

Development of IP-LC-TQMS methodology as biomarker readout to quantify Tau phosphorylation around T217 in CSF clinical study samples from Alzheimer diseased patients

**Sebastiaan Bijttebier**, Clara Theunis, Farid Jahouh, Dina Rodrigues Martins, Marc Verhemeldonck, Karolien Grauwen, Lieve Dillen, Marc Mercken

13<sup>th</sup> EBF Open Symposium - November 2020



# Alzheimer

Lack of knowledge of the mechanisms involved in disease pathogenesis

Aggregation of  $amyloid \ \beta$  and  $phosphorylated \ Tau$  in brain

Linked to neurodegeneration



> **Project aim**: develop Ab specific for pTau to prevent aggregation

Hanger et al., 2009, Trends in Molecular Medicine 15, 112-119 Lee et al., 2019, Future Medicinal Chemistry 11, 1845-1848

janssen 🔽

PHARMACEUTICAL COMPANIES

# Anti-pTau Ab



## **Humanized Ab X dosed in clinic**



janssen

PHARMACEUTICAL COMPANIES OF Johnson-Johnson

4

## **IP-LC-MS/MS** approach



- Expected pTau concentration 1-10pM



# **LC-MSMS systems**

### **AB Sciex 6500**



### Advantages:

- Most sensitive system in development BA
- High throughput
- Compatible to a wide pH range

### Disadvantages:

- Works at classical UHPLC flow rates

### Waters TQS multi-D LC system



Sensitivity

### Advantages:

- High samples loading capacity
- Elution at a low flow rate (best sensitivity of the system)

### **Disadvantages**:

- Not possible to work at high pH
- Complexity of the system (novelty)
- Longer run time



## **Tryptic fragments of extended peptides**



relative abundance relative to the most abundant ion per peptide:

	-	p217	P214/p217	p212/p217	p212/p214	P212/p214/p217	p210/p214/p217
TPSLPTPPTR	100	100	100	2.5	2.3	-	75*
SRTPSLPTPPTR	-	-	53	100	100	100	100
TPSLPTPPTREPK	12	18	32	-	-	-	26*
SRTPSLPTPPTREPK	-	-	19	50	15	64	52

\*loss of phospho-moiety

Major influence of phosphorylation on trypsinization – site dependent

PHARMACEUTICAL COMPANIES

# **Chromatography at pH 3**



janssen 🖌

# **Chromatography at pH 11**



janssen\_

# **Optimization of immunoprecipitation**

First optimization experiments were carried out on **brain homogenates of transgenic mouse expressing human Tau**, diluted in aCSF:



- Higher (p)Tau concentrations
- Availability for method optimization

### Sample preparation optimization

- Amount of DTT
- Ab concentration
- Amount of beads
- On-bead digestion or elution



Focus on pT212 and/or pT217



## **IP experiments: human CSF**



#### Detection of **di-phospho peptide** in CSF not expected:

- Not reported in literature
- Ab highest affinity for Tau with pT212/pT217

FOCUS on "2 p 2 m" peptide

- Reference standard + SIL ordered
- High noise levels and ionisation suppression





### Mono-phospho peptides not detected!



## Focus on "2 p 2 m peptide" – multi-dimensional LC



## **Quality control criteria**

**Method validation not possible in the traditional way** due to scarcity of human CSF and endogenous presence of pTau.

#### **Quality control criteria:**

- Use of stable isotope internal standard (SIL)
- **Calibration curve:** method blanks (IP-ed artificial CSF) spiked at 0.5, 1, 2, 4, 6, 10 pM. Linear regression,  $1/X^2$ . Acceptance criteria: | %RE $| \le 20\%$  (LLOQ  $\le 25\%$ ), at least 4 standards accepted.
- Blank: method blank, no SIL
- Zero: method blank with SIL
- Carry over
- QC samples:
  - IP depletion samples were analysed with SIMOA to confirm all pTau is captured during IP
  - **Human CSF samples** from CSF pools with **low, medium and high (p)Tau** concentrations. Evaluation criterium: concentration 2 p 2 m peptide: low Tau CSF < medium Tau CSF < high Tau CSF
  - **Repeatability:** 3 replicates of 2-fold diluted medium Tau CSF. Acceptance criterium: at least 2 out of 3 should be ≤ 20% of the mean value.
  - QC for batch acceptance: method blanks spiked at 4 pM and 8 pM, analysis before and after samples. Acceptance criteria: |%RE| ≤ 20%, at least 2 accepted, 1 of each set and 1 of each concentration.



## **Results clinical samples IP-LC-MSMS**



Total pTau measured with IP LC-MS/MS correlates with Simoa measurement



## Acknowledgments

### Neurosciences

### **Discovery Bioanalysis**

Clara Theunis

Dina Rodrigues Martins

**Tine Loomans** 

Farid Jahouh

**Development Bioanalysis** 

Marc Verhemeldonck

Luc Diels

Lieve Dillen

Marc Mercken

Karolien Grauwen

