NMR-BASED METABOLOMICS APPROACH TO EXPLORE BRAIN METABOLIC CHANGES INDUCED BY PRENATAL EXPOSURE TO AUTISM-**INDUCING CHEMICALS AS A FUNCTION OF AGE AND SEX**



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Introduction

SD

Autism spectrum disorders (ASD) are a heterogeneous group of neurodevelopmental disorders characterized by deficits in social interaction, social and verbal communication along with the presence of repetitive, restricted and stereotyped patterns of interests and/or behaviors. Its origin is largely unknown, but current theories pose that autism can be caused by environmental factors, like the exposure to some chemicals. Valproic acid (VPA), an antiepileptic drug, and chlorpyrifos (CPF), an organophosphorus pesticide, are linked to greater occurrence of ASD in humans. Identification of biomarkers can be a challenge considering the complexity and diversity of molecular pathways implicated in most neurological disorders such as ASD, so metabolomics works in this way. This technique assures the characterization of an individual metabolic phenotype, that permits the detection of rapid biochemical pathway alterations and unravels multiple biomarker panels. In this study, we aimed to explore brain metabolic changes in a rat model of ASD induced by prenatal exposure to VPA and CPF in rats at different postnatal ages in the metabolome of different tissues of the brain (hippocampus and cerebellum). The biochemistry in these two anatomical regions is expected to be disturbed to different extents by the administration of these xenobiotics, and also depending on the age and sex. The metabolomic analysis was achieved by an analytical platform based on a liquid **high-resolution NMR spectrometer** and a high-sensitive cryoprobe, which is the method of choice for efficient quantification of tissue metabolites.



Results and discussion



PLS-DA scores plots reveals discrimination between cerebellum tissues from B and C brains from control and CPF groups.

plot shows the discrimination **OPLS-DA** scores between tissues of hippocampus and cerebellum from B and C brains from control and VPA groups.

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00	C	e-Control 🔲 Ce-CPF	Ce-AVP	Ce-Control	Ce-CPF [Ce-AVP	
Control 🔲 CPF	AV H	i-Control 🔲 Hi-CPF	Hi-AVP	Hi-Control	Hi-CPF [Hi-AVP	

brain regions in all age groups, after administration of VPA and/or CPF comparing to control. Impaired glutamate/GABA-glutamine cycle have been linked to ASD related phenotypes and behavior.

Conclusions

- VPA and CPF prenatal exposure may evoke both specific and common metabolic responses associated to an increased risk of ASD occurrence in different tissues of the brain, depending on the aging process, but no correlation was found with sex.
- Concerning the exposure to VPA and CPF, changes in some metabolites were common in all group ages and brain tissues: NAA generally increased while acetate and choline generally decreased with VPA and/or CPF exposure.
- Reduced GABA along with differences in glutamate and Gln concentrations might indicate a cortical excitation/inhibition imbalance, which may contribute to the development of ASDs.
- These observations provided broad insight for systemic effects of the exposure to important ASD-inducing chemicals on brain metabolism.

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