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Application of a metabolomic multiplatform to investigate Alzheimer's disease pathogenesis

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Application of a metabolomic multiplatform to investigate Alzheimer's disease pathogenesis





Abstract:

Alzheimer's disease (AD) is the most common neurodegenerative disorder, but nowadays there is no cure mainly because its etiology is still unclear. With the aim to get a comprehensive overview of pathological mechanisms associated with AD, complementary metabolomic platforms were developed, including screening procedures based on direct mass spectrometry analysis and hyphenated approaches with orthogonal separation mechanisms such as liquid chromatography, gas chromatography and capillary electrophoresis. The application of these techniques to serum samples from patients suffering from Alzheimer's disease and mild cognitive impairment enabled the identification of numerous metabolic alterations linked to pathogenesis of this disorder and its progression from pre-clinical stages, including abnormalities in the composition of membrane lipids, deficits in energy metabolism and neurotransmission, and oxidative stress, among others. In turn, these metabolomics perturbations were also observed in multiple biological compartments from the APP/PS1 model, including serum, brain, liver, kidney, spleen and thymus, thus demonstrating the utility of these transgenic mice to model Alzheimer's disease. The comparison of different brain regions evidenced that the most affected areas are hippocampus and cortex, but other regions were also significantly perturbed to a lesser extent. Furthermore, alterations detected in peripheral organs confirm the systemic nature of this neurodegenerative disorder.

Keywords: metabolomics; mass spectrometry; Alzheimer's disease



Introduction

Alzheimer's disease (AD): most common neurodegenerative disorder among older people

- Insidious onset
- Progressive decline of cognitive functions



Mild cognitive impairment (MCI)

- Incipient dementia
- Preclinical phase of AD

- Loss of neurons and synapses
- Unknown causes
- Multifactorial pathology
- Systemic disease
- Genetic factors
- Inflammation
- Oxidative stress
- Metal homeostasis
- > Amyloid hypothesis
- Tau hypothesis



Introduction



*NINCDS-ADRDA: National Institute of Neurological and Communicative Disorders and Stroke and Alzheimer's Disease and Related Disorders Association



Introduction

Metabolomics: comprehensive study of the entire set of metabolites from a biological system as well as of metabolic changes produced in response to a genetic or environmental perturbation

- Chemical heterogeneity
- Wide range of concentrations
- Temporal and inter-individual variability



Analytical Techniques in Metabolomics

- Sensitivity
- Versatility











ESI(+)

ESI(-)

Anal Bioanal Chem 2014, 406:7137-7148

FIA-APPI(+/-)-QTOF-MS



$$D + h\nu \rightarrow D^{\bullet +}$$

$$D^{\bullet +} + AB \rightarrow D + AB^{\bullet +}$$

$$D^{\bullet +} + MP \rightarrow [D - H]^{\bullet} + [MP + H]^{+}$$

$$[MP + H]^{+} + AB \rightarrow MP + [AB + H]^{+}$$





Talanta 2015, **131**:480-489

UPLC/GC/CE-MS



- Serum: similar metabolic alterations between AD patients and APP/PS1 mice
- Brain: hippocampus and cortex are the most affected regions
- > Peripheral organs: systemic nature of AD





J Pharm Biomed Anal 2015, **107**:378-385

Electrophoresis 2015, **36**:577-587









SFA/PUFA-PL imbalance





Oxidative stress Energy Metabolism \downarrow antioxidants ↑ glucose GLUCOLYSIS \geq Uric acid $\rightarrow \uparrow$ alanine ↑ lactate < pyruvate Histidine & imidazole \geq carnosine Cystine & pyroglutamic acid glutathione LIPID \uparrow acyl-carnitines \longrightarrow acetyl-CoA β-ΟΧΙDΑΤΙΟΝ \downarrow carnitine \longrightarrow ↑ fatty acids ↑ oxidation products ATP-CREATINE SYSTEM Eicosanoids (prostaglandins, LTB4) citrate lipid \succ phosphocreatine peroxidation oxalacetate ↑ isocitrate nucleotides Adenosine \geq oxidation ATP ↓ creatine ↑ keto-glutarate **_** malate **KREBS** CYCLE succinate ↑ creatinine



Hyperammonemia



Conclusions

- Metabolomic platforms based on direct mass spectrometry analysis (DI-ESI-MS, FIA-APPI-MS) show a great potential in order to perform a first metabolic screening due to its wide metabolome coverage, reduced analysis time and instrumental simplicity
- The combination of orthogonal separation techniques allows performing a more comprehensive investigation of the entire metabolome

RP-UHPLC-MS GC-MS CE-MS

The application of these metabolomic approaches enabled the detection of numerous metabolic alterations associated to AD pathogenesis and progression from MCI (abnormal metabolism of membrane lipids, failures in neurotransmission, deficit in energy metabolism, oxidative stress)



Conclusions

- Metabolomic study of the APP/PS1 transgenic mouse allowed performing a holistic investigation about pathological mechanisms associated with the development of Alzheimer's disease in multiple biological compartments
- Serum metabolomic profiles from patients and APP/PS1 mice showed great similarities, thus demonstrating the potential of this transgenic mouse to model AD
- Comparative analysis of different brain regions showed that the most affected areas by the characteristic neuropathology of Alzheimer's disease in the APP/PS1 mouse were hippocampus and cortex, although other regions were also disrupted to a lesser extent, including the striatum, cerebellum and olfactory bulbs.
- Metabolomic profiles of liver, kidney, spleen and thymus showed significant changes in levels of multiple metabolites, common to those previously described in serum and brain, corroborating the systemic nature of this neurodegenerative disorder



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