

Reduced Cocaine Reinforcement in the Male Offspring of Cocaine-Experienced Sires

Mounting evidence suggests that parental ingestion of abused drugs influences the physiology and behavior of future generations in the absence of prenatal exposure (Vassoler *et al*, 2014). However, few studies have examined potential mechanisms of transmission of addiction-related phenotypes. Therefore, we developed a rat model to delineate a heritable phenotype resulting from the self-administration of cocaine. Our research indicates that the male offspring of cocaine-experienced male rats find cocaine-less reinforcing, leading them to consume considerably less cocaine than controls (Vassoler *et al*, 2013). Increased levels of cortical brain-derived neurotrophic factor (BDNF) may be the underlying cause of the cocaine resistance observed in the sons. These findings show that cocaine-induced changes in physiology can be inherited by sons from their fathers. The reason for the sex specificity is unclear, but may be due to intergenerational effects on gene transcription interacting with subsequent hormonal influences.

We usually think about inherited changes in physiology occurring via natural selection on an evolutionary timescale. However, a growing body of evidence indicates that environmental information can be transmitted from one generation to the next. For example, epidemiological data show that a fetus exposed to famine early in pregnancy will tend to be born small but will be more prone to obesity, diabetes, and mental health issues as an adult (Lumey *et al*, 2011). Some of these health problems also plague the grandchildren of mothers malnourished in early pregnancy (Lumey *et al*, 2011). The latter is a potential example of epigenetic inheritance, defined as changes in phenotype caused by mechanisms other than alterations in DNA sequence.

In our paradigm, male rats self-administered cocaine for 60 days (controls were administered saline) and were then paired with naive females. The offspring of these matings were tested for acquisition of cocaine self-administration. Our results indicated that the male, but not female, offspring of cocaine-experienced sires acquired cocaine self-administration more slowly and had decreased levels of cocaine intake relative to controls. Moreover, control animals were willing to work significantly harder for single cocaine infusions than the cocaine-sired rats, suggesting a decrease in the reinforcing effectiveness of cocaine. The cocaine-sired rats did not have generalized learning deficits, as there was no difference in acquisition of food self-administration. We next looked at BDNF expression in the prefrontal cortex of naive littermates. The cocaine-sired male offspring had increased histone acetylation association with a *Bdnf* promoter and augmented *Bdnf* mRNA, which enhanced BDNF protein levels in the prefrontal cortex. Importantly, blocking the action of BDNF reversed the cocaine-resistance phenotype.

These findings raise the question of how paternal cocaine exposure influenced the behavior of the male offspring. Intriguingly, our results indicate that there were changes in histone acetylation of *Bdnf* promoters in the sperm of cocaine-experienced sires, which might lead to increases in BDNF protein expression in the brains of the offspring. This finding indicates that cocaine causes epigenetic changes in sperm, which may alter the physiology and behavior of offspring in the absence of changes in DNA sequence. Taken together, these results indicate that paternal exposure to toxins such as cocaine can have profound effects on gene expression and behavior of the offspring.

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Lumey LH, Stein AD, Susser E (2011). Prenatal famine and adult health. *Annu Rev Public Health* **32**: 237–262.

Vassoler FM, Byrnes EM, Pierce RC (2014). The impact of exposure to addictive drugs on future generations: Physiological and behavioral effects. *Neuropharmacology* **76**: 269–275.

Vassoler FM, White SL, Schmidt HD, Sadri-Vakili G, Pierce RC (2013). Epigenetic inheritance of a cocaine-resistance phenotype. *Nat Neurosci* **16**: 42–47.

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De Novo Mutations in Schizophrenia Disrupt Genes Co-Expressed in Fetal Prefrontal Cortex

We recently reported that damaging *de novo* mutations in persons with schizophrenia from otherwise healthy families disrupt genes that orchestrate neurogenesis in fetal prefrontal cortex (Gulsuner *et al*, 2013). By sequencing genomic DNA from entire families, we identified point mutations and copy number variants that appeared *de novo* in 105 persons with schizophrenia and in 84 of their healthy siblings. Patients were more likely than unaffected siblings to harbor damaging *de novo* mutations (47/105 vs 30/84, OR = 1.91, X² = 4.45; *p* = 0.035). The proportion of schizophrenia attributable to damaging *de novo* mutations in this sample was 21%.

Even more striking than the difference in mutation frequencies was the distinctive functional relationship among the genes harboring mutations. The genes disrupted by damaging *de novo* mutations in patients formed a network defined by protein interaction (Mostafavi *et al*, 2008) and by

transcriptional co-expression (BrainSpan: Atlas of the Developing Human Brain, 2013) in the dorsolateral and ventrolateral prefrontal cortex during fetal development. Interactions among these genes were not significantly enriched in other brain regions or during other developmental periods, nor were interactions enriched among genes harboring benign *de novo* events. Of the 54 genes disrupted by damaging *de novo* mutations in patients, 50 mapped to this network. These genes are active in pathways critical to neurogenesis, including neuronal migration, synaptic transmission, signaling, transcriptional regulation, and transport. Many network genes share a pattern of high expression in prefrontal cortex during the early fetal development, with transcription levels declining in the late fetal development and childhood only to rise again during young adulthood (Figure 1), coinciding with the typical age of onset of the illness.

The results suggest that aberrant prefrontal cortical development is critical to the pathogenesis of schizophrenia. The prefrontal cortex is highly interconnected with other brain regions, and organizes information to coordinate executive skills, including working memory, attention span, problem solving, and self-regulation (Catts *et al*, 2013). Given the clearing-house role of prefrontal cortex in

brain function, disruptions in this region during early development likely result in the overall loss of neocortical integrity and connectivity. Impairments in executive functions are characteristic of schizophrenia, suggesting that higher-order cognitive deficits are early manifestations of the syndrome, with psychosis emerging as critical brain regions mature.

Some genes with *de novo* mutations in patients function in neurotransmitter pathways that suggest possible avenues for treatment, including GLS (glutamate synthesis), ADCY9 (glutamate and GABA signaling), and SLC18A2 (serotonin, dopamine, norepinephrine, epinephrine, and histamine transport). *CACNA1I*, a brain-specific, T-type calcium channel that regulates neuronal firing in the thalamus, striatum, nucleus accumbens, and prefrontal cortex, was the only gene disrupted in two unrelated probands, each harboring a different *de novo* event. Some antipsychotic medications, including clozapine, inhibit T-type calcium channels (Choi and Rhim, 2010).

Key mechanisms underlying complex psychiatric disorders can be identified by characterizing brain pathways disrupted by mutant genes in affected persons. By integrating genomic analyses with brain mapping strategies, we were able to define

possible disease-related processes and to identify potential targets for treatment. Applying the same approach in large-scale sequencing studies will help elucidate basic neurobiological mechanisms underlying normal brain circuitry and neuropsychiatric disease.

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BrainSpan: Atlas of the Developing Human Brain (2013); www.brainspan.org.

Catts VS, Fung SJ, Long LE, Joshi D, Vercammen A, Allen KM *et al* (2013). Rethinking schizophrenia in the context of normal neurodevelopment. *Front Cell Neurosci* 7: 60.

Choi KH, Rhim H (2010). Inhibition of recombinant Ca(v)3.1 (alpha1G) T-type calcium channels by the antipsychotic drug clozapine. *Eur J Pharmacol* 626: 123–130.

Gulsuner S, Walsh T, Watts AC, Lee MK, Thornton AM, Casadei S *et al* (2013). Spatial and temporal mapping of *de novo* mutations in schizophrenia to a fetal prefrontal cortical network. *Cell* 154: 518–529.

Mostafavi S, Ray D, Warde-Farley D, Grouios C, Morris Q (2008). GeneMANIA: a real-time multiple association network integration algorithm for predicting gene function. *Genome Biol* 9(Suppl 1): S4.

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Repetitive Transcranial Magnetic Stimulation as a Treatment for Auditory Hallucinations

With transcranial magnetic stimulation (TMS) a rapidly fluctuating magnetic field is delivered over a specific part of the brain, which can change brain activity in the underlying cortex. When targeting the motor cortex, TMS

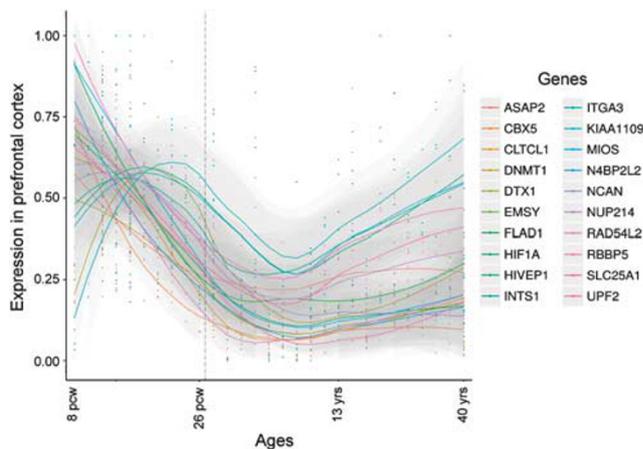


Figure 1. Expression levels of selected genes with damaging *de novo* mutations in dorsolateral prefrontal cortex throughout development (8 post-conception weeks to 40 years). Many network genes were highly expressed during early fetal prefrontal cortical development, with expression declining in late fetal development and childhood, and rising again during adulthood, coinciding with the typical age of onset of schizophrenia. Data were obtained from BrainSpan: Atlas of the Developing Human Brain (2013). RPKM values were max-min normalized and Loess smoothed across time points.