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## Negative Regulator of MAP Kinase is Increased in Depression and Is Necessary and Sufficient for Expression of Depressive Behavior

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### Abstract

Lifetime prevalence (~16%)<sup>1</sup> and the economic burden (\$100 billion annually)<sup>2,3</sup> associated with major depressive disorder (MDD) make it one of the most common and debilitating neurobiological illnesses. To date, the exact cellular and molecular mechanisms underlying the pathophysiology of MDD have not been identified. Here we use whole genome expression profiling of postmortem tissue and demonstrate significantly increased expression of mitogen-activated protein kinase (MAPK) phosphatase-1 (*MKP-1*) in the hippocampal subfields of MDD subjects compared to matched controls. MKP-1, also known as DUSP1, is a member of a family of dual-specificity phosphatases (DUSP) that dephosphorylate both threonine and tyrosine residues and thereby serves as a key negative regulator of MAPK cascade<sup>4</sup>, a major signaling pathway involved in neuronal plasticity, function and survival<sup>5,6</sup>. The significance of altered MKP-1 was tested in rodent models of depression and demonstrates that increased hippocampal MKP-1 expression, as a result of stress or viral-mediated gene transfer, causes depressive behaviors. Conversely, chronic antidepressant treatment normalizes the stress-induced MKP-1 expression and behavior, and mice lacking MKP-1 are resilient to stress. These postmortem and

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### Author Contributions

V.D prepared the original draft of the manuscript and was involved in all aspects of the experimental design and research, including execution of all microarray and molecular experiments, as well as behavioral tests. M.B. conducted behavioral aspects of rat CUS study, assisted with animal surgeries, and was involved in analysis and interpretation of behavioral tests. P.L. was responsible for optimization, construction and preparation of recombinant AAVs. H.D.S. conducted baseline behavior tests in *Mkp-1*<sup>-/-</sup> mice. C.A.S. was responsible for human tissue generation and preparation of relevant human subjects' information tables and methodology. A.A.S. conducted statistical analysis of microarray experiments. S.S.N. assisted in the development and optimization of microarray experiments. R.S.D. was involved in all aspects of study design, data analysis, interpretation of results and preparation of the manuscript and figures. All authors discussed the results presented in the manuscript.

### Competing Financial Interests

The authors declare no financial interests.

preclinical studies identify MKP-1 as a critical factor in MDD pathophysiology and as a novel target for therapeutic interventions.

## Keywords

depression; hippocampus; postmortem; stress; rat; mouse

Brain imaging and postmortem studies have provided evidence of changes in the cellular architecture of several limbic brain regions, most notably atrophy of hippocampal pyramidal neurons and a corresponding reduction in volume of this region in patients with MDD<sup>7–10</sup>. Preclinical studies also demonstrate that stress causes atrophy of the apical dendrites of pyramidal neurons and decreases neurogenesis in the dentate gyrus of the adult hippocampus<sup>11–13</sup>. Such alterations of the structure and function of the hippocampus could contribute to certain aspects of MDD, including disruption of cognition, depressed mood, helplessness, anhedonia, and control of the HPA axis<sup>14–18</sup>.

To characterize the molecular changes underlying the pathophysiology of MDD, we conducted whole genome expression analysis of postmortem hippocampal tissues from 21 depressed patients and 18 healthy controls that were matched for age, gender, tissue pH, and postmortem interval (Supplementary Tables 1 and 2). To decrease tissue heterogeneity, the analysis was conducted on two microdissected (micropunches) hippocampal subfields, the dentate gyrus (DG) granule cell layer and CA1 pyramidal cell layer. Rodent studies have demonstrated that stress causes atrophy of CA3 pyramidal cells, but this cell layer could not be reliably dissected from human sections and therefore was not analyzed. Total RNA was extracted and the resulting cDNA used for whole genome microarray analysis (48,958 probes). We identified *MKP-1* (*DUSP1*) as significantly dysregulated in both the DG (2.3 fold,  $P = 0.038$ ) and CA1 (2.4 fold,  $P = 0.004$ ) of MDD subjects (Fig. 1a). Of the subjects with depression, 12 had a prescription for an antidepressant drug filled in the last month of life, but only one depressed subject had measurable levels of an antidepressant (Supplementary Table 2). Expression levels of other members of the DUSP family were also examined. Levels of *DUSP2* and *DUSP19* were increased in the DG, while *DUSP9*, *DUSP12* and *DUSP24* were significantly regulated in the CA1 (Fig. 1a) (see Supplementary Table 3 for complete list). *MKP-1* was the only DUSP that was significantly increased in both hippocampal subregions. Secondary validation of the microarray results using qPCR confirmed that *MKP-1* mRNA was increased by over two-fold in the DG and CA1 of MDD subjects (Fig. 1b). *MKP-1* expression was also assessed by *in situ* hybridization (ISH) in a separate cohort of MDD subjects and matched healthy controls (Supplementary Table 4). The results showed that levels of *MKP-1* mRNA in the DG and CA1 of MDD subjects are increased by 31% ( $P = 0.016$ ) and 16% ( $P = 0.128$ ), respectively (Fig. 1c).

Because MKP-1 is a major negative regulator of the neurotrophic factor-MAP kinase cascade, other components of this pathway were also examined (Fig. 1d–f). Significant down-regulation of *MEK2* was observed in the CA1 of subjects with MDD, while *ERK2*, a MAP kinase directly regulated by MKP-1, was decreased in the DG. Sustained induction of MKP-1 would lead to inhibition of ERK signaling, which has been demonstrated in previous

postmortem studies of suicide/MDD hippocampus (i.e., decreased levels of phospho-ERK)<sup>19–21</sup>. Moreover, reduced expression levels of other known MAPK signaling target proteins (*MSK1*), downstream transcription factors (*CREB*, *CREBL1*) and growth factor genes (*BDNF*, *VGF*, *VEGF*) were also observed in depressed subjects, consistent with previous reports<sup>22–25</sup>, and could subsequently contribute to the functional consequences of reduced ERK signaling. All of the down-regulated genes contain a cAMP response element (CRE) (Supplementary Table 5), suggesting that decreased MAPK-CREB signaling could account for decreased expression of these genes in MDD. However, most of the genes are decreased in only one hippocampal subfield, and other genes containing a CRE are not regulated in either subfield, indicating that the mechanisms underlying altered gene expression are more complex than a simple reduction in CRE-CREB activity. Together the results indicate a disruption of MAP kinase signaling at multiple levels, including the expression of selected target genes.

To further examine the regulation and function of MKP-1, studies were conducted in a rodent chronic unpredictable stress (CUS) model (Fig. 2a), one of the most valid and relevant models of depression<sup>26–28</sup>. CUS results in depressive-like behaviors, notably anhedonia and helplessness, core symptoms of MDD that are reversed by chronic, but not acute antidepressant administration<sup>26–28</sup>. Exposure to CUS (35 d) decreased sucrose preference and increased escape failures in an active avoidance test, measures of anhedonia and helplessness, respectively (Fig. 2b,  $P < 0.05$ ). Analysis of the different hippocampal subfields shows that CUS exposure causes a significant increase in levels of *Mkp-1* mRNA in the DG (47%,  $F_{1,14} = 22.48$ ,  $P = 0.0003$ ), CA1 (71%,  $F_{1,14} = 27.29$ ,  $P = 0.0001$ ) and CA3 (62%,  $F_{1,14} = 17.30$ ,  $P = 0.001$ ) (Fig. 2c). The results also demonstrate that administration of fluoxetine, which blocks the CUS-induced anhedonia and helpless behavior (Fig. 2b), also reverses the CUS-induced up-regulation of *Mkp-1* mRNA in the DG, and partially normalizes the increase in CA1, but not in CA3 cell layers (Fig. 2c). Two-way ANOVA analysis shows a significant interaction between CUS  $\times$  fluoxetine in the DG and CA1 ( $F_{1,14} = 22.40$ ,  $P = 0.0003$ ;  $F_{1,14} = 8.65$ ,  $P = 0.0107$ , respectively) and a trend in CA3 ( $F_{1,14} = 3.52$ ,  $P = 0.081$ ). CUS animals treated with fluoxetine showed ~30% reductions in *Mkp-1* mRNA levels within both DG and CA1 compared to CUS alone ( $P = 0.0016$  and  $P = 0.023$ , respectively). Neither stress nor fluoxetine had an effect on *Mkp-1* gene expression in the cortex, demonstrating that this is not a global effect (Fig. 2c). A parallel set of animals displaying similar depressive-like behavioral deficits (data not shown) was generated and used for assessing *Mkp-1* protein levels. Western blot analysis performed on whole hippocampal homogenates (Fig. 2d) shows that CUS induced a significant 30% increase in *Mkp-1* protein levels ( $F_{1,16} = 9.36$ ,  $P = 0.003$ ). Although not significant, a trend was observed when assessing the interaction between CUS  $\times$  fluoxetine ( $F_{1,16} = 3.56$ ,  $P = 0.077$ ), indicating that administration of fluoxetine only partially attenuated CUS-induction of *Mkp-1* protein levels. CUS-mediated increases in hippocampal *Mkp-1* mRNA and protein levels suggests a potential role for stress- and depression-induced elevation of adrenal glucocorticoids, which is often observed in MDD patients<sup>29,30</sup>, and consistent with reports that *MKP-1* is a stress- and glucocorticoid-responsive immediate-early gene<sup>31–33</sup>.

Despite the strong evidence that *MKP-1* is dysregulated in MDD and CUS, there is no data linking altered MKP-1 or other DUSP subtypes with depressive behaviors. To directly address this issue, we used both viral vector and mutant mouse approaches to determine the influence of increased expression or deletion of MKP-1 on depression behaviors in rodent models. A viral vector was used to locally express *Mkp-1* in the hippocampal subfields (Fig. 3a). Infusions of rAAV-*Mkp-1* were targeted to the DG cell layer, because of the opposing regulation of *Mkp-1* by CUS and antidepressant treatment (Fig. 2). Viral infusions increased *Mkp-1* primarily in the DG, although increases were also observed in the CA1, probably as a result of the virus traveling up the cannula track (Fig. 3b,c). Behavioral analysis shows that rAAV-*Mkp-1* infusion into unstressed rats produced anhedonic responses evident from significantly decreased sucrose preference (Fig. 3d,  $P = 0.002$ ), and increased escape failures in the active avoidance test (Fig. 3e,  $P = 0.021$ ), behaviors similar to those observed in animals exposed to CUS (Fig. 2b). Infusion of rAAV-*Mkp-1* also increased latency to feed in the novelty suppressed feeding test (Fig. 3f,  $P = 0.093$ ) and significantly increased immobility in the forced swim test (see Supplementary Fig. 1,  $P = 0.021$ ). There were no significant effects in the elevated plus maze or on locomotor activity, indicating no change in overall ambulatory behavior (see Supplementary Fig. 1). Subsequent studies demonstrate that infusions of rAAV-*Mkp-1* into the CA1 subfield also decreases sucrose preference (data not shown). These results demonstrate that targeted, viral expression of *Mkp-1* in the DG subfield of nonstressed rats produces profound depressive-like responses similar to the effect of CUS.

The influence of MKP-1 deletion on behavior was examined in constitutive *Mkp-1* null mice (*Mkp-1*<sup>-/-</sup>). Previous studies report that *Mkp-1*<sup>-/-</sup> mice have no obvious behavioral or histological abnormalities<sup>34</sup>, and display normal levels of locomotor activity and food intake, although there is a reduction in weight with age due to an increase in fat metabolism<sup>35</sup>. Our preliminary baseline behavioral analysis (before initiation of the CUS paradigm) was consistent with these reports (i.e., no gross differences between *Mkp-1*<sup>-/-</sup> and wild type (WT or *Mkp-1*<sup>+/+</sup>) littermate controls in the open field, forced swim, or elevated plus maze tests; see Supplementary Fig. 2). Experiments were conducted to determine if deletion of *Mkp-1* influenced the response to CUS (Fig. 4a). Prior to stress, no difference between *Mkp-1*<sup>-/-</sup> and WT mice was observed on sucrose consumption, but exposure to CUS resulted in a progressive, significant reduction in WT mice, indicative of stress-induced anhedonia (Fig. 4b,  $P < 0.05$ ). However, *Mkp-1*<sup>-/-</sup> mice exposed to CUS consumed sucrose volumes similar to non-stress levels and were significantly higher than the WT group (Fig. 4b,  $P < 0.05$ ). Similar results were seen on days 17 and 30 of CUS, indicating that the effects were persistent. In contrast, there was no significant effect on water consumption (Fig. 4b) or time spent in an open field (center vs. peripheral zones; Supplementary Fig. 3). In the elevated plus maze *Mkp-1*<sup>-/-</sup> mice exposed to CUS spent significantly more time in the open arms compared to WT ( $P = 0.050$ ), but there was no effect on the number of entries into the open arms (Fig. 4c). The results demonstrate that *Mkp-1* deletion mutant mice are normal in the absence of stress and are resistant to CUS-induced behavioral deficits.

The functional state of MAPK signaling was assessed by analysis of phospho-Erk in the hippocampus. Exposure to CUS decreased levels of both phospho-Erk1 and phospho-Erk2 (Fig. 4d). The CUS effect was more robust and statistically significant for pERK2 levels in WT compared to nonstressed controls ( $P = 0.049$ ), or to *Mkp-1*<sup>-/-</sup> deletion mutants ( $P = 0.014$ ). There was no significant effect of CUS on phospho-Erk1/2 in *Mkp-1*<sup>-/-</sup> mice compared to nonstressed controls, and there were no significant effects on total Erk under any of the conditions tested. The results are consistent with the hypothesis that decreased ERK signaling, as well as sucrose consumption, in response to CUS requires MKP-1. The results are also consistent with previous studies demonstrating that pharmacological blockade or null mutation of MEK-ERK signaling prevents antidepressant responses<sup>36,38</sup>, although these studies have been confounded by the locomotor activating effects of chemical inhibitors as well as deletion of ERK<sup>38,40</sup>.

The results indicate that induction of MKP-1 is not only a direct consequence of stress but is also an important negative regulator of MAPK that contributes to the expression of depressive symptoms. ERK signaling and function have been linked with synaptic plasticity and survival of neurons<sup>5,6</sup>, and sustained disruption of this pathway via MKP-1 would be expected to have negative consequences on the function of pyramidal and granule cells in the hippocampus. The stress-resistance observed in *Mkp-1* deletion mice also indicates that pharmacological blockade of MKP-1 would produce a resilient or antidepressant response to stress, or possibly an enhanced response to other classes of antidepressants. Although kinases have received more attention in the control of biological processes, the enzymatic power of phosphatases is much greater (100 to 1,000 times) because dephosphorylation is a direct and more efficient process than phosphorylation<sup>4</sup>. Phosphatases such as MKP-1 are powerful negative regulators of intracellular signaling that represent exciting novel drug targets for treating depression and possibly other mood disorders.

## Online Methods

### Human subjects and tissue preparation

Tissues from 28 depressed subjects and 25 age-matched psychiatrically healthy control subjects were obtained at autopsy from the Coroner's Office of Cuyahoga County, Cleveland, Ohio, USA. An ethical protocol approved by the Institutional Review Board of the University Hospitals of Cleveland was used, and informed written consent was obtained from the next-of-kin for all subjects. All depressed subjects (12 women and 16 men) met diagnostic criteria for MDD according to the Diagnostic and Statistical Manual of Mental Disorders IV (American Psychiatric Association, 1994). The control subjects (12 women and 13 men), never met criteria for an Axis I disorder at any time in their lives. For the microarray analysis and qPCR, samples from 15 pairs of subjects for the dentate gyrus (DG) and CA1 were matched for age, gender, tissue pH, or postmortem interval (Supplementary Tables 1 and 2). For the microarray and real-time PCR (qPCR) studies, we collected punches from the granule cell layer of the DG and the CA1 pyramidal cell layers. For *in situ* hybridization, we used 20  $\mu$ m thick frozen, hippocampal sections from a separate cohort of seven pairs of subjects matched for age, gender, tissue pH and postmortem interval

(Supplementary Table 3). For full description of human subject selection process, MDD diagnosis criteria and tissue collection please see the Supplementary Methods online.

### Microarray analysis

We used human whole genome expression MI Ready microarrays (Microarray, Inc.) to analyze changes in gene expression. A total of 30 two-channel arrays was used to hybridize all DG and CA1 samples. Data were analyzed using R/Bioconductor; statistical analysis was executed by 1,000 permutation tests using a high performance computing cluster. *P* values were then adjusted to control false discovery rate (FDR) at 0.05 using the Q-value package. *P* values were calculated using distributions generated using permutation methods and standard error estimates were therefore not used in the *P* value calculations (see the Supplementary Methods online for full details of microarray experimental conditions and analysis).

### Quantitative real-time PCR (qPCR) and *in situ* hybridization analysis

qPCR was performed utilizing a hot-start SYBR Green (Qiagen) method. *MKP-1* gene fold changes in MDD vs. controls were determined by utilizing Ct (Ct = cycle number at threshold) analytical method that includes normalization against house-keeping genes *cyclophilin* and *GAPDH*. For detail description of primer design and sequences, *in situ* hybridization procedure, test conditions and analysis please see the Supplementary Methods online.

### Western blot analysis and immunohistochemistry

Proteins from fresh mouse hippocampal tissue were electrophoretically separated on an SDS-PAGE gel (10% Tris-HCl; Bio-Rad) and transferred to polyvinylidene difluoride membranes (0.2  $\mu$ m pores; Millipore) for western blot analysis.

Coronal rat brain sections (60  $\mu$ m) were immunohistochemically stained against green fluorescent protein (Gfp). Images were captured using Olympus Fluoview FV1000 confocal microscope (Olympus Corporation) and Zeiss Axioskop 2 fluorescent microscope with AxioVision 3.1 software (Carl Zeiss Imaging Solutions GmbH).

For complete technical details of experimental conditions, antibodies used and analysis please see the Supplementary Methods online.

### Construction, preparation and infusion of recombinant AAV

The rat *Mkp-1* cDNA was amplified from rat hippocampal cDNA library and subcloned into an AAV2 backbone, containing two CMV promoters to independently drive the expression of target protein (Mkp-1) and EGFP. The same backbone carrying no *Mkp-1* cDNA was used as a control (rAAV-control). For full description of recombinant AAV 2/1 pseudo-typed virus preparation and aseptic infusion surgeries please see the Supplementary Methods online.

## Chronic unpredictable stress and behavioral testing

Male Sprague-Dawley rats (Charles River), wild-type (*Mkp-1<sup>+/+</sup>*) and homozygotic null (*Mkp-1<sup>-/-</sup>*) mice were housed in groups of 2–4 per cage under a 12 h light/dark cycle at constant temperature (25 °C) and humidity with *ad libitum* access to food and water (except when indicated). Prior to any treatments or experiments, animals were allowed at least one week of habituation to the housing conditions. All animals were age and weight matched (rats: 250–300 g, mice: 29–33 g) at the time of the first stressor. The maintenance of rat and mouse colonies and all animal treatments and procedures were in accordance with NIH laboratory care standards and approved by the Yale University Care and Use of laboratory animals (YACUC) guidelines.

CUS is a rodent model of depression where animals are exposed to sequence of mild and unpredictable stressors designed to prevent habituation<sup>26,28</sup>. Animals were subjected to the sequence of 12 different stressors (rats: two per day; mice: three per day) for 35 days as previously described<sup>28</sup> (see Supplementary Table 6).

For full description of rodent stress models and behavioral tests used in this study (*rats*: sucrose preference test, active avoidance test and novelty suppressed feeding test; *mice*: sucrose and water consumption tests, elevated plus maze, open field test and forced swim test) please see the Supplementary Methods online.

## Statistical Analysis

Data from molecular and behavioral experiments were analyzed using Student's *t*-test for two-group comparisons. Two-way analysis of variance (ANOVA) with Fisher's PLSD *post-hoc* comparison tests was used in experiments with four groups, while one-way ANOVA followed by Student-Newman-Keuls' *post hoc* analysis was performed in experiments with three treatment groups. In behavioral experiments where multiple tests were conducted on the same sets of animals, repeated-measures ANOVA with Dunnett's *post hoc* test was used. Significance was set at  $P = 0.05$  (StatView 5.0.1, SAS Institute).

## Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

## Acknowledgments

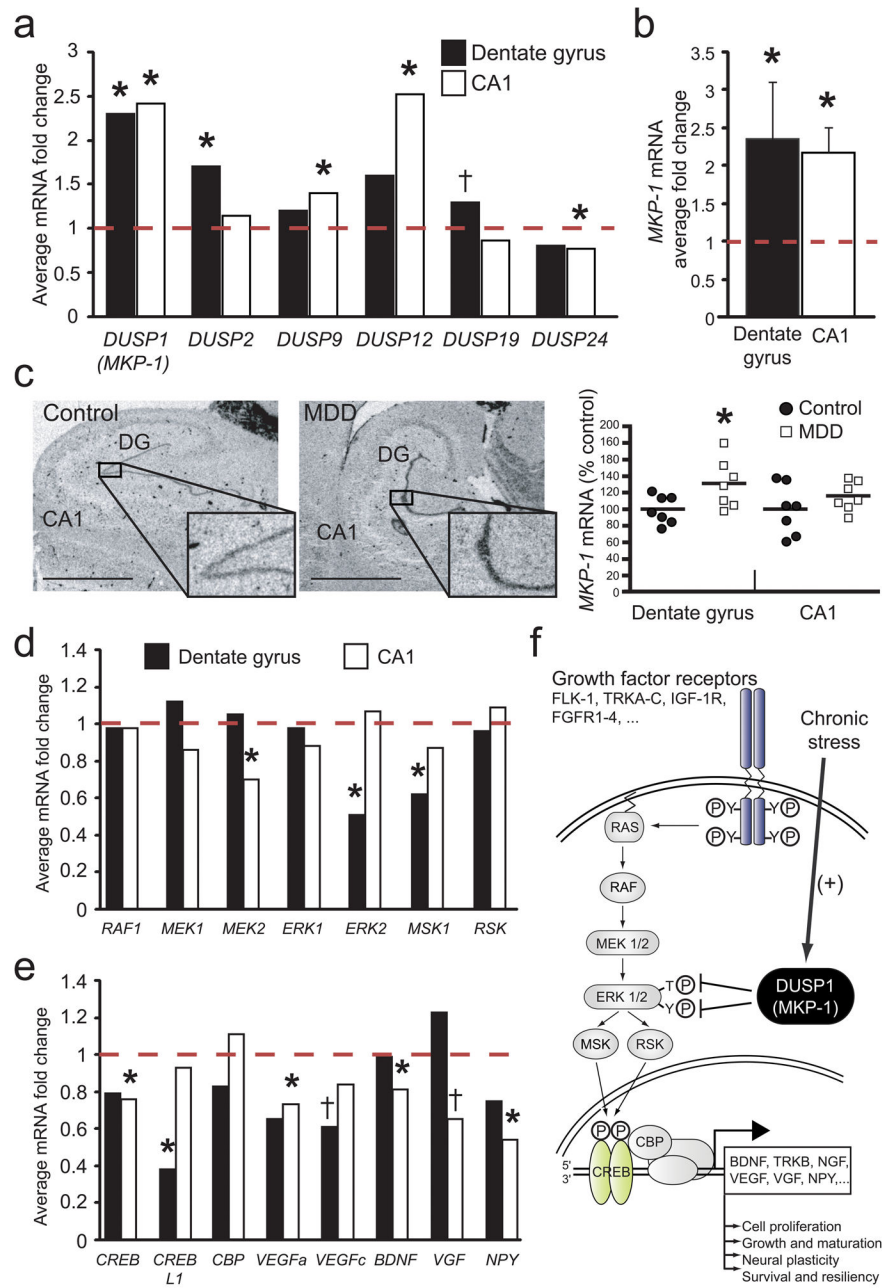
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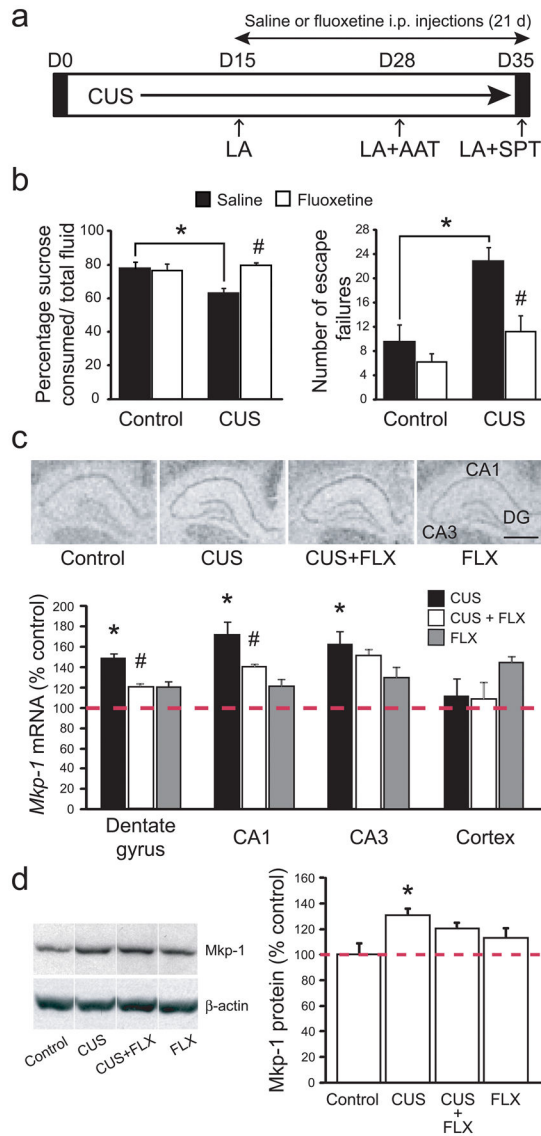


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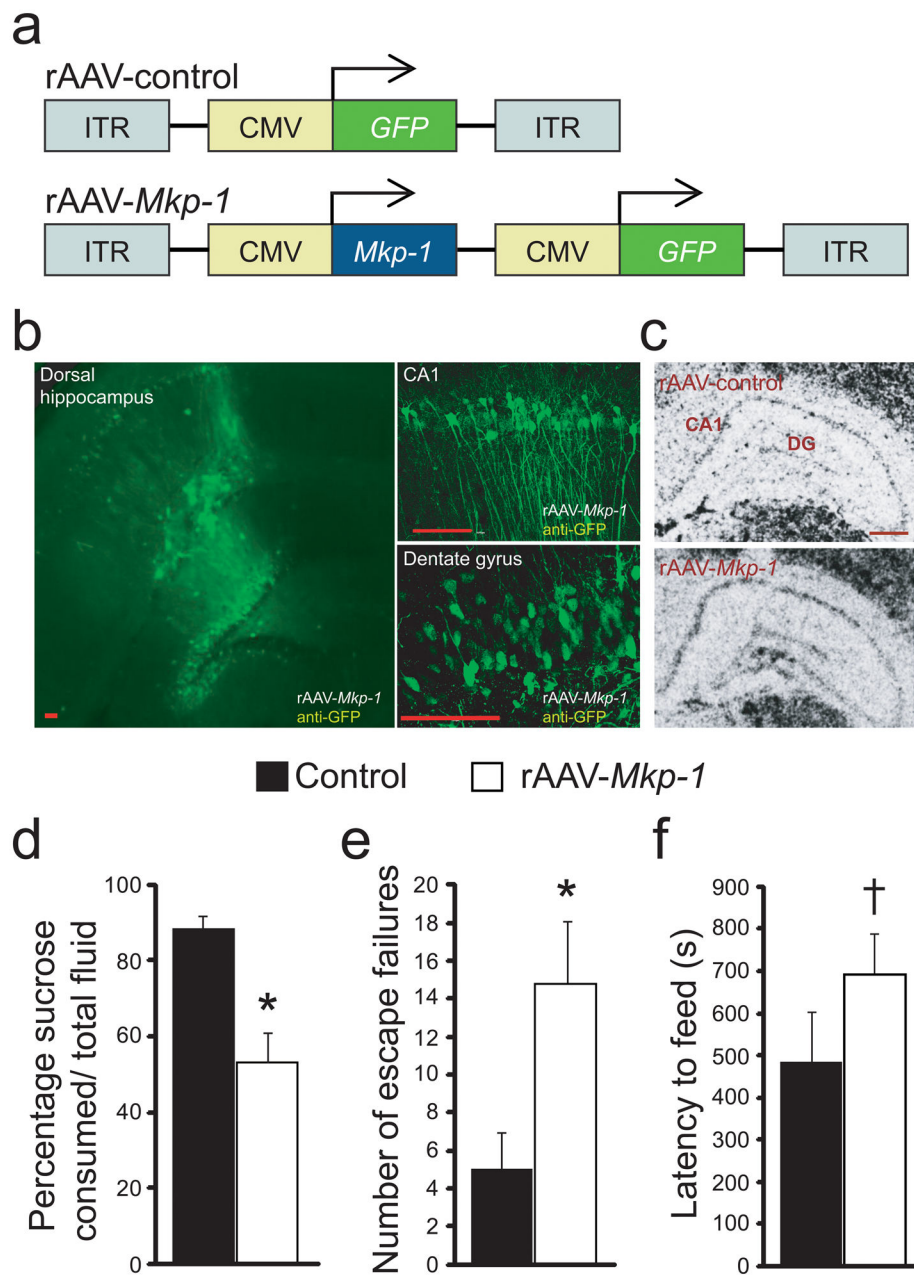
**Figure 1.** MKP-1 is dysregulated in major depressive disorder (MDD). **a**) Microarray analysis of MDD postmortem brain samples demonstrates significant alterations in the expression of DUSP genes in hippocampal subfields. **b**) Microarray findings for *MKP-1* gene expression were validated by qRT-PCR of samples from the same cohort. Data are expressed as mean fold change  $\pm$  S.E.M. ( $n = 6$ );  $*P < 0.05$  compared to the healthy controls (Student's *t*-test). **c**) Representative autoradiographs and quantitative analysis of hippocampal *MKP-1* mRNA levels by *in situ* hybridization in a separate cohort of MDD subjects and matched controls (scale bar = 5 mm). Results are shown as percent increase for each control and MDD subject.  $*P < 0.02$  compared to the healthy controls (Student's *t*-test). Microarray-based

expression levels of (d) MAP kinases and (e) downstream transcription factors and target genes. (f) Model for neurotrophic/growth factor receptor activation of MAPK, down-stream transcription factors, and target genes that play a key role in neuronal proliferation, survival and plasticity. Microarray results (a, d, and e) are shown as an average fold change (dentate gyrus,  $n = 14$ ; CA1,  $n = 15$ );  $*P < 0.05$ ,  $^{\dagger}P < 0.06$  compared to the healthy controls (permutation tests, p-value adjusted to FDR at 0.05). Fold change for specific splice variants is reported for *DUSP19.2*, *DUSP24.2*, *RPS6KA5.2 (MSK1)* and *VEGFA.2*. BDNF, brain-derived neurotrophic factor; CREB, cyclic-AMP response element binding protein; CBP, CREB binding protein; CREBL, CREB-like; ERK, extracellular signal-regulated kinase; MAPK, mitogen activated protein kinase; MEK, MAPK kinase; MSK, mitogen and stress-activated protein kinase; NPY, neuropeptide Y; RAF, v-raf-1 murine leukemia viral oncogene homolog 1; RSK, ribosomal S6 kinase; VEGF, vascular endothelial growth factor; VGF, VGF nerve growth factor inducible.



**Figure 2.**

Influence of chronic unpredictable stress (CUS) and antidepressant treatment on behavior and MKP-1 expression. **a**) Rats were exposed to CUS or control conditions and then were administered either saline or fluoxetine (FLX) for 21 d. Locomotor activity (LA), active avoidance test (AAT), and sucrose preference test (SPT) behaviors were determined. **b**) Behavioral results for AAT and SPT, expressed as mean  $\pm$  S.E.M. ( $n = 8$ ). **c**) Representative autoradiographs and quantitative analysis of *Mkp-1* mRNA levels by *in situ* hybridization on coronal sections of rat hippocampus (scale bar = 1.0 mm). Results are expressed as mean  $\pm$  S.E.M. ( $n = 4$  or 5). **d**) Western blot analysis showing the effects of CUS and FLX treatments on hippocampal MKP-1 protein levels. Tissue levels of  $\beta$ -actin were used as loading controls. Data are expressed as mean  $\pm$  S.E.M. percent change over non-stressed control group ( $n = 5$ );  $*P < 0.05$  compared to the non-stressed control group,  $\#P < 0.05$  compared to CUS group (two-way ANOVA and Fisher's PLSD *post hoc* analysis).

**Figure 3.**

Influence of Mkp-1 over-expression on behavior in rodent models of depression. **a**) Recombinant adeno-associated virus was engineered to locally over-express MKP-1 (rAAV-*Mkp-1*), and compared to a control vector that expresses green fluorescent protein (rAAV-*GFP*). Rats received bilateral intrahippocampal infusions of rAAV-*Mkp-1* or rAAV-*GFP*. Expression levels of GFP protein (**b**) and *Mkp-1* mRNA (**c**) are shown [representative figures; **b** scale bars = 100  $\mu$ m, **c** scale bar = 500  $\mu$ m]. Effects of rAAV-*Mkp-1* infusions on animal behavior, compared to rAAV-*GFP* controls, was evaluated for (**d**) the percent sucrose consumed compared to total fluid consumption (water and sucrose) in the SPT, (**e**) number of escape failures in the AAT, and (**f**) latency to feed in the novelty suppressed

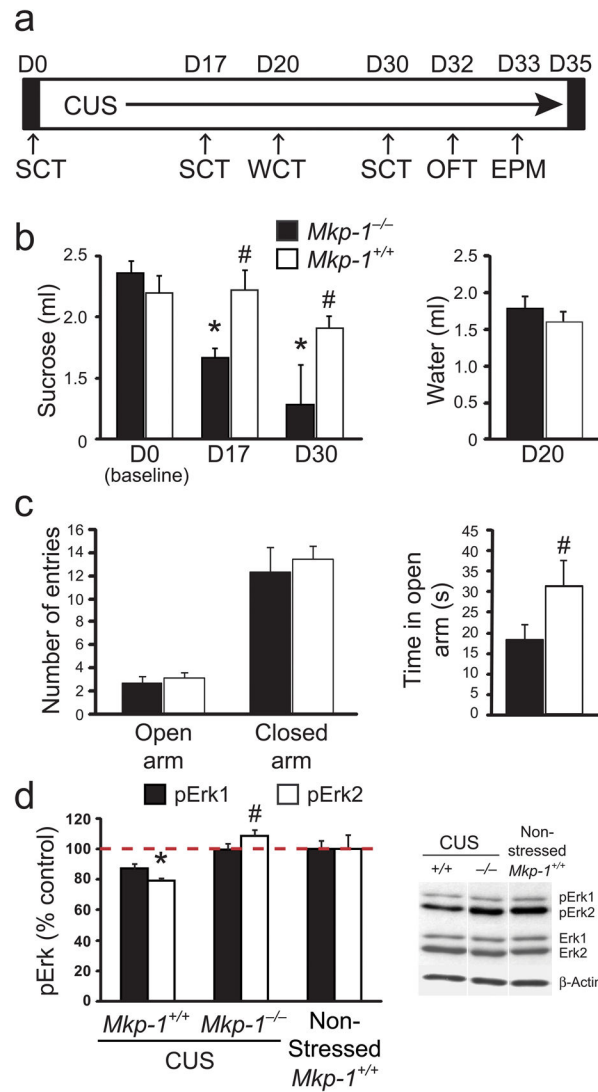
feeding (NSF) test. Behavioral data are expressed as mean  $\pm$  S.E.M. ( $n = 6-9$ );  $*P < 0.02$ ,  $^{\dagger}P < 0.10$  compared to the rAAV-*GFP* control group (Student's *t*-test). ITR, inverted terminal repeats; CMV, cytomegalovirus promoter.

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**Figure 4.** Influence of MKP-1 deletion on behavioral models of depression. **a**) Experimental paradigm for behavioral testing and CUS exposure of *Mkp-1* knockout mice (*Mkp-1<sup>-/-</sup>*;  $n = 9-10$ ) and wildtype (WT) littermates (*Mkp-1<sup>+/+</sup>*;  $n = 8$ ). **b**) Baseline sucrose consumption was tested on day 0, followed by post-stress measurements conducted on days 17 and 30. Water consumption was also measured throughout the stress paradigm (data shown for water test on day 20). **c**) Both genotypes were further tested in the elevated plus maze test; the number of entries into the open or closed arms, and the total time spent in the open arms are shown. Results are expressed as mean  $\pm$  S.E.M.; \* $P < 0.05$  compared to the WT control group and # $P < 0.05$  compared to the WT stress group (sucrose and water consumption: repeated-measures ANOVA and Dunnett's; elevated plus maze: Student's *t*-test). **d**) Representative images and quantitative results of western blot analysis showing the effects of CUS on hippocampal phospho-Erk levels in WT and *Mkp-1<sup>-/-</sup>*, compared to non-stressed WT control mice. Tissue levels of total Erk and beta-actin were used as loading controls. Optical density values are expressed as a ratio of the pErk and total Erk. Data are expressed as mean

± S.E.M. percent change over non-stressed wildtype control ( $n = 3$ ); \* $P < 0.05$  compared to WT control group and # $P < 0.05$  compared to the WT stress group (ANOVA and Student-Newman-Keuls' *post hoc* analysis). SCT, sucrose consumption test; WCT, water consumption test; OFT, open field test; EPM, elevated plus maze.

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