

Cocaine Abuse in Humans Is Not Associated with Increased Microglial Activation: An 18-kDa Translocator Protein Positron Emission Tomography Imaging Study with [^{11}C]PBR28

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Basic science investigations have consistently shown that repeated exposure to psychostimulant drugs, such as cocaine, activate the immune response and lead to inflammatory changes in the brain. No previous *in vivo* studies have confirmed this observation in chronic cocaine-abusing humans. To test this hypothesis, we used positron emission tomography imaging to measure the binding of [^{11}C]PBR28 to the 18 kDa translocator protein (TSPO), a marker for microglial activation in a group of 15 recently abstinent cocaine abusers and 17 matched healthy controls. [^{11}C]PBR28 volumes of distribution expressed relative to total plasma ligand concentration (V_T) were measured in subjects with kinetic analysis using the arterial input function. Subjects were also genotyped for the *TSPO* alanine147 threonine (Ala147Thr, rs6971) polymorphism that has been shown to influence the *in vivo* binding of PBR28 to TSPO. Consistent with previous reports, the *TSPO* Ala147Thr genotype predicted the *in vivo* binding of [^{11}C]PBR28. No significant differences in [^{11}C]PBR28 V_T were observed in the cortical and subcortical regions in cocaine abusers compared with healthy controls. The results of this *in vivo* study do not support increased TSPO expression and, by extension, microglial activation in chronic cocaine-abusing humans. Further research with more direct markers of microglial activation is necessary to conclusively rule out neuroinflammation in cocaine dependence.

Key words: [^{11}C]PBR28; cocaine dependence; inflammation; PET; TSPO

Introduction

Positron emission tomography (PET) imaging studies have demonstrated decreased dopamine transmission in the striatum of chronic cocaine abusers relative to healthy comparison subjects (Volkow et al., 1997; Malison et al., 1999). These reports have been furthered with data suggesting that less dopamine release is associated with higher relapse rates in cocaine abusers (Martinez et al., 2007, 2011). One possible mechanism that contributes to decreased dopamine transmission in cocaine abuse may involve activation of microglia in the brain (Lee et al., 2009; Yao et al.,

2011). For example, inflammatory cytokines released by activated microglia (and astrocytes) have been shown to decrease dopamine synthesis and release by a variety of mechanisms, such as oxidization of tetrahydrobiopterin, a cofactor involved in the dopamine synthesis pathway; altering the expression and function of the vesicular monoamine transporter, Type 2 and dopamine transporter; and enhancing the production of kynurenic acid, which in turn decreases glutamate transmission and impacts dopamine release (for detailed review, see Felger and Miller, 2012). Little et al. (2009) investigated this issue in postmortem human brain tissue and reported a twofold to fourfold increase in activated microglia and macrophages in the anterior midbrain of cocaine abusers compared with controls. No previous *in vivo* studies have reported on whether or not there is an increase in activated microglia in the brains of cocaine abusers.

To evaluate this issue, we used [^{11}C]PBR28 and PET to contrast the *in vivo* status of the 18 kDa translocator protein (TSPO) in 15 cocaine abusers and 17 healthy comparison subjects matched for age, gender, race, and nicotine smoking status. TSPO, which is a high-affinity cholesterol transporter located in the mitochondrial membrane of steroid-producing cells, is an ideal target because it is upregulated in activated microglia in inflammation (Imaizumi et al., 2007; Ching et al., 2012). Thus, increased TSPO binding in cocaine abusers would indicate greater activated microglia and triggering of the inflammatory

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cascade of the brain. Furthermore, the localization of increased TSPO in brain regions, such as the midbrain, striatum, and prefrontal cortex, which are part of the mesolimbic dopaminergic pathways and implicated in addiction, would suggest a role for inflammation in decreased dopamine transmission in cocaine dependence.

Materials and Methods

Human subjects. Thirty-two subjects were enrolled in this study who were either cocaine abusers ($n = 15$) or healthy comparison ($n = 17$) subjects. The study was conducted following the approvals of the University of Pittsburgh Institutional Review Board and Radioactive Drug Research Committee. All subjects provided written informed consent. Cocaine abusers were recruited through flyers displayed at local community centers, buses, and addiction medicine clinics. Study criteria for cocaine abusers were as follows: (1) males or females between 18 and 55 years of age, of all ethnic and racial origins; (2) fulfill DSM-IV criteria for cocaine dependence as assessed by SCID; (3) a positive urine screen for cocaine; (4) no DSM-IV Axis I disorder other than cocaine abuse or dependence, including abuse or dependence to alcohol or other drugs (nicotine dependence was allowed); (5) no current (as confirmed by urine drug screen at screening) use of opiates, cannabis, sedative-hypnotics, amphetamines, MDMA, and PCP; (6) not currently on any prescription or over-the-counter medications; (7) no current or past severe medical or neurological or infectious illness as assessed by a complete medical assessment, which included a review of past medical records, complete physical examination, electrocardiogram, blood and urine tests; (8) not currently pregnant; (9) no history of significant radioactivity exposure (nuclear medicine studies or occupational exposure); and (10) no metallic objects in the body that are contraindicated for MRI. All eligible cocaine-dependent subjects completed a minimum of 14 days of outpatient abstinence monitored with witnessed urine toxicology (all subjects underwent urine drug screens for cocaine and other recreational drugs 3 times per week for 2 consecutive weeks) before the PET scan. Healthy control subjects with no past or present neurological or psychiatric illnesses, including substance abuse, underwent the PET scan as outpatients.

Image acquisition and analysis. Before PET imaging, a magnetization prepared rapid gradient echo structural MRI scan was obtained using a Siemens 3 Tesla Trio scanner for determination of regions of interest. MRI segmentation was performed using the automated segmentation tool implemented in the FMRIB Software Library version 4.0 (Smith et al., 2004).

Briefly, [^{11}C]PBR28 was synthesized using the methods reported previously (Briard et al., 2008). The maximum injected mass for [^{11}C]PBR28 was restricted to $\leq 8.7 \mu\text{g}$. PET imaging sessions were conducted with the ECAT EXACT HR+ camera. After a transmission scan, subjects received an intravenous bolus injection of [^{11}C]PBR28 and emission data were collected for 90 min (Fujita et al., 2008). Arterial blood samples were collected for [^{11}C]PBR28 to derive a metabolite-corrected input function. After centrifugation of the samples, plasma was collected and activity measured in 200 μl aliquots on a gamma well counter. Subsets of the samples (1, 2, 4, 10, 20, 40, and 60 min) were processed using high performance liquid chromatography for determination of the fraction of activity corresponding to the parent compound (Fujita et al., 2008). These measured parent fractions were then fitted using a Hill model (Gunn et al., 1998). The input function was then calculated as the product of total counts and interpolated parent fraction at each time point. The measured input function values were fitted to a sum of three exponentials from the time of peak plasma activity and the fitted values were used as the input to the kinetic analysis. The clearance of the parent compound (L/h) was calculated as the ratio of the injected dose to the area under the curve of the input function (Abi-Dargham et al., 1994). The free fraction of radiotracer in the plasma (f_p) was determined by ultracentrifugation as described previously (Gandelman et al., 1994).

PET data were reconstructed and processed with the image analysis software MEDx (Sensor Systems) and SPM2 (www.fil.ion.ucl.ac.uk/spm) as de-

scribed previously (Narendran et al., 2009). Frame-to-frame motion correction for head movement and MR-PET image alignment were performed using a mutual information algorithm implemented in SPM2. Cortical and subcortical regions of interest were restricted to those that are part of the mesolimbic dopaminergic pathways and implicated in addiction. These regions included the midbrain, limbic striatum (ventral striatum), associative striatum (the precommissural caudate, precommissural putamen, and postcommissural caudate), sensorimotor striatum (postcommissural putamen), dorsolateral prefrontal cortex, orbital frontal cortex, medial prefrontal cortex, anterior cingulate cortex, and medial temporal lobe (which included the amygdala and hippocampus). In addition, the cerebellum, a region that is relatively devoid of dopaminergic receptors, was included in the analysis as a control region. Cortical and subcortical regions of interest were defined on the MRI using a segmentation-based and direct identification method described previously (Abi-Dargham et al., 2002; Martinez et al., 2003). Regional volumes and time-activity curves were then generated in MEDx as outlined previously (Abi-Dargham et al., 2002).

TSPO availability was estimated using the PET outcome measure, V_T , which is total distribution volume expressed relative to total plasma ligand concentration (Innis et al., 2007). [^{11}C]PBR28 V_T can be described as follows:

$$V_T = f_p * \left(\frac{B_{\text{avail}}}{K_D} \right) + V_{ND}$$

where f_p is free fraction in the plasma, B_{avail} is the density of TSPO receptors available to bind to [^{11}C]PBR28, K_D is the equilibrium dissociation constant of [^{11}C]PBR28, and V_{ND} is nonspecific binding. There is no reference region that is devoid of TSPO receptors that can be used to estimate and separate the nonspecific binding component from [^{11}C]PBR28 V_T . However, this is less of an issue because $\sim 95\%$ of [^{11}C]PBR28 V_T in the brain has been shown to represent specific binding (Imaizumi et al., 2008). The TSPO Ala147Thr polymorphism has been shown to predict PBR28 binding affinity in human platelets and brain V_T in a trimodal distribution (high C/C, low T/T, and mixed affinity C/T binders) (Owen et al., 2010, 2012). Thus, all participants were genotyped so that it could be included as a factor in the analysis. The inclusion of genotype as a factor allowed for the detection of differences in TSPO density between cocaine abusers and controls.

DNA analysis. Genomic DNA from all subjects was isolated using QIAamp DNA Blood Mini Kits (QIAGEN), from whole blood samples stored in DMSO. The Ala147Thr SNP (rs6971) was assayed as described previously (Costa et al., 2009). Briefly, a PCR-amplified product was digested with NruI restriction enzyme according to the manufacturer's recommendations, and the digested products separated using 2% agarose gel electrophoresis. For quality control, 3 CEPH samples were sequenced and used as positive controls.

Statistical analysis. Group demographic and baseline scan parameter (such as injected dose, mass, plasma clearance, V_{ND}) comparisons were performed with unpaired t tests. Group differences in V_T were analyzed using a linear mixed-model analysis with regions of interest as a repeated measure, and diagnostic group and genotype as fixed factors (IBM SPSS Statistics). Correlations between [^{11}C]PBR28 V_T and clinical variables, such as duration and amount of money spent on cocaine abuse in addicts, were performed using Pearson Product moment correlation coefficient. A two-tailed probability value of $p < 0.05$ was selected as the significance level for all analyses.

Results

Fifteen cocaine-dependent subjects (8 women and 7 men, mean age 39.9 ± 9.0 years) and 17 healthy comparison subjects (9 women and 8 men, mean age 38.4 ± 8.1 years) were enrolled in this study. Subjects were matched on both ethnicity (cocaine abusers: 8 black and 7 white; healthy controls: 8 black and 9 white) and smoking status (11 smokers/group matched on number of cigarettes smoked per day rounded to the nearest one-half pack, i.e., 10 cigarettes). The genotypes for the TSPO Ala147Thr

Table 1. [^{11}C]PBR28 PET scan parameters^a

Parameter	Healthy comparison subjects ($n = 17$)	Cocaine abusers ($n = 15$)
Injected dose (mCi)	15.8 \pm 0.3	15.6 \pm 0.7
Specific activity (Ci/mmol)	3122 \pm 1556	2731 \pm 1182
Injected mass (μg)	2.1 \pm 0.8	2.5 \pm 1.7
Free fraction (%)	3.4 \pm 0.8	3.2 \pm 1.1
Clearance (L/h)	100.0 \pm 35.8	83.1 \pm 28.8

^aValues are mean \pm standard deviation.

polymorphism that predicts PBR28 binding affinity were not significantly different in patients and controls (cocaine abusers: 8 C/C, high affinity, 5 C/T, intermediate affinity, and 2 T/T, low affinity; controls: 12 C/C, 4 C/T, and 1 T/T; $\chi^2 = 1.12$, $df = 2$, $p = 0.57$). These subjects were not preselected based on their genotype before the PET scans. The distribution of genotype was consistent with that reported in previously published studies when ethnicity is considered.

The cocaine abusers reported smoking crack cocaine on average of 17 ± 7 years and were spending $\$346 \pm 269$ weekly.

Baseline parameters

PET scan parameters are listed in Table 1. [^{11}C]PBR28-injected dose, specific activity at time of injection, and injected mass did not differ between the groups. No significant between-group differences were observed in the clearance rate of [^{11}C]PBR28 from the plasma compartment, or in [^{11}C]PBR28 f_p .

No significant between-group differences were found in the regions of interest volumes determined from the MRI scans (data not shown, all p values ≥ 0.1), suggesting lack of measurable volumetric changes in cocaine abusers.

Measurement of TSPO availability

As shown in Figure 1, significant differences in [^{11}C]PBR28 V_T were observed with TSPO genotype, but not diagnostic group (linear mixed model: effect of diagnosis, $F_{(1,26)} = 0.04$, $p = 0.85$; effect of genotype, $F_{(2,26)} = 14.72$, $p < 0.001$; effect of region, $F_{(9,279)} = 45.80$, $p < 0.001$; genotype \times diagnosis interaction, $F_{(2,26)} = 0.16$, $p = 0.86$). Excluding the low binders from the analysis (linear mixed model: effect of diagnosis, $F_{(1,25)} = 0.35$, $p = 0.56$; effect of genotype, $F_{(1,25)} = 11.26$, $p = 0.003$; effect of region, $F_{(9,252)} = 57.32$, $p < 0.001$; genotype \times diagnosis interaction, $F_{(1,25)} = 0.22$, $p = 0.64$) or using V_T/f_p as an outcome measure (linear mixed model: effect of diagnosis, $F_{(1,26)} = 0.36$, $p = 0.55$; effect of genotype, $F_{(2,26)} = 11.61$, $p < 0.001$; effect of region, $F_{(9,279)} = 49.01$, $p < 0.001$; genotype \times diagnosis interaction, $F_{(2,26)} = 0.25$, $p = 0.78$) did not change the results.

Genotype-corrected correlation analyses revealed no significant associations between [^{11}C]PBR V_T in regions of interest and the duration in years, or amount in dollars of cocaine use.

Discussion

In this PET study, we failed to demonstrate increased [^{11}C]PBR28 binding to TSPO in cocaine abusers compared with matched healthy controls. Previous protein and gene expression data from animals have shown that repeated exposure to psychostimulant drugs, such as cocaine, activate the immune response and lead to inflammatory changes in the brain (for detailed review, see Clark et al., 2013). Based on these data and a postmortem study that reported an increase in activated microglia in the midbrain of chronic cocaine abusers (Little et al., 2009), we evaluated [^{11}C]PBR28 binding to TSPO in cocaine dependence. To the

extent that TSPO expression is a valid marker for activated microglia in the CNS (Venet et al., 2013), the results of this study do not support greater microglial activation in cocaine abusers. An important question, with respect to this negative finding, is whether [^{11}C]PBR28 PET is sensitive enough to detect activated microglia in diseased conditions in humans. In the postmortem studies by Little et al. (2009), a twofold to fourfold increase in activated microglia and macrophages was observed in cocaine abusers compared with controls. Based on prior work that suggests a linear relationship between activated microglia/macrophages and TSPO expression (Venet et al., 2008), this increase in cocaine abusers is within the twofold increase in TSPO specific binding reported in high-affinity binders compared with mixed-affinity binders (Owen et al., 2014). The fact that [^{11}C]PBR28 can robustly distinguish binding (V_T) between high- and mixed-affinity binders suggests that this radioligand is sensitive enough to detect the twofold to fourfold increase in activated microglia reported in postmortem cocaine brains. There are methodological differences that may have contributed to the discordant results between postmortem and human imaging studies. One such difference relates to the inclusion of the brains of cocaine abusers who were actively using cocaine before death as opposed to the inclusion of abstinent cocaine abusers in the imaging studies. Thus, the possibility of microglial activation reverting back to control levels after 14 days of abstinence cannot be ruled out from these imaging data. Another factor that may have contributed to increased microglia in postmortem cocaine brain samples relates to the medical cause of death, such as cocaine overdose, cocaine-related coronary spasm, and cerebrovascular events, acute trauma, etc., despite the best efforts to match control brains on this variable. Finally, the effect of comorbid drug and alcohol abuse in the postmortem cocaine sample, which is difficult to exclude using retrospective interviews, may be contributory as well.

The results of this study in cocaine abusers is in sharp contrast to a [^{11}C]PK11195 imaging study that reported a 264%, 313%, and 1530% increase in TSPO in the midbrain, striatum, and orbital frontal cortex in methamphetamine abusers (Sekine et al., 2008). These results that show greater microglial activation in the mesolimbic dopamine pathway support a role for inflammation in decreased dopamine transmission in methamphetamine dependence. Nevertheless, the use of an unconventional modeling method to arrive at the PET outcome measure, binding potential in this study, limits the conclusions that can be drawn from this dataset. This relates to the use of a normalized [^{11}C]PK11195 time-activity curve from the cortex of healthy controls as a reference-tissue input function to model regions of interest in methamphetamine abusers. The problem with this approach is that it assumed that the nonspecific binding for [^{11}C]PK11195 is the same in controls and methamphetamine abusers. Such an assumption fails to account for any between-group differences that may exist in [^{11}C]PK11195 plasma parameters (e.g., metabolism, plasma clearance, and free fraction) and influx/efflux across the blood–brain barrier (e.g., kinetic rate constants K_1 and k_2), all of which can influence nonspecific binding. Typically, this issue is addressed in clinical PET studies by normalizing the region of interest specific binding in patients and controls to their respective total plasma concentration or reference region nonspecific binding. Furthermore, more recent [^{11}C]PK11195 studies in humans question the presence of a region of reference that is devoid of TSPO and uses clusters of brain voxels with the most rapid tissue clearance to represent nonspecific binding (Turkheimer et al., 2007). Thus, the possibility of specific binding

to TSPO in the cortex leading to a biased between-group comparison in the Sekine et al. (2008) study cannot be ruled out either. We are not able to analyze the current dataset using the methods in Sekine et al. (2008) because [^{11}C]PBR28 has no reference region that is devoid of specific binding. Also, the use of a normalized input function derived from controls to model both patient and control data, which exist in three different TSPO genotypes shown to predict [^{11}C]PBR28 V_T , would lead to assumptions that are further problematic. Another issue that deserves discussion, with respect to the discrepant imaging findings in chronic cocaine and methamphetamine abusers, is the fact that basic investigations consistently suggest greater toxicity to dopamine neurons from methamphetamine than cocaine administration (Ryan et al., 1988; Bennett et al., 1993). Consistent with this notion, rodent studies have shown increased microglial activation and neurotoxicity to dopamine nerve endings in the striatum after chronic methamphetamine, but not cocaine, administration (Thomas et al., 2004). Furthermore, human PET studies are consistent in reporting a reduction in striatal dopamine transporter, a marker that correlates with dopamine neurons, in abstinent methamphetamine but not cocaine abusers (Volkow et al., 1996, 2001; Wang et al., 1997). However, arguing against this is recent PET data that report lower striatal vesicular monoamine transporter, Type 2, which is a more stable and exclusively presynaptic dopamine neuronal marker, in abstinent methamphetamine and cocaine abusers (Johanson et al., 2006; Narendran et al., 2012). Further study of TSPO using rigorous imaging methodology is necessary to confirm the presence of microglial activation reported in methamphetamine dependence.

The strengths of this study are the inclusion of a relatively homogeneous sample of cocaine abusers with no comorbid medical, psychiatric, or drug abuse; monitored abstinence before imaging; the use of [^{11}C]PBR28, a well-validated second-generation TSPO radioligand with relatively high specific binding compared with [^{11}C]PK11195; documentation of TSPO genotype that influences *in vivo* binding; and use of compartmental modeling with an arterial input function to derive PET outcome measures. The limitations of the study are the generalizability of findings because individuals with comorbid disorders were excluded; and inability to rule out between-group differ-

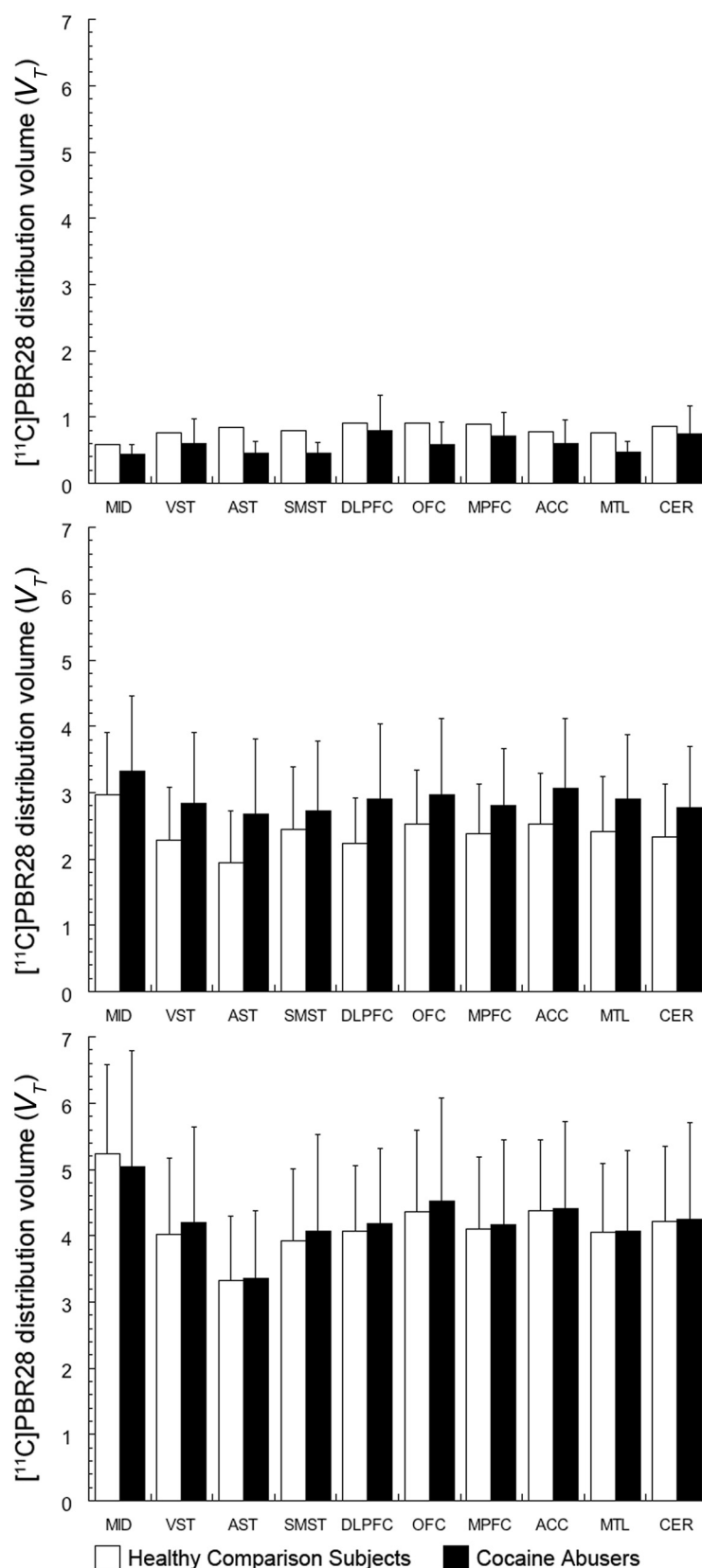


Figure 1. There is no significant difference in [^{11}C]PBR28 V_T in cocaine abusers (black bars, mean \pm standard deviation) relative to healthy comparison subjects (white bars) in low- (top), mixed- (middle), and high-affinity binders (bottom). Consistent with prior reports, TSPO Ala147Thr (rs6971) genotypes predicted [^{11}C]PBR28 binding *in vivo* (low < mixed < high binders, i.e., [^{11}C]PBR28 V_T values in top < middle < bottom). Regions shown include the midbrain (MID), limbic striatum (VST), associative striatum (AST), sensorimotor striatum (SMST), dorsolateral prefrontal cortex (DLPFC), orbital frontal cortex (OFC), medial prefrontal cortex (MPFC), anterior cingulate cortex (ACC), medial temporal lobe (MTL), and cerebellum (CER).

ences in V_{ND} as a possible confound to increased microglial activation in cocaine abusers.

In conclusion, we found no differences in TSPO binding in brain regions that are involved in the mesolimbic dopamine pathway in cocaine abusers compared with controls. The results of these studies question the role of inflammation-mediated mechanisms in decreased dopamine transmission in psychostimulant addiction. Further studies with more direct markers for microglial activation are necessary to conclusively rule out inflammation in cocaine dependence.

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