Calcineurin/NFAT-induced up-regulation of the Fas ligand/Fas death pathway is involved in methamphetamine-induced neuronal apoptosis

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Methamphetamine [METH ("speed")], an abused psychostimulant, can affect psychostimulant, cognitive, and psychomotor impairment in humans. These signs and symptoms are thought to be related to dysfunctions in basal ganglionic structures of the brain. To identify possible molecular bases for these clinical manifestations, we used cDNA microarray technology to measure METH-induced transcriptional responses in the striatum of rats treated with an apoptosis-inducing dose of the drug. METH injection resulted in increased expression of members of the Jun, Egr, and Nur77 subfamilies of transcription factors (TFs), changes that were confirmed by quantitative PCR. Because pathways linked to these factors are involved in the up-regulation of Fas ligand (FasL), FasL mRNA was quantified and found to be increased. Immunohistochemical studies also revealed METH-induced increased FasL protein expression in striatal GABAergic neurons that express enkephalin. Moreover, there were METH-mediated increases in calcineurin, as well as shutting of nuclear factor of activated T cells (NFAT)c3 and NFATc4 from the cytosol to the nucleus of METH-treated rats, mechanisms also known to be involved in FasL regulation. Furthermore, METH induced cleavage of caspase-3 in FasL- and Fas-containing neurons. Finally, the METH-induced changes in the FasL/Fas death pathway were attenuated by pretreatment with the dopamine D1 receptor antagonist, SCH23390, which also caused attenuation of METH-induced apoptosis. These observations indicate that METH causes some of its neurodegenerative effects, in part, via stimulation of the Fas-mediated cell death pathway consequent to FasL up-regulation mediated by activation of multiple TFs.

calcium | neurodegeneration | gelsolin | Egr

Methamphetamine [METH ("speed")], a psychostimulant that is abused throughout the US and the world. Its use can result in euphoria, decreased appetite, and increased alertness, whereas long-term abuse of METH can result in neuropsychiatric complications such as paranoia, coma, stroke, and even death (1, 2). The acute euphoric and intoxicating effects of the drug are thought to be related to the release of dopamine (DA), a neurotransmitter that is very abundant in the mammalian striatum (3). In contrast, the long-term changes that occur in human abusers might be due to neurotoxic or neurodegenerative effects of the drug on monoaminergic terminals (4, 5). Abnormalities that have been implicated in animal models of METH toxicity (6). Recent animal studies have also suggested that METH can damage neuronal cell bodies located in the frontal cortex and striatum (6), abnormalities that might also have an impact on the clinical signs and symptoms observed with chronic abuse of the drug. These suggestions are supported by observations that recovery of indices of DA depletion is not associated with significant improvement in neuropsychological parameters in METH abusers (7) and by reports that METH abusers show metabolic abnormalities in other brain regions in addition to the striatum (8, 9). A recent postmortem study has also provided evidence of METH-induced degeneration of nonmonoaminergic cells in the brains of METH abusers (10). So far, however, only a few studies have tried to unravel the cellular and molecular bases of METH-induced neuronal death. Thus, the purpose of this paper is to report that a dose of METH, known to negatively impact on monoaminergic terminals, can also cause apoptosis in the rat striatum. We also provide evidence that METH-induced cell death depends, in part, on calcineurin/nuclear factor of activated T cells (NFAT)-mediated increases in Fas ligand (FasL) expression and activation of the Fas-dependent apoptotic pathway.

Materials and Methods

Animals and Drug Treatment. Male Sprague–Dawley rats (Charles River Breeding Laboratories), weighing 250–300 g, were used. Experiments were carried out in a room with temperature maintained at 22°C. Rats were housed individually and received food and water ad libitum. Rats were given one injection of either METH (40 mg/kg) or saline i.p. This dose was chosen because it has been shown to cause long-term depletion of monoaminergic terminals in the rat brain (19) and to induce apoptosis in the mouse brain (15, 18). This dose of METH was lethal in the majority of the rats. To assess the effects of a drug known to protect against METH-induced striatal depletion on some parameters measured in the present study, we pretreated some animals with the DA D1 receptor antagonist, SCH2339 (0.5 mg/kg), 30 min before administering a saline or METH injection. Rectal temperature was measured by using a Yellow Springs Instruments (Yellow Springs, OH) telethermometer; see Supporting Text, which is published as supporting information on the PNAS web site, for more details. All animal use procedures were according to the National Institutes of Health Guide for the Care and Use of Laboratory Animals and were approved by the local animal care committee.

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Abbreviations: METH, methamphetamine; DA, dopamine; TF, transcription factor; FasL, Fas ligand; ENK, enkephalin; NFAT, nuclear factor of activated T cells; SP, Substance P; GAD, glutamic acid decarboxylase; Egr, early growth response gene.

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Array and RT-PCR Analyses. For the array experiments, animals were killed 1 h after drug treatment. To confirm some of the array data and to measure the levels of several transcripts, other groups of rats were injected with METH and were killed at various times afterward. Detailed cDNA array preparation and RT-PCR analyses are provided in the Supporting Text. See Table 1, which is published as supporting information on the PNAS web site, for a list of the primers used.

HPLC Measurements. DA and its metabolites were measured by using HPLC with electrochemical detection (see Supporting Text).

TUNEL Histochemistry. Animal death (time points are in Figs. 1–5) and section preparations were performed according to previously reported methods (20). The number of TUNEL-positive cells in the striatum (one side only, randomly chosen) was counted by using a Zeiss fluorescent microscope. For statistical analyses, the total number of TUNEL-positive cells in each rat striatum, at Bregma 1.60, 0.48, and −0.92 mm levels, was added to indicate cell death observed in each individual animal.

Double-Label Immunohistochemistry. To identify the neurotransmitter contents of the cells in which METH induced FasL expression, we carried out double-label immunocytochemical experiments as described in the Supporting Text by using antibodies against NeuN (monoclonal antibody, Chemicon), glutamic acid decarboxylase (GAD), enkephalin (ENK), and Substance P (SP) (polyclonal antibodies from Chemicon), all of which were costained with FasL (polyclonal from Oncogene Research Products; monoclonal from BD Biosciences). We also tested the possibility that FasL and Fas proteins might be expressed in cells that exhibited staining with an antibody against active caspase-3. The antibodies used were a polyclonal anti-cleaved caspase-3 antibody (Cell Signaling Technology, Beverly, MA), a monoclonal antibody against Fas (Santa Cruz Biotechnology), and a monoclonal anti-FasL antibody (BD Biosciences). Animal death and section preparations were performed according to methods published by us (16).

Western Blot Analysis. Nuclear and cytosolic extracts were prepared by using NE-PER nuclear and cytoplasmic extraction reagent (Pierce). The fractions were obtained from individual striatal samples of six animals per time point. The rest of the procedures were essentially as described by us (18). Antibodies used include anticleaved caspase 8 (Cell Signaling Technology), rabbit polyclonal anti-NFATc3; NFATc4; goat polyclonal calcineurin panA (Chemi-con). To confirm equal protein loading, blots were reprobed with α-tubulin antibody (Sigma). Signal intensity was measured by using densitometric analysis and quantitated by using LabWorks, Ver. 4.5 (BioImaging System, Ultraviolet Products).

Statistical Analyses. All data are presented as means ± SEM. The data were analyzed by ANOVA followed by Fisher’s protected least-significant difference test by using the program STATVIEW, Ver. 4.02 (SAS Institute, Cary, NC).

Results

METH Administration Causes Cell Death in the Rat Striatum. METH injections have been reported to cause cell death in the mouse brain via activation of apoptotic mechanisms (13, 18, 20). There is, however, no study that has investigated these processes in the rat striatum. We thus used a dose of METH that has previously been shown (19) to be toxic to monoaminergic systems in the rat to evaluate the possibility that this dose might also cause death of intrinsic striatal neurons. Fig. 1 Upper shows that this dose of the drug did indeed cause the appearance of TUNEL-positive cells in the striatum when examined at various intervals after the injection of the drug. The quantitative data for the appearance of TUNEL-positive cells in the rat brain are also shown in Fig. 1 Lower.

METH Administration Causes Induction of Various Transcription Factors (TFs) in the Rat Striatum. The cDNA array approach was used to identify genes whose transcripts might be regulated in the rat striatum after injection of this toxic METH regimen. We found that several transcripts showed either increases (n = 39) or decreases (n = 22) 1 h after METH injection. Fig. 6, which is published as supporting information on the PNAS web site, shows the cluster analysis of the genes that were affected by METH. These transcripts include genes that fall within multiple functional classes, including genes that code for proteins involved in metabolic pathways, transcriptional regulation, and regulation of apoptosis. The class of TFs includes c-jun, junB, early growth response gene (Egr)-1 and -2, and Nur77, among others (Fig. 6). These results are consistent, in part, with previous observations from experiments in METH-treated rodents (17, 21, 22).

To confirm the array results, we used quantitative PCR to measure transcript levels of the three members of the Jun family of TFs, namely c-Jun, JunB, and JunD. These proteins have been implicated in regulating apoptosis (23). We also extended these studies by using different groups of animals that were killed at various time points after the injection of the drug. Fig. 7, which is published as supporting information on the PNAS web site, shows that these transcripts are affected in a time-dependent fashion. We also confirmed the expression of members of the
induces FasL protein expression in GABAergic neurons that expressed FasL (data not shown). These observations indicate that METH caused increases in FasL mRNA translated to increased protein expression. If so, we hypothesized that METH-induced changes in FasL expression might be due, in part, to METH-induced calcium-mediated calcineurin-dependent NFAT activation (39) followed by increases in FasL mRNA expression (28). These ideas were tested by measuring the levels of NFAT and calcineurin protein levels, because calcineurin-induced NFAT dephosphorylation is essential to NFAT shuttling from the cytoplasm to the nucleus (39, 40), and because calcineurin overexpression has also been shown to predispose neurons to apoptosis (41).

To determine whether the METH-induced changes observed in the various families of immediate early genes might have resulted in up-regulation of FasL, we measured FasL mRNA in the striatum of the rats injected with METH. Fig. 7E shows there were indeed METH-induced increases in the expression of FasL mRNA. These changes reached ~4–5-fold increases in animals killed 2–4 h after METH administration. We also measured possible METH-induced changes in the expression of FasL, ENK, and SP, which is a member of the TNF superfamily (29). As can be seen in Fig. 7E, FasL mRNA levels showed significant decreases at 4 h, reverted to normal by 8 h, and showed small increases at 12 h after METH injection (see Fig. 7E).

We also wanted to know whether the increases observed in FasL mRNA translated to increased protein expression. If so, we wanted to determine in which striatal cell types the increases had occurred. As can be seen in Fig. 2, METH caused increases in FasL in cells that stain for NeuN, GAD, and ENK. However, neither SP- nor somatostatin-containing cells were colabeled with FasL (data not shown). In addition, cells that express markers of the cholinergic system were also not labeled with FasL (data not shown). These observations indicate that METH induces FasL protein expression in GABAergic neurons that express ENK but not in those that express SP.

**METH, Calcineurin, and NFATs.** In addition to Egr, Nur77, and AP-1, NFAT family members have been shown to be involved in the regulation of cytokine expression (35). At present, five members of the NFAT family have been identified. These include NFAT1 (NFATp or NFATc2), NFAT2 (NFATc1), NFAT3 (NFATc4), NFAT4 (NFATc3 or NFATx), and NFAT5 (35, 36). Although originally described in T cells, the NFATs are now known to participate in the regulation of calcium- and calcineurin-mediated transcriptional activity in the nervous system (37). Because both oxidative stress and calcium dysregulation are also involved in causing METH-induced toxicity (38), we reasoned that METH-induced changes in FasL expression might be due, in part, to METH-induced calcium-mediated calcineurin-dependent NFAT activation (39) followed by increases in FasL mRNA expression (28). These ideas were tested by measuring the levels of NFAT and calcineurin protein levels, because calcineurin-induced NFAT dephosphorylation is essential to NFAT shuttling from the cytoplasm to the nucleus (39, 40), and because calcineurin overexpression has also been shown to predispose neurons to apoptosis (41).

**METH Administration Causes Activation of Caspase-3 in FasL- or Fas-Containing Cells.** Because FasL/Fas-induced cell death depends on the formation of a death-inducing signaling complex, which causes the autoproteolytic activation of procaspase-8 with subsequent activation of caspase-3 (42), we also assessed the status of caspase-8 by Western blot analysis. As can be seen in Fig. 4A, there was METH-induced cleavage of caspase-8. These changes in caspase-8 were blocked by pretreatment with SCH23390 (Fig. 4B). We also tested the possibility that FasL and Fas might be expressed on cells that express the penultimate executioner, caspase-3. As shown in Fig. 4B, there were time-dependent increases in FasL expression in the striatum of METH-induced increases in the expression of FasL and caspase-3 in rat striatal cells (Fig. 4B). It is important to note that all sections taken from control rats showed the consistent presence of a few cells that express FasL and active caspase-3, although colocalization of these two proteins was never observed in control animals (Fig. 4B, Saline). Prior treatment with SCH23390 caused significant inhibition of the METH-induced increases in the expression of FasL and caspase-3 in rat striatal cells (Fig. 4B; see Fig. 4D for quantitative data).

Fig. 4C shows METH-induced changes in Fas expression. There was almost no detectable Fas-like immunostaining in the striatum of control rats. However, METH-treated rats showed
against calcineurin A fractions. Time-dependent increases were observed by using antibodies Meth injection completely blocked METH-induced increases in the nuclear contents of NFATc3 and NFATc4. Pretreatment with SCH23390 almost completely eliminated METH expression in striatal cells of METH-treated rats (Fig. 4C; see Fig. 4D for quantitative data).

METH Administration Causes Proteolysis of Caspase-3 Targets. Because activation of terminal caspases leads to the cleavage of several cytoplasmic and nuclear proteins, we investigated the effects of METH on the status of gelsolin and lamin B, which are known targets of these caspases. When cleaved to an active form by caspase-3, gelsolin severs actin filaments and is thought to participate in some of the structural changes observed in the cytoplasm during apoptosis (43). Proteolysis of lamin B is thought to be involved in the nuclear changes observed during apoptosis (44). Fig. 5A shows the cleavage product of gelsolin, with the appearance of the cleaved (85-kDa) band occurring 2 h after METH administration. Fig. 5B shows the cleavage product of lamin B.

Discussion

Apoptosis is a suicide program that is involved in the elimination of superfluous or traumatized cells (45). This process is intimately involved in embryonic development, the maintenance of tissue homeostasis, and adaptive responses to injurious events. Apoptosis is mediated by various molecular pathways that cause the activation of several members of the caspase family of proteolytic enzymes (45). Because these pathways are thought to play intimate roles in the causation or progression of neurodegenerative processes (46), knowledge gleaned from the dissection of these molecular events might influence the development of therapeutic approaches to human disorders characterized by accelerated cell death. Because such an argument is relevant to observations of cognitive deficits reported in patients who abuse METH (1), we have been conducting mechanistic studies aimed at elucidating the molecular and cellular bases of METH-induced neuronal apoptosis observed in vitro and in vivo (see ref. 6 for a recent review). So far, our efforts had identified mitochondria- and endoplasmic reticulum-mediated events as important culprits in causing cell death in the rodent brain (15, 18). Thus, the present observations extend our previous work in mouse by showing that METH can regulate the expression of several pro-death transcripts in the rat striatum. Members of the Egr, AP1, and Nur77 subfamilies of TFs were found to sustain very early and profound METH-induced up-regulation. These increases preceded changes in FasL protein according to a time course that reflects the appearance of cell death in the rat striatum.

Several of the METH-responsive TFs have been shown to participate in various models of apoptosis. These include the Egr, AP1, Nr4a, and NFAT subfamilies of TFs (see above). Of direct relevance to our thesis, these TFs have been shown to be more intimately involved in degenerative processes. The changes in FasL protein occurred according to a time course that reflects the appearance of cell death in the rat striatum.

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early up-regulation of these factors, with subsequent increases in FasL expression. It is also to be noted that NFAT activity can be potentiated by calcium ionophores that cause increases in intracellular calcium (35–37). This occurs through the activation of the calmodulin-dependent phosphatase, calcineurin, which dephosphorylates NFAT and exposes a nuclear localization sequence, with resulting translocation of NFATs from the cytosol to the nucleus (39, 40). Our test of the idea that similar events might occur in the METH toxicity model revealed that METH does cause marked changes in calcineurin levels that were associated with shuttling of NFATc3 and NFATc4 from the cytosol to the nucleus. These results are also consistent with previous reports that METH administration can cause marked increases in glutamate release in the striatum (47), events known to be associated with dysregulation of calcium homeostasis (38). This thesis is also consistent with our previous demonstration (18) that endoplasmic reticulum-mediated events are involved in METH-induced neuronal apoptosis in mice. This suggestion is also supported by our observations that an agent, SCH23390, which causes significant reduction of TUNEL-positive cells in the striatum, can also inhibit METH-induced effects on the calcineurin/NFAT/FasL death cascade. It is of interest to point out that the drug caused complete inhibition of the effects of METH on the dopaminergic system, whereas it caused partial inhibition of the appearance of METH-induced TUNEL-positive cells. These observations suggest there are some differences in the mechanisms involved in METH-induced degeneration of presynaptic terminals and of postsynaptic neurons. These mechanisms might involve METH-induced activation of the mitochondria-dependent death pathway in postsynaptic neurons in mice (20) and in rats (unpublished observations). This discussion is also consistent with the observation that pretreatment with SCH23390 also blocks METH-induced expression of Fas in striatal cells but only partially suppressed activation of caspase-3 (see Fig. 4D). That SCH23390 also blocks METH-induced hyperthermia (see Fig. 8C, which is published as supporting information on the PNAS web site), which is known to play a role in METH-induced striatal DA depletion, might, in part, be relevant to the partial protection that the drug caused against METH-induced neuronal apoptosis.

Fig. 4. METH injection causes significant increases in the expression of FasL and Fas in caspase-3-expressing striatal cells. (A) Western blot analyses were used to measure the effects of METH and SCH23390 on the cleavage of caspase-8. Cleavage of caspase-8 (43 kDa) was detected 2 h after METH injection. Pretreatment with SCH23390 completely blocked these changes. Statistical analyses were conducted as described in the text. *, P < 0.05; **, P < 0.01; ***, P < 0.001, in comparison to the respective control group. Double-labeled experiments showed that METH induced FasL (B) and Fas (C) expression in cells that express the executioner caspase-3.

Fig. 5. METH leads to cleavage of the caspase targets, gelsolin (A) and lamin B (B), in the rat striatum. Analyses were conducted as described in the text. *, P < 0.05; **, P < 0.01; ***, P < 0.001, in comparison with the control group.
It is of interest that immunohistochemical studies showed significant increases in the expression of the Fas protein in the striata of METH-treated animals, whereas Fas mRNA levels showed decreases early after METH injection and only small increases later on. Early decreases in Fas mRNA might be related to compensation or down-regulation of Fas mRNA in response to overstimulation of Fas receptor by FasL, which was induced early by METH. In contrast, the somewhat delayed increase in the expression of the Fas protein might be related to METH-induced posttranslational modifications of the Fas receptor. These posttranslational changes might have led to Fas induced early by METH. In contrast, the somewhat delayed response to overstimulation of Fas receptor by FasL, which was Fas related to compensatory down-regulation of Fas mRNA might be consistent with previous data documenting variable degrees (0.356–0.71) of correlations between mRNA and protein levels in various systems (49, 50).

Conclusion

This paper shows that METH administration can cause calcineurin-mediated shutting of NFAT from the cytosol to the nucleus, with associated increases in the expression of FasL at both transcript and protein levels. In addition, the observation that METH-induced FasL expression and caspase-3 activation are coincident in a specific striatal neuronal subpopulation suggests that FasL expression is induced in enkephalineric neurons on their journey toward death.
