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The potential association of psychoactive pharmaceuticals in the environment with human neurological disorders

Gaurav Kaushik^{1,2,#,§}, Michael A. Thomas¹

¹Department of Biological Sciences, Idaho State University, Stop 8007, 921 S 8th Ave, Pocatello, ID 83209-8007, USA

²Stem Pharm, Incorporated, Madison, WI 53711 USA

Abstract

Psychoactive pharmaceuticals release into the environment and reach humans through a variety of routes, including sewage, drinking water, contaminated irrigation water, biosolids, soil and food. It was assumed that these compounds via the environment could induce genetic effects in the etiology of human neurological disorders. With the help of *in vitro*, *in vivo* and *in silico* approaches, we demonstrated that psychoactive pharmaceuticals in drinking water can cross maternal biological barriers and alter *in vitro* molecular and genetic mechanisms that potentially have a key role in the development, growth and regulation of neuronal systems during embryonic brain development.

Keywords

Psychoactive pharmaceuticals; Fluoxetine; Venlafaxine; Carbamazepine; Drinking water; Environmental toxicology

Introduction

Psychoactive pharmaceuticals (especially SSRIs, SNRIs and AEDs) are one of the mostly widely prescribed classes of drugs in the United States. Excretions from clinical patients contain active metabolites and isoforms with long half-lives (Calisto and Esteves, 2009; Thomas and Klaper, 2012). Sewage treatment plants (STP) release treated water containing pharmaceuticals into rivers and lakes, thus introducing contamination into aquatic systems. Due to the excretion of pharmaceuticals and their metabolites by humans and their inefficient removal by STP, these pharmaceuticals might reach potable water (Calisto and Esteves, 2009; Thomas and Klaper, 2012). By reusing sludge as biosolids and by irrigation with polluted surface and groundwater, these contaminants end up in the soil and accumulate in food crops (Goldstein et al., 2014; Riemenschneider et al., 2017). SSRI antidepressants

§ Corresponding author kaugaur@isu.edu.

#Current address

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including their metabolites tend to accumulate in brain tissues of fish (Arnnok et al., 2017; Brooks et al., 2005; Lajeunesse et al., 2011; Schultz et al., 2010; Silva et al., 2015; Valdés et al., 2016), other food organisms like mussels (Bringolf et al., 2010; Silva et al., 2016), and in food crops (Goldstein et al., 2014; Malchi et al., 2014; Riemenschneider et al., 2017). Previous laboratory studies demonstrated that gene sets associated with neuronal systems were up- and down-regulated in the brains of fathead minnows treated with psychoactive pharmaceuticals (fluoxetine, venlafaxine and carbamazepine) at low concentrations (Thomas et al., 2012; Thomas and Klaper, 2012). We hypothesized that exposure to psychoactive pharmaceuticals via environment would induce genetic effects associated with human neurological disorders including autism. Using *in vitro*, *in silico*, and *in vivo* approaches, we determined the extent to which psychoactive pharmaceuticals induced molecular patterns similar to neurological disorders (Kaushik et al., 2017, 2016a, 2016b, 2015).

Methods

We cultured human neuronal SK-N-SH cells on a dish and differentiated them into pure neuronal cells with retinoic acid (3 µg/L) for two weeks. We then treated them with a mixture of psychoactive pharmaceuticals (fluoxetine 10µg/L, venlafaxine 50µg/L and carbamazepine 100µg/L) for 48 hrs. We extracted the RNA of treated samples and used them for the RNA sequencing (Kaushik et al., 2016b). In parallel, we analyzed the expression of key synaptic proteins using flow cytometry (Kaushik et al., 2017). With the help of the GAGE enrichment analysis tool, we determined if any neuronal gene set was significantly up- and down-regulated under the treatments (Kaushik et al., 2016b). We then created an autism-associated protein-protein interaction network using Cytoscape and analyzed interactions of induced genes (or, proteins) (Kaushik et al., 2015). To determine the extent to which these pharmaceuticals can cross maternal biological barriers, we added ²H isotope labeled pharmaceuticals into the drinking water of female mice *in vivo*, and measured the $\delta^2\text{H}$ isotope signal in maternal liver and embryonic brains (Kaushik et al., 2016a).

Results

In Table 1, RNA-sequencing results from *in vitro* study showed that psychoactive pharmaceuticals in a mixture treatment altered the expression of neurological gene sets significantly. Those gene sets were associated with human neurological disorders including Idiopathic Autism, Alzheimer's disease and Schizophrenia (Kaushik et al., 2016b). Network analysis showed that genes in human cell cultures enriched by pharmaceutical mixtures and valproate (which was used as a positive control at clinical dosages) had similar network signatures and greater connectedness than genes in the overall network (Kaushik et al., 2015). In addition, we found that the expression of autism-associated synaptic proteins (HTR1B, HTR2C, OXTR, NMDAR1, GABRB3, PSD95 and SV2A) were altered significantly in cultured human neuronal cells by psychoactive pharmaceuticals (Kaushik et al., 2017). After analyzing mouse maternal liver and embryonic brains with mass spectrometry, we observed that carbamazepine presented in the maternal drinking water crossed intestinal and placental barriers and reached developing embryonic brains (Kaushik et al., 2016a).

Discussion

This study examined the potential association of psychoactive pharmaceuticals (FLX, CBZ and VNX) with neurological disorders. We hypothesized that psychoactive pharmaceuticals from drinking water and food can cross maternal biological barriers and alter *in vitro* neuronal protein and gene expression associated with neurological disorders. To address this overarching hypothesis, we determined the extent to which psychoactive pharmaceuticals can induce the gene or protein expression patterns associated with neurological disorders in human neuronal cells. The information presented in previous literature concerning the role of psychoactive pharmaceuticals in the etiology of neurological disorders is very limited. Therefore, this study sought to address the issue with different approaches to improve upon limited knowledge of these chemical contaminants present in the environment.

In our findings, we showed that these pharmaceuticals can induce *in vitro* expression of synaptic proteins and neuronal genes that are associated with neurological disorders like Autism, Alzheimer's disease and others (Kaushik et al., 2017, 2016b). We also found that the drug-induced gene expression changes in human neuronal cells represent higher connectedness in an ASD-associated protein-protein interaction network (Kaushik et al., 2015). Due to higher connectedness, the altered gene expression would further perturb more downstream connected proteins, thus creating profound effects in ASD-associated network because of the ripple effect. In addition, we also demonstrated that carbamazepine present in the drinking water can cross maternal intestinal and placental barriers and reached developing embryonic brains (Kaushik et al., 2016a).

Our findings are innovative and significant because they considered the ways in which psychoactive pharmaceuticals altered fundamental molecular expressions that may result in abnormal neuronal growth, regulation, and development, which are implicated in the etiology of human neurological disorders including idiopathic autism. To date, several studies have shown that mutations in candidate genes and other stochastic factors are responsible for only a few cases of idiopathic autism (Gompers et al., 2017, 2016; Kaushik and Zarbalis, 2016; Napoli et al., 2018), but the majority of cases result from the presence of an unknown environmental trigger (especially in the first trimester of pregnancy) in genetically susceptible individuals (Landrigan, 2010).

In the perspective of the bioaccumulation potential of the tested drugs and especially of their metabolites, it may be considered in the future to adjust the concentrations of the model substances. Given the lower BAC/BCF values of carbamazepine and fluoxetine, the test concentration of carbamazepine could be lowered, and the test concentration of fluoxetine can therefore be increased to make the test concentrations more environmentally relevant. Since the metabolites accumulate more strongly and can be more toxic, testing with metabolites may also be considered. Some researchers have also observed the strong accumulation of sertraline and in particular, norsesertraline in the brain tissues (Brooks et al., 2005; Schultz et al., 2010), this drug could be a good candidate for the follow-up testing.

Other future studies would include performing mice studies using pharmaceuticals (carbamazepine, fluoxetine and venlafaxine) labeled with different isotopes at different

isotopic concentrations (10%, 20%, 50% and 100%) to understand the transfer rate when those drugs are administered individually and, in a mixture to pregnant mice' drinking water and derive a mathematical relationship. And, in the continuation, it would be useful to further analyze newly born pups behavior and brain samples for in-depth understanding of association of pharmaceuticals at environmental relevant concentrations with human neurological disorders. In addition, many researchers have been creating embryonic brain-mimic models (also known as organoids) using human induced pluripotent stem cells (iPSCs) derived neurons, endothelial cells and microglia (Schwartz et al., 2015). With the help of recently developed tools such as label-free imaging and machine learning, these brain-mimic models can be treated with different neurotoxins at environment-relevant concentrations for high-throughput toxicity screening (Kaushik et al., 2019a, 2019b; Schwartz et al., 2015). The outcomes for these studies would provide more insights into altered genetic effects by environmental contaminants.

Conclusions

As a broader perspective, the current study suggests that psychoactive pharmaceuticals can interact with genetic factors causing altered neuronal growth, regulation and development associated with human neurological disorders.

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Highlights

- Psychoactive pharmaceuticals have been detected at low concentrations in wastewater, streams and drinking water.
- Psychoactive pharmaceuticals at low concentrations could cross maternal barriers and alter neuronal gene sets significantly during embryonic brain development.
- Altered gene sets are associated with human neurological disorders.

Table 1:

Enrichment of human neurological gene sets

| Source | Neurological Disorders gene set (previously published) | Size | Function/Description | Significant change in the expression of the gene set | Significance level |
|----------|--|------|---|--|--|
| GSE12457 | ADHD_down | 32 | Down-regulated genes by molecular alterations in genetic and environmental rat models of ADHD | Down-regulated | <i>P</i> -value = 0.000 <i>Q</i> -value = 0.003 |
| GSE12457 | ADHD_up | 44 | Up-regulated genes by molecular alterations in genetic and environmental rat models of ADHD | Down-regulated | <i>P</i> -value = 0.007 <i>Q</i> -value = 0.022 |
| GSE1297 | Alzheimers | 308 | Genes upregulated in the CA1 region of the hippocampus in Alzheimer's disease | Up-regulated | <i>P</i> -value = 0.004 <i>Q</i> -value = 0.027 |
| | Autism_idiopathic | 439 | Combination of Chakrabarti, Hu and ASD_2class; excluding duplicates | Up-regulated | <i>P</i> -value = 0.000 <i>Q</i> -value = 0.001 |
| | Parkinsons | 130 | Genes associated with Parkinsons | Down-regulated | <i>P</i> -value = 0.000 <i>Q</i> -value = 0.000 |
| | Schizophrenia | 29 | Differentially expressed proteins in the brains of SCZ patients | Down-regulated | <i>P</i> -value = 0.000 <i>Q</i> -value = 0.000 |
| GSE15402 | ASD_2Class | 354 | Differentially expressed genes (significantly) from a SAM 2-class analysis of the data from combined autistic samples and neurotypical controls | Up-regulated | <i>P</i> -value = 0.000 <i>Q</i> -value = 0.000 |
| GSE15402 | ASD_Mild | 306 | Differentially expressed genes (significantly) from a SAM 2-class analysis of the data from mild autistic samples and neurotypical controls | Up-regulated | <i>P</i> -value = 0.000 <i>Q</i> -value = 0.000 |

The table represents the analyses of gene sets associated with neurological disorders. Source indicates the database from where the gene set was derived, Gene Ontology (GO) or Molecular Signatures Database (MSigDB). Size represents the number of genes in each gene set. Significant change indicates the expression of gene sets which were significantly found up-regulated and down-regulated in the mixture treatment of pharmaceuticals on cultured human neuronal cells. Gene sets with *P*-value < 0.01 and *Q*-value < 0.1 were considered as statistically significantly enriched.