Mass spectrometry-based protein analysis in research of Alzheimer's disease

<u>Markéta Nezvedová ⁽¹⁾, Tereza Váňová ^(2,3), Dáša Bohačiaková ⁽²⁾, Zdeněk Spáčil ⁽¹⁾</u>

(1) Masaryk University, Faculty of Science, RECETOX Centre, Brno, Czech Republic (2) Masaryk University, Faculty of Medicine, Dept. of Histology and Embryology, Brno, Czech Republic (3) International Clinical Research Center (ICRC) St. Anne's University Hospital, Brno, Czech Republic marketa.nezevdova@recetox.muni.cz

RECETOX

OVERVIEW

Aim: Identification of cell protein markers to characterize the 3D cell model system of the brain used to study Alzheimer's disease (AD). Quantify a new set of protein biomarkers related to AD in cell systems and clinical samples.

Methods: Ultra-high performance LC, tandem mass spectrometry (UHPLC-SRM-MS/MS) Achievements: Development of multiplex assay targeting several proteins of interest: cell-specific and AD-related proteins.

BACKGROUND

RESULTS

CEREBRAL ORGANOIDS

Fig. 3: Characterization of cerebral organoids (COs, n=4 per time point) using cell-specific protein markers. (A) Cell markers identified in COs derived from healthy (wild type, WT) cell lines at various developmental stages showed the usual course of neurodevelopment. Decreasing tissue levels of NSCs markers and increasing RGCs markers indicate ongoing neuronal differentiation with a culmination in D110, same as neuronal markers. Astrocyte markers showed an increasing trend with the highest levels in the last time point. (B) Cell markers indicate normal neurodevelopment in both, WT and diseased (mutation in PSEN1, MUT) organoids. (C) Successful identification of 27 of 40 selected protein markers in each analyzed cerebral organoid, including the smallest one (6 μ g).

- The dementia epidemic affects around 47 million people worldwide, with increasing incidence. Alzheimer's disease (AD) is the most common form of dementia with an unknown cause.^[1]
- Recent advances in mass spectrometry and cell biology opened new avenues to investigate neurodegeneration. ^[2,3]
- **Cerebral organoids** (COs) are three-dimensional cell cultures representing an emerging model system to study biological processes causing neurological diseases.
- COs recapitulate the brain tissue's cytoarchitecture, mimicking the brain development in vivo.
- Immune-based assays are frequently used to analyze proteins.^[4]
- Several protein targets can be analyzed simultaneously using the system of ultra-high performance liquid chromatography (UHPLC) coupled to tandem mass spectrometry in the mode of selected reaction monitoring (SRM-MS/MS).

EXPERIMENTAL DESIGN **AND METHODS**

Fig. 1: Formulation of working hypothesis using cerebral organoids and confirmation of working hypothesis in clinical samples (cerebrospinal fluid, serum).

SAMPLE COLLECTION:

ANALYTICAL CHEMISTRY:

STATISTICAL ANALYSIS:

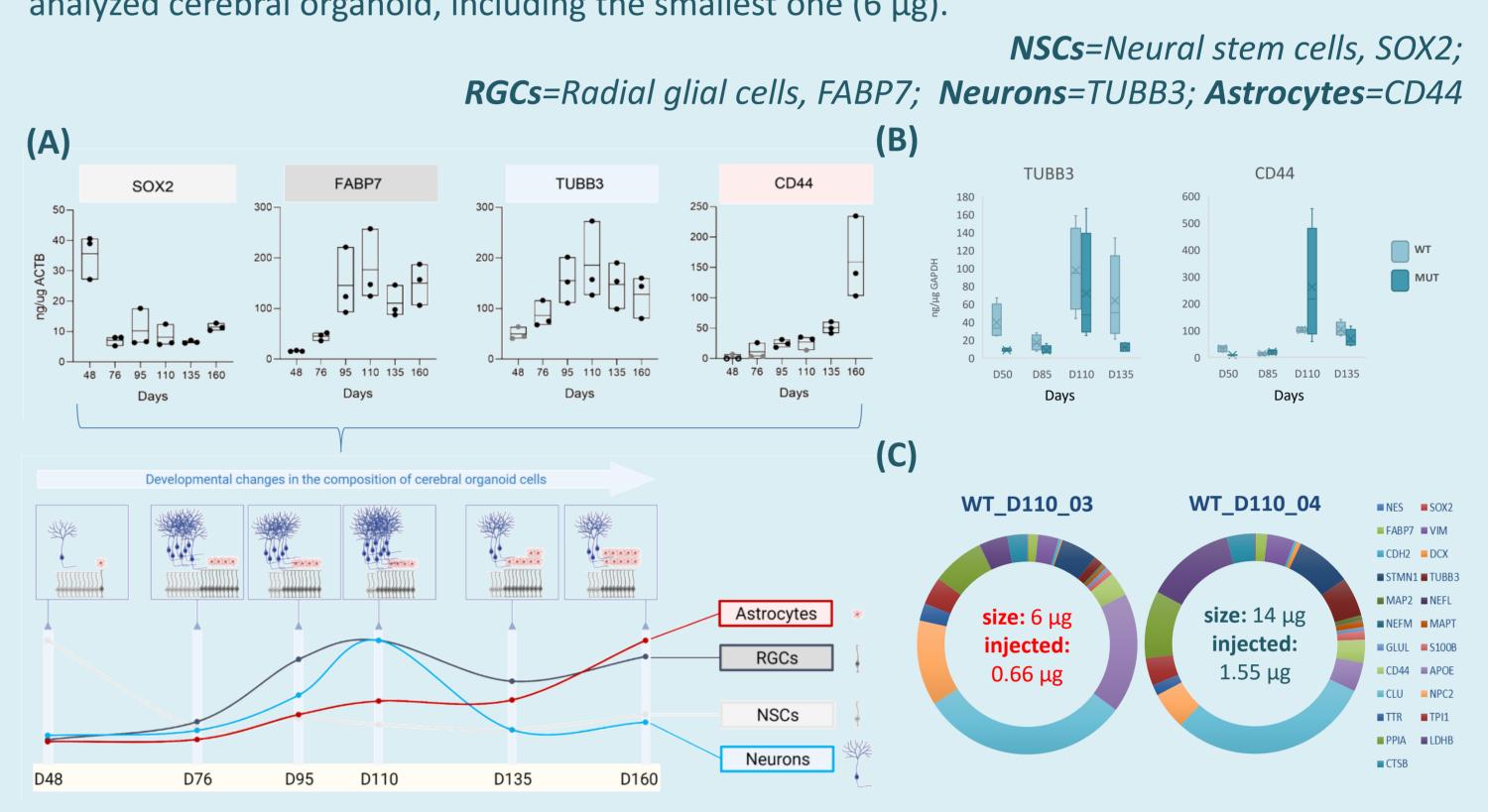
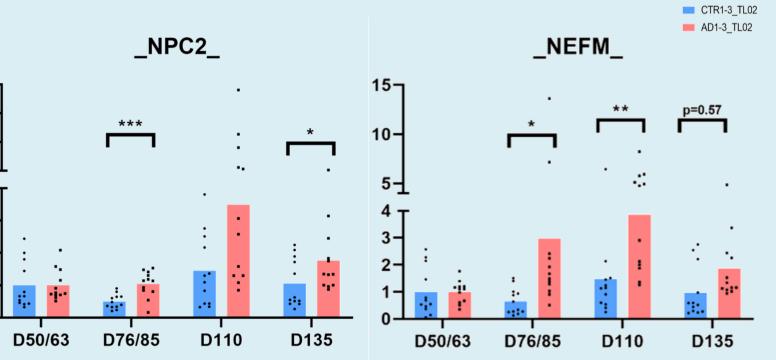
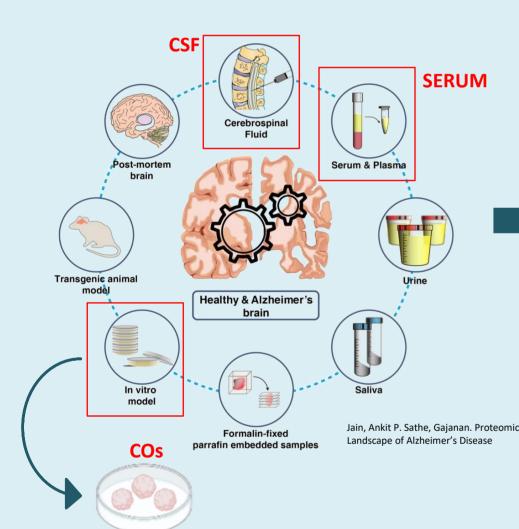
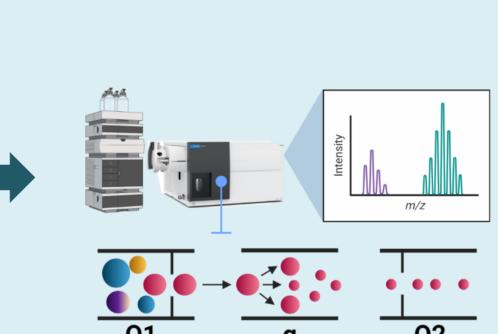


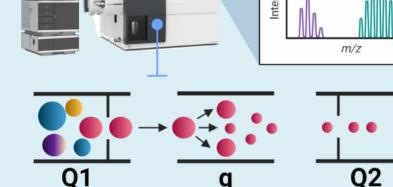
Fig. 4: AD-related proteins in three different cell lines from healthy controls (CTR1-3, n=12) and patients Alzheimer's disease with (AD1-3, **n=12).** Levels of markers related mainly (NPC2), lipids brain and to neurofilaments showed (NEFM) increased levels in AD organoids.



Days







Sample types used to study proccesses occuring in the brain are highlighted.

UHPLC (C18 Peptide CSH column) coupled to **tandem** mass spectrometer (Agilent) was used for targeted analysis.

Use of appropriate **bioinformatics** tools to demonstrate significance in the obtained data sets.

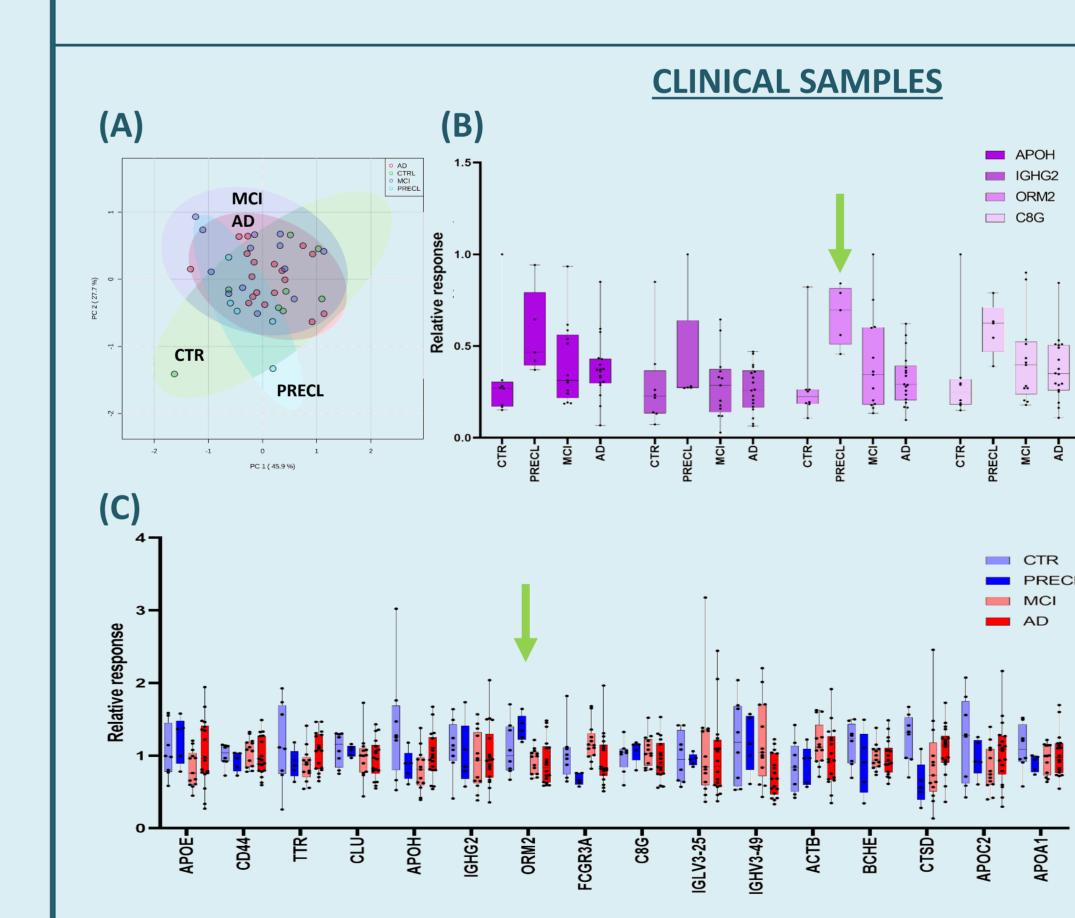


Fig. 5: Analysis of CSF (A, B) serum (C) samples and derived from healthy control (CTRL, n=8), preclinical stage (PRECL, n=5), mild cognitive impairment (MCI, 13) and patients with AD (n=18). (A) PCA analysis did not show separated groups for CSF samples. (B) Selected proteins (n=4 out of 29) showing increased levels in **PRECL CSF** samples.

Days

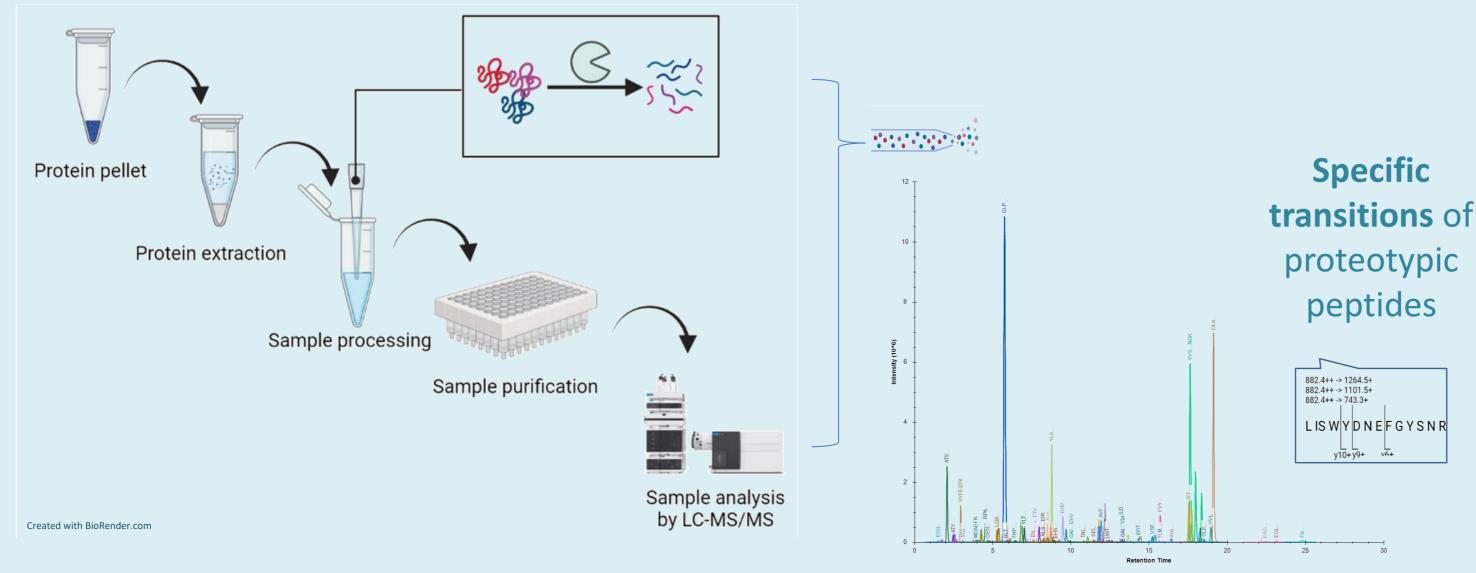
(C) Proteins 13) (**n**= determined in serum samples highlighted with ORM2 showing similar a trend as in CSF.

Fig. 2: Bottom-up proteomics. The sample preparation protocol consisted of the enzymatic digestion by trypsin to obtain peptides to investigate protein cell markers. SRM-MS/MS assay development to **analyze peptides unique for** targeted **proteins**.

SUMMARY AND PLANS

• The COs were found as in vitro model systems that recapitulate in vivo developmental features (same in CTR vs. diseased COs) and thus suitable for studying biological processes

Targeted proteins and its selected **proteotypic peptides**



occurring in human brains during ageing.

- Analysis of COs brought a set of markers with altered levels of protein markers related mainly to **lipid metabolism and/or amyloid β binding**.
- In CSF and serum samples, another spectrum of protein markers was observed, including proteins related to the **immune system**.
- The newly discovered potential protein biomarkers found in COs, CSF, and serum samples will be further investigated in terms of their role in the pathogenesis of AD.

References

[1] World Health Organization [online]. WHO: ©2019 (cit. 12. 07. 2019). [2] Shi, T.; Song, E.; Nie, S.; Rodland, K. D.; Liu, T.; Qian, W.; Smith, R. D. Proteomics **2016**, *16* (15–16), 2160–2182. [3] Qian, X.; Song, H.; Ming, G. Development 2019, 146 (8). [4] Kim, H.; Xu, R.; Padmashri, R.; Dunaevsky, A.; Liu, Y.; Dreyfus, C. F.; Jiang, P. Stem Cell Reports 2019, 12 (5), 890–905.

Acknowledgements

This work was supported by the Grant Agency of Masaryk University (GAMU project No. MUNI/G/1131/2017), the Czech Health Research Council (AZV project No. NV19-08-00472), the RECETOX research infrastructure (the Czech Ministry of Education, Youth, and Sports-MEYS, LM2018121), CETOCOEN EXCELLENCE Teaming (Horizon2020, 857560 and MEYS, 02.1.01/0.0/0.0/18_046/0015975), by the Czech Science Foundation (GACR; no. 18-25429Y, GA20-15728S, and 21-21510S), by the European Regional Development Fund - Project INBIO (No. CZ.02.1.01/0.0/0.0/16_026/0008451).