Sex Differences in Nucleus Accumbens Transcriptome Profiles Associated with Susceptibility versus Resilience to Subchronic Variable Stress

Citation

As Published
http://dx.doi.org/10.1523/jneurosci.1392-15.2015

Publisher
Society for Neuroscience

Version
Final published version

Accessed
Sat Feb 09 17:07:16 EST 2019

Citable Link
http://hdl.handle.net/1721.1/110520

Terms of Use
Creative Commons Attribution 4.0 International License

Detailed Terms
http://creativecommons.org/licenses/by/4.0/
Behavioral/Cognitive

Sex Differences in Nucleus Accumbens Transcriptome Profiles Associated with Susceptibility versus Resilience to Subchronic Variable Stress

Georgia E. Hodes,1 Madeline L. Pfau,1 Immanuel Purushothaman,1 H. Francisca Ahn,1 Sam A. Golden,1 Daniel J. Christoffel,1 Jane Magida,1 Anna Brancato,1,6 Aki Takahashi,1,2 Zachary S. Lorsch,1,6 Jian Feng,1 Mitra Heshmati,1 Minghui Wang,3 Gustavo Turecki,4 Rachel Neve,3 Bin Zhang,3 Li Shen,1,6 Eric J. Nestler,1 and Scott J. Russo1

1Fishberg Department of Neuroscience and Friedman Brain Institute, Icahn School of Medicine at Mount Sinai, New York, New York 10029, 2Laboratory of Behavioral Neuroendocrinology, University of Tsukuba, Tsukuba, Ibaraki 305-8577, Japan, 3Genetics and Genomic Sciences, Icahn School of Medicine at Mount Sinai, New York, New York 10029, 4McGill Group for Suicide Studies, Douglas Mental Health University Institute, Department of Psychiatry, Montreal, Quebec H4H 1R3, Canada, 5Department of Brain and Cognitive Sciences, Massachusetts Institute of Technology, Cambridge, Massachusetts 02139, and 6Department of Science for Health Promotion and Mother and Child Care, University of Palermo, 90127 Palermo, Italy

Depression and anxiety disorders are more prevalent in females, but the majority of research in animal models, the first step in finding new treatments, has focused predominantly on males. Here we report that exposure to subchronic variable stress (SCVS) induces depression-associated behaviors in female mice, whereas males are resilient as they do not develop these behavioral abnormalities. In concert with these different behavioral responses, transcriptional analysis of nucleus accumbens (NAc), a major brain reward region, by use of RNA sequencing (RNA-seq) revealed markedly different patterns of stress regulation of gene expression between the sexes. Among the genes displaying sex differences was DNA methyltransferase 3a (Dnmt3a), which shows a greater induction in females after SCVS. Interestingly, Dnmt3a expression levels were increased in the NAc of depressed humans, an effect seen in both males and females. Local overexpression of Dnmt3a in NAc rendered male mice more susceptible to SCVS, whereas Dnmt3a knock-out in this region rendered females more resilient, directly implicating this gene in stress responses. Associated with this enhanced resilience of female mice upon NAc knock-out of Dnmt3a was a partial shift of the NAc female transcriptome toward the male pattern after SCVS. These data indicate that males and females undergo different patterns of transcriptional regulation in response to stress and that a DNA methyltransferase in NAc contributes to sex differences in stress vulnerability.

Key words: behavior; depression; epigenetics; nucleus accumbens; sex differences; stress

Significance Statement

Women have a higher incidence of depression than men. However, preclinical models, the first step in developing new diagnostics and therapeutics, have been performed mainly on male subjects. Using a stress-based animal model of depression that causes behavioral differences in females but not males, we demonstrate a sex-specific transcriptional profile in brain reward circuitry. This transcriptional profile can be altered by removal of an epigenetic mechanism, which normally suppresses DNA transcription, creating a hybrid male/female transcriptional pattern. Removal of this epigenetic mechanism also induces behavioral resilience to stress in females. These findings shed new light onto molecular factors controlling sex differences in stress response.

Introduction

Men and women manifest different symptoms and coping responses to episodes of depression (Martin et al., 2013); and based on current diagnostic schemes, women have twice the incidence of depression and anxiety disorders (Kessler et al., 1994). Despite this sex-based skew in the occurrence of stress-related illness, basic research has lagged in including female animals in stress studies (Beery and Zucker, 2011). When females are included,
research has demonstrated numerous sex differences in stress responses between males and females, including different cellular responses to stress (Bangasser and Valintino, 2012; Chow et al., 2013; Howerton et al., 2014), different brain circuits involved in stress responses (Bangasser and Shors, 2008; Shansky et al., 2010; Kelly et al., 2014; Stevens et al., 2014), sex-specific effects of stress on synaptic and neural plasticity (Shors et al., 2004; Autry et al., 2009; Carvalho-Netto et al., 2011; Chow et al., 2013; Galea et al., 2013; Farrell et al., 2015; McEwen et al., 2015), and myriad differences in the cognitive and emotional behavioral effects of stress exposure (Bowman et al., 2001; 2003; Monteggia et al., 2007; Dalla et al., 2008, 2011; LaPlant et al., 2009). Together, these studies raise the possibility that transcriptional regulation differs between the sexes and that such differences may contribute to stress vulnerability and resilience.

There is growing evidence for sex differences in the nucleus accumbens (NAc), a brain area important for reward and stress processing (Russo and Nestler, 2013). Males and females show different susceptibility to addiction, and this is thought to relate to differences in the brain’s reward and stress circuitry (Anker and Carroll, 2011; Becker et al., 2012). Females exhibit structural differences in NAc neural plasticity at baseline (Wissman et al., 2012) and after cocaine exposure (Wissman et al., 2011), and they are far more sensitive to the addictive properties of cocaine (Lynch and Carroll, 2000; Lynch et al., 2000; Russo et al., 2003). Less is known about the molecular basis of sex differences in stress susceptibility; and to date, most studies examining sex differences in molecular correlates of addiction or stress behavior in NAc have used a candidate gene approach (LaPlant et al., 2009; Sato et al., 2011; Rappeneau et al., 2015). It is not currently known how males and females compare with respect to the molecular cascades in the NAc that are altered by stress exposure.

Epigenetic mechanisms have been implicated in sex differences in gene expression and sexual differentiation of the brain (Tsai et al., 2009; Ghahraramani et al., 2014; Morrison et al., 2014; Nugent et al., 2015; Shen et al., 2015). Sexual differentiation in the brain is triggered by a gonadal hormone surge (Rhees et al., 1990; MacLennan et al., 1997), which drives demethylation and subsequent masculinization. The process of masculinizing the brain involves methylation of the estrogen receptor α (Kurian et al., 2010; Schwarz et al., 2010) along with sex differences in histone acetylation (Murray et al., 2009; Matsuda et al., 2011). These early epigenetic sex differences result in sex-specific sexual behaviors in adulthood (Matsuda et al., 2011; Nugent et al., 2015) and have been implicated in vulnerability to mental disorders in humans (Kim et al., 2015). Epigenetic regulation is also implicated in vulnerability to repeated social defeat stress during adulthood (Tsankova et al., 2006; Elliott et al., 2010; LaPlant et al., 2010; Golden et al., 2013), but these preclinical studies have been limited to males.

Using the subchronic variable stress (SCVS) model, which consists of 6 d of alternating stressors, we explored sex differences in stress responses on a battery of depression- and anxiety-like behaviors and on transcriptional regulation in the NAc with RNA sequencing (RNA-seq). We hypothesized that sex differences in the transcriptional profile of the NAc are associated with sex differences in stress susceptibility. Our findings implicate an important role of the DNA methyltransferase, Dnmt3a, in mediating female–male differences in stress susceptibility and in transcriptional responses to stress.

**Materials and Methods**

**Animals.** C57BL/6J female and male mice (The Jackson Laboratory) at 8–12 weeks of age were used for all experiments, except Dnmt3a knock-out studies. For Dnmt3a conditional deletion, Dnmt3a<sup>lox/lox</sup> mice were bred at the Ichan School of Medicine from a line originally generated in the laboratory of Dr. Li at Novartis Institutes of Biomedical Research (Dodge et al., 2005). They were backcrossed with 129Jae mice for 8 generations to generate a common genetic background. Dnmt3a<sup>lox/lox</sup> mice were between 8 and 20 weeks old at the time of behavioral experiments. One week before the onset of each experiment, mice were group housed and maintained on a 12:12 light/dark cycle with ad libitum access to food and water, except when explicitly stated for behavioral testing. All mice that underwent behavioral testing were single housed following the splash test, the first portion of the behavioral test battery. Mouse procedures were performed in accordance with the Institutional Animal Care and Use Committee guidelines of the Ichan School of Medicine at Mt. Sinai.

**Subchronic variable stress.** SCVS was performed as described previously (LaPlant et al., 2009), which consists of three different stressors over 6 d (Fig. 1a). Stressors alternated during the 6 d to prevent stress habituation. Stressors were administered in the following order: 100 random mild foot shocks at 0.45 mA for 1 h (10 mice to a chamber), a tail suspension stress for 1 h and restraint stress, placed inside a 50 ml falcon tube, for 1 h within the home cage. The three stressors were then repeated for the next 3 d in the same order. In some experiments, we used an abbreviated (3 d) subthreshold variable stress (STVS) to assess stress susceptibility.

**Behavioral assessments: splash test.** Testing was based on a published protocol (Isingrini et al., 2010). The test was performed under red light (230 V, 15 W). Mice were habituated to the room for 1 h before testing. Mice were sprayed on the back with a 10% sucrose solution 3 times. Mice were then placed into an empty housing cage, and behavior for 5 min was recorded via videotape. The total amount of time grooming over the 5 min period was recorded and hand scored by an observer blind to experimental conditions. Mice were immediately single housed after the test.

**Novelty suppressed feeding.** Testing was adapted from a published protocol (Santarelli et al., 2003). Mice were food restricted overnight before testing. On the day of testing, mice habituated to the testing room for 1 h. Under red light conditions, mice were then placed into a plastic box 50 × 50 × 20 cm with bedding. A single pellet of food was placed in the center of the box. Mice were placed in the corner of the box, and the latency to eat was scored up to 10 min during testing. Mice were then immediately transferred to their home cage in standard lighting conditions, and the latency to eat was recorded.

**Sucrose consumption test.** Testing was conducted according to previously published protocols (Krishnan et al., 2007; Vialou et al., 2010). Immediately after the splash test, mice were separated and individually housed. They were given 2 bottles filled with water for a 24 h habitation period. The following day, immediately after novelty suppressed feeding (NSF) testing, one of the two 50 ml bottles was replaced with a 1% sucrose bottle for 24 h. The 2 bottles were then weighed, and position was switched for an additional 24 h. The total duration of the test was 48 h. Sucrose was calculated by determining the percentage of total sucrose consumption divided by total liquid consumption (sucrose + water).

**Forced swim test (FST).** The FST was conducted according to previously published protocols (LaPlant et al., 2010). At 24 h after the NSF test, animals were placed in the test room for an hour before behavioral testing. Mice were tested in a 4 L Pyrex glass beaker, containing 2 L of water at 25 ± 1°C for 6 min. Behavior was videotaped and hand scored using a 5 s sampling method for percentage time spent immobile by an observer blind to experimental conditions.

**Elevated plus maze (EPM).** Mice were acclimated to the testing facility for 1 h before testing. Animals were placed in the EPM under red light conditions for 5 min. Each arm of the maze measured 12 × 50 cm. The black Plexiglas cross-shaped maze consisted of two open arms with no walls and two closed arms (40 cm high walls) and was on a pedestal 1 m above floor level. Behavior was tracked using an automated system (Noldus Ethovision; Noldus Interactive Technologies). Behavior was mea-
measured as total time in combined open arms and total time in combined closed arms.

**Locomotor activity.** Locomotor activity (n = 8 per group) was measured in a separate cohort of animals exposed to SCVS. One day after the last stressor, mice were acclimated to the testing room 1 h and tested under red light. They were placed into clear testing chambers (44.45 cm length × 17.78 cm width × 25.4 cm height), and the number of photo-beam breaks on the x and y planes were measured for 30 min using an automated system (PAS, San Diego Instruments).

**Surgery.** Herpes simplex virus (HSV)-mediated Dnmt3a overexpression. Male and female C57BL/6J mice (n = 9 or 10 per group splash test, NSF sucrose, FST; cohort 1; cohort 2, n = 8 per group EPM/locomotor activity).
activity were anesthetized with a mixture of ketamine (100 mg/kg) and xylazine (10 mg/kg) and positioned in a small-animal stereotaxic instrument (David Kopf Instruments) with the skull surface exposed. Thirty-three-gauge syringe needles (Hamilton) were used to bilaterally infuse 0.5 μL of HSV (1.5 × 1011 infectious units/ml) expressing a control green fluorescent protein (GFP) or Dnmt3a in to NAc (bregma coordinates: anteroposterior, +1.5 mm; mediolateral, +1.6 mm; dorsoventral, −4.4 mm) at a rate of 0.1 μL/min.

Adeno-associated virus (AAV) Cre-mediated Dnmt3a knock-out. Male and female Dnmt3a2loxPlox mice (n = 12 mice per group for RNA-seq and 8–11 mice per group for splash test, NSF, sucrose, FST; cohort 1; cohort 2, n = 5–7 for EPM/locomotor activity) were anesthetized with a ketamine/xylazine mixture described above, and surgery was performed as described for HSV. Animals were bilaterally infused with 0.5 μL of AAV (1.5 × 1012 infectious units/ml) expressing a control GFP or Cre/GFP in to NAc (coordinates listed above). Viral vectors have been tested and validated in vivo and in vitro (LaPlant et al., 2010).

Corticosterone ELISA. Submandibular vein bleeds (Golde et al., 2005) were taken 24 h after the last stressor, and serum was collected as previously described (Hodes et al., 2014).

Corticosterone (CORT) levels were measured in serum with a commercially available sandwich ELISA kit (ImmuNoDiagnostics Systems) according to the manufacturers’ instructions. Intra-assay variability for the corticosterone assay ranged from 3.8% to 6.6%; interassay variability according to the manufacturers’ instructions. Intra-assay variability for commercially available sandwich ELISA kit (ImmunoDiagnostic Systems) was obtained using the HTSeq python package (Anders et al., 2015). Before differential analysis, only genes with >5 reads in at least 80% of samples in any one of the experimental conditions were included. Counts were converted to precision weighted log2 counts per million using the voom transformation, a function of the Bioconductor R package limma (Law et al., 2014; Ritchie et al., 2015). The limma package was used to fit a 2 × 2 factorial design interaction model with stress and sex as main factors to determine the effect of stress in males and in females separately. The same design was used to investigate the effect of Dnmt3a knock-out in stressed males and stressed females with sex and genotype as main factors. An uncorrected p value <0.05 and a fold change threshold of 1.3 were used to determine differential expressions between genes.

Tissue collection and RNA extraction: mouse. NAc samples were collected and processed as described previously (Golden et al., 2013). Bilateral 14-gauge NAc dorsal striatum punches were collected on ice after rapid decapitation and then immediately placed on dry ice and stored at −80°C until use. RNA was isolated using homogenization in Trizol (Invitrogen) followed by chloroform layer separation. The clear RNA layer was then processed as described previously (Golden et al., 2005). Tissue samples were normalized to GAPDH. Primer pairs are available upon request.

Corticosterone ELISA. Submandibular vein bleeds (Golde et al., 2005) were taken 24 h after the last stressor, and serum was collected as previously described (Hodes et al., 2014).

Corticosterone (CORT) levels were measured in serum with a commercially available sandwich ELISA kit (ImmuNoDiagnostics Systems) according to the manufacturers’ instructions. Intra-assay variability for the corticosterone assay ranged from 3.8% to 6.6%; interassay variability according to the manufacturers’ instructions. Intra-assay variability for commercially available sandwich ELISA kit (ImmunoDiagnostic Systems) was obtained using the HTSeq python package (Anders et al., 2015). Before differential analysis, only genes with >5 reads in at least 80% of samples in any one of the experimental conditions were included. Counts were converted to precision weighted log2 counts per million using the voom transformation, a function of the Bioconductor R package limma (Law et al., 2014; Ritchie et al., 2015). The limma package was used to fit a 2 × 2 factorial design interaction model with stress and sex as main factors to determine the effect of stress in males and in females separately. The same design was used to investigate the effect of Dnmt3a knock-out in stressed males and stressed females with sex and genotype as main factors. An uncorrected p value <0.05 and a fold change threshold of 1.3 were used to determine differential expressions between genes.

Quantitative gene overlap. Genes differentially expressed between conditions were divided into upregulated and downregulated groups. Using custom software in R, lists were combined pairwise, generating a total of 120 unique comparisons. For each comparison, the gene IDs in each list were extracted, and the quantitative overlap between the two lists was determined. Subsequently, a Fisher’s exact test was used to statistically analyze the overlap based on the number of genes in common, the size of each gene list, and the total number of background genes, examining whether the observed gene overlap was significantly (p < 0.05) larger than expected by chance. For all comparisons, the number of background genes was kept constant at 18,724 reflecting the total number of candidate genes analyzed in the differential expression analysis. Additionally, the fold change between observed gene overlap and expected gene overlap was recorded.

Pathway analysis. Pathway and network analysis were performed on differentially regulated genes using Ingenuity Pathway Analysis (Qiagen; www.qiagen.com/ingenuity).

Statistical analysis. Differences between two groups were compared using unpaired t tests (two-tailed). Comparisons of multiple factors or repeated measures were analyzed by bivariate ANOVAs with a Bonferroni post test for post hoc analysis. All statistical analyses were performed using Graph Pad Prism 5.0 software (Graphpad). Statistical significance was set at a p < 0.05. Grubbs outlier test was performed and samples that varied >2 SDs from the mean were removed.

Results

Female but not male mice are susceptible to SCVS

We showed previously that 6 d of SCVS increased passive coping behavior in female but not male mice in the FST (LaPlant et al., 2009), a test commonly used to screen for antidepressant drug efficacy. Here we expanded on these findings by putting male and female mice through a behavioral test battery of anxiety, locomotor, and depression associated behaviors following SCVS (Fig. 1a). The initial test battery included the splash test, NSF, sucrose preference, and EPM. Locomotor activity was measured subse-
quently in a separate cohort of mice to confirm that behavioral effects in the above mentioned tests were not due to sex- or stress-related differences in physical activity. For the splash test, animals were sprayed with a sticky 10% sucrose solution, and subsequent grooming behavior was examined; stressed mice groomed less than unstressed mice (Surget et al., 2008). Mice that underwent NSF were food deprived overnight and then placed in a novel environment where latency to eat is examined; stressed animals have a longer latency to eat. This test has been implicated in both anxiety and depression-associated behavior (Santarelli et al., 2003). Sucrose preference was examined as a measure of anhedonia, a key symptom of depression. The EPM was used as a measure of exploratory behavior related to anxiety (File, 2001). Female mice that underwent SCVS exhibited a series of depression-like behaviors, including decreased grooming in the splash test (Fig. 1b), indicated by a significant interaction between stress and sex ($F_{1,33} = 5.48, p = 0.02$). Female mice that underwent SCVS also displayed increased latency to eat in the novelty suppressed feeding test (Fig. 1c) as indicated by a significant interaction between stress and sex ($F_{1,30} = 4.96, p = 0.03$). SCVS decreased sucrose preference in females (Fig. 1d) as indicated by a significant interaction between stress and sex ($F_{1,32} = 4.22, p = 0.05$). Furthermore, SCVS increased levels of corticosterone only in female mice (Fig. 1e) as demonstrated by a significant interaction ($F_{1,33} = 7.97, p = 0.008$). Male mice subjected to identical SCVS exhibited none of these abnormalities in depression-like behavior or stress hormone levels ($p > 0.05$). Neither sex displayed altered anxiety-like behavior as indicated by the EPM (Fig. 1f; $p > 0.05$). Additionally, there were no differences in locomotor activity between male and female mice or between stressed and unstressed mice (Fig. 1g; $p > 0.05$).

**Figure 2.** Male and female mice express different transcriptional responses in NAc after SCVS. *a,* Heatmap of genes differentially regulated by SCVS in females compared with the same genes in males. *b,* Heatmap of genes differentially regulated by SCVS in males compared with females. *c,* Venn diagram of total number of significantly upregulated genes in stressed males and females. *d,* Venn diagram of total number of downregulated genes in stressed males and females. *e,* Representation of the top 10 gene ontology networks regulated by SCVS in males and females. Libraries were created from pooled mRNA samples ($n = 4$ mice/library and run in independent biological replicates of 3 libraries per sex/stress).

SCVS induces different transcriptional profiles in male and female mice
To discover unbiased biological correlates of sex differences in susceptibility versus resilience to SCVS, we used RNA-seq to measure all polyA-containing transcripts in NAc of control and stressed animals. Males and females were exposed to SCVS and NAc tissue was sampled 24 h after the last stressor. Heatmaps of significantly regulated genes were constructed from the global transcriptome analysis (Fig. 2a,b). Overall, 17% more genes in the NAc were regulated by stress compared to same sex controls for males than for females, indicating a more active transcriptional process in males exposed to SCVS. The majority of genes (~60%) were upregulated in females exposed to SCVS com-
pared with nonstressed controls (Fig. 2a). In males, 40% of genes were upregulated, whereas the remainder (60%) were downregulated compared with nonstressed controls (Fig. 2b). Only ~3% of the genes regulated by stress in females significantly overlapped with the same genes in males regardless of the direction of transcriptional changes (upregulated, \( p = 3.62 \times 10^{-8}; \) downregulated, \( p = 4.72 \times 10^{-10}; \) Fig. 2c,d). Even fewer genes were oppositely regulated by stress (0.5%) in males and females (data not shown, \( p > 0.05 \)). Examination of the most differentially expressed genes by stress within each sex indicated that only one gene, GM1A4027, was upregulated in both males and females (Table 1). These data indicate that, rather than the same genes being either commonly or even oppositely regulated by stress in males and females, different molecular cascades are sex-specifically associated with the stress response. Examination of the gene ontology of regulated transcripts indicated that for the top 10 enriched networks ~40% were regulated in both sexes; however, different sets of specific genes were regulated within these similar networks (Fig. 2e). DNA methyltransferase 3a is altered in NAc by SCVS in mice and major depressive disorder in humans

A potential mechanism contributing to sex differences in transcriptional profiles is DNA methylation. Dnmts are enzymes involved in catalyzing the addition of a methyl group to the 5-position on cytosine. Addition of this methyl group can lead to direct transcriptional silencing by occluding transcription factor binding sites, although more recent research has demonstrated more complex roles for DNA methylation in transcriptional control (Hervouet et al., 2009; Baubec et al., 2015; Schübeler, 2015). Dnmt1 maintains previous methylation patterns in daughter cells by methylating hemi-methylated sites, whereas Dnmt3a and 3b are involved in de novo methylation (Bestor, 2000; Robertson and Wolffe, 2000). Dnmt expression has been shown to differ during development in males and females, leading to masculinization and feminization of brain structures (McCarthy et al., 2009; Nugent et al., 2015). Furthermore, there is evidence that in males Dnmt3a contributes to susceptibility to social stress and drugs of abuse (LaPlant et al., 2010). We found here that mRNA
levels for Dnmt3a were increased in the NAc of both male and female mice by SCVS at both 4 h ($F(1,26) = 4.64, p = 0.04$; Fig. 3a) and 24 h ($F(1,27) = 12.26, p = 0.0016$; Fig. 3b) after stress exposure. We also found a main effect of sex on Dnmt3a, where female mice had overall higher Dnmt3a levels in NAc compared with male mice under combined control and SCVS conditions at 4 h ($F(1,26) = 4.79, p = 0.03$) and 24 h after the stressor ($F(1,27) = 9.07, p = 0.0056$). We examined expression of Dnmt3b and Dnmt1 to determine whether these enzymes might also contribute to sex differences in the effects of stress on the NAc transcriptome. There was no significant effects of stress or sex on Dnmt3b expression 4 h after SCVS ($p > 0.05$). Dnmt3b was equally elevated by stress in both sexes 24 h after SCVS ($F(1,24) = 10.27, p = 0.003$), whereas Dnmt1 was not significantly affected by stress in male or female mice either 4 or 24 h after SCVS ($p > 0.05$). Additionally, we compared expression of Dnmt3a directly with Dnmt3b and Dnmt1 at the 4 and 24 h time periods in controls. We normalized all data to average Dnmt levels expressed in control males for each time point. Two-way ANOVA was used to examine Dnmt expression by sex. We found a significant interaction between Dnmt expression and sex at 4 h ($F(2,42) = 3.55, p = 0.037$; data not shown) and 24 h ($F(2,41) = 4.47, p = 0.017$; Fig. 3c) Post hoc analysis indicated that at both time points Dnmt3a was expressed at higher levels than all other Dnmts in both males and females but to a greater degree in females than in males.

Dnmt3a was not significantly elevated by SCVS in the medial prefrontal cortex (mPFC) of mice ($p > 0.05$, data not shown), suggesting that stress does not globally upregulate Dnmt3a equally in all areas of the brain. However, future research will need to determine whether stress affects Dnmt3a expression in other stress-related brain regions, such as the central nucleus of the amygdala and the hippocampus. An increase in Dnmt3a expression was seen in the NAc of humans with major depressive disorder ($F(1,26) = 10.71, p = 0.0002$; Fig. 3d), with a trend for antidepressant treatment to partially reverse this abnormality. We did not observe a main effect of sex on Dnmt3a levels in human NAc tissue, as was the case for mice. We also did not find any significant increase in expression of Dnmt3b or Dnmt1 in the NAc of depressed patients ($p > 0.05$). Examination of relative expression of Dnmts in control patients indicated that only Dnmt3a expression was elevated in NAc of both males and females ($F_{(2,33)} = 64.33, p < 0.0001$; Fig. 3e).

Overexpression of Dnmt3a makes both sexes susceptible to subthreshold variable stress

In male mice, viral-mediated overexpression of Dnmt3a in the NAc has been shown to induce a prosusceptible behavioral phenotype in response to a subthreshold form of social defeat stress (LaPlant et al., 2010). Here we expressed HSV-Dnmt3a or −green fluorescent protein (GFP/control) in the NAc (Fig. 4a) of male and female mice and exposed all animals to a 3 d STVS. Overexpression of Dnmt3a by HSV resulted in a significant increase in Dnmt3a expression 3 d after viral injection ($F_{(1,19)} = 44.38, p < 0.0001$; Fig. 4b). Mice injected with HSV-Dnmt3a exhibited 6-fold to 8-fold higher levels of Dnmt3a than those injected with HSV-GFP, with approximately comparable induction seen in the two sexes. Although STVS was not sufficient to induce depression- or anxiety-associated behavior in either sex injected intra-NAc with HSV-GFP, both male and female mice injected intra-NAc with HSV-Dnmt3a displayed a stress susceptible phenotype across all behavioral measures. Dnmt3a overexpression decreased grooming in the splash test (Fig. 4c) as indicated by a
main effect of virus ($F_{(1,34)} = 7.8, p = 0.008$), increased latency to eat in the NSF test (Fig. 4d) as indicated by a main effect of virus ($F_{(1,34)} = 5.73, p = 0.02$), decreased sucrose preference ($F_{(1,34)} = 7.4, p = 0.01$; Fig. 4e), and increased passive coping responses (Fig. 4f) in the FST ($F_{(1,34)} = 6.64, p = 0.01$). Overexpression of Dnmt3a in NAc followed by STVS did not lead to sex or stress differences in exploratory anxiety-associated behavior in the EPM ($p > 0.05$; Fig. 4g) or locomotor activity ($p > 0.05$; Fig. 4h).

**Dnmt3a knock-out in the female NAc promotes behavioral resilience to SCVS**

As overexpression of Dnmt3a was sufficient to induce a stress susceptible state in both sexes, we next tested whether the enzyme was also necessary for the greater susceptibility of female mice to SCVS. Male and female $Dnmt3a^{2lox/2lox}$ mice were injected intra-NAc with AAV-Cre to knock-out $Dnmt3a$ expression specifically in adult NAc neurons, which we confirmed experimentally (Fig. 5a, b; main effect of virus, $F_{(1,29)} = 13.38, p = 0.001$). After a previously validated 2 week period of recovery to allow for viral expression (Feng et al., 2010; LaPlant et al., 2010), animals were exposed to 6 d of SCVS. Female mice that were given injections of AAV-GFP exhibited depression-associated behaviors (similar to responses seen in SCVS females in Fig. 1), whereas knock-out of $Dnmt3a$ in the NAc of adult females promoted resilience. Stressed AAV-GFP injected females displayed decreased grooming behavior, whereas knock-out of $Dnmt3a$ increased time spent grooming to male-like levels ($F_{(1,33)} = 14.56, p = 0.0006$; Fig. 5c). SCVS increased the latency to eat in the NSF test in AAV-GFP injected mice, whereas knock-out of $Dnmt3a$ significantly increased latency to eat in the NSF test in both males and females.

**Figure 4.** Overexpression of Dnmt3a in NAc is sufficient to induce depression- and anxiety-associated behaviors in males and females exposed to STVS. 

<table>
<thead>
<tr>
<th>a</th>
<th>Schematic of the 3 d STVS procedure and behavioral testing schedule.</th>
</tr>
</thead>
<tbody>
<tr>
<td>b</td>
<td>Validation of viral-mediated overexpression of HSV-Dnmt3a by mRNA expression in NAc.</td>
</tr>
<tr>
<td>c</td>
<td>Overexpression of Dnmt3a in NAc decreased time grooming in the splash test in both males and females.</td>
</tr>
<tr>
<td>d</td>
<td>Dnmt3a overexpression increased latency to eat in a novel environment in both males and females.</td>
</tr>
<tr>
<td>e</td>
<td>Overexpression of Dnmt3a decreased sucrose preference in both males and females.</td>
</tr>
<tr>
<td>f</td>
<td>Overexpression of Dnmt3a increased percentage of time spent immobile in the FST in both sexes ($n = 9$ or $10$/sex/virus). &quot;Main effect of virus (two-way ANOVA).&quot;</td>
</tr>
<tr>
<td>g</td>
<td>Dnmt3a overexpression or sex did not alter time spent in the open arm of the EPM.</td>
</tr>
<tr>
<td>h</td>
<td>There were no effects of Dnmt3a overexpression or sex on locomotor activity.</td>
</tr>
</tbody>
</table>

---

Hodes et al. • Sex Differences in Stress-Induced NAc Transcriptome J. Neurosci., December 16, 2015 • 35(50):16362–16376 • 16369
females, but knock-out of Dnmt3a reversed this effect ($F_{(1,33)} = 4.35, p = 0.04$; Fig. 5a). Stressed AAV-GFP injected females showed a decrease in sucrose preference that was blocked by knock-out of Dnmt3a ($F_{(1,33)} = 6.41, p = 0.01$; Fig. 5e). Knock-out of Dnmt3a in females also increased active coping response in the FST ($F_{(1,33)} = 6.13, p = 0.01$; Fig. 5f). In striking contrast to female mice, male mice exhibited no significant behavioral effects upon NAc knock-out of Dnmt3a as they were already resilient to SCVS. In a separate cohort of animals, we demonstrated that NAc specific knock-out of Dnmt3a had no effect on exploratory anxiety-associated behavior in the EPM or on locomotor activity following SCVS ($p > 0.05$; Figs. 5g,h).

**Dnmt3a knock-out in female NAc creates a mixture of male- and female-like transcriptional responses to SCVS**

Based on these findings that Dnmt3a knock-out from the NAc induces behavioral resilience to SCVS in females, making them behaviorally resemble males, we next examined the effects of Dnmt3a knock-out on NAc transcriptional responses to SCVS in both sexes. The goal was to determine whether stressed females without Dnmt3a in NAc are transcriptionally similar to resilient stressed males or whether Dnmt3a knock-out affected distinct sets of genes in females. Adult male and female Dnmt3a$^{2lox/2lox}$ were injected intra-NAc with AAV-Cre or AAV-GFP and allowed 2 weeks for maximal viral expression. All animals were subjected

---

**Figure 5.** Dnmt3a knock-out from NAc in females promotes resilience to SCVS. a, Schematic of surgery, SCVS procedure, and behavioral testing. b, Validation of Dnmt3a knock-out by mRNA expression levels in NAc ($n = 5–11$ per condition). c, Dnmt3a knock-out from NAc blocks the decrease in grooming caused by SCVS in females ($n = 8–11$/sex/virus for behavioral testing). d, Dnmt3a knock-out from NAc blocks the increased latency to eat in the novelty suppressed feeding test in females. e, Dnmt3a knock-out from NAc blocks the decreased sucrose preference in females. f, Dnmt3a knock-out from NAc blocks the increase in passive coping in the FST in females. No effect of Dnmt3a knock-out was evident in males. g, There was no effect of excising Dnmt3a or sex on anxiety associated exploratory behavior in the EPM. h, There were no effects of Dnmt3a knock-out or sex on locomotor activity. *Significant interaction between sex and virus (two-way ANOVA followed by Bonferroni post hoc analysis). ∧ indicates a main effect of virus.
to our standard 6 d SCVS procedure, after which NAc was analyzed by RNA-seq. We first compared SCVS males that were injected intra-NAc with AAV-GFP to SCVS females that were injected with AAV-GFP to obtain a direct measure of genes that differed in stressed males versus stressed females. Genes that differed between stressed females with or without Dnmt3a were then overlapped with the genes that differed in males to determine whether the same or different genes were altered by removing Dnmt3a. Dnmt3a knock-out increased the number of genes that were similarly regulated in stressed males and females (Fig. 6a). When genes that were upregulated by stress were examined, 7% now overlapped (p = 9.72E-30; Fig. 6b), a doubling of the per-
To determine which genes regulated by SCVS in females were affected by removal of Dnmt3a, we compared gene profiles from the first RNA-seq experiment (Stress/Control) with the second RNA-seq experiment (Stress/Control) with the second RNA-seq experiment (Stress/Control). We found that, in females, removal of Dnmt3a led to neutralization of transcription regardless of whether these genes were activated or suppressed by stress (Fig. 6c).

Next, we examined how Dnmt3a knock-out in the female NAC altered the top 10 gene ontology pathways that were regulated by stress. Using Ingenuity pathway analysis, we explored whether patterns of gene expression in NAC lacking Dnmt3a resembled wild-type males that were stressed (i.e., resilience) or wild-type females that were stressed (i.e., susceptibility). Seven of the top 10 canonical pathways affected by SCVS in wild-type females were changed to male levels upon removal in females. Overall, network analysis

<table>
<thead>
<tr>
<th>Gene name</th>
<th>Fold change</th>
<th>p value</th>
<th>Gene name</th>
<th>Fold change</th>
<th>p value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Dnmt3a</td>
<td>-0.355863384</td>
<td>0.038272611</td>
<td>Klf19</td>
<td>2.298627522</td>
<td>0.028274182</td>
</tr>
<tr>
<td>Lgk85</td>
<td>2.168052913</td>
<td>0.021273717</td>
<td>Dnmt3a</td>
<td>-0.355863384</td>
<td>0.038272611</td>
</tr>
<tr>
<td>Lgk85</td>
<td>2.168052913</td>
<td>0.021273717</td>
<td>Dnmt3a</td>
<td>-0.355863384</td>
<td>0.038272611</td>
</tr>
<tr>
<td>Lgk85</td>
<td>2.168052913</td>
<td>0.021273717</td>
<td>Dnmt3a</td>
<td>-0.355863384</td>
<td>0.038272611</td>
</tr>
<tr>
<td>Lgk85</td>
<td>2.168052913</td>
<td>0.021273717</td>
<td>Dnmt3a</td>
<td>-0.355863384</td>
<td>0.038272611</td>
</tr>
<tr>
<td>Lgk85</td>
<td>2.168052913</td>
<td>0.021273717</td>
<td>Dnmt3a</td>
<td>-0.355863384</td>
<td>0.038272611</td>
</tr>
<tr>
<td>Lgk85</td>
<td>2.168052913</td>
<td>0.021273717</td>
<td>Dnmt3a</td>
<td>-0.355863384</td>
<td>0.038272611</td>
</tr>
<tr>
<td>Lgk85</td>
<td>2.168052913</td>
<td>0.021273717</td>
<td>Dnmt3a</td>
<td>-0.355863384</td>
<td>0.038272611</td>
</tr>
<tr>
<td>Lgk85</td>
<td>2.168052913</td>
<td>0.021273717</td>
<td>Dnmt3a</td>
<td>-0.355863384</td>
<td>0.038272611</td>
</tr>
<tr>
<td>Lgk85</td>
<td>2.168052913</td>
<td>0.021273717</td>
<td>Dnmt3a</td>
<td>-0.355863384</td>
<td>0.038272611</td>
</tr>
</tbody>
</table>
SCVS alters different transcriptional pathways in males and females

Although males do not show behavioral susceptibility to SCVS, they exhibit robust transcriptional changes after stress. Indeed, more genes were regulated in NAc by SCVS compared with unstressed controls in males than in females, and this may reflect a more active transcriptional response that contributes to stress resilience. Few of the genes that were regulated by stress in males overlapped with the same genes regulated by stress in females. The genes that were significantly downregulated in both males and females by stress were for the most part activity-dependent early response genes such as cFos, Arc, and Npas4, many of which have been demonstrated to affect a multitude of different downstream molecular cascades (Spiegel et al., 2014). Genes that were upregulated in both sexes included several involved in G-protein-coupled receptor signaling. Network analysis demonstrated that molecules involved with the cardiovascular system, DNA regulation, cancer and nervous system development and function were among the top 10 networks regulated by stress in both sexes as indicated by enrichment scores. Some networks, such as the cardiovascular system, received similar enrichment scores in both males and females, indicating a similar number of genes in each network were involved, although different genes were activated or suppressed by stress within each sex. Other networks, such as nervous system development and function, were enriched to a much greater degree in females than males. We believe that identification of sex-specific changes in these broad network categories provides a rationale for developing individualized diagnostic tests and treatment strategies for male and female depression.

Dnmt3a in NAc controls behavioral susceptibility to stress

Both chronic cocaine exposure and repeated social defeat stress increase Dnmt3a expression in NAc of male mice (LaPlant et al., 2010). Dnmt3a is the most abundantly transcribed DNA methyltransferase in NAc of male (LaPlant et al., 2010) and female mice and humans. Here we demonstrate that SCVS increases levels of Dnmt3a in the NAc of both male and female mice at least 4–24 h after stressor cessation. Dnmt3a expression levels in NAc were also increased in humans suffering from major depressive disorder. In both sexes, these effects were partially attenuated by antidepressant treatment. These findings are interesting in light of the recent report that single nucleotide polymorphisms in the human Dnmt3a gene, extracted from peripheral tissues, are associated with the ability to buffer the effects of stress contributing to negative affect (Pishva et al., 2014).

Earlier studies have associated increased Dnmt3a levels in response to maternal stress during the neonatal period with subsequent increased anxiety-like behavior in males through lasting epigenetic regulation of the hypothalamic-pituitary-adrenal axis (Jensen Peña et al., 2012; Wang et al., 2013). Alternatively, early life stress can downregulate Dnmt3a expression in the mPFC of mice, although causal links have not yet been made with depression or anxiety behavior (Blaze and Roth, 2013). In contrast to early life stress, exposure to SCVS on Dnmt3a in adulthood reported here seems to be specific to the NAc as no effects were observed in the mPFC. Further studies will be needed to determine the effects of stress on Dnmt3a levels in subregions of mPFC (infraalimbic vs prelimbic) as well as other stress responsive brain regions associated with mood disorders. In adult male animals, overexpression of Dnmt3a in the NAc increased social avoidance behavior following a subthreshold social stress (LaPlant et al., 2010). Here we expand upon these findings and demonstrate that
Dnmt3a overexpression in NAc functionally contributes to stress susceptibility in both sexes. Males and females were injected intra-NAc with HSV-Dnmt3a and then exposed to 3 d STVS. As females are already susceptible to the 6 d version of SCVS, we used this subthreshold procedure that normally does not induce depression and anxiety-related behavior to uncover whether the animals had shifted to a more susceptible phenotype. Both males and females overexpressing Dnmt3a in NAc exhibited depression-like behaviors after STVS across a behavioral test battery that included the splash test, NSF, sucrose preference, and FST. Together, these data suggest that the higher transcriptional expression of Dnmt3a is sufficient to induce a stress susceptible state that may be specific to depression-like behavior.

While overexpression of Dnmt3a in the NAc induces stress susceptibility in both males and females, conditional deletion of the Dnmt3a gene from NAc neurons induced behavioral resilience in females. Males do not display behavioral susceptibility to stress under normal conditions and therefore did not show any changes in behavior upon Dnmt3a knock-out. Previous research demonstrated that pharmacologically inhibiting Dnmt3a in NAc, through infusion of RG108, in males susceptible to social defeat stress, reversed avoidance behavior (LaPlant et al., 2010). These effects were similar to those produced by 28 d of systemic administration of the standard antidepressant fluoxetine (LaPlant et al., 2010), indicating that blocking DNA methylation is antidepressant-like in stressed male animals.

Removing Dnmt3a from the female NAc shifts transcriptional patterns after SCVS

Although excising Dnmt3a from the NAc made females stress resilient, it was not clear from the behavioral data whether this was due to a more male-like transcriptional pattern in the female NAc upon Dnmt3a knock-out or to distinct transcriptional mechanisms. Therefore, we performed RNA-seq on NAc from separate groups of male and female Dnmt3aΔlocΔia mice that were injected intra-NAc with either AAV-GFP or AAV-Cre and then subjected to SCVS. AAV-GFP-expressing females exposed to SCVS have mostly different patterns of transcriptional activation and suppression than AAV-GFP-expressing males, similar to observations in noninjected SCVS animals (Fig. 2). Removing Dnmt3a from the female NAc, which leads to behavioral resilience, dramatically alters transcriptional profiles in this brain region. Females lacking Dnmt3a from NAc display a hybrid of male and female stress-specific transcriptional profiles. For example, there is a doubling (upregulation) to tripling (downregulation) of the percentage of overlapping genes occurring between stressed males and stressed Dnmt3a knock-out females. These changes in transcription lead to a more male-like expression of canonical pathways, with Dnmt3a knock-out in females inducing a male-like pattern in 7 of the top 10 regulated gene ontology pathways. Despite this partial shift toward male-like patterns, Dnmt3a knock-out from the female NAc also leads to many unique changes in transcription associated with behavioral resilience in the mutant females.

In conclusion, these data demonstrate a sex-specific transcriptional profile in NAc that mirrors sex-specific behavioral stress susceptibility. This transcriptional profile can be altered by removal of the de novo DNA methyltransferase Dnmt3a from this brain region, which creates a hybrid male/female transcriptional pattern. Such removal also induces behavioral resilience to stress in females. These findings shed new light onto molecular factors controlling sex differences in stress responses, the first step in defining therapeutic strategies selective for stress-related disorders in women.

References


File SE (2001) Prefrontal-DNA methyltransferase Dnmt3a from this brain region, which creates a hybrid male/female transcriptional pattern. Such removal also induces behavioral resilience to stress in females. These findings shed new light onto molecular factors controlling sex differences in stress responses, the first step in defining therapeutic strategies selective for stress-related disorders in women.


