.001$ compared to M-AEA; & $p < 0.05$, && $p < 0.01$, &&& $p < 0.001$ compared to CP. All comparisons used a one-way repeated measures ANOVA followed by Tukey's Multiple Comparison Test. Agonist-stimulated [^{35}S]GTP γ S binding autoradiography was performed as described in *Methods*

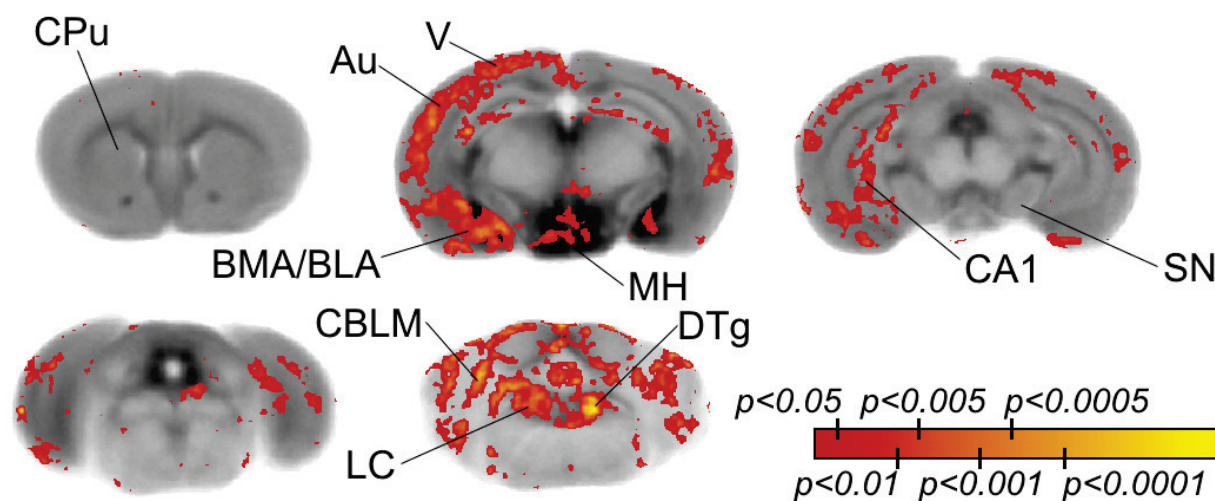


Figure 2.7. SPM analysis showing the regional distribution of significant differences between WIN-stimulated (10 μ M) and basal [35 S]GTP γ S binding ($p < 0.05$, ANOVA, $n=8$) in $CB_1^{-/-}$ mouse brains. Representative coronal sections with colored overlays (red to yellow) show significant differences (WIN > basal) corresponding to a p -value scale. Corresponding bregma coordinate from top left anterior-most slice to bottom right posterior-most slice are: 1.34 mm, -1.82 mm, -3.28 mm, -4.84 mm, -5.34 mm (Paxinos et al., 2008). Au (auditory ctx), BMA/BLA (basomedial and basolateral amygdala), CA1 (CA1 field of hippocampus), CBLM (cerebellum), CPu (caudate-putamen), DTg (tegmental nucleus, dorsal), LC (locus coeruleus), MH (medial hypothalamus), SN (substantia nigra), V (visual cortex), WIN, WIN55,212-2. Agonist-stimulated [35 S]GTP γ S binding autoradiography was performed as described in *Methods*

2.3 WIN55,212-2-stimulated G-protein activity in wild-type mice is blocked by SR141716.

The aminoalkylindole WIN activated G-proteins in $CB_1^{-/-}$ mice, providing evidence for non- CB_1 sites in a genetic model. To validate this finding, a pharmacological approach was applied by incubating wild-type mouse brain sections with WIN in the presence or absence of the CB_1 antagonist SR141716A (SR1), and resulting G-protein activity was compared using SPM in the reconstructed $CB_1^{+/+}$ mouse brain (N=8). In CB_1 antagonist studies 0.5 μ M SR141716A was used, which is 1,000-fold greater than its K_D value and at this concentration does not exhibit inverse agonism in [35 S]GTP γ S autoradiographic assays, as previously determined in our laboratory (Sim-Selley et al., 2001).

SR1 (0.5 μ M) alone did not significantly stimulate or inhibit [35 S]GTP γ S binding compared to basal binding in any brain region (Fig. 2.8). WIN-stimulated G-protein activity was robust and widespread in CB_1 receptor containing regions in the absence of SR1, as discussed above (Fig. 2.8). WIN-stimulated [35 S]GTP γ S binding in the presence of SR1 (WIN/SR1) was reduced in all brain regions and did not significantly differ from basal as determined by SPM. It is possible that WIN might exhibit lower potency and/or efficacy for putative non- CB_1 sites (Breivogel et al., 2001). Therefore, a higher concentration of WIN (50 μ M) was used in the presence or absence of 0.5 μ M SR1 in select brain regions that demonstrated non- CB_1 binding sites as determined in $CB_1^{-/-}$ mice (Table 2.3, Fig. 2.7). WIN alone produced greater G-protein activation compared to basal in all regions, except for dorsal tegmentum where only an insignificant trend was observed (Fig. 2.9). Variability in measured signal in this particular region was probably due to the general difficulty in collecting representative sections at the same level of dorsal tegmentum from different animals. ROI analyses of all these regions, however,

showed no significant stimulation of [³⁵S]GTP γ S binding in the presence of 50 μ M WIN + SR1 (Fig. 2.9). These findings suggest that SR1 might also bind to putative non-CB₁ sites.

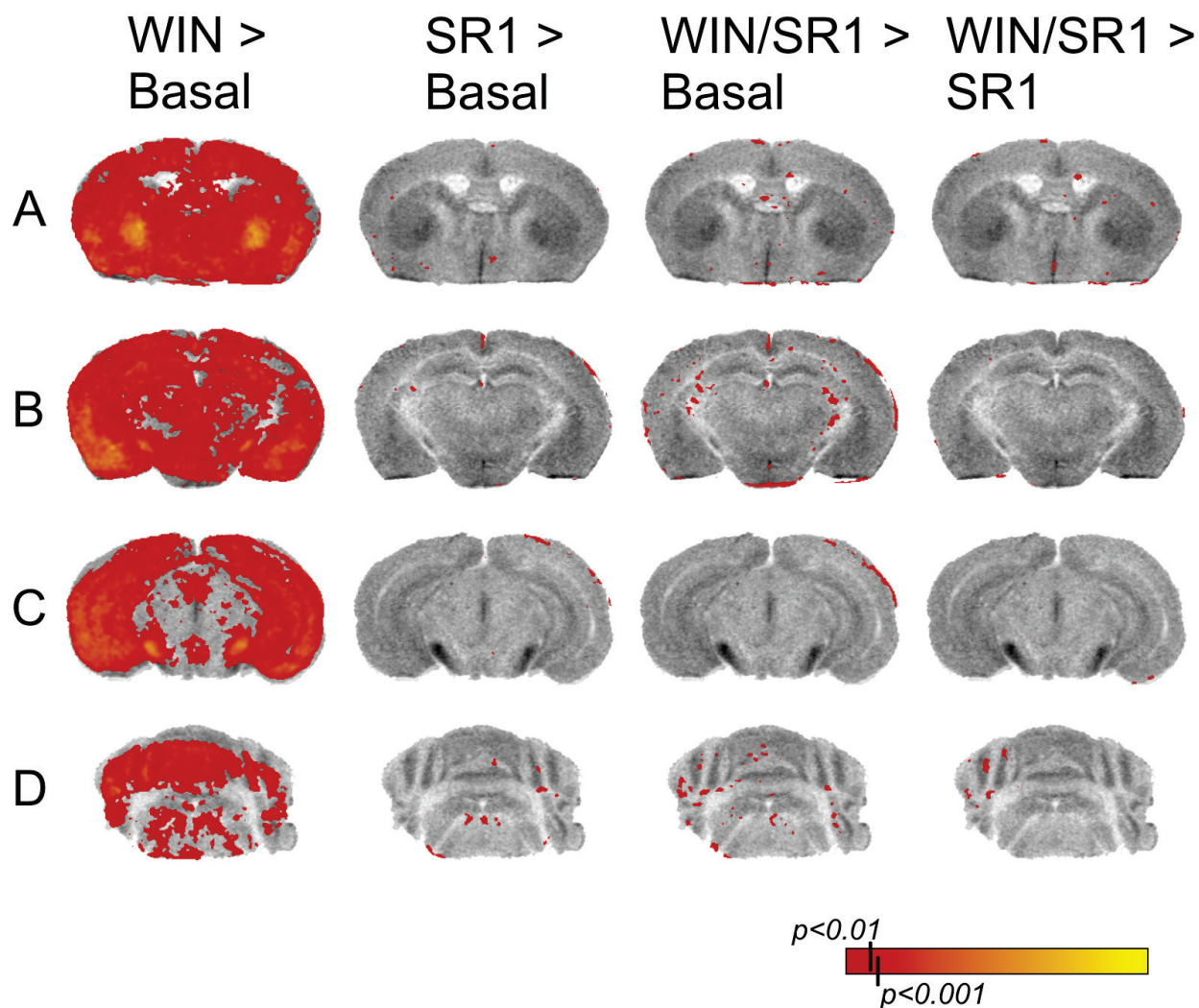


Figure 2.8. SPM analysis showing various comparisons between WIN (10 μ M), WIN in the presence of the CB₁ antagonist SR1 (WIN/SR1; 0.5 μ M), SR1 alone (0.5 μ M), or basal (no agonist) ($p < 0.01$, ANOVA, $n=8$) in CB₁^{+/+} mouse brains. Representative coronal sections are shown at the level of the striatum (A), hippocampus (B), substantia nigra (C), and cerebellum (D). Colored overlays (red to yellow) show significant differences corresponding to a p -value scale. Corresponding bregma coordinate from top- to bottom-most row are: -0.34 mm, -1.7 mm, -3.28 mm, -5.52 mm. WIN, WIN55,212-2; SR1, SR141716A. Agonist-stimulated [³⁵S]GTP γ S binding autoradiography was performed as described in *Methods*

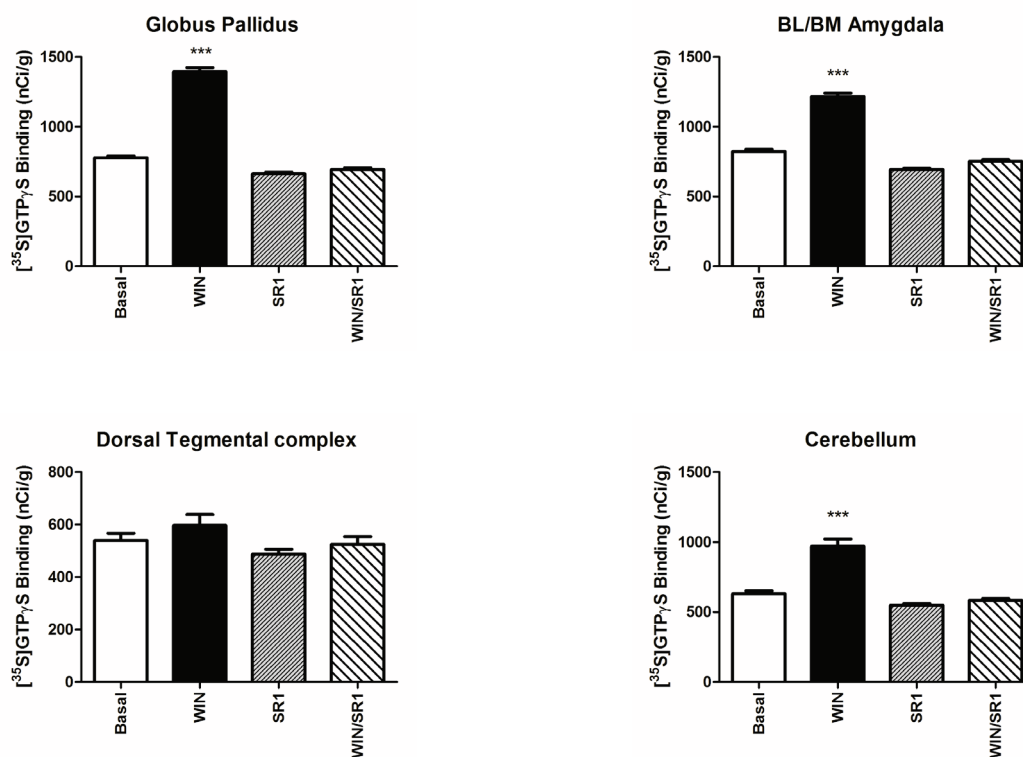


Figure 2.9. SR141716A (0.5 μ M) blocked 30 μ M WIN-stimulated [³⁵S]GTP_γS binding (represented as the mean \pm SEM) in naive CB₁^{+/+} mice (N = 7). * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$ compared to basal. All comparisons used a one-way repeated measures ANOVA followed by Tukey's Multiple Comparison Test. Agonist-stimulated [³⁵S]GTP_γS binding autoradiography was performed as described in *Methods*

2.4 The inactive isomer WIN55,212-3 does not produce G-protein activation in cerebellum of $CB_1^{-/-}$ mice

To confirm the stereoselectivity of the aminoalkylindole WIN55,212-2 for putative non- CB_1 sites, we used its inactive stereoisomer WIN55,212-3 to stimulate [35 S]GTP γ S binding in $CB_1^{-/-}$ mice. Compared to basal (354.5 ± 11.63 nCi/g), 10 μ M of WIN55,212-3 produced no differences in receptor-stimulated [35 S]GTP γ S binding (381 ± 14.1 nCi/g). The full CB_1 agonist and active isomer WIN55,212-2, however, produced significantly greater G-protein activation (443.3 ± 14.06 nCi/g) when compared to either basal or WIN55,212-3 (Fig. 2.10). As a positive control, the synthetic μ opioid receptor agonist DAMGO (10 μ M) stimulated greater [35 S]GTP γ S binding (1150 ± 9.2 nCi/g) compared to basal (686.2 ± 24.2 nCi/g) in the medial thalamus of $CB_1^{-/-}$ mice (Fig. 2.10). These results suggest that putative non- CB_1 sites in the cerebellum of $CB_1^{-/-}$ mice show stereoselectivity to the active isomer WIN55,212-2 in regard to G-protein activation. This stereoselectivity also supports the fact that G-protein activation of non- CB_1 sites is receptor-mediated.

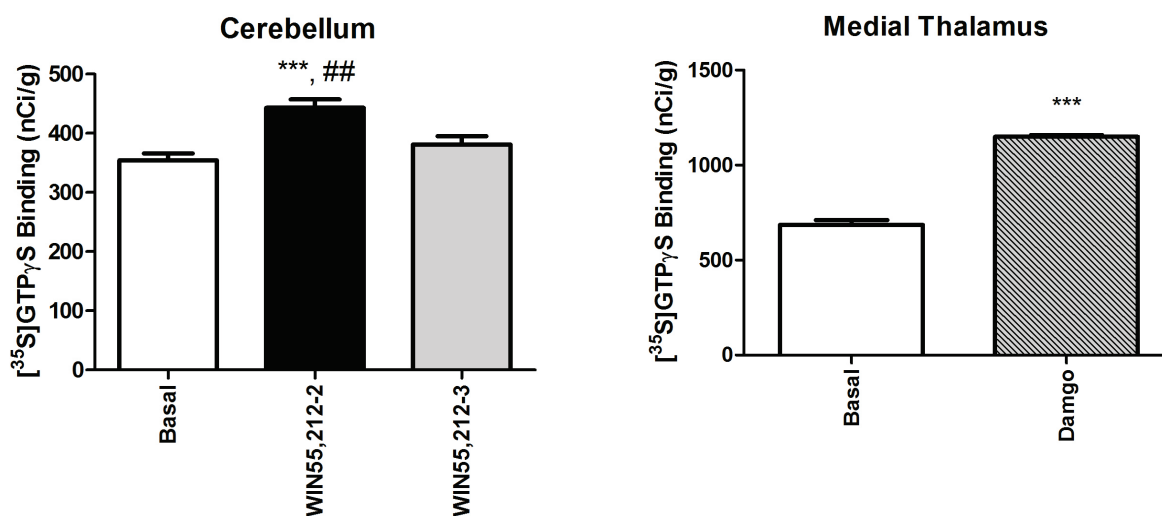


Figure 2.10. Stereoselectivity of WIN55,212-2 in stimulating [³⁵S]GTP_γS binding in naive CB₁^{-/-} mice. WIN55,212-2 (10 μM) produced greater [³⁵S]GTP_γS binding (shown as the mean ± SEM) compared to either basal or its inactive isomer WIN55,212-3 (10 μM) in the cerebellum from naive CB₁^{-/-} mice (N = 8). The synthetic μ opioid receptor agonist DAMGO (10 μM) was used as a positive control. *** *p* < 0.001 compared to basal. ## *p* < 0.01 compared to WIN55,212-3. Cerebellum analysis used a one-way repeated measures ANOVA followed by Tukey's Multiple Comparison Test and Medial Thalamus used a pair-wise t-test. Agonist-stimulated [³⁵S]GTP_γS binding autoradiography was performed as described in *Methods*

2.5 Discussion

The primary goal of this study was to elucidate regional differences in the relative efficacy of receptor-mediated G-protein activity produced by cannabinoids differing in intrinsic efficacy and chemical structure. The potential contribution of non-CB₁ sites to agonist-stimulated G-protein activity was then evaluated in the CB₁^{-/-} mouse model. This was accomplished using a novel approach, in which Statistical Parametric Mapping (SPM) was adapted for whole-brain analysis of 3D reconstructed agonist-stimulated [³⁵S]GTPγS autoradiographic data. SPM revealed regional differences in the efficacy of cannabinoids to activate G-proteins in brains of wild-type mice and localized novel WIN-stimulated [³⁵S]GTPγS binding sites in CB₁^{-/-} mouse brains. This approach provided the dual advantages of creating a functional map of receptor-activated G-proteins in the reconstructed brain, with an unbiased statistical comparison of levels of G-protein activity, thereby providing new data on cannabinoid-mediated activity in the mouse brain.

SPM has previously been adapted for the analysis of reconstructed autoradiographic datasets mapping cerebral blood flow (Nguyen et al., 2004), and successfully applied to functionally map brain activity in small animals (Dubois et al., 2008; Holschneider et al., 2006; Soto-Montenegro et al., 2008; Yang et al., 2007). Applying SPM analysis to *in vitro* agonist-stimulated [³⁵S]GTPγS autoradiographic data offers unique advantages compared to conventional region of interest (ROI) analysis. ROI analysis is generally assessed within predefined anatomical boundaries, but effects of interest might not always conform to anatomically defined regions. For heterogenous distributions of receptor-mediated activity, the size and shape of ROIs and plane(s) of data might be difficult to define a priori in order to maximize signal detection. In addition, if regions of receptor activity are substantially smaller than the defined ROI,

significance might be missed when signal is averaged with surrounding background that is included within the ROI. Moreover, the anatomical precision of this approach is illustrated in the motor and somatosensory cortices, where voxels with the most significant and greatest magnitude of cannabinoid-stimulated [^{35}S]GTP γ S binding in CB $_1^{+/+}$ mice were localized in specific cortical laminae (Fig. 2.4A) in a pattern consistent with previous reports showing the highest concentration of CB $_1$ receptor protein in the superficial (II, III) and deep (VI) layers of cortex (Herkenham et al., 1991; Tsou et al., 1998). It is important to note that most of the significant differences between cannabinoid-stimulated [^{35}S]GTP γ S binding showed bilateral symmetry. This neuroanatomical property, in addition to the known expression profile of CB $_1$ receptor protein, further strengthens the validity of SPM for analyzing agonist-stimulated [^{35}S]GTP γ S binding autoradiographic data.

Initial studies revealed regional differences in the relative efficacies of WIN-, CP-, and M-AEA-stimulated [^{35}S]GTP γ S binding. SPM comparison identified an efficacy profile of WIN > CP > M-AEA in areas including globus pallidus, hypothalamus, and periaqueductal gray. However in other brain areas including caudate-putamen, cerebellum, hippocampus, amygdala, substantia nigra and cortex, the relative efficacy for cannabinoid-stimulated G protein activity was WIN = CP > M-AEA. A different finding emerged in the thalamus, where the profile WIN = CP = M-AEA was found. A previous study using membrane preparations from cerebellum, hippocampus, and hypothalamus also reported regional differences in the relative efficacy and potency of WIN, CP, and M-AEA (Breivogel and Childers, 2000). However, the relative stimulation of receptor-activated G-proteins for these cannabinoid agonists differed somewhat from the current study. This discrepancy could be due to differences in the anatomical resolution of autoradiography versus [^{35}S]GTP γ S binding in membranes prepared from grossly dissected

brain regions. While the mechanism(s) underlying regional differences in relative agonist efficacy are not known, CB₁ receptors have been shown to exhibit domain selectivity for coupling to different subtypes of G $\alpha_{i/o}$, and in various brain regions, activate different subtypes of G-proteins with varying efficacy and potency after agonist stimulation (Mukhopadhyay et al., 2000; Prather et al., 2000). Cannabinoid-selective G-protein signaling has also been demonstrated using recombinant expression of CB₁ receptors in situ with reconstitution of purified G-protein subunits (Glass and Northup, 1999). In that study, the relative efficacies of different cannabinoid agonists differed between G α_i versus G α_o activation. One can thus envision ligand- and region-specific CB₁ receptor signaling based on the stoichiometric complement of various G α subtypes.

An alternative explanation for the higher efficacy of certain cannabinoids is the contribution of multiple receptors (e.g. CB₁ + non-CB₁ receptors) to the overall agonist-stimulated activity. To explore this question further, SPM was used to determine the extent to which WIN, CP, and M-AEA, would activate G-proteins in CB₁^{-/-} mouse brains. Of these cannabinoid agonists, only the aminoalkylindole WIN significantly stimulated [³⁵S]GTP γ S binding when compared to basal activity (absence of agonist). In this study, WIN stimulated [³⁵S]GTP γ S binding in a subset of brain regions in CB₁^{-/-} mouse brains that only partially overlapped the distribution of activity in CB₁^{+/+} brains. The greatest magnitudes of WIN-stimulated G-protein activity were noted within the dorsal tegmental complex and locus coeruleus, which contain acetylcholine and norepinephrine producing neurons, respectively. Relatively high levels of G-protein activation were also found in the cerebellum, which appear to correspond to the molecular layer. Modest G-protein activation was found in the cortex, amygdala, hippocampus, and hypothalamus. Interestingly, the hypothalamus was a brain region in which SPM analysis of brains from CB₁^{+/+}

mice found significantly greater WIN- versus CP-stimulated [^{35}S]GTP γ S binding, suggesting a possible contribution of additional non-CB $_1$ sites to the greater efficacy for WIN in G-protein activation. However, for other brain areas in CB $_1^{-/-}$ mice with significant WIN-stimulated [^{35}S]GTP γ S binding, such as amygdala and cerebellum, there were no differences in efficacy for G-protein activation between WIN and CP in the CB $_1^{+/+}$ mice. For these brain areas, it is possible that differences in regional G-protein coupling may enhance the efficacy of CP in CB $_1^{+/+}$ mice. Interestingly, no significant WIN-stimulated [^{35}S]GTP γ S binding in CB $_1^{-/-}$ mice was found in the nuclei of the basal ganglia, which normally contain the highest levels of CB $_1$ receptors (Herkenham et al., 1991). In contrast, the brainstem contains relatively low to moderate levels of CB $_1$ receptors (Herkenham et al., 1991) but the greatest magnitude of WIN-stimulated activity was detected in certain pontine nuclei. These findings are also consistent with previous reports that WIN stimulated [^{35}S]GTP γ S binding, but CP had no effect, in membrane homogenates prepared from CB $_1^{-/-}$ mice (Breivogel et al., 2001). Although previous studies have also found that anandamide (AEA) stimulated G-protein activity in CB $_1^{-/-}$ mice (Breivogel et al., 2001; Di Marzo et al., 2000), the stable analog M-AEA had no effect in this study. Brain areas with significant WIN-stimulated [^{35}S]GTP γ S binding compared to basal in this study (Table 2) were similar to those previously reported by Breivogel and colleagues (Breivogel et al., 2001). Both studies found WIN-stimulated G-protein activity in the brainstem, cortex, hypothalamus, and hippocampus, and no significant WIN-stimulated [^{35}S]GTP γ S binding in the basal ganglia. However, no significant WIN-stimulated [^{35}S]GTP γ S binding was found in the cerebellum by Breivogel and colleagues, whereas in this study significance was localized in bands that appear to correspond to the molecular layer of the cerebellum (Fig 4). The slight discrepancy in results could be due to differences in the analytical techniques, where SPM assesses changes at the

individual voxel-level in intact brain tissue sections versus the [³⁵S]GTPγS binding assay for homogenized gross brain areas.

Interestingly, non-CB₁ WIN-stimulated [³⁵S]GTPγS binding sites detected by SPM appeared to be distributed in certain functional systems. The localization of non-CB₁ sites in the locus coeruleus (LC) and its projection regions including frontal cortex, amygdala, hypothalamus, hippocampus, and cerebellum, might suggest a possible neuromodulatory role of these non-CB₁ sites within the noradrenergic system. Noradrenergic projections from the LC to forebrain regions are especially relevant to regulation of cognition, attention and anxiety (Aston-Jones et al., 1999; Bremner et al., 1996; Foote et al., 1983). Previous studies by Van Bockstaele and colleagues have shown that systemic WIN administration increased *cfos* expression in tyrosine hydroxylase positive LC neurons, indicating that WIN was affecting the coeruleo-cortical pathway. In addition, administration of WIN systemically (Oropeza et al., 2005) or directly into the frontal cortex (Page et al., 2008) increased norepinephrine release in an SR1-sensitive manner. Interestingly, CB₁ receptors are generally associated with presynaptic inhibition of neurotransmitter release (Schlicker and Kathmann, 2001) and inhibit NE release in the hippocampus (Schlicker et al., 1997). While it is possible that enhanced WIN-mediated NE release in the frontal cortex occurs via an indirect mechanism, it is also possible that NE release is regulated by both CB₁ and non-CB₁ receptors in this region. Approximately 30% of CB₁ receptor immunoreactive terminals in the frontal cortex also contain the catecholamine-synthesizing enzyme dopamine-β-hydroxylase (Oropeza et al., 2007), and if non-CB₁ WIN sites predominated in remaining terminals, the net result could be enhanced NE release. However, this question would need to be further examined in CB₁^{-/-} mice. Thus, the anatomical profile of non-

CB₁ WIN sites found in the current study could subserve a distinct modulatory function from the endogenous cannabinoid system that has yet to be fully characterized.

Because WIN was active in CB₁^{-/-} mice, pharmacological studies were conducted in CB₁^{+/+} mice to assess WIN-stimulated [³⁵S]GTPγS binding in the presence of the CB₁ receptor antagonist SR141716A (SR1). However, no significant G-protein activation was detected with WIN in the presence of SR1, nor did SR1 alone produce any change in [³⁵S]GTPγS binding compared to basal activity. Thus, it is possible that SR1 might bind to both CB₁ and non-CB₁/CB₂ sites. In fact, previous studies have shown that certain non-CB₁ mediated effects of WIN are inhibited by pretreatment with SR1 (Hajos et al., 2001; Hoffman et al., 2005; Pistis et al., 2004). It is further possible that multiple non-CB₁ WIN-stimulated [³⁵S]GTPγS binding sites exist, based on pharmacological and species specificity as defined in the literature (Hoffman et al., 2005). Although the molecular identity of non-CB₁ WIN-binding sites in the current study is unknown, several conclusions can be reached regarding their pharmacology. WIN is an agonist of unknown efficacy, SR1 appears to be an antagonist or very low efficacy partial agonist, and CP and M-AEA are not agonists. Further, these sites are presumably coupled to inhibitory G-proteins of the Gα_{i/o} class because agonist-stimulated [³⁵S]GTPγS autoradiography in brain does not appear to detect other classes of receptor-activated G-proteins due to the high abundance of Gα_o in brain and the kinetics of binding under the conditions of the assay (Sim-Selley and Childers, 2002). Insensitivity to CP indicates that these sites are unlikely to be CB₂ receptors (Govaerts et al., 2004), despite previous reports that CB₂ receptors are expressed in brainstem (Van Sickle et al., 2005). These sites are also unlikely to be GPR55, which has been shown to activate G_q and G₁₂ and does not respond to WIN in various *in vitro* assays (Ross, 2009). Thus, the present results provide anatomical and functional evidence supporting the existence of a

novel non-CB₁/CB₂/GRP55 WIN-stimulated [³⁵S]GTPγS binding site in defined regions of mouse brain.

In summary, Statistical Parametric Mapping (SPM) was used to assess and spatially map regional differences in cannabinoid-mediated G-protein activity in reconstructed mouse brain images derived from agonist-stimulated [³⁵S]GTPγS binding autoradiography. SPM analysis, combined with conventional ROI analysis, demonstrated regional differences in the relative efficacies of various cannabinoid agonists, and showed that certain cannabinoid agonists activate functional non-CB₁ sites, in addition to CB₁ receptors. The unique pharmacology and functional neuroanatomical distribution of non-CB₁ sites indicates that this novel system might have distinct physiological roles from the endogenous cannabinoid system that have yet to be characterized. Furthermore, the neuroanatomical distribution of these putative non-CB₁ sites suggests that this system could be exploited therapeutically. Lastly, this study demonstrates SPM as a powerful tool for the neuroanatomical analysis and functional mapping of G-protein coupled receptors in 3D reconstructed mouse brain images derived from [³⁵S]GTPγS autoradiography.

VI. Chapter 3: β -arrestin 2 regulation of the CB₁ receptor following chronic administration of THC

In the previous chapter, whole brain analysis of CB₁ receptor activity revealed region-specific differences in the relative efficacy of different classes of cannabinoid agonists. Regional differences in the relative efficacy of receptor-mediated G-protein activation suggest unique signaling properties of the CB₁ receptor that could result in differential receptor regulation by brain region. This hypothesis could have implications for the regulation of CB₁ receptor adaptation during repeated cannabinoid administration, which could affect the magnitude and/or rate of tolerance development following repeated administration of cannabinoids. Chronic administration of THC and other cannabinoid agonists generally leads to the development of tolerance to its *in vivo* effects. Tolerance has also been demonstrated to various cannabinoid-mediated effects including antinociception, hypothermia, catalepsy, spontaneous motor hypoactivity, and memory. Previous work in our laboratory demonstrated region-specific differences in the attenuation or desensitization of CB₁ receptor activity following chronic administration of THC (McKinney et al., 2008; Sim-Selley and Martin, 2002; Sim-Selley et al., 2006; Sim et al., 1996a). However, a mechanistic link between desensitization and tolerance has not been determined for cannabinoids. Studies in cell models have shown that β -arrestin 2 (β arr2) regulates CB₁ receptors *in vitro* (Jin et al., 1999; Kouznetsova et al., 2002), but evidence for involvement of β arr2 in regulation of CB₁ receptors in brain is very limited. In this chapter, we will test the hypothesis that the regulatory protein β arr2 mediates the functional adaptation of CB₁ receptors to chronic stimulation by THC in certain brain regions where the two are co-distributed. Further, we propose that β arr2-mediated regulation of CB₁ receptors contributes to the development of tolerance to THC-mediated *in vivo* effects.

3.1 β -arrestin 2 attenuates tolerance to specific THC-mediated effects *in vivo*

One study has reported the potential role of β arr2 in acute cannabinoid-mediated effects. Breivogel et al. (Breivogel et al., 2008) showed that loss of β arr2 enhanced THC-mediated antinociception and hypothermia in β arr2 knockout (KO) mice compared to wild-type (WT) mice. Similarly, Bohn et al. reported enhanced and prolonged antinociception after morphine administration, as well as greater morphine-mediated hypothermia in mice lacking β arr2 compared with their wild-type littermates (Bohn et al., 2000; Bohn et al., 2002; Bohn et al., 1999). The role of β arr2 in cannabinoid-mediated effects following repeated cannabinoid administration has not been examined, but evidence from the μ opioid system suggests possible outcomes. In those studies, β arr2 KO mice did not develop tolerance to morphine-mediated antinociception as determined in the hot-plate test, but interestingly only delayed tolerance when assessed using the warm-water tail immersion test. These results suggest that β arr2 regulates nociceptive function through the μ opioid receptor and may have differential effects within various anatomical systems. Mu opioid receptors and CB₁ receptors both belong to the superfamily of GPCRs and interact in certain physiological responses (reviewed in (Corchero et al., 2004)). However, it is unclear whether common mechanisms regulate these receptor classes. We therefore tested the hypothesis that β arr2 is involved in producing tolerance to various THC-mediated effects.

To test this hypothesis, β arr2 KO mice and their WT littermates were treated twice daily for 6.5 days with an intraperitoneal (i.p.) administration of either vehicle (1:1:18, ethanol:cremaphor:saline) or 10 mg/kg THC. Drug dosing and *in vivo* tests were done in collaboration by Dr. Laura Bohn's laboratory (Scripps Research Institute, FL). On the morning of

the 7th day, 24 hrs following drug treatment, THC-mediated effects were assessed using a cumulative dosing paradigm (3, 7, 20, 26, 44 mg/kg for doses of 3, 10, 30, 56, 100 mg/kg i.p.) in 40 minute intervals, in which behaviors were assessed 30 minutes after each injection. The following behaviors were assessed: 1) antinociception using the tail warm-water withdrawal assay at 52°C, 2) hypothermia using rectal temperature, and 3) catalepsy using the ring immobility test. *In vivo* procedures are outlined in *Section III - Methods*.

Results revealed that abrogation of β arr2 produced effect-specific alterations in both vehicle control and THC-treated mice. Interestingly in the vehicle treated groups, β arr2 KO animals displayed a greater sensitivity to the hypothermic effect of THC compared to WT [F(1,84) = 7.39, $p < 0.01$]. In contrast, mice in the vehicle treated groups, showed no difference in antinociception or immobility between genotypes. Assessment of tolerance to these effects following repeated THC treatment also showed effect-specific alterations in tolerance in β arr2 KO compared to WT mice. However in this case, only tolerance to antinociception was affected by loss of β arr2. Although both WT [F(1,84) = 92.45, $p < 0.0001$] and β arr2 KO [F(1,84) = 14.72, $p < 0.001$] animals developed tolerance to the antinociceptive effects of THC (Fig. 3.1C), tolerance to antinociception was attenuated in the THC-treated β arr2 KO group, which was significantly less than the THC-treated WT group [F(1,84) = 13.25, $p < 0.001$]. When tested for catalepsy, both WT [F(1,84) = 18.13, $p < 0.0001$] and β arr2 KO [F(1,84) = 53.76, $p < 0.0001$] animals developed tolerance that was of similar magnitude (Fig. 3.1B). In contrast to acute results, both WT [F(1,84) = 51.15, $p < 0.0001$] and β arr2 KO [F(1,84) = 44.48, $p < 0.0001$] animals developed tolerance to THC-mediated hypothermia following the chronic THC dosing paradigm (Fig. 3.1A) and the tolerance was similar in magnitude. These results show that β arr2 may be involved in the acute effects of THC-mediated hypothermia, whereas tolerance to

antinociception is attenuated in β arr2 KO mice. Therefore, attenuation in tolerance occurred in a behavior-specific manner, suggesting that β arr2 may regulate CB₁ receptors in a region-specific manner as well in brain.

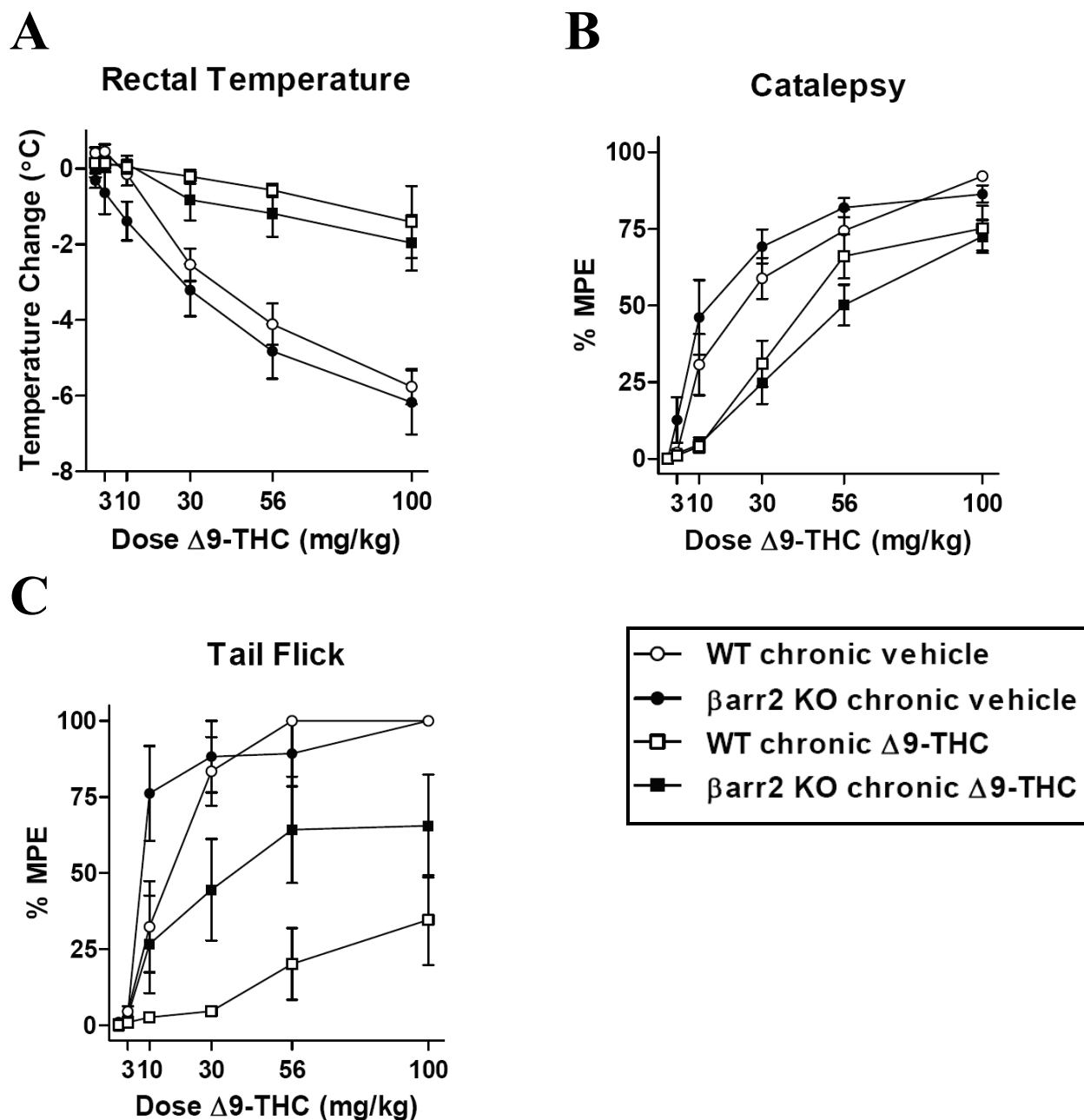


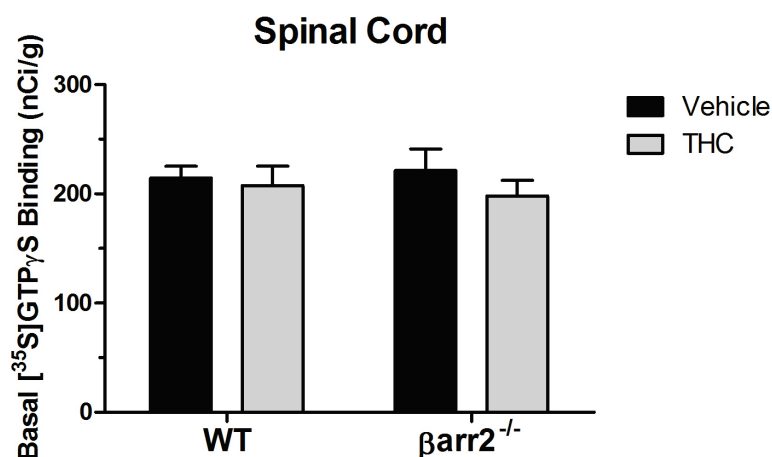
Figure 3.1. THC-mediated *in vivo* effects in β Arr2 KO and WT animals following 6.5 day administration of 10 mg/kg THC or vehicle treatment (i.p.) given twice daily. THC-mediated effects including change in rectal temperature, percentage of time of ring immobility (catalepsy), and percent of maximum possible antinociceptive effect were measured. Both β Arr2 KO and WT animals developed tolerance to THC-mediated hypothermia (A) and catalepsy (B). However, tolerance to THC-mediated antinociception (C) was significantly attenuated in β Arr2 KO animals compared to WT. Data reflect the mean \pm SEM (N = 8 per group)

3.2 β -arrestin 2 regulates CB_1 receptor desensitization in mouse spinal cord following chronic administration of THC

Persistent exposure to an agonist leads to characteristic changes at the level of the GPCR in order to dampen its signaling capacity, and thereby maintain equilibrium. The mechanisms underlying the regulation of GPCRs, specifically receptor desensitization (uncoupling of G-proteins) and downregulation (receptor degradation), have been studied extensively in cell models (Ferguson and Caron, 1998; Gainetdinov et al., 2004). In the classical sense, receptor desensitization occurs when a receptor is phosphorylated by a GPCR kinase (GRK), which leads to the binding of an arrestin protein and subsequent uncoupling of the G-protein from its cognate receptor. These same mechanisms appear to contribute to regulation of CB_1 receptors in response to persistent stimulation by an agonist. Previous work by Mackie and colleagues has shown that co-expression of both GRK3 and β arr2, using a *Xenopus Oocyte* expression system, was required for the rapid desensitization of CB_1 -receptor mediated potassium currents following exposure to the full CB_1 agonist WIN55,212-2 (Jin et al., 1999). In the current study, the attenuation in tolerance to THC-mediated antinociception, as measured by tail withdrawal in β arr2 KO mice, also suggests that β arr2 regulates CB_1 receptors in anatomical circuits that may mediate this behavior. The tail withdrawal assay is largely a spinally-mediated reflex, suggesting that β arr2-mediated regulation of CB_1 receptors in the spinal cord could contribute to this observation. To test this hypothesis, whole spinal cords were collected from mice 24 hours after the behavioral tests described above. Membrane preparations from homogenized spinal cord were then used to generate concentration-effect curves of cannabinoid-stimulated [35 S]GTP γ S binding to assess changes in CB_1 receptor-mediated G-protein activity (conducted as described in *Section III - Methods*). No significant differences were found in basal (no agonist) [35 S]GTP γ S binding

between genotypes or drug treatment groups, thus indicating no gross alteration in constitutive G-protein coupling (Fig 3.2). These data also indicate that residual THC did not remain in the sample because it would stimulate [³⁵S]GTP γ S binding above basal levels seen in vehicle-treated mice. CP55,940 (CP)-mediated G-protein activity was first compared between vehicle-treated mice to determine whether loss of β arr2 altered baseline (e.g. no drug treatment) CB₁ receptor activity. Results showed that CP-stimulated [³⁵S]GTP γ S binding did not differ between genotypes in vehicle-treated mice, with E_{max} values (expressed as %Net Stimulation, see *Methods*) of 45.04 ± 1.91% in WT and 46.41 ± 2.13% in β arr2 KO animals (Fig. 3.3A, Table 3.1). Chronic treatment with THC lead to significant desensitization of receptor-mediated G-protein activity in β arr2 WT mice, with an E_{max} value for CP-stimulated [³⁵S]GTP γ S binding of 27.88 ± 3.64% in WT compared to 41.10 ± 1.80% in β arr2 KO animals, which represented an approximately 38% decrease in receptor-mediated activity (Fig. 3.3A, Table 3.1). Interestingly, CB₁ receptor desensitization was attenuated in the β arr2 KO mice, where its E_{max} value for CP-stimulated [³⁵S]GTP γ S binding was reduced by approximately 11% of its respective vehicle control. Further, this E_{max} value did not significantly differ from its respective vehicle control, but did differ from THC-treated WT mice. No differences were found in the EC₅₀ values for CP-stimulated [³⁵S]GTP γ S binding between treatment groups (Table 3.1). This important observation indicates that there was satisfactory washout of drug prior to performing *in vitro* studies. Similar results were obtained when using the full CB₁ agonist WIN55,212-2 (WIN) to assess receptor-stimulated [³⁵S]GTP γ S binding (Fig. 3.3B). Again, WIN-stimulated [³⁵S]GTP γ S binding did not differ between genotypes in vehicle-treated mice, with E_{max} values of 75.46 ± 6.82% in WT and 80.87 ± 11.55% in β arr2 KO animals (Fig. 3.3B, Table 3.1). Chronic treatment also led to significant desensitization of CB₁ receptors β arr2 WT mice with an E_{max} value of

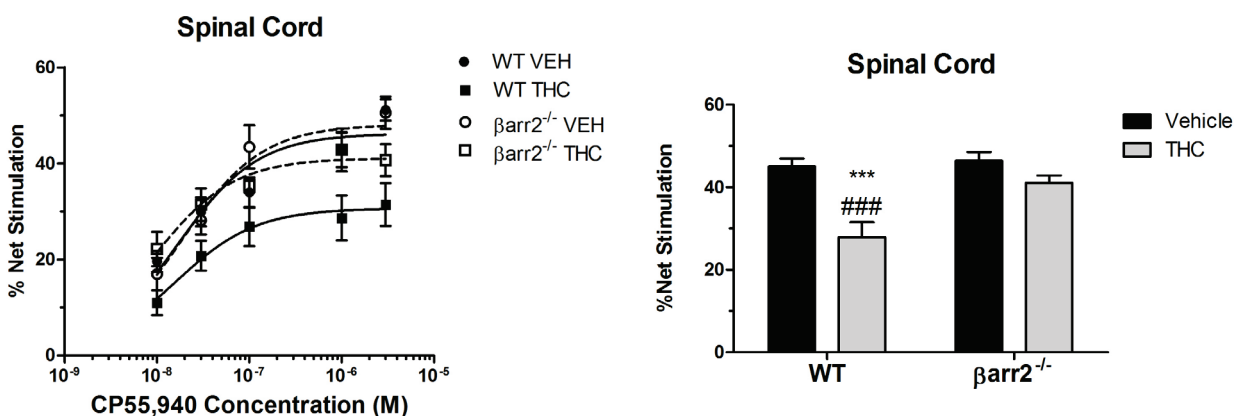
49.39 ± 4.41%, or an approximately 35% decrease in receptor-mediated G-protein activity, compared to no change in the β arr2 KO animals (E_{\max} value of 72.53 ± 5.99%, or an approximately 10% decrease in receptor-mediated G-protein activity). When comparing E_{\max} values between THC-treated β arr2 WT and KO mice, a close trending difference was also found ($p = 0.052$). Lastly, a significant interaction between Drug x Genotype was found [$F(1,24) = 5.68, p < 0.05$], suggesting that β arr2 is involved in mediating CB₁ receptor desensitization of G-protein coupling following THC treatment in spinal cord. Thus β arr2 regulation of CB₁ receptor desensitization may be one mechanism that contributes to THC-mediated antinociceptive tolerance.



| Basal [³⁵ S]GTPγS Binding (nCi/g) | | | |
|---|---------------|------------------------------------|--------------------------------|
| WT Vehicle | WT THC | βarr2^{-/-} Vehicle | βarr2^{-/-} THC |
| 214.7 ± 10.6 | 207.5 ± 17.9 | 221.3 ± 19.8 | 198 ± 14.5 |

Figure 3.2. Basal [³⁵S]GTPγS binding in spinal cord of βArr2 KO and WT animals following chronic THC or vehicle treatment. βArr2 KO and WT animals received 6.5 day administration of 10 mg/kg THC or vehicle treatment (i.p.) given twice daily. No differences were found in basal (no agonist) [³⁵S]GTPγS binding by genotype or drug treatment as determined by 2-way ANOVA. Binding values represent the mean ± SEM (N = 6).

A



B

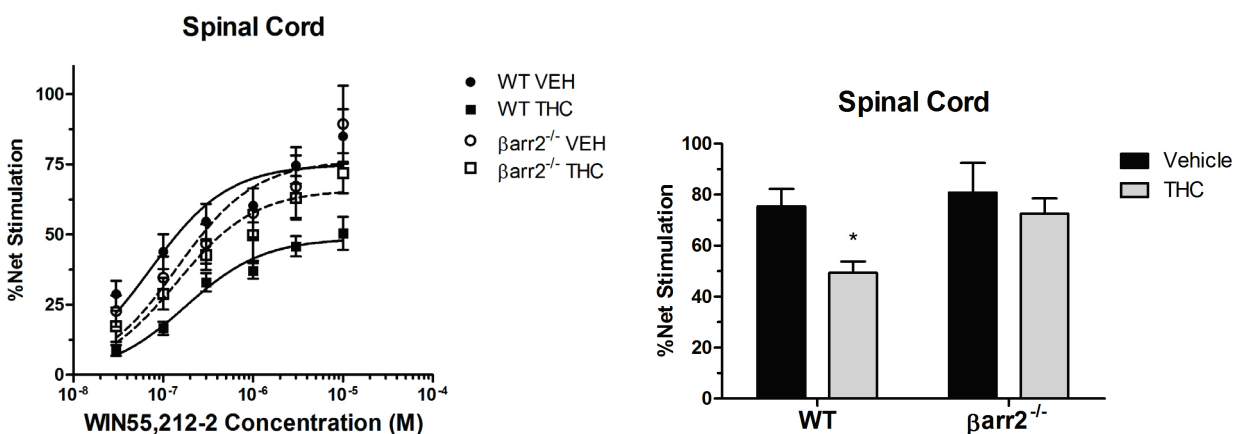


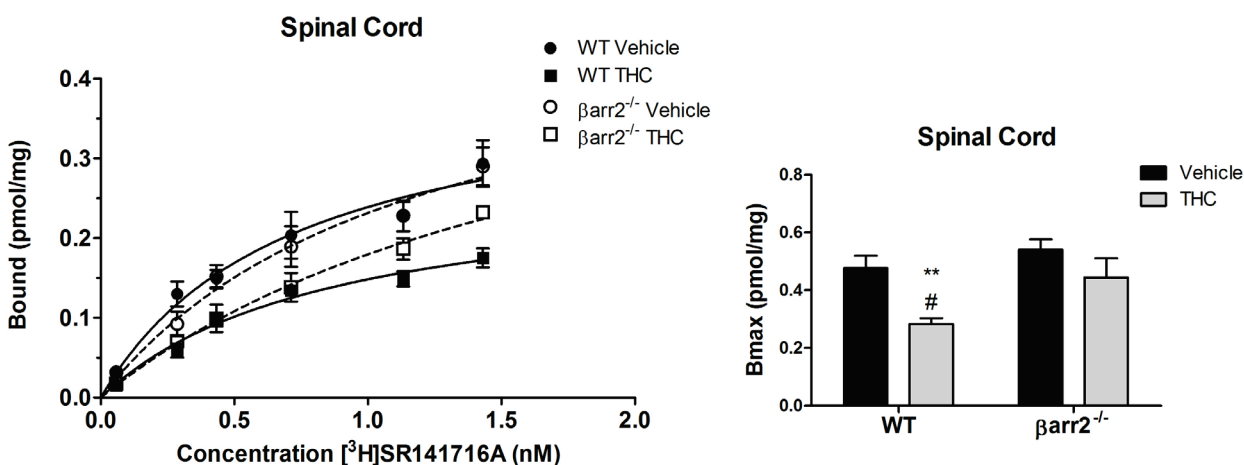
Figure 3.3. Desensitization of CB₁ receptor-mediated G-protein activation was attenuated in spinal cords of β arr2 KO animals following chronic treatment of THC. β Arr2 KO and WT animals received 6.5 day administration of 10 mg/kg THC or vehicle treatment (i.p.) given twice daily. Agonist-stimulated [³⁵S]GTP γ S binding curves using CP55,940 (A) or WIN55,212-2 (B) are shown and values are expressed as %Net stimulation [(agonist - basal)/basal x 100%]. Each point represents the mean \pm SEM (N = 6-7 in each point) [³⁵S]GTP γ S binding value. E_{max} [³⁵S]GTP γ S binding values were calculated using non-linear regression analyses in Prism and are shown in the bar graphs (right). * $p < 0.05$, *** $p < 0.001$, compared to respective vehicle control; ### $p < 0.001$ versus KO THC (2-way ANOVA, Student-Newman Keuls post-hoc). Agonist-stimulated [³⁵S]GTP γ S binding curves were generated as described in *Methods*.

Table 3.1. Desensitization of CB₁ receptor-mediated G-protein activation was attenuated in spinal cords of β arr2 knockout animals following chronic treatment of THC. β Arr2 KO and WT animals received 6.5 day administration of 10 mg/kg THC or vehicle treatment (i.p.) given twice daily. Concentration-effect curves were constructed and analyzed for best-fit E_{max} and EC_{50} values using Prism and described in *Methods*. Values represent the mean \pm SEM (N = 6-7 in each point). E_{max} [³⁵S]GTP γ S binding values are expressed as %Net stimulation [(agonist - basal)/basal x 100%]. * $p < 0.05$, *** $p < 0.001$, versus respective vehicle control group; ### $p < 0.001$ versus KO THC (2-way ANOVA, bonferroni post-test).

| Group | EC_{50} (μ M) | E_{max} (% Net Stim.) | % Vehicle |
|-------------------------------------|----------------------|--------------------------------------|------------------|
| CP55,940 | | | |
| WT Vehicle | 0.04 \pm 0.01 | 45.04 \pm 1.91 | 100 \pm 4.25 |
| WT THC | 0.02 \pm 0.01 | 27.88 \pm 3.64 ^{***, ###} | 61.89 \pm 8.08 |
| β arr2 ^{-/-} Vehicle | 0.02 \pm 0.01 | 46.41 \pm 2.13 | 100 \pm 4.60 |
| β arr2 ^{-/-} THC | 0.01 \pm 0.01 | 41.10 \pm 1.80 | 88.56 \pm 3.88 |
| WIN55,212-2 | | | |
| WT Vehicle | 0.08 \pm 0.02 | 75.46 \pm 6.82 | 100 \pm 9.04 |
| WT THC | 0.20 \pm 0.04 | 49.39 \pm 4.41 [*] | 65.45 \pm 5.84 |
| β arr2 ^{-/-} Vehicle | 0.34 \pm 0.19 | 80.87 \pm 11.55 | 100 \pm 14.28 |
| β arr2 ^{-/-} THC | 0.22 \pm 0.07 | 72.53 \pm 5.99 | 89.67 \pm 7.41 |

3.3 β -arrestin 2 regulates CB_1 receptor downregulation in mouse spinal cord following chronic administration of THC

β arr2 may also serve other physiological functions in the regulation of GPCR signaling. For example, β arr2 has previously been demonstrated as an adaptor protein, targeting phosphorylated β_2 adrenergic receptors towards degradation via clathrin-mediated endocytosis (Lin et al., 1997). Reduction in cell surface receptor levels, or downregulation, could therefore be another mechanism contributing to drug tolerance. We therefore evaluated the effect of β arr2 deletion on CB_1 receptor downregulation in whole spinal cord following chronic THC administration. Receptor binding saturation curves were generated using the CB_1 receptor antagonist SR141716A (SR1). No differences were found in [3 H]SR141716A binding between genotypes in vehicle treated mice, with B_{max} values (pmol/mg) of 0.47 ± 0.04 in WT and 0.54 ± 0.04 in β arr2 KO mice (Fig. 3.4). Chronic THC treatment resulted in significant CB_1 receptor downregulation in β arr2 WT mice ($B_{max} = 59.4\%$ of vehicle control) that was attenuated in β arr2 KO mice ($B_{max} = 82.3\%$ of vehicle control) (Fig. 3.3). Furthermore, no differences in receptor affinity were found between groups (Fig. 3.3), indicating adequate washout of drug and that downregulation was due primarily to a reduction in bound CB_1 receptor protein. It is important to note that SR1 recognizes both high and low affinity binding states of the receptor, and therefore is independent of receptor desensitization. These results thus indicate that β arr2 is also involved in regulating CB_1 receptor downregulation within the spinal cord, thus contributing to the attenuation in THC-mediated antinociceptive tolerance.



| Group | K _D (nM) | B _{max} (pmol/mg) | % Vehicle |
|-------------------------------------|---------------------|-----------------------------|---------------|
| WT Vehicle | 1.03 ± 0.24 | 0.47 ± 0.04 | 100 ± 9.07 |
| WT THC | 0.91 ± 0.11 | 0.28 ± 0.02 ^{**,#} | 59.40 ± 4.12 |
| β arr2 ^{-/-} Vehicle | 1.43 ± 0.27 | 0.54 ± 0.04 | 100 ± 6.67 |
| β arr2 ^{-/-} THC | 1.51 ± 0.34 | 0.44 ± 0.07 | 82.30 ± 12.21 |

Figure 3.4. Chronic administration of THC led to downregulation of CB₁ receptors in spinal cords of WT animals, but was abolished in β arr2 KO mice. β Arr2 KO and WT animals received 6.5 day administration of 10 mg/kg THC or vehicle treatment (i.p.) given twice daily. CB₁ receptor binding curves (as described in *Methods*) were generated using [³H]SR141716A. B_{max} (pmol/mg) and K_D (nM) values were calculated with Prism using a one site hyperbola function and displayed as the mean ± SEM (N = 6-7 per point). ** $p < 0.01$, compared to respective vehicle control; # $p < 0.001$ versus KO THC (2-way ANOVA, Student-Newman Keuls post-hoc)

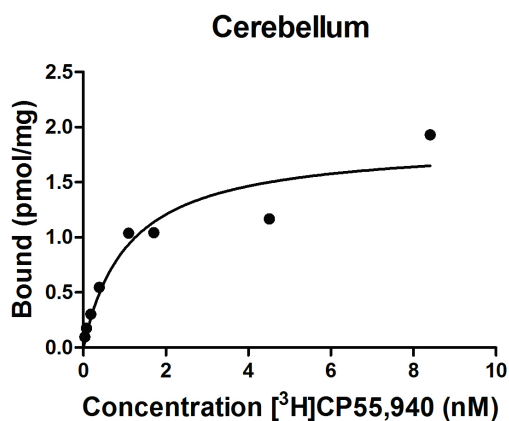
3.4 Method for 3D reconstruction of agonist-stimulated [^{35}S]GTP γ S and [^3H]CP55,940 binding autoradiography

Results of *in vivo* studies showed that β arr2 deletion altered THC-mediated effects in an effect-specific manner. The attenuation in THC-mediated antinociceptive tolerance, but not tolerance to catalepsy or hypothermia, suggests that β arr2 may differentially regulate CB $_1$ receptor signaling within different neuronal populations. For example, cannabinoid-mediated antinociception is likely to be mediated by circuits that include the PAG and spinal cord (Lichtman et al., 1996). Results in membrane homogenates of spinal cord support a role for β arr2-regulated CB $_1$ receptor desensitization/downregulation in this region in antinociceptive tolerance. Based on *in vivo* findings, we predict that deletion of β arr2 would reduce desensitization in regions including PAG. Conversely, we do not predict that β arr2 would affect desensitization in regions such as hypothalamus and basal ganglia that contribute to hypothermia and catalepsy, respectively. To test this hypothesis, we utilized Statistical Parametric Mapping (SPM) analysis to determine whether β arr2 regulates CB $_1$ receptor function and levels following chronic THC treatment, using reconstructed images derived from agonist-stimulated [^{35}S]GTP γ S and [^3H]CP55,940 binding autoradiography, respectively.

3D reconstructions of agonist-stimulated [^{35}S]GTP γ S binding were conducted as outlined in Chapters 1-2. CP55,940 (CP) was used to stimulate [^{35}S]GTP γ S binding, since we showed that it exhibits similar efficacy as the full CB $_1$ agonist WIN55,212-2 (WIN) for G-protein activation in a number of CB $_1$ receptor containing brain regions (see Chapter 2, Fig. 2.4) but does not activate non-CB $_1$ /CB $_2$ sites as shown in mice lacking CB $_1$ receptors (see Chapter 2, Fig. 2.7). [^{35}S]GTP γ S binding values in reconstructed images were expressed as net differences (agonist-stimulated minus basal [^{35}S]GTP γ S binding). These reconstructions of net values were derived

by image subtracting basal images from their respective CP-stimulated images, both of which were spatially normalized to the same coordinate space. Estimation of spatial normalization parameters were derived from CP-stimulated images, as these provided the most contrast between anatomical structures. The image average of all CP-stimulated reconstructions from all treatment groups was used to create the template for estimation of spatial normalization of individual CP-stimulated reconstructions. These parameters were then applied to basal images that were coregistered to their respective CP-stimulated brain image. To remove artifactual binding values, such as negative numbers that result from inadequate overlap of basal and CP-stimulated images, these values were set to zero. These occurred most frequently along the contour of sections, where artifacts related to slice preparation were predominately found. Setting negative voxel values to zero thus allows the SPM program to ignore these data points and view them as background, which by default has a voxel value of zero.

To quantitate CB₁ receptor density, [³H]CP55,940 (3 nM) was incubated with brain sections, in the presence (non-specific binding) or absence (total binding) of 10 μM CP55,940. Images of total binding values (specific + non-specific) were used to reconstruct images derived from [³H]CP55,940 binding autoradiography. This was done because non-specific activity was low, therefore reconstructions derived from non-specific binding sections would be suboptimal given the extremely low contrast and poor structural information following image quantitation (Fig. 3.5B). Average non-specific activity ranged from 0.49% to 3.6% of total binding across all sampled brain regions of interest (see next section). This would present a technical challenge for creating image reconstructions derived from specific binding values. Reconstructions of total [³H]CP55,940 binding used similar approaches as in agonist-stimulated [³⁵S]GTPγS binding images (outlined in Chapter 2).

A

| K_D (nM) | B_{max} (pmol/mg) |
|------------|---------------------|
| 1.084 | 1.862 |

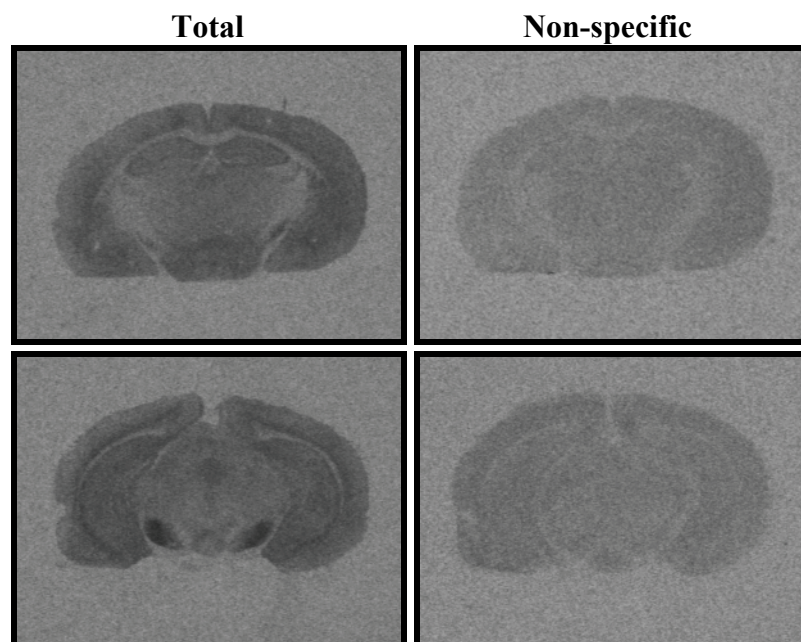
B

Figure 3.5. (A) CB_1 receptor B_{max} and K_D values were determined in mouse cerebellum with $[^3H]CP55,940$ using a one site hyperbola function in Prism. (B) $[^3H]CP55,940$ autoradiographic images are shown for total (left column) and non-specific (right column) binding. $[^3H]CP55,940$ autoradiography and receptor-binding were conducted as described in Methods, Section III.

3.5 β -arrestin 2 regulates CB_1 receptor desensitization in a region-specific manner

Previous studies from our laboratory demonstrated that CB_1 receptors undergo desensitization following chronic THC administration, with regional differences in the magnitude of reduction in CB_1 receptor-mediated G-protein activation (McKinney et al., 2008; Sim-Selley and Martin, 2002; Sim et al., 1996a). Based on *in vivo* results from this study and agonist-stimulated [35 S]GTP γ S binding results in spinal cord, one would postulate that β arr2 could produce region-specific regulation of CB_1 receptor desensitization in the CNS. To answer this question, CB_1 receptor-mediated G-protein activity was assessed in the reconstructed mouse brain using SPM with subsequent region of interest (ROI) analyses in brains from vehicle- and THC-treated β arr2 WT and KO mice.

Under basal conditions with no agonist, there were no observed differences by genotype or drug treatment in all sampled brain areas in regards to basal [35 S]GTP γ S binding (Fig. 3.6). Within vehicle control groups, significant differences between genotypes in CP-stimulated [35 S]GTP γ S binding were found in certain sampled brain regions. The biggest difference was found in the piriform cortex where greater CB_1 receptor-mediated G-protein activity was found in the β arr2 KO animals (380 ± 18 nCi/g) versus WT animals (225 ± 32 nCi/g) (Fig. 3.7). In the auditory/visual (A/V) cortex, significantly greater CB_1 receptor-mediated G-protein activity was also found in the β arr2 KO animals (249 ± 26 nCi/g) versus WT animals (188 ± 20 nCi/g). Interestingly, intra-regional differences in the vehicle treated groups were found in the hippocampus, where significant differences in CB_1 receptor-mediated G-protein activity were only noted in the caudal extent. In the caudal sub-region of the hippocampus, CP-stimulated [35 S]GTP γ S binding was 362 ± 27 nCi/g in β arr2 KO animals versus 279 ± 31 nCi/g in the WT

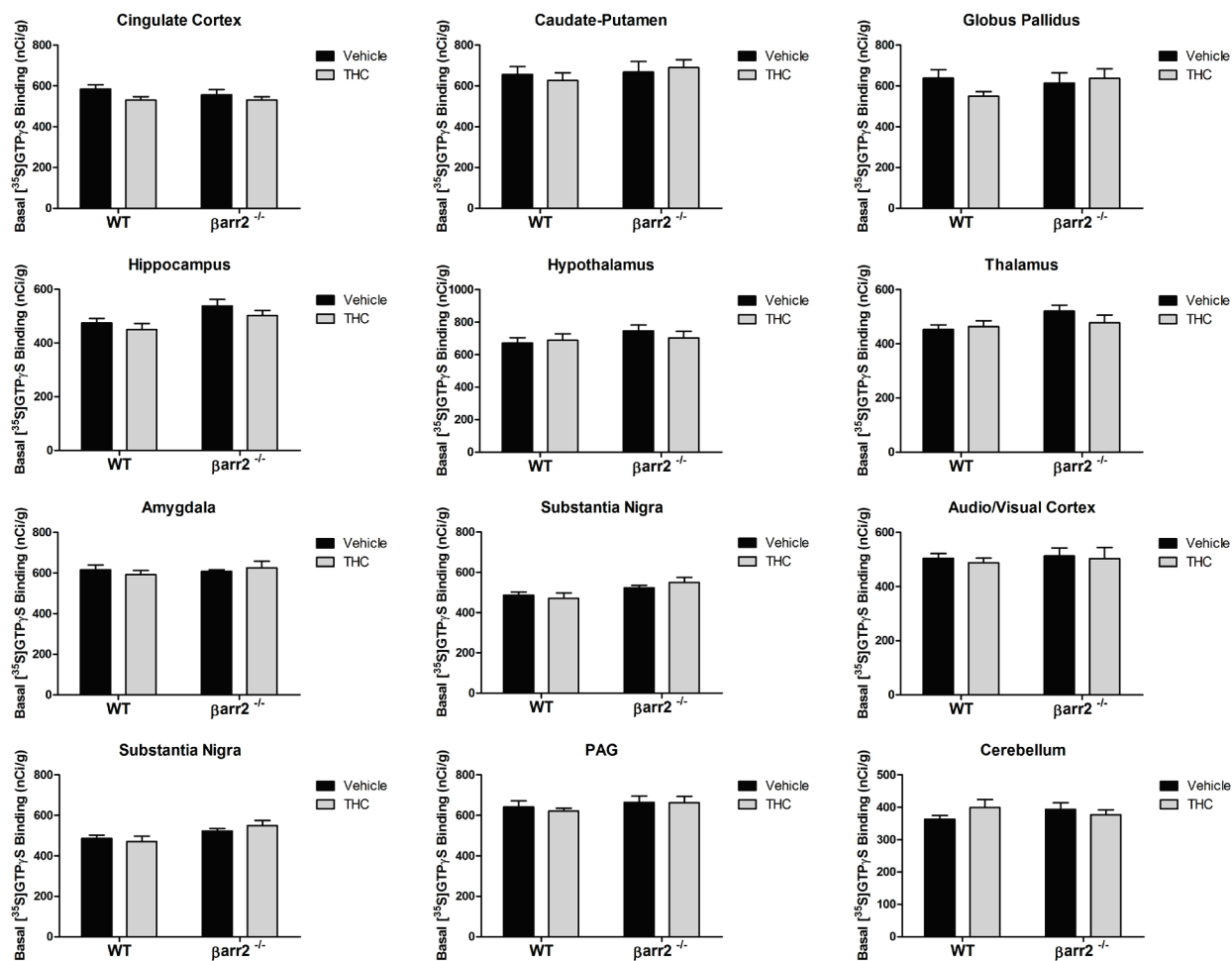


Figure 3.6. Basal $[^{35}\text{S}]\text{GTP}\gamma\text{S}$ binding values in βArr2 KO and WT animals following chronic administration of THC or vehicle. No differences in basal $[^{35}\text{S}]\text{GTP}\gamma\text{S}$ binding were found by either genotype or drug treatment in various brain regions as determined by 2-way ANOVA. Binding values represent the mean \pm SEM in various sampled brain regions from βarr2 WT and KO mice following 6.5 day chronic administration of either vehicle or 10 mg/kg THC (N = 8 per group) twice daily.

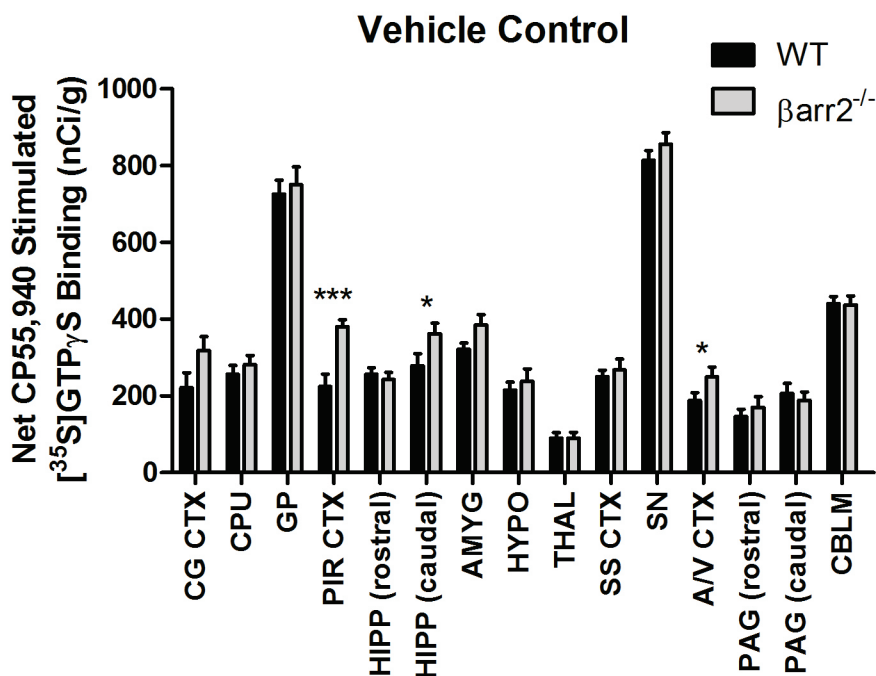


Figure 3.7. Net (agonist - basal) CP55,940-stimulated [³⁵S]GTP γ S binding values (mean \pm SEM) in sampled brain regions from β arr2 WT and KO mice following 6.5 day treatment with vehicle twice daily (N = 8 per group). *** $p < 0.001$, * $p < 0.05$; Two way ANOVA, Student-Newman Keuls Post-hoc. CG CTX, cingulate cortex; CPU, caudate-putamen; GP, globus pallidus; PIR CTX, piriform cortex; HIPP, hippocampus; AMYG, amygdala; HYPO, hypothalamus; THAL, thalamus; SS CTX, somatosensory cortex; SN, substantia nigra; A/V CTX, auditory/visual cortex; PAG, periaqueductal gray; *CBLM*, cerebellum

animals. Similar non-significant trends of greater CB₁ receptor-mediated G-protein activity were also noted in the cingulate cortex ($p = 0.051$), somatosensory cortex ($p = 0.078$), and amygdala ($p = 0.058$) of β arr2 KO animals versus WT (Fig. 3.7). Overall, these results showed regionally restricted differences in agonist-stimulated [³⁵S]GTP γ S binding between genotypes that were generally small in magnitude.

SPM with subsequent ROI analyses was then applied to assess agonist-stimulated [³⁵S]GTP γ S binding in vehicle- and THC-treated β arr2 WT and KO mice to compare the regional profile and magnitude of desensitization between genotypes. Comparing volumetric reconstructions derived from the image average of all subjects within each group, visual decreases in CB₁ receptor-stimulated [³⁵S]GTP γ S binding can be appreciated in brain areas including the hippocampus, amygdala, and rostral periaqueductal gray (PAG), within both β arr2 WT and KO animals following THC treatment (Fig. 3.8-3.9). Overall, SPM analysis revealed region-specific receptor desensitization in CB₁ receptor-mediated G-protein activity (Fig. 3.10) with a similar regional relationship in magnitude of desens as previously reported: hippocampus > cerebellum > striatum/basal ganglia (McKinney et al., 2008; Sim et al., 1996a). Also, the distribution of receptor desensitization coincided with regions known to contain CB₁ receptors (Herkenham et al., 1991), as well as the anatomical distribution of CB₁ receptor activity (Chapter 2).

A subset of regions showed a similar response as seen in spinal cord and were consistent with the prediction that β arr2 regulates CB₁ receptor desensitization. The clearest example of this was in the cerebellum. SPM detected moderate desensitization in WT animals (Fig. 3.10), where

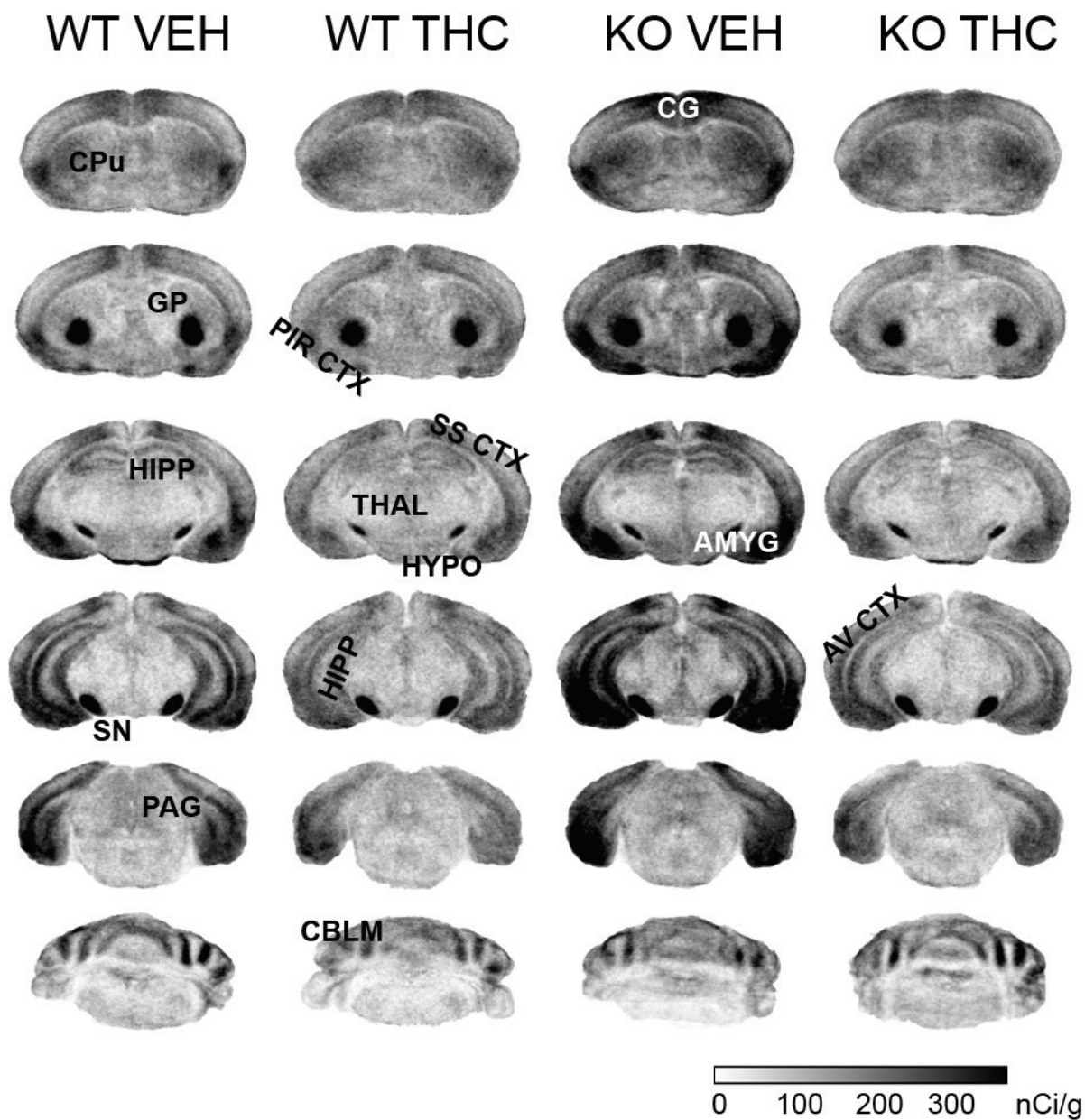


Figure 3.8. Net cannabinoid-stimulated $[^{35}\text{S}]\text{GTP}\gamma\text{S}$ binding reconstructions derived from the image average of all subjects within each group ($N = 8$). $\beta\text{arr}2$ WT and KO mice were treated for 6.5 day administration of either vehicle or 10 mg/kg THC twice daily. Original autoradiographic images are shown in grayscale and correspond to the scale (bottom right). *CG CTX*, cingulate cortex; *CPu*, caudate-putamen; *GP*, globus pallidus; *PIR CTX*, piriform cortex; *HIPP*, hippocampus; *AMYG*, amygdala; *HYPO*, hypothalamus; *THAL*, thalamus; *SS CTX*, somatosensory cortex; *SN*, substantia nigra; *A/V CTX*, auditory/visual cortex; *PAG*, periaqueductal gray; *CBLM*, cerebellum.

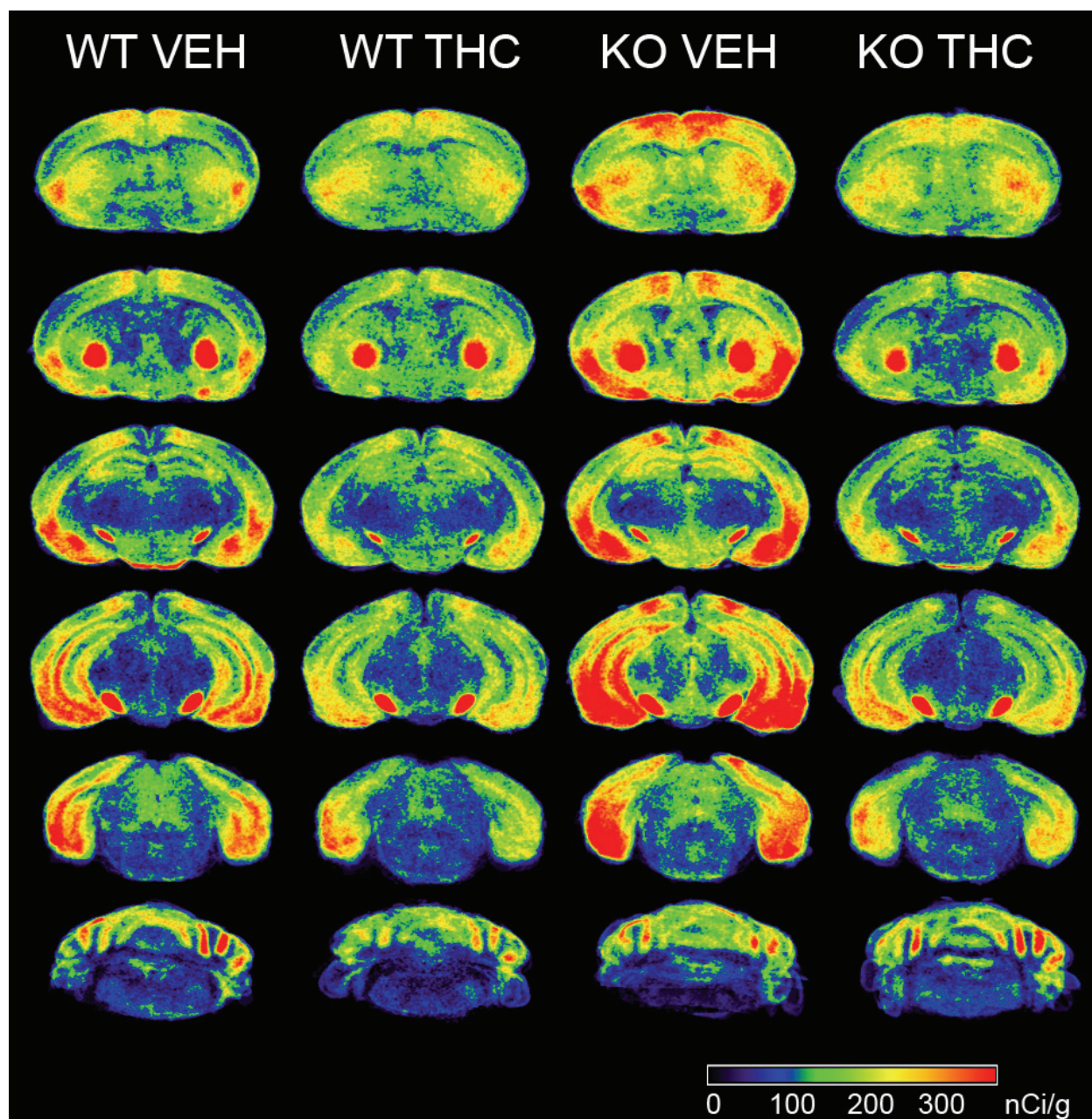


Figure 3.9. Net cannabinoid-stimulated [35 S]GTP γ S binding reconstructions derived from the image average of all subjects within each group (N = 8). β arr2 WT and KO mice were treated for 6.5 day administration of either vehicle or 10 mg/kg THC twice daily. Images are shown in pseudocolor and correspond to the color scale (bottom right). Anatomical reference labels are shown in Fig. 3.8.

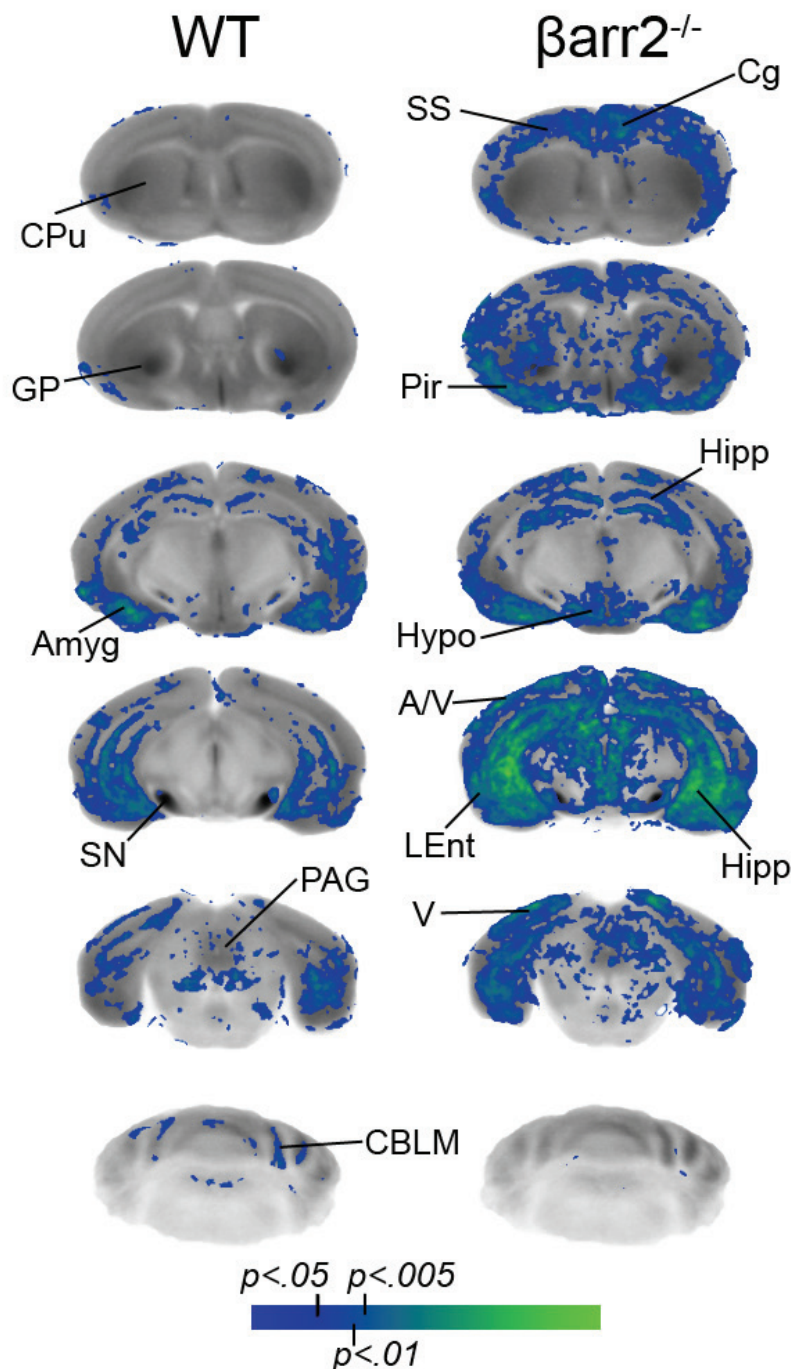


Figure 3.10. SPM analysis revealed both region- and genotypic-specific differences in desensitization of CB₁ receptor-mediated G-protein activation in the reconstructed mouse brain of β arr2 WT and KO mice following 6.5 day chronic administration of either vehicle or 10 mg/kg THC (N = 8 per group) twice daily. Brain regions within each genotype demonstrating significant desensitization ($p < 0.05$, 2-way ANOVA, N = 8) are colored in blue/green and correspond to the significance scale (bottom). *AMYG*, amygdala; *A/V CTX*, auditory/visual cortex; *CBLM*, cerebellum; *CG*, cingulate cortex; *CPU*, caudate-putamen; *GP*, globus pallidus; *HIPP*, hippocampus; *HYPO*, hypothalamus; *PAG*, periaqueductal gray; *PIR*, piriform cortex; *SN*, substantia nigra; *SS*, somatosensory cortex; *THAL*, thalamus; *V*, visual cortex;

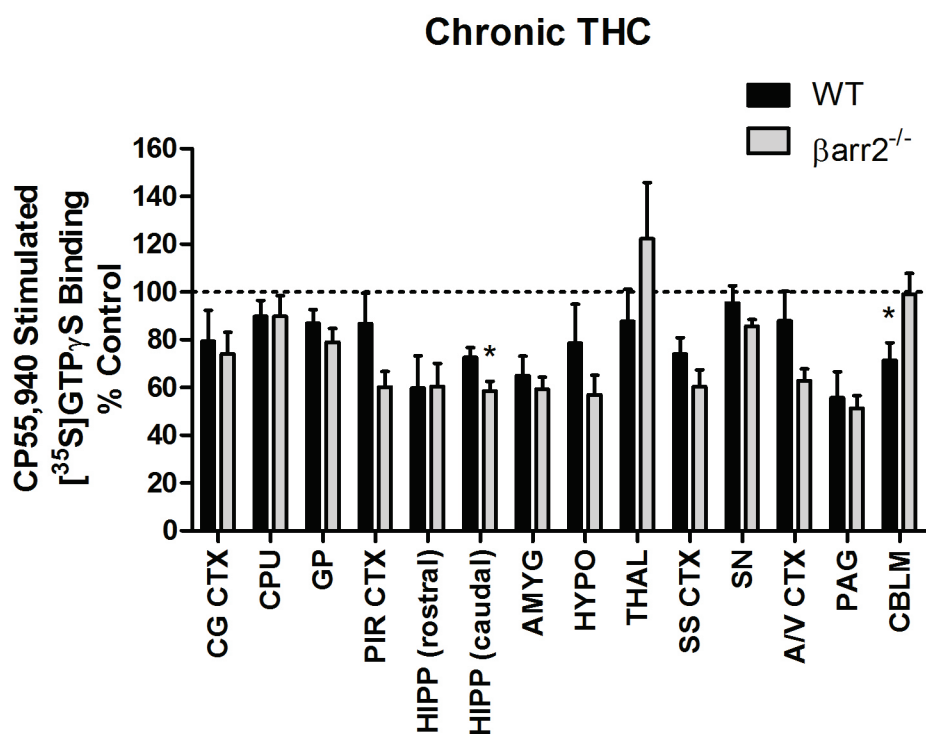


Figure 3.11. Region- and genotypic-specific differences were found in the magnitude of CB₁ receptor desensitization following chronic 6.5 day THC treatment twice daily in both β arr2 WT and KO mice (N = 8 per group). CP55,940-stimulated [³⁵S]GTP γ S binding values are shown normalized to vehicle and represent the mean \pm SEM (N = 8). * $p < 0.05$, Student's two-sample t -test. *CG CTX*, cingulate cortex; *CPU*, caudate-putamen; *GP*, globus pallidus; *PIR CTX*, piriform cortex; *HIPP*, hippocampus; *AMYG*, amygdala; *HYP0*, hypothalamus; *THAL*, thalamus; *SS CTX*, somatosensory cortex; *SN*, substantia nigra; *AV CTX*, auditory/visual cortex; *PAG*, periaqueductal gray; *CBLM*, cerebellum.

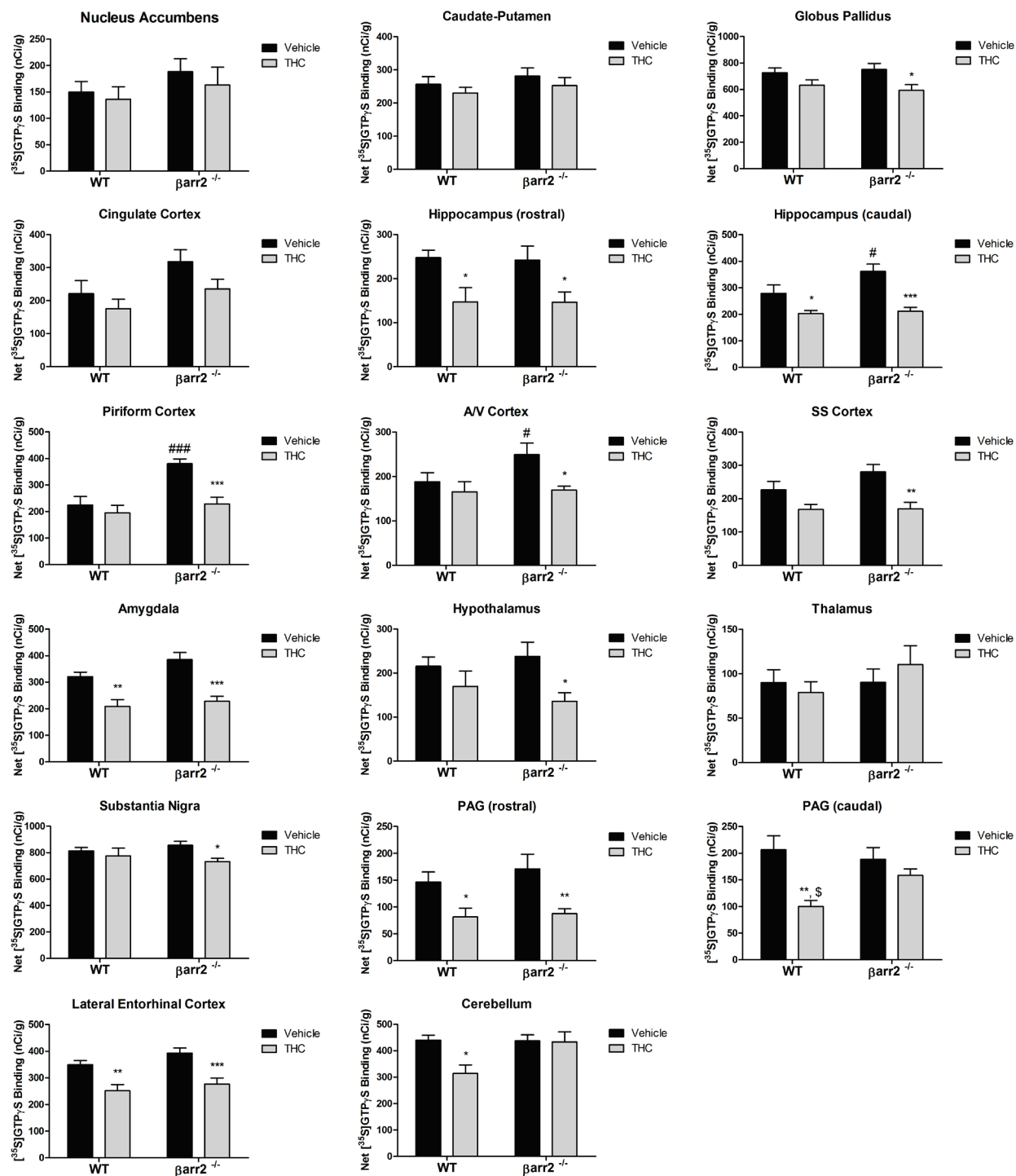


Figure 3.12. Net CP55,940-stimulated [35S]GTP γ S binding values (mean \pm SEM) in sampled brain regions (N = 8 per group) of β arr2 WT and KO mice following 6.5 day chronic administration of either vehicle or 10 mg/kg THC twice daily. *** $p < 0.001$, ** $p < 0.01$, * $p < 0.05$ versus respective vehicle; ### $p < 0.001$, # $p < 0.05$ versus WT vehicle; \$ versus KO THC (Two way ANOVA, Student-Newman Keuls Post-hoc). A/V, auditory/visual; SS, somatosensory

Table 3.2

Net CP55,940-stimulated [^{35}S]GTP γ S binding values in brain tissue sections from β arr2 WT and KO mice following 6.5 day chronic administration of either vehicle or 10 mg/kg THC (N = 8 per group) twice daily

Brain sections were incubated with 0.04 nM [^{35}S]GTP γ S, 3 μM CP55,940, and 2 mM GDP as described under *III. Methods*. [^{35}S]GTP γ S binding values represent the mean \pm SEM.). *** $p < 0.001$, ** $p < 0.01$, * $p < 0.05$ versus respective vehicle; #### $p < 0.001$, # $p < 0.05$ versus WT vehicle; \$ versus KO THC (N = 8 per group, two way ANOVA, Student-Newman Keuls Post-hoc)

| Region | Vehicle | | THC | |
|----------------|--------------|-----------------------|-------------------|-----------------------|
| | WT | β arr2 $^{-/-}$ | WT | β arr2 $^{-/-}$ |
| NAc | 150 \pm 20 | 189 \pm 24 | 136 \pm 24 | 163 \pm 33 |
| CPu | 256 \pm 23 | 282 \pm 24 | 230 \pm 17 | 252 \pm 25 |
| GP | 726 \pm 36 | 751 \pm 47 | 631 \pm 41 | 593 \pm 43* |
| CG CTX | 221 \pm 39 | 318 \pm 36 | 176 \pm 29 | 235 \pm 29 |
| HIPP (rostral) | 248 \pm 17 | 242 \pm 32 | 147 \pm 32* | 146 \pm 23* |
| HIPP (caudal) | 279 \pm 31 | 362 \pm 27# | 203 \pm 12* | 212 \pm 14*** |
| PIR CTX | 225 \pm 32 | 380 \pm 18### | 195 \pm 29 | 229 \pm 25*** |
| A/V CTX | 188 \pm 21 | 249 \pm 26 | 165 \pm 23# | 169 \pm 9* |
| SS CTX | 226 \pm 25 | 281 \pm 22 | 168 \pm 15 | 169 \pm 20** |
| AMYG | 321 \pm 17 | 385 \pm 27 | 209 \pm 26** | 228 \pm 19*** |
| HYP0 | 216 \pm 21 | 238 \pm 32 | 169 \pm 35 | 136 \pm 20* |
| THAL | 90 \pm 15 | 90 \pm 15 | 79 \pm 12 | 110 \pm 21 |
| SN | 814 \pm 26 | 856 \pm 30 | 776 \pm 58 | 733 \pm 24* |
| PAG (rostral) | 146 \pm 19 | 171 \pm 28 | 81 \pm 16* | 88 \pm 9** |
| PAG (caudal) | 207 \pm 26 | 189 \pm 22 | 100 \pm 12**,\$ | 158 \pm 12 |
| LEnt CTX | 350 \pm 16 | 393 \pm 19 | 252 \pm 23** | 277 \pm 23*** |
| CBLM | 440 \pm 19 | 437 \pm 23 | 314 \pm 32* | 434 \pm 38 |

ROI analysis showed that CB₁ receptor-mediated G-protein activity in THC-treated WT mice was $71 \pm 7\%$ of vehicle levels. In contrast, CB₁ receptor desensitization was nearly abolished in β arr2 KO mice following chronic treatment with THC, and CB₁ receptor-mediated G-protein activity was comparable in β arr2 KO and WT mice. A significant interaction of Drug treatment X Genotype was also found [$F(1,28) = 4.51, p < 0.05$], suggesting that β arr2 is involved in mediating CB₁ receptor desensitization within the cerebellum following this treatment paradigm. Interestingly, intra-regional differences in the magnitude of CB₁ receptor desensitization were revealed by SPM analysis, which underscores an advantage of using a whole-brain approach to assess the regulatory role of β arr2 in mediating CB₁ receptor desensitization in highly different neuroanatomical systems and brain regions. In these regions, β arr2 attenuated desensitization in certain aspects of the nucleus, whereas desensitization was similar between genotypes in other subregions. For example, initial ROI examination of the caudal sub-region of the PAG showed that chronic THC lead to a greater reduction in CB₁ receptor-mediated activity in the WT animals ($48 \pm 5\%$ of respective vehicle) versus β arr2 KO animals ($84 \pm 6\%$ of respective vehicle) (Fig. 3.8). However, in more rostral portions of the PAG, SPM analysis revealed significant desensitization within the β arr2 KO animals ($51 \pm 5\%$ of respective vehicle). Subsequent ROI analysis substantiated these findings, demonstrating significant desensitization within both β arr2 WT and KO mice (Fig. 3.12, Table 3.2).

Other regions showed no difference between β arr2 KO and WT mice either because both genotypes exhibited desensitization (i.e. amygdala) or neither genotype exhibited desensitization (i.e. striatum). Consistent with previous reports using similar dosing paradigms (McKinney et al., 2008; Sim-Selley and Martin, 2002; Sim et al., 1996a), there were no differences in CB₁ receptor-mediated G-protein activity in the caudate-putamen and nucleus accumbens within

either genotype, as determined by both SPM and ROI analyses. Interestingly, different results were found in the striatal/basal ganglia output nuclei, as discussed below. In the thalamus, a brain area with relatively sparse concentrations of CB₁ receptors (Herkenham et al., 1991), there were also no differences in CP-stimulated [³⁵S]GTPγS binding following THC treatment in either genotype. Similar magnitudes of desensitization were found in the amygdala region within both genotypes, where there was slightly greater desensitization in βarr2 KO (59 ± 5% of respective control) versus WT animals (65 ± 8% of respective control). Among all sampled cortical regions in this study, including cingulate, somatosensory, piriform, and auditory/visual cortex, CB₁ receptor G-protein activity in the WT mice was apparently reduced following THC treatment, ranging between 74-87%, but did not differ from vehicle-treated mice. Significant desensitization however was found in the lateral entorhinal cortex within WT THC-treated animals. Interestingly, there was a trend towards greater desensitization in the βarr2 KO mice, particularly in the piriform (60 ± 6% of vehicle) and auditory/visual cortex (68 ± 3% of vehicle), as demonstrated by SPM analysis and subsequently confirmed by an independent ROI analysis (Fig. 3.10, Fig. 3.11). This appeared to result from the slightly higher, but insignificant difference from WT level of CP-stimulated [³⁵S]GTPγS binding in vehicle-treated βarr2 KO mice. As noted above, the piriform cortex was also a brain region where CP-stimulated [³⁵S]GTPγS binding in the vehicle treated groups was greater in the βarr2 KO versus WT mice (Fig. 3.7).

Unexpectedly, SPM analysis identified enhanced desensitization in certain regions of βarr2 KO mice. SPM showed significant desensitization of CB₁ receptor-mediated G-protein activation in the hypothalamus of βarr2 KO animals (57 ± 8% of vehicle), but not in WT mice (79 ± 16% of vehicle) This was subsequently confirmed by ROI analysis, which showed no

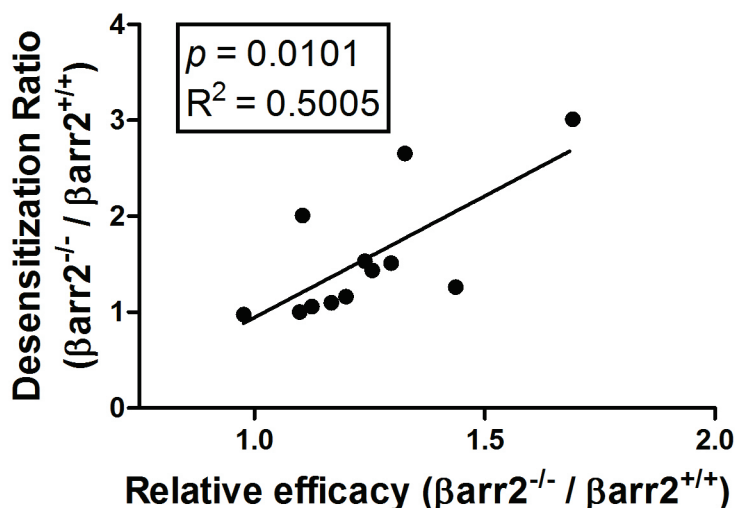
difference in CP-stimulated [^{35}S]GTP γ S binding between vehicle- and THC-treated WT animals. The basal ganglia output nuclei, including the substantia nigra and globus pallidus, contain the highest concentrations of CB $_1$ receptors (Herkenham et al., 1991) and are relatively insensitive to changes in CB $_1$ receptor activity following THC treatment. Although WT animals exhibited no changes in CB $_1$ receptor-mediated G-protein activity after THC treatment, β arr2 KO animals interestingly displayed a significant reduction in the substantia nigra ($85 \pm 3\%$ of respective vehicle) and a trend in the globus pallidus ($79 \pm 6\%$, $p = 0.053$). Subregional differences in desensitization were also found in the hippocampus. In this region, desensitization was more robust in the caudal extent of β arr2 KO mice (Fig. 3.10). This was confirmed by a subsequent ROI analysis, which showed significantly greater desensitization in the caudal aspects of the hippocampus in β arr2 KO mice ($58.6 \pm 4\%$ of vehicle), compared to WT mice ($72.6 \pm 4\%$ of vehicle). Significant reductions in CP-stimulated [^{35}S]GTP γ S binding were also found in the rostral hippocampus of β arr2 KO and WT animals, where both exhibited about a 40% reduction following chronic THC treatment.

Increases in the apparent efficacy of CP-stimulated [^{35}S]GTP γ S binding in various brain regions in β arr2 KO mice appeared to be associated with the enhancement or unmasking of CB $_1$ receptor desensitization in the these same brain regions following chronic administration of THC. Interestingly, the relative magnitude of desensitization of β arr2 KO when normalized to WT animals was positively correlated with the relative efficacy of CP-stimulated [^{35}S]GTP γ S binding in β arr2 KO mice when normalized to WT animals ($p = 0.0101$, $R^2 = 0.5$; Fig. 3.13). For example, a 1.5 fold increase in the relative efficacy of CP-stimulated [^{35}S]GTP γ S binding in β arr2 KO mice was equal to about a 2 fold increase in the relative magnitude of desensitization in β arr2 KO mice. This suggests that increases in the apparent efficacy of cannabinoid agonists

in β arr2 KO mice may enhance other regulatory pathways thus producing greater CB₁ receptor desensitization.

Together, these results suggest a regional-specificity in the regulation of CB₁ receptors by β arr2 at the level of G-protein coupling. However, it is unclear whether β arr2 may regulate other mechanisms of CB₁ receptor adaptation, such as receptor downregulation or degradation of proteins.

Regional correlation analysis



| Brain Region | Desensitization Ratio | Relative efficacy |
|-------------------------------|-----------------------|-------------------|
| Cingulate cortex | 1.44 ± 0.16 | 1.26 ± 0.44 |
| Somatosensory cortex | 1.24 ± 0.10 | 1.53 ± 0.27 |
| Auditory-Visual cortex | 1.33 ± 0.14 | 2.65 ± 0.30 |
| Piriform cortex | 1.69 ± 0.08 | 3.01 ± 0.49 |
| Lateral Entorhinal cortex | 1.12 ± 0.05 | 1.06 ± 0.21 |
| Amygdala | 1.20 ± 0.08 | 1.16 ± 0.14 |
| Hippocampus (rostral) | 0.98 ± 0.13 | 0.97 ± 0.24 |
| Hippocampus (caudal) | 1.30 ± 0.10 | 1.51 ± 0.14 |
| Periaqueductal gray (rostral) | 1.17 ± 0.19 | 1.10 ± 0.12 |
| Caudate Putamen | 1.10 ± 0.09 | 1.00 ± 0.85 |
| Hypothalamus | 1.10 ± 0.15 | 2.01 ± 0.38 |
| Nucleus Accumbens | 1.26 ± 0.16 | 1.44 ± 1.91 |

Figure 3.13. Relative efficacy of CP-stimulated $[^{35}\text{S}]\text{GTP}\gamma\text{S}$ binding is positively correlated with the relative magnitude of CB_1 receptor desensitization in $\beta\text{arr}2$ KO mice following chronic THC administration (top graph). $\beta\text{Arr}2$ KO and WT animals received 6.5 day administration of 10 mg/kg THC or vehicle treatment (i.p.) given twice daily. Each point in the graph represents a brain area (listed in the table above) corresponding to its mean Desensitization Ratio and mean Relative efficacy. The Desensitization Ratio was calculated by normalizing the magnitudes of desensitization in $\beta\text{arr}2$ KO mice to the mean magnitude of desensitization in $\beta\text{arr}2$ WT mice. The Relative efficacy was calculated by normalizing the magnitudes of CP-stimulated $[^{35}\text{S}]\text{GTP}\gamma\text{S}$ binding in vehicle treated $\beta\text{arr}2$ KO mice by the mean magnitude of CP-stimulated $[^{35}\text{S}]\text{GTP}\gamma\text{S}$ binding in vehicle treated $\beta\text{arr}2$ WT mice. Calculated ratios in the table represent the mean ± SEM (N = 8). Linear regression analysis was performed in Graphpad Prism 5.

3.6 β -arrestin 2 is involved in CB_1 receptor downregulation in the cerebellum

β arr2 targeting of GPCRs towards internalization and subsequent degradation represents another mechanism by which GPCRs respond to persistent stimulation by agonists. To investigate whether there were changes in CB_1 receptor levels within the brain following THC treatment, SPM and ROI analyses of [3 H]CP55,940 binding were performed. Results in sampled brain regions showed that [3 H]CP55,940 binding did not differ between genotypes in vehicle-treated mice (Fig. 3.14). Comparing volumetric reconstructions derived from the image average of all subjects within each group, visual decreases in [3 H]CP55,940 binding can be seen in the cortex, hippocampus, and PAG (Figs. 3.15-3.16). Again, striatal regions including the caudate-putamen and basal ganglia output nuclei (globus pallidus, substantia nigra), demonstrated minimal changes in [3 H]CP55,940 binding.

In the cerebellum, CB_1 receptors were significantly downregulated ($55 \pm 10\%$ of vehicle) and this response was virtually abolished in β arr2 KO mice. In addition, a significant interaction of Drug treatment X Genotype was found in the cerebellum [$F(1,28) = 4.277, p < 0.05$], suggesting that β arr2 is involved in mediating CB_1 receptor downregulation in this particular brain area (Fig 3.18, Table 3.3).

In general, there were no significant differences in CB_1 receptor levels according to SPM analysis (data not shown) and in all sampled brain regions using ROI, within β arr2 KO mice following chronic THC treatment. Within WT mice, only an insignificant trend towards decreased receptor levels were found following THC treatment in the hypothalamus ($71 \pm 20\%$ of respective vehicle), hippocampus ($75 \pm 17\%$ of respective vehicle), and PAG ($68 \pm 15\%$ of respective vehicle) (Fig. 3.17). Collectively, these results suggest that β arr2 may be involved in mediating receptor downregulation in the cerebellum.

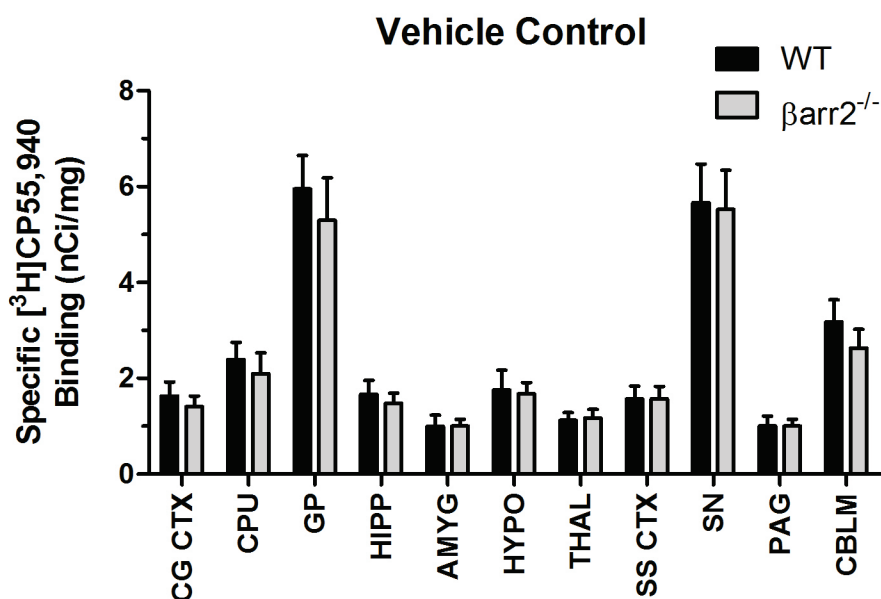


Figure 3.14. [³H]CP55,940 binding values (mean \pm SEM) in sampled brain regions from β arr2 WT and KO mice following 6.5 day chronic administration of either vehicle or 10 mg/kg THC twice daily (N = 8 per group). *CG CTX*, cingulate cortex; *CPU*, caudate-putamen; *GP*, globus pallidus; *HIPP*, hippocampus; *AMYG*, amygdala; *HYPO*, hypothalamus; *THAL*, thalamus; *SS CTX*, somatosensory cortex; *SN*, substantia nigra; *PAG*, periaqueductal gray; *CBLM*, cerebellum. [³H]CP55,940 autoradiography was performed as described in *Methods*

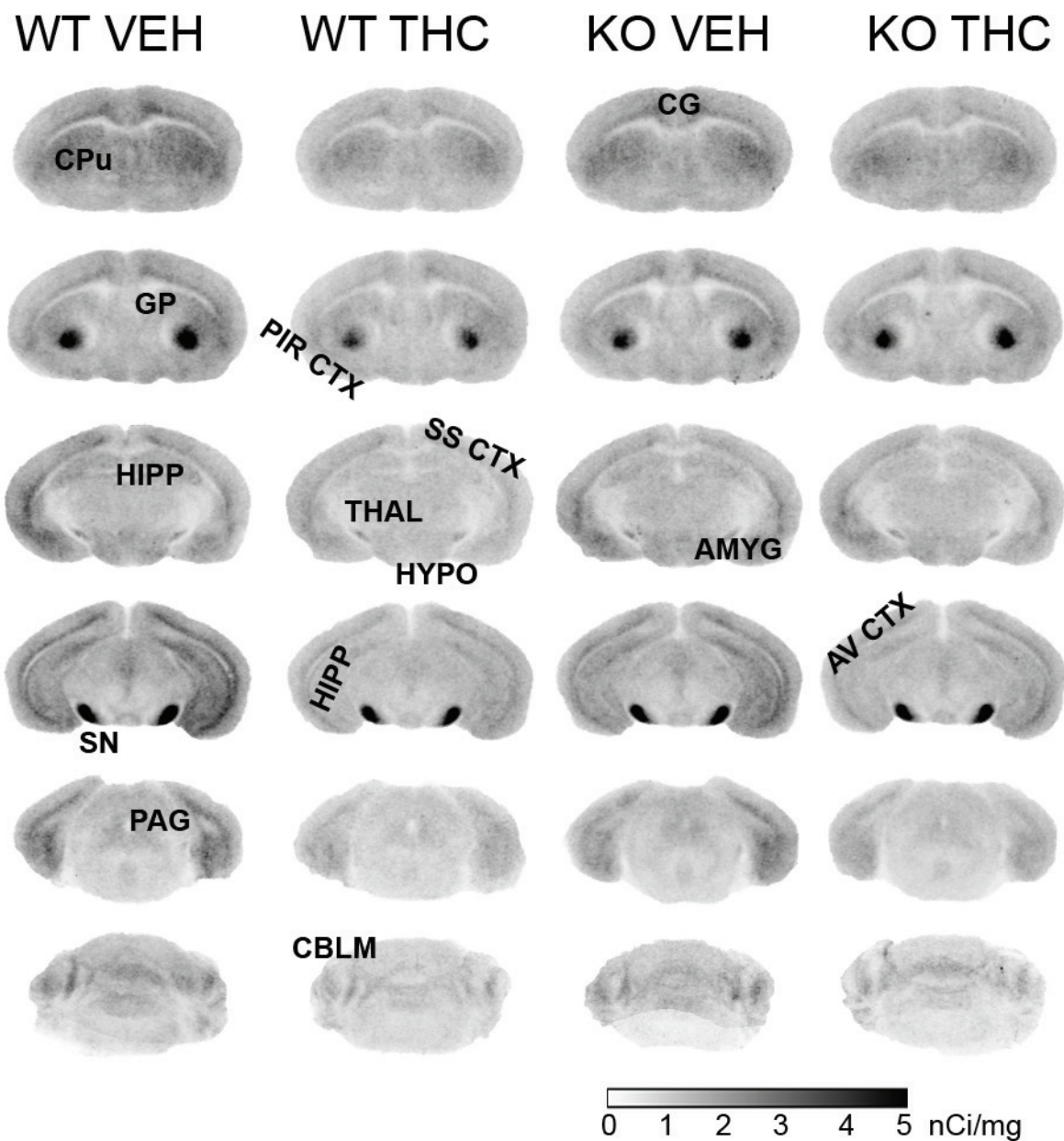


Figure 3.15. $[^3\text{H}]\text{CP55,940}$ receptor binding reconstructions derived from the image average of all subjects within each group ($N = 8$ per group). $\beta\text{arr}2$ WT and KO mice were treated 6.5 days with either vehicle or 10 mg/kg THC twice daily. Original autoradiographic images are shown in grayscale and correspond to the scale of binding values (bottom right). *CG CTX*, cingulate cortex; *CPu*, caudate-putamen; *GP*, globus pallidus; *PIR CTX*, piriform cortex; *HIPP*, hippocampus; *AMYG*, amygdala; *HYPO*, hypothalamus; *THAL*, thalamus; *SS CTX*, somatosensory cortex; *SN*, substantia nigra; *A/V CTX*, auditory/visual cortex; *PAG*, periaqueductal gray; *CBLM*, cerebellum. $[^3\text{H}]\text{CP55,940}$ autoradiography was performed as described in *Methods*

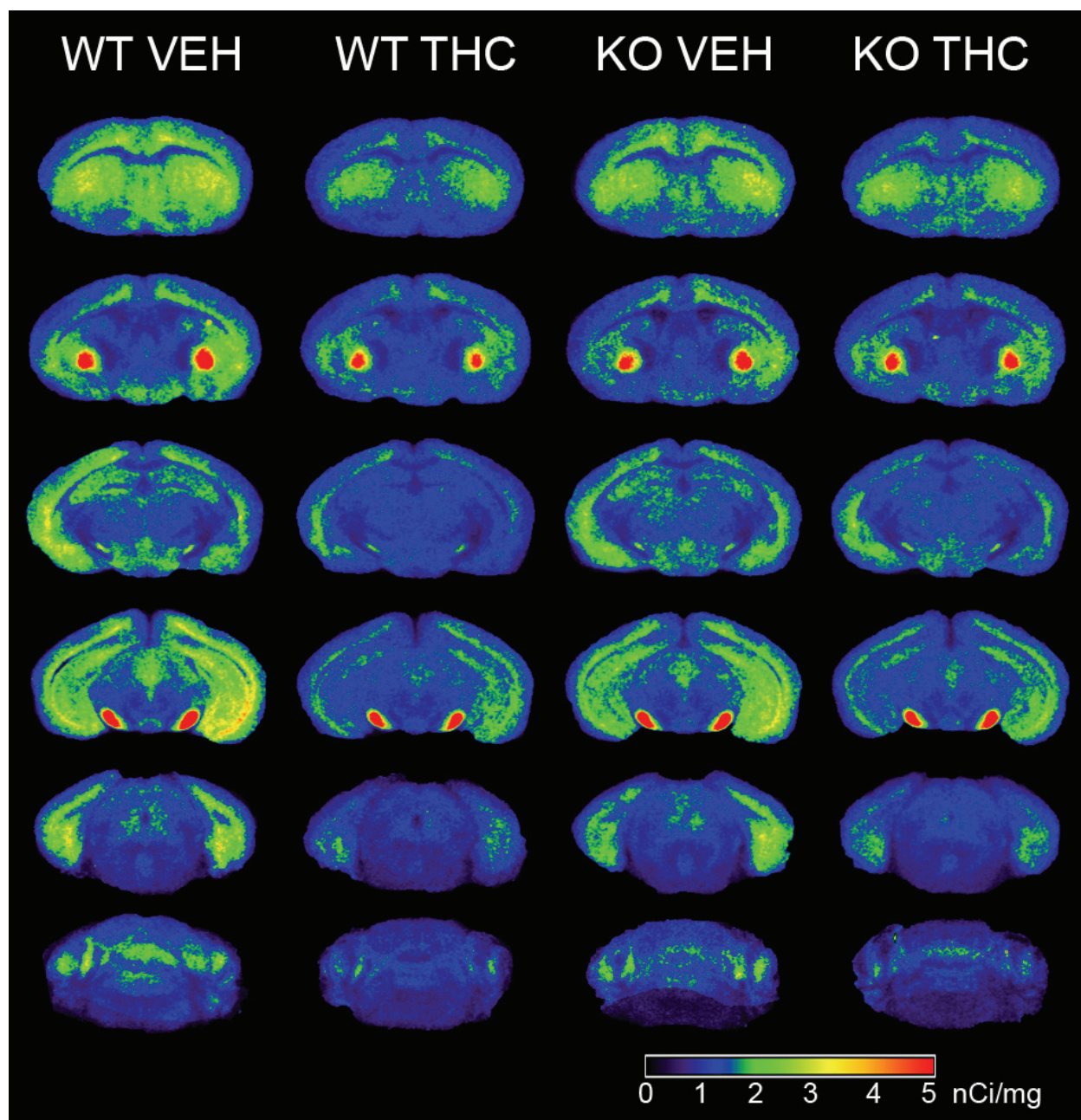


Figure 3.16. [^3H]CP55,940 receptor binding reconstructions derived from the image average of all subjects within each group ($N = 8$ per group). β arr2 WT and KO mice were treated 6.5 day with either vehicle or 10 mg/kg THC twice daily. Images are shown in pseudocolor and correspond to the color scale of binding values (bottom right). Anatomical reference labels are shown in Fig. 3.15. [^3H]CP55,940 autoradiography was performed as described in *Methods*

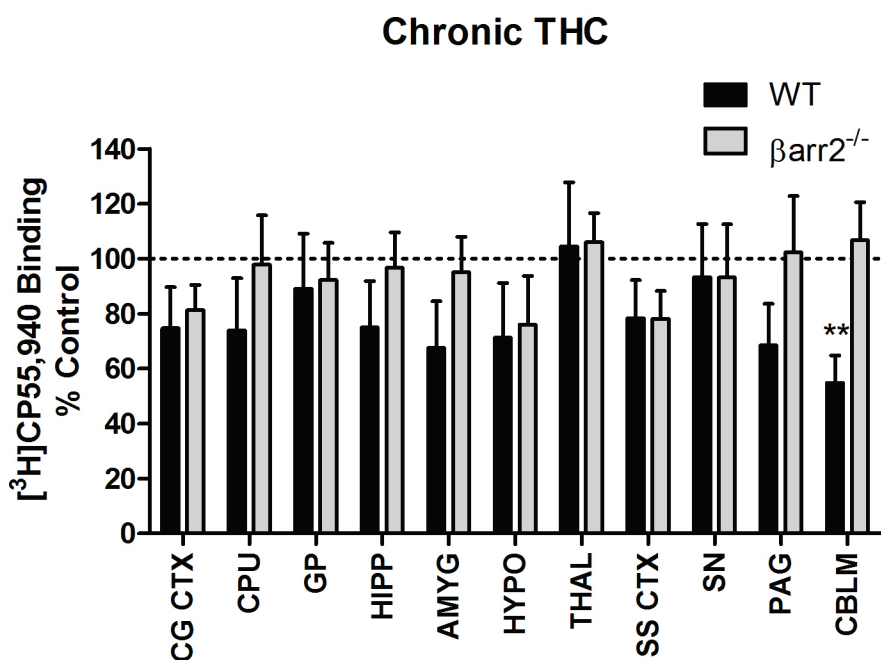


Figure 3.17. [³H]CP55,940 binding values normalized to vehicle (mean \pm SEM) in sampled brain regions from β arr2 WT and KO mice following 6.5 day chronic administration of either vehicle or 10 mg/kg THC twice daily (N = 8 per group). ** $p < 0.05$, Student's two-sample t -test. *CG CTX*, cingulate cortex; *CPU*, caudate-putamen; *GP*, globus pallidus; *PIR CTX*, piriform cortex; *HIPP*, hippocampus; *AMYG*, amygdala; *HYPO*, hypothalamus; *THAL*, thalamus; *SS CTX*, somatosensory cortex; *SN*, substantia nigra; *PAG*, periaqueductal gray; *CBLM*, cerebellum. [³H]CP55,940 autoradiography was performed as described in *Methods*

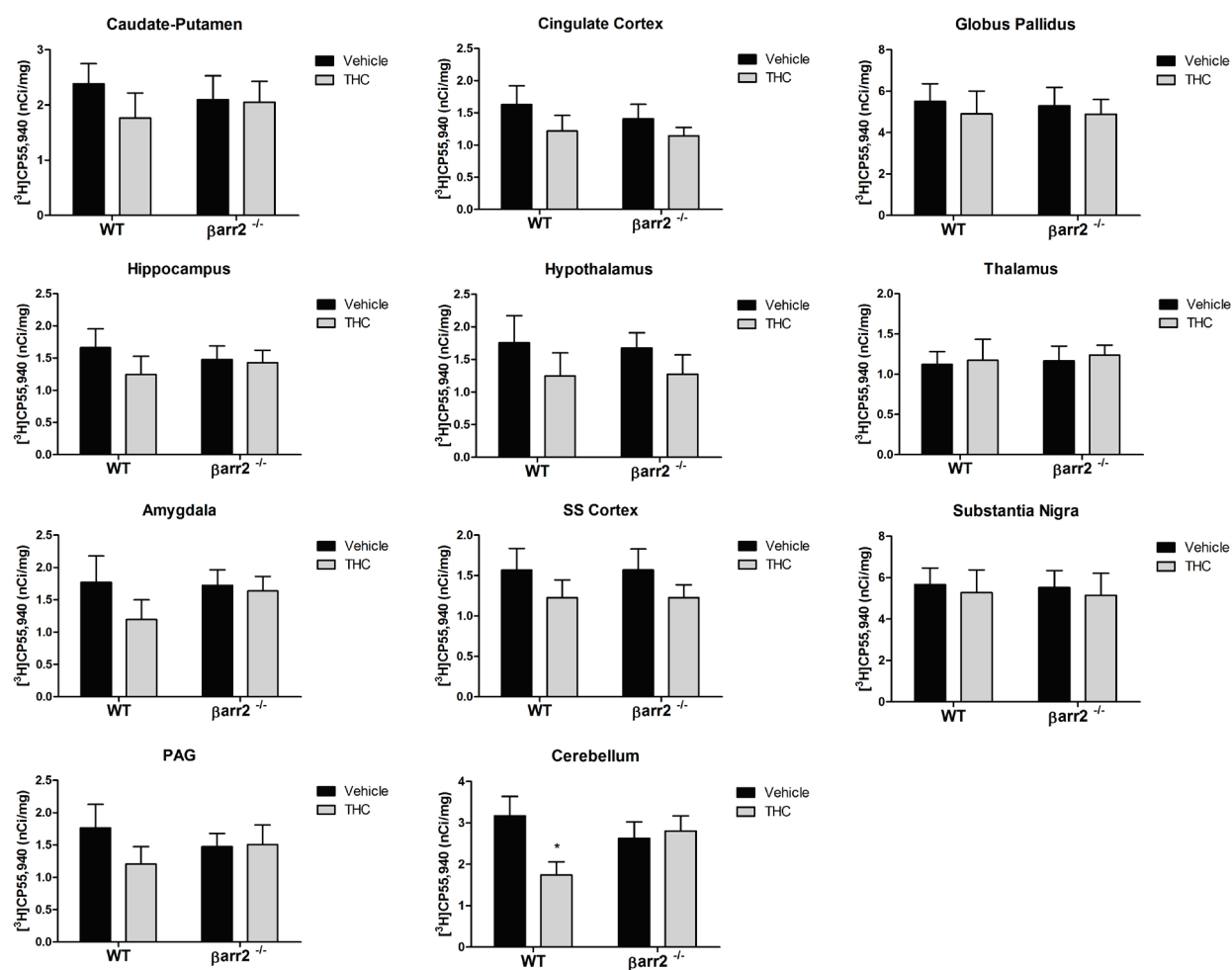


Figure 3.18. [³H]CP55,940 binding values (mean ± SEM) in sampled brain regions (N = 8 per group) from βarr2 WT and KO mice treated 6.5 day with either vehicle or 10 mg/kg THC twice daily.. * *p* < 0.05 versus respective vehicle (Two way ANOVA, Student-Newman Keuls Post-hoc). SS, somatosensory. [³H]CP55,940 autoradiography was performed as described in *Methods*

Table 3.3

[³H]CP55,940 binding values in brain tissue sections from β arr2 WT and KO mice treated 6.5 day with either vehicle or 10 mg/kg THC twice daily (N = 8 per group).

Brain sections were incubated with 3 nM [³H]CP55,940 as described under *Methods*. [³H]CP55,940 binding values represent the mean \pm SEM. $p < 0.05$ versus respective vehicle (Two way ANOVA, Student-Newman Keuls Post-hoc). *CG CTX*, cingulate cortex; *CPU*, caudate-putamen; *GP*, globus pallidus; *PIR CTX*, piriform cortex; *HIPP*, hippocampus; *AMYG*, amygdala; *HYPO*, hypothalamus; *THAL*, thalamus; *SS CTX*, somatosensory cortex; *SN*, substantia nigra; *PAG*, periaqueductal gray; *CBLM*, cerebellum.

| Region | Vehicle | | THC | |
|--------|-----------------|-----------------------------|------------------|-----------------------------|
| | WT | β arr2 ^{-/-} | WT | β arr2 ^{-/-} |
| CPU | 2.39 \pm 0.36 | 2.10 \pm 0.43 | 1.76 \pm 0.46 | 2.05 \pm 0.38 |
| CG CTX | 1.63 \pm 0.29 | 1.41 \pm 0.22 | 1.22 \pm 0.24 | 1.14 \pm 0.13 |
| GP | 5.51 \pm 0.86 | 5.29 \pm 0.89 | 4.90 \pm 1.11 | 4.88 \pm 0.72 |
| HIPP | 1.66 \pm 0.29 | 1.48 \pm 0.21 | 1.24 \pm 0.28 | 1.43 \pm 0.19 |
| HYPO | 1.75 \pm 0.42 | 1.67 \pm 0.23 | 1.25 \pm 0.35 | 1.27 \pm 0.29 |
| THAL | 1.12 \pm 0.16 | 1.17 \pm 0.18 | 1.17 \pm 0.26 | 1.24 \pm 0.12 |
| AMYG | 1.77 \pm 0.40 | 1.72 \pm 0.24 | 1.20 \pm 0.30 | 1.64 \pm 0.22 |
| SS CTX | 1.57 \pm 0.27 | 1.57 \pm 0.25 | 1.23 \pm 0.22 | 1.23 \pm 0.16 |
| SN | 5.66 \pm 0.80 | 5.52 \pm 0.82 | 5.28 \pm 1.09 | 5.15 \pm 1.07 |
| PAG | 1.76 \pm 0.37 | 1.47 \pm 0.21 | 1.21 \pm 0.27 | 1.51 \pm 0.30 |
| CBLM | 3.18 \pm 0.46 | 2.63 \pm 0.40 | 1.74 \pm 0.32* | 2.80 \pm 0.36 |

3.7 Discussion

The overall finding of this study is that β arr2-mediated CB₁ receptor adaptation following chronic THC treatment occurs in a region-specific manner, which was also reflected in differential effects on tolerance. Deletion of β arr2 resulted in the loss of desensitization in the cerebellum, rostral PAG, and spinal cord. In addition, CB₁ receptor downregulation occurred in only the spinal cord and cerebellum, and was attenuated in β arr2 KO animals following chronic THC treatment. Whole-brain analysis using SPM revealed that other brain regions retained the ability to desensitize in β arr2 KO animals following chronic THC treatment, suggesting other potential regulatory mechanisms either compensating for the absence of β arr2 or serving as the primary mediator of desensitization in these specific populations of neurons. For example, the hippocampus, amygdala, and rostral PAG retained the ability to desensitize to chronic THC treatment despite the absence of β arr2. Interestingly, desensitization was found in the hypothalamus and almost all examined cortical regions of β arr2 KO, but not WT animals. Further, a greater magnitude of desensitization was noted in the caudal hippocampus and amygdala of β arr2 KO animals. Regional differences in β arr2-mediated CB₁R adaptation were associated with differential effects on tolerance, where THC-mediated antinociception, but not catalepsy or hypothermia, was attenuated in β arr2 KO mice. These results demonstrate not only inter-regional, but intra-regional differences in the involvement of β arr2-mediated regulation of CB₁ receptor signaling.

Deletion of β arr2 resulted in a region-specific loss in desensitization of CB₁ receptor-mediated G-protein activity after chronic administration of THC. This occurred in the cerebellum, caudal aspects of the PAG, and spinal cord of β arr2 KO animals. This is consistent with previous reports in cell models demonstrating that desensitization of CB₁ receptor-mediated

activation of K_{ir3} channels is dependent on both G-protein receptor kinase 3 (GRK3) and β arr2 (Jin et al., 1999). In addition, other reports have shown decreases in the rate and extent of desensitization of various GPCRs in cells with reduced concentrations of β -arrestin (Mundell and Benovic, 2000; Mundell et al., 1999), and conversely augmentation of desensitization following overexpression of β -arrestin (Pippig et al., 1993). Results from studies in cell models thus demonstrate that when in proximity with other important components of the desensitization machinery (i.e. GRKs), β arr2 plays an important regulatory role in the desensitization of receptors following persistent stimulation with an agonist. Mechanistically, this may also have important implications regarding the development of tolerance. In this study, β arr2 KO mice exhibited an attenuation in tolerance to THC-mediated antinociception, which is related to the loss in CB_1 receptor desensitization in the spinal cord and caudal PAG and loss of downregulation in the spinal cord. These are two brain areas that serve important functions in modulating the perception of pain (Lichtman et al., 1996).

The hippocampus, amygdala, rostral PAG, and lateral entorhinal cortex, were brain areas where desensitization occurred in both genotypes following chronic THC treatment. The finding that desensitization of CB_1 receptor-mediated G-protein can still occur despite deletion of β arr2, suggests that other mechanisms may be present. One possibility is the involvement of the other non-visual arrestin isoform, β arr1, which shares structural similarity (78% amino acid homology) and has a very similar anatomical distribution as β arr2 (Attramadal et al., 1992; Gurevich et al., 2002). In addition, the expression of β arr1 exceeds β arr2 by two to three fold in the CNS (Gurevich et al., 2002). Knockout of either β arr1 or β arr2 results in a viable phenotype, whereas the deletion of both isoforms is embryonic lethal (Kohout et al., 2001). This suggests that either isoform can substitute for the other, however emerging data (reviewed in (DeWire et al., 2007))

and results in this study indicate that they may not completely substitute, since CB₁ receptor desensitization was not present in all examined brain regions.

Unexpectedly, CB₁ receptor-mediated G-protein activity was desensitized in the hypothalamus and cortical regions, including the cingulate, piriform, auditory/visual, and somatosensory cortex, of β arr2 KO animals but not WT animals. In some instances, desensitization was greater in magnitude in particular brain regions in β arr2 KO compared to WT, such as the caudal extent of the hippocampus and amygdala. Thus it appears that deletion of β arr2 enhanced CB₁ receptor desensitization in these particular brain areas. It's interesting to note that the relative abundance of β arr2 is highest and overlaps the expression profile of CB₁ receptors in areas such as the hypothalamus, amygdala, and cortex (Gurevich et al., 2002), suggesting a potential association between deletion of β arr2 and the observed enhancement of desensitization. One possible explanation is that under normal conditions, β arr2 may shift the population of CB₁ receptors toward an inactive state, such that in its absence, the available pool of functional CB₁ receptors are increased. In fact, studies in HEK-293 cells showed that constitutively active CB₁ receptors undergo constitutive endocytosis and recycling to the membrane, with a substantial proportion of CB₁ receptors localized in intracellular vesicles (Leterrier et al., 2004). A subsequent report later showed that this constitutive endocytosis was required for the proper axonal targeting of CB₁ receptors in hippocampal neurons (Leterrier et al., 2006), indicating an important functional role for the constitutive endocytosis and recycling of CB₁ receptors. In other GPCRs, constitutively active mutant isoforms of the 5HT_{2C} serotonin receptor also displayed constitutive endocytosis that was β arr2 dependent (Marion et al., 2004).

If deletion of β arr2 results in an overall increase in the population of functional CB₁ receptors, this may possibly increase the apparent efficacy of an agonist. Potential increases in

the apparent efficacy of cannabinoids in β arr2 KO animals suggest an involvement of β arr2 in the acute regulation of CB₁ receptor signaling. Such increases in the apparent efficacy of an agonist may result in an increase in the magnitude of desensitization. Interestingly, Breivogel et al. found that acute treatment with THC produced greater decreases in body temperature and antinociception in β arr2 KO versus WT mice (Breivogel et al., 2008). This enhancement in the sensitivity of THC was not replicated by other structurally different classes of cannabinoids, including the bicyclic analogue CP55,940, metabolically stable synthetic endocannabinoid derivatives methanandamide and O-1812, and the aminoalkylindole JWH-073. This suggests a possible ligand-specific sensitivity to some cannabinoid *in vivo* effects. Similarly, previous reports utilizing β arr2 KO mice showed greater morphine-mediated hypothermia and enhanced analgesia, with associated increases in μ -opioid receptor-mediated G-protein activation produced by the selective μ -opioid receptor agonist [D-Ala², MePhe⁴, Gly⁵-*ol*]enkephalin (DAMGO) (Bohn et al., 1999). Follow up studies also found ligand-specific prolonged and enhanced antinociceptive responses in β arr2 KO mice upon administration with equipotent doses of morphine and the structurally similar agonist heroin, but not upon administration with etorphine, fentanyl, or methadone (Bohn et al., 2004). Paradoxically, the lower efficacy μ -opioid receptor agonists morphine and heroin generally do not promote receptor internalization yet produces rapid development of tolerance (Finn and Whistler, 2001; Zhang et al., 1998). Similarly, low efficacy cannabinoid agonists such as anandamide and THC induce little internalization compared to higher efficacy cannabinoid agonists such as WIN, CP, HU210, and 2-AG, which promote more rapid and greater internalization (Hsieh et al., 1999; Wu et al., 2008). In the current study, although both genotypes displayed relatively equal degrees of tolerance to THC-mediated hypothermia, significant differences between the genotypes were found within the

vehicle treated groups. Specifically, vehicle treated β arr2 KO animals produced a greater decrease in body temperature compared to WT animals when tested with THC, consistent with results by Breivogel and colleagues (Breivogel et al., 2008). This may also be related to the observation of desensitization in β arr2 KO but not WT animals in the hypothalamus, which is a brain area that likely mediates the hypothermia effects of THC. One possibility is that the increase in apparent efficacy of cannabinoid agonists within the hypothalamus of β arr2 KO mice may unmask desensitization in this brain region, whereas in the wild-type animals reduction in stimulated G-protein activity was only moderate following the current treatment paradigm. Vehicle treated β arr2 KO animals also had greater CP-stimulated G-protein activity compared to WT animals in other brain regions including the hippocampus and cortex, indicating that deletion of β arr2 had enhanced the apparent efficacy of CP in stimulating G-protein activity in these particular brain areas.

Other mechanisms involving second-messenger dependent kinases may also mediate CB_1 receptor desensitization and contribute towards the development of tolerance. In one study, inhibiting cAMP-dependent kinase (PKA) or Src family tyrosine kinase inhibitor reversed THC-induced antinociceptive tolerance (Lee et al., 2003). Further, no effects were seen when inhibiting other kinases, including protein kinase C (PKC), cGMP-dependent protein kinase (PKG), GRK inhibitor, and phosphatidylinositol-3 kinase (PI3-K), indicating involvement of specific kinases in the development of THC-mediated antinociception. The involvement of PKA in mediating antinociceptive tolerance is supported by the fact that there is an enhanced activation of the cAMP pathway in brain regions of animals tolerant to the analgesic effect of THC (Rubino et al., 2000). In a related study, inhibition of PKA reversed tolerance to THC-induced antinociception, catalepsy, and hypoactivity, but not hypothermia (Bass et al., 2004).

The differential effects on cannabinoid tolerance from PKA inhibition suggests involvement of distinct signaling pathways in different neuronal populations. Interestingly, reversal of tolerance to hypoactivity occurred as early as after 1.5 day treatment with THC, whereas for antinociceptive tolerance reversal was apparent after the 6.5 day treatment time point (Bass et al., 2004). The differences in the time course of these two behavioral measures indicate that the relative contribution of PKA in mediating tolerance may vary among different neuronal populations. For example, brain regions involved in pain sensation may predominately involve PKA at a later time point compared to regions subserving motor function in the development of tolerance. Other studies have noted increased basal levels of cAMP and PKA activity in membrane homogenates of striatum, cortex, and cerebellum following chronic administration of THC (Rubino et al., 2000), further suggesting an involvement of PKA during the development of cannabinoid tolerance.

Emerging evidence suggests that phosphorylation-independent mechanisms may also contribute to the regulation of GPCR function (reviewed in (Ferguson, 2007)). In a recent report, GRK2-mediated desensitization and internalization of mGluR5 in striatal neurons occurred independently of receptor phosphorylation, and rather via GRK2 RH domain interactions with $G\alpha_{q/11}$ binding (Ribeiro et al., 2009). GRK2 is highly abundant throughout the CNS and is the most highly expressed GRK isoform in the brain (Arriza et al., 1992). The anatomical co-distribution of CB₁ receptors and GRK2, as well as the subcellular localization of GRK2 in the cytoplasm and presynaptic axon terminals (Arriza et al., 1992), suggest that these two proteins may colocalize and that GRK2 may serve a function in the regulation of CB₁ receptor signaling. This is supported by evidence demonstrating that presynaptic expression of a dominant negative GRK2 reduced desensitization of WIN55,212-2-induced presynaptic inhibition of glutamatergic

neurotransmission in rat hippocampal neurons (Kouznetsova et al., 2002). Further, GRK2 expression is particularly high in regions such as the hippocampus (Murga et al., 1998), which in the current study was a brain region that demonstrated desensitization of CB₁ receptor-mediated G-protein activity (particularly pronounced in the more caudal extent) despite the absence of β arr2. In addition, GRK2 is also abundant throughout the cortex (Arriza et al., 1992). Although the THC treatment paradigm used in this study did not produce desensitization in almost all cortical regions examined (except lateral entorhinal cortex) in WT animals, desensitization was apparent in β arr2 KO animals. It is possible that GRK2-dependent regulatory mechanisms become more prominent following THC treatment in the absence of β arr2.

In this study we have demonstrated region-specific differences in the involvement of β arr2 in the regulation of CB₁ receptor adaptations following chronic administration of THC. In the absence of β arr2, CB₁ receptors in β arr2 KO animals still retained the ability to desensitize and downregulate in specific brain areas, suggesting that additional signaling pathways may also contribute towards its regulation. Moreover, deletion of β arr2 did not attenuate any acute effects of THC, suggesting that it does not mediate THC-induced effects including antinociception, hypothermia, and catalepsy. Involvement of multiple regulatory pathways in different neuronal populations illustrates the complexity and fine tuning of CB₁ receptor signaling. Diverse regulation of CB₁ receptor signaling among highly distinct anatomical brain regions, further support the importance of performing an anatomically inclusive analysis of CB₁ receptor signaling and the power of utilizing a whole-brain unbiased analytical approach. Investigating the complete regulation of CB₁ receptor signaling within various anatomical contexts will further facilitate our understanding of the neuromodulatory role of CB₁ receptors as well as provide

exciting therapeutic avenues in the design of drugs for the selective enhancement and/or attenuation of tolerance development of specific cannabinoid-mediated effects.

VII. Conclusion and Perspectives

In the preceding studies we proposed that regional-differences in the acute and chronic signaling of CB₁ receptors reflect differences in its regional regulation, and that this specificity would be revealed using a novel whole-brain unbiased approach. This was successfully accomplished by adapting Statistical Parametric Mapping (SPM) to study CB₁ receptors in reconstructed mouse brain images derived from autoradiographic data, which previously has not been described. Using this approach to investigate the acute signaling properties of CB₁ receptors, regional differences in the relative efficacy of cannabinoid agonists were demonstrated. In addition, the aminoalkylindole WIN55,212-2 (WIN), activated G-protein coupled non-CB_{1/2}/GPR55 sites in specific brain regions that partially overlapped with CB₁ receptor containing regions. Moreover, the presence of these putative novel sites in brainstem nuclei, including the lateral dorsal tegmental nuclei and locus coeruleus, suggest a possible role in regulating the release of neurotransmitters such as acetylcholine and norepinephrine, respectively. Regional differences in the relative efficacy of cannabinoid agonists to produce CB₁ receptor-mediated G-protein activation suggests unique signaling properties of the CB₁ receptor within various brain areas. This may have important implications regarding the chronic regulation of CB₁ receptors, as well as the development of cannabinoid tolerance, particularly if the contribution of different regulatory mechanisms has regional-specificity. Another possible explanation for regional differences in CB₁ receptor regulation is the co-localization of CB₁ receptors with specific signaling or regulatory proteins. This question was investigated by examining the role of β -arrestin-2 (β arr2) on CB₁ receptor adaptation using a β arr2 knockout (KO) mouse model. Interestingly, studies using β arr2 KO animals showed that involvement of

β arr2 in the regulation of CB₁ receptor adaptations, including desensitization of receptor-mediated G-protein activity and downregulation of CB₁ receptors, have regional-specificity as well. Deletion of β arr2 resulted in a loss of desensitization in the cerebellum, caudal PAG, and spinal cord, with a corresponding attenuation in THC-mediated antinociception. However in regions such as the amygdala and rostral hippocampus, desensitization was found in both genotypes and did not differ in magnitude. Unexpectedly, in regions such as the hypothalamus, caudal hippocampus, and cortex, desensitization appeared to be enhanced in β arr2 KO mice. CB₁ receptor downregulation was found only in the cerebellum and spinal cord of wild-type mice after chronic treatment with THC, and this was lost in β arr2 KO mice. Tolerance to THC-mediated catalepsy and hypothermia were further unaffected in the absence of β arr2. Collectively, these results in β arr2 KO mice suggest that β arr2 may play a role in the regulation of CB₁ receptor signaling in specific brain areas, whereas in other brain regions different mechanisms of regulation may exist with anatomical and perhaps temporal specificity.

Regional differences in the signaling and regulation of CB₁ receptors is not perhaps surprising, given the highly diverse cellular architecture, and its co-localization and interaction with various signaling components. From a biological and signaling perspective, this might be expected for a highly abundant GPCR in the CNS that has an important neuromodulatory function in the fine tuning and physiological action of other receptor systems. Due to the high degree of interaction of CB₁ receptors with other functionally distinct receptor systems, complex and overlapping pathways likely exist to regulate and fine-tune cannabinoid-mediated signaling.

Studies in CB₁ KO mice demonstrated that non-CB_{1/2}/GPR55 sites exhibited a unique pharmacology and neuroanatomical localization. One important question is the functional relevance of non-CB₁ sites. For example, given the anatomical localization and systems

connectivity of non-CB_{1/2}/GPR55 sites in the cortex and its afferent projections from the locus coeruleus and amygdala, one hypothesis is that these putative novel cannabinoid sites may modulate behaviors such as attention or emotional learning. Another unanswered question is the potency and efficacy of WIN at non-CB_{1/2}/GPR55 sites revealed by SPM analysis. Thus, full concentration-effect curves using WIN or structurally similar agonists in these specific regions is needed. Perhaps most important would be the molecular identification and cloning of this putative novel cannabinoid receptor, which might be assisted by results in this dissertation mapping the functional distribution of non-CB_{1/2}/GPR55 sites. Identification of "WIN-binding" sites, which is probably one of several apparently distinct novel cannabinoid sites, may reveal unique physiological roles of the endocannabinoid system and its therapeutic exploitation.

SPM analysis revealed a number of interesting observations from chronic THC studies using β arr2 KO mice, and results have generated multiple questions regarding the regulation of CB₁ receptor signaling. For example, to what extent is β arr1 involved in mediating CB₁ receptor adaptations to chronic THC treatment? Do second-messenger dependent kinases contribute to the development of tolerance of some THC-mediated effects, and if so can it be reversed in β arr2 KO mice if we disrupted these kinase-dependent pathways? What is the time course of action for adaptation through other putative regulatory mechanisms in β arr2 KO mice and how does it vary by brain region? Interestingly, deletion of β arr2 resulted in an enhancement of desensitization in areas such as the hippocampus. What role does β arr2 play in learning and memory? These are a few important and exciting questions that will further our understanding of the regulation of CB₁ receptor signaling.

Whole-brain based analytical approaches are not only important to the study of CB₁ receptor signaling, but other receptor systems as well. Voxel-based analyses provide an

unprecedented level of anatomical precision, which is highly suitable for answering questions and investigating the nature of receptor signaling among various distinct populations of neurons. Doing so may potentially give important insight as to the physiological function and role of receptors and/or their signaling proteins. This is particularly advantageous for the cannabinoid system due to its neuromodulatory role and widespread abundance throughout the CNS. In addition, this paradigm allows an important translation of knowledge gained from mechanistic studies in well defined cellular systems into different anatomical contexts within the brain. Such an approach can be termed "Functional Anatomic", inspiring the next step in the study of biological systems. Fundamentally speaking, this concept is similar to other large-scale data mining paradigms including proteomics, functional genomics, lipidomics, bioinformatics, etc. One interesting idea would be the integration of gene expression databases, such as the Allen Brain Atlas, to identify potential interactions or involvement of specific proteins, for example based on their overlapping subcellular localization in different brain regions.

Understanding the relationship between structure and function within the human brain as well as the integration of distinct neuronal populations has historically been a challenging effort. Yet, accumulating evidence of receptor functional selectivity further points to the importance of understanding the regulation of signal transduction within various anatomical contexts. Studies in this dissertation demonstrated regional specificity in the acute and chronic signaling and regulation of CB₁ receptors in the reconstructed mouse brain. These results not only highlight the importance of performing an anatomically inclusive analysis, but suggest that mechanisms of CB₁ receptor signaling and regulation are diverse among different neuronal populations. This has extremely important implications in regard to understanding the cannabinoid system in relevance to human health and disease, as well as the potential design of cannabinoid-based therapeutics to

maximize clinical efficacy and minimize their side effects. It is important to note that repeated use of cannabinoids for management of chronic clinical conditions, such as multiple sclerosis, pain, etc., is susceptible to the development of tolerance, and possibly dependence and addiction. Because of diverse CB₁ receptor regulatory mechanisms among various brain regions, tolerance is likely to develop differentially for various cannabinoid-mediated effects with respect to relative magnitude, and to its onset and duration following cessation of cannabinoid administration. Lastly, understanding the regional regulation of CB₁ receptor signaling may allow better insight into the possibility of thwarting tolerance to the desired therapeutic effects of cannabinoids.

VIII. Appendix

This section contains supplementary thesis data from various collaborative studies. The reader is referred to the primary reference of each study for further details when appropriate. Supporting information for thesis chapters are also included.

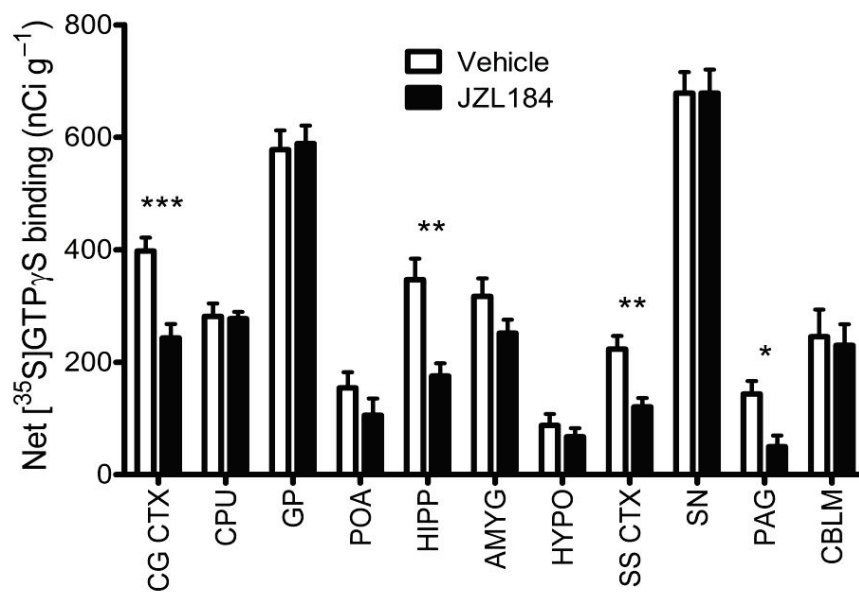
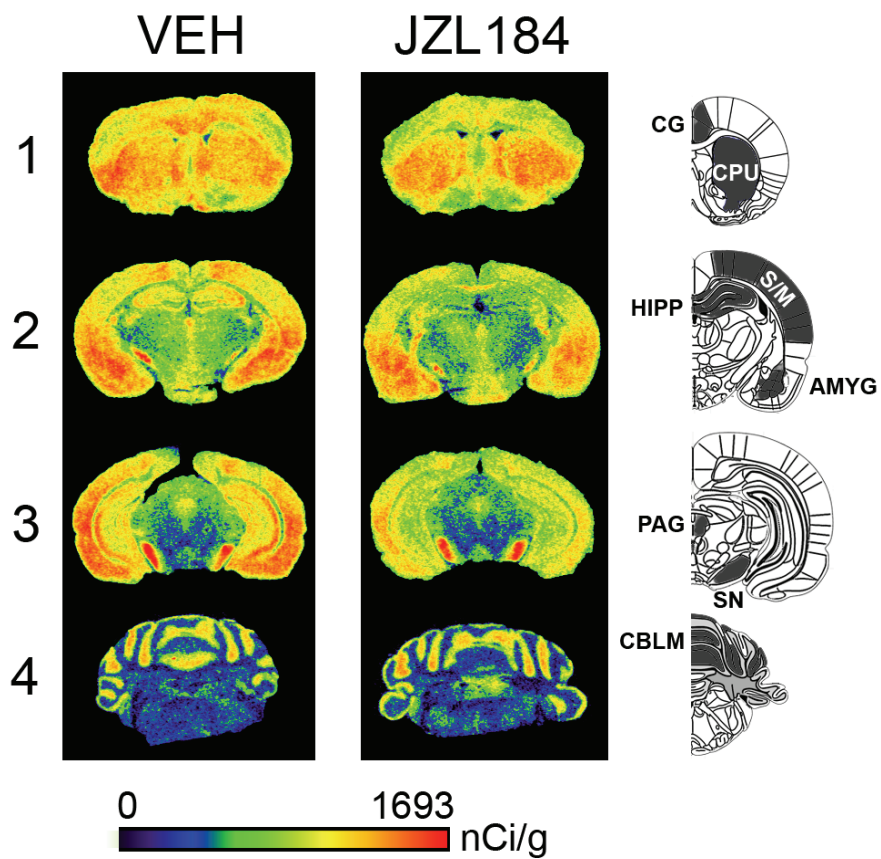


Figure A1. Regional changes in cannabinoid agonist-stimulated [³⁵S]GTPγS binding following chronic disruption of MAGL by the MAGL inhibitor JZL 184. (Top) Representative autoradiograms showing CP55,940-stimulated [³⁵S]GTPγS binding in coronal brain sections following either chronic vehicle (left column) or JZL 184 (right column) treatment. Pseudocolor images indicate levels of receptor-mediated G-protein activity and highlight significant decreases in CB₁ receptor activation in the cingulate cortex (CG CTX, row 1), hippocampus (HIP, row 2) and periaqueductal gray (PAG, row 3), while no differences are apparent in the caudate-putamen (CPU, row 1) or cerebellum (CBLM, row 4). Colors correspond to a quantitative scale depicting [³⁵S]GTPγS binding values (nCi/g). Line cartoons in the rightmost column are shown for anatomical reference and areas shaded in gray are sampled regions of interest (Bottom) Densitometric analysis of CP55,940-stimulated [³⁵S]GTPγS binding in selected brain regions, including: cingulate cortex (CG CTX), caudate putamen (CPU), globus pallidus (GP), preoptic area of the hypothalamus (POA), hippocampus (HIP), amygdala (AMYG), hypothalamus (HYPO), somatosensory cortex (SS CTX), substantia nigra (SN), periaqueductal gray (PAG), & cerebellum (CBLM). Data are presented as means ± SEM (N = 8 per group, sampled in triplicate slices for each targeted region). * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$ versus vehicle treatment for specific region (Student's t-test).

Work in collaboration with Dr. Liu's laboratory (Medical College of Wisconsin), Dr. Lichtman's laboratory (Virginia Commonwealth University), and Dr. Cravatt's laboratory (Scripps Research Institute).

Source: Chronic monoacylglycerol lipase blockade causes functional antagonism of the endocannabinoid system. J.E. Schlosburg, J.L. Blankman, J.Z. Long, D.K. Nomura, B. Pan, S.G. Kinsey, P.T. Nguyen, D. Ramesh, L. Booker, J.J. Burston, E.A. Thomas, D.E. Selley, L.J. Sim-Selley, Q. Liu, A.H. Lichtman, B.F. Cravatt. 2010. *In press, Nature Neuroscience.*

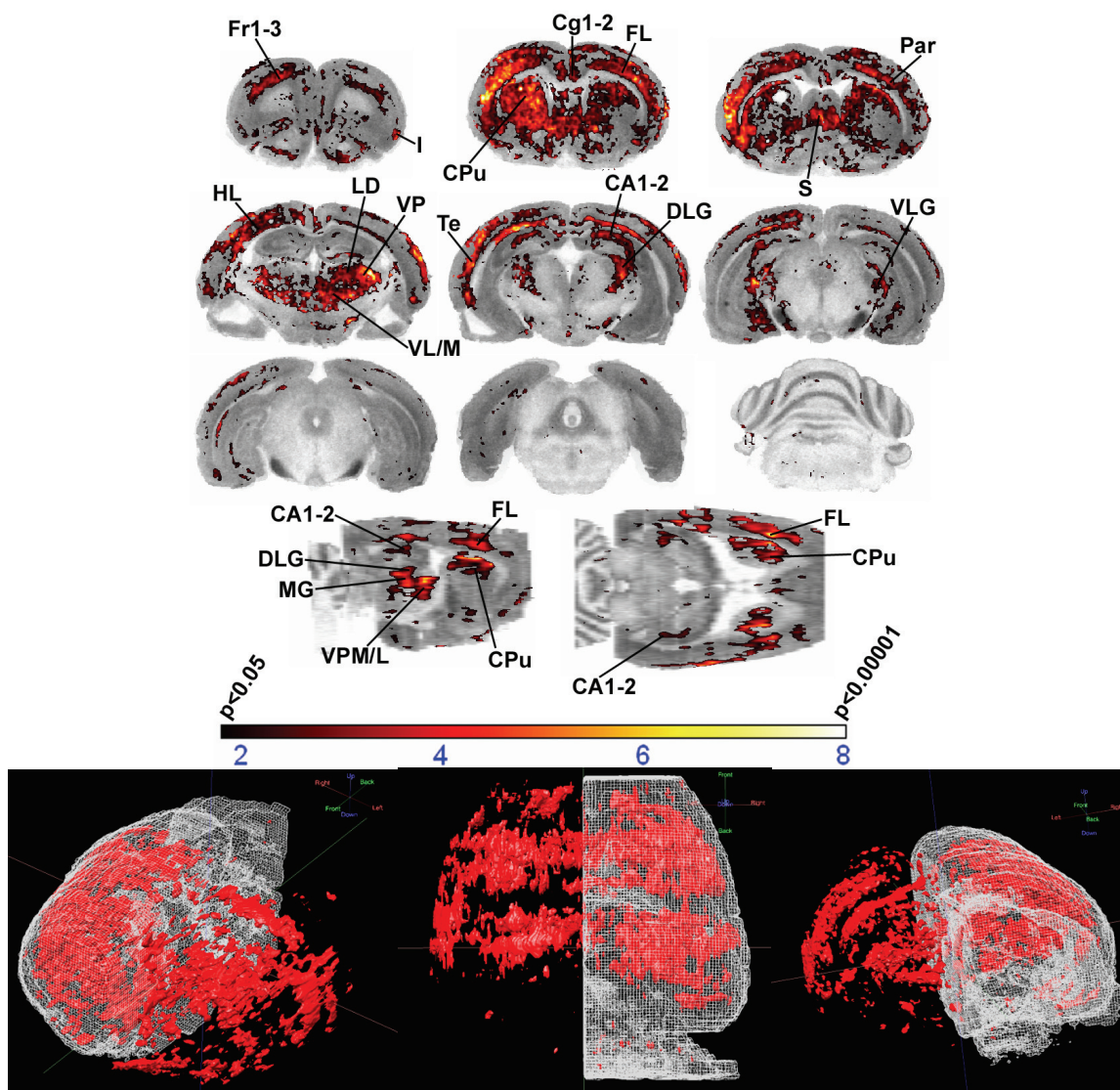


Figure A2. Statistical Parametric Mapping (SPM) reveals greater CB_1 receptor-mediated activity in epileptic animals versus controls in discrete forebrain regions. SPM analysis illustrates regions with significantly greater net WIN55,212-2-stimulated $[^{35}S]GTP\gamma S$ binding in epileptic rats when compared to control. Representative coronal sections (top panel) and volumetric rendered images (bottom panel) illustrate the spatial extent of differences in magnitude of G-protein activation shown as colored overlays (red to yellow) that correspond to significance level. Fr1-3 (frontal cortex, areas 1-3), I (insular cortex), Cg1-2 (cingulate gyrus, areas 1-2), CPU (caudate putamen), FL (forelimb cortex), S (septum), Par (parietal cortex), HL (hindlimb cortex), LD (laterodorsal thalamic nucleus), VL/M (ventrolateral/medial thalamic nuclei), Te (temporal cortex), hippocampal area CA3, DLG (dorsal lateral geniculate nucleus), VLG (ventral lateral geniculate nucleus), MG (medial geniculate nucleus), VPM/L (ventral posterolateral/medial thalamic nuclei).

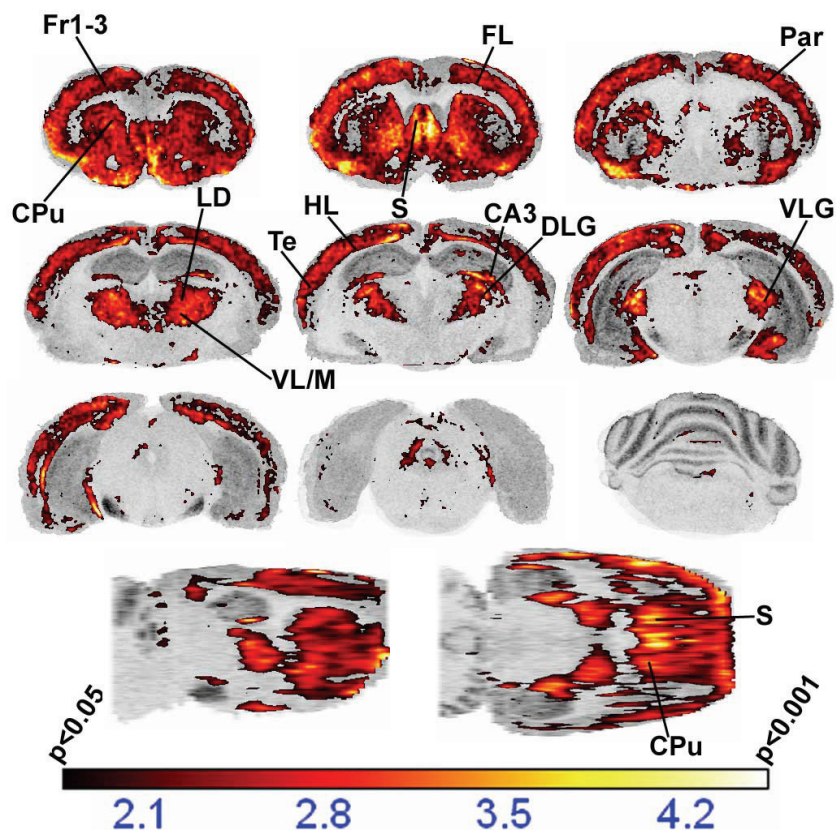


Figure A3. Statistical Parametric Mapping (SPM) reveals increases in CB₁ receptors in discrete forebrain regions of epileptic animals versus controls. SPM analysis illustrates regions with greater total [³H]WIN55,212 binding in epileptic rats when compared to control. Representative coronal sections and volumetric rendered sagittal and transverse images illustrate the spatial extent of differences in magnitude of CB₁ receptor binding shown as colored overlays (red to yellow) that correspond to significance level. Fr1-3 (frontal cortex, areas 1-3), I (insular cortex), Cg1-2 (cingulate gyrus, areas 1-2), CPu (caudate putamen), FL (forelimb cortex), S (septum), Par (parietal cortex), HL (hindlimb cortex), LD (laterodorsal thalamic nucleus), VL/M (ventrolateral/medial thalamic nuclei), Te (temporal cortex), hippocampal area CA3, DLG (dorsal lateral geniculate nucleus), VLG (ventral lateral geniculate nucleus), MG (medial geniculate nucleus), VPM/L (ventral posterolateral/medial thalamic nuclei).

Table A1. Region of interest (ROI) analysis reveals increases in specific [³H]WIN55,212 binding and net WIN55,212-stimulated [³⁵S]GTP γ S binding in forebrain regions of epileptic animals. ROI analysis was conducted and compared to SPM to evaluate increases in [³⁵S]GTP γ S binding observed in epileptic animals. Overall, several regions were confirmed using ROI analysis, such as the stratum radiatum of the hippocampus, whole thalamus, and caudate putamen. * $p < 0.05$, Student's two-sample t -test.

| Region | ³ H]WIN binding (nCi/mg) | | Net [³⁵ S]GTP γ S binding (nCi/g) | |
|----------------------|-------------------------------------|--------------|--|-----------|
| | Control | Epileptic | Control | Epileptic |
| Whole Hippocampus | 2.10 ± 0.35 | 2.80 ± 0.23 | 290 ± 39 | 370 ± 26 |
| Stratum Radiatum | 1.92 ± 0.32 | 3.33 ± 0.35* | 366 ± 38 | 513 ± 28* |
| Whole Thalamus | 0.50 ± 0.15 | 1.04 ± 0.18* | 130 ± 21 | 239 ± 28* |
| Cerebellum Mol Layer | 4.30 ± 0.72 | 4.38 ± 0.42 | 409 ± 43 | 436 ± 24 |
| Substantia Nigra | 5.20 ± 1.00 | 5.04 ± 0.67 | 789 ± 43 | 754 ± 50 |
| Caudate Putamen | 1.37 ± 0.20 | 2.40 ± 0.32* | 293 ± 46 | 436 ± 19* |
| Globus Pallidus | 4.39 ± 0.84 | 5.70 ± 0.87 | 969 ± 55 | 736 ± 51* |
| Cingulate Cortex | 1.52 ± 0.23 | 2.33 ± 0.27* | 354 ± 44 | 236 ± 53 |
| Periaqueductal Gray | 0.62 ± 0.15 | 0.80 ± 0.11 | 173 ± 31 | 58 ± 15* |
| Deep (HL) Cortex | 1.30 ± 0.29 | 3.55 ± 0.28* | 396 ± 45 | 506 ± 42 |
| Entorhinal Cortex | 0.86 ± 0.10 | 1.53 ± 0.21* | 464 ± 72 | 329 ± 51 |

Data presented in Figures A2 and A3, and Table A1 were done in collaboration with Dr. Falenski in Dr. DeLorenzo's laboratory (Virginia Commonwealth University).

Source: Statistical Parametric Mapping of the Regional Alterations in Cannabinoid CB₁ Receptor Expression, Binding, and G-Protein Activation in the 3D Epileptic Rat Brain. Falenski KW, Nguyen PT, Sim-Selley LJ, DeLorenzo RJ. 2010. *Manuscript in preparation.*

Table A2. Internet links to downloadable analytical software and resources on brain imaging

| Software | |
|----------------------|--|
| ImageJ | http://rsbweb.nih.gov/ij/ ImageJ is a multi-operating system (MAC, PC, Linux) image analysis suite with an online library of plugins that are created and updated by an extensive user base. |
| MRICro/MRIcron | http://www.cabiatl.com/mricro/ MRIcron (MRICro is the original older name) is a free brain imaging viewer that has 3D rendering capabilities, region/volume of interest creation, and image header viewing/editing functions. MRIcron can also overlay results from SPM analyses (i.e. SPM statistical maps) onto reference brain images |
| Spamalize | http://brainimaging.waisman.wisc.edu/~oakes/spam/spam_frames.htm Image viewer that has 3D volumetric rendering capabilities. Requires the program IDL |
| SPM | http://www.fil.ion.ucl.ac.uk/spm/ Statistical Parametric Mapping (SPM) homepage also includes documentation, bibliography, and links to download the free software (requires the program Matlab). |
| Documentation | |
| Brain imaging wikis | http://imaging.mrc-cbu.cam.ac.uk/imaging/CbuImaging Wiki on image preprocessing, SPM beginner tutorials and documentation http://en.wikibooks.org/wiki/SPM Another SPM wiki |
| SPM Forum | https://www.jiscmail.ac.uk/cgi-bin/webadmin?A0=spm SPM community forums |

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Vita

Peter Tiendung Nguyen was born on September 22, 1980, in San Gabriel Valley, California. Peter graduated from Nogales High School, La Puente, California, in 1998. He then attended the University of California Irvine, Irvine, California, and graduated in 2003 as a double major in Chemistry and Biological Sciences. In 2004, Peter began his physician-scientist M.D./Ph.D. training at the Medical College of Virginia (MCV) Campus, Virginia Commonwealth University (VCU) School of Medicine, Richmond, Virginia. He entered the Neuroscience Graduate Program in 2006 through the Department of Pharmacology and Toxicology and began his dissertation work on cannabinoid receptors in the laboratory of Dr. Laura Sim-Selley. Peter will defend his dissertation and begin the clinical year of his medical training in August of 2010.

Peter has presented abstracts at several national and international scientific conferences, including the International Cannabinoid Research Society, Society for Neuroscience, Experimental Biology (The American Society for Pharmacology and Experimental Therapeutics), American Physician Scientists Association, and the Association of University Professors of Neurology. He was on the MCV Campus X-Ray yearbook staff from 2005-2008, where he served as Editor-in-Chief during the last two years and established the first web-based yearbook production platform at MCV in collaboration with Jostens publishing. He was also an executive board member of the MCV Campus Student Government Association from 2006-2008 and participated in committees including the establishment of student services in the new Hunton Student Center and newly renovated Larrick Student Center. In 2007, he created the official Neuroscience Graduate Program website and has served as webmaster. Peter has received awards and recognition, including multiple student travel awards and honors at scientific conferences, recognition at VCU Watts Day and at the Central VA Society for Neuroscience symposium, VCU University Service Award, induction into Phi Kappa Phi honor society, and the Anthony Ambrose and Lauren A. Woods awards for the top 3rd year and graduating Ph.D. student in the Department of Pharmacology and Toxicology, respectively. His first publication at VCU, based on initial work with Statistical Parametric Mapping and CB₁ receptors, made the journal cover in the October 2010 issue of *NeuroImage*. He also received a Ruth L. Kirschstein National Research Service Award Predoctoral Fellowship (National Institute of Drug Abuse F30DA023758: 5/08-5/12) entitled "Cannabinoid Regulation of CB₁ Receptor Function".

Research Papers

Nguyen PT, Schmid C, Raehal K, Selley DE, Bohn L, Sim-Selley LJ. 2010. Beta-arrestin 2 regulates CB1 receptor desensitization and downregulation and THC-mediated antinociceptive tolerance. *Manuscript in preparation*.

Falenski K, **Nguyen PT**, Sim-Selley LJ, DeLorenzo R. 2010. Statistical Parametric Mapping of the Regional Alterations in Cannabinoid CB₁ Receptor Expression, Binding, and G-Protein Activation in the 3D Epileptic Rat Brain. *Manuscript in preparation*.

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Nguyen PT, Schmid C, Raehal K, Selley DE, Bohn L, Sim-Selley LJ, 2009. Beta-arrestin 2 regulates CB1 receptor desensitization and THC-mediated antinociceptive tolerance. International Cannabinoid Research Society 19th Meeting. *Oral Presentation*.