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Frequencies of cerebrospinal fluid ATN biomarker profiles and their assocation with memory function in persons without dementia

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Facts & Figures

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Contributions	
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Challenge

Recently, a classification system of pathological events in Alzheimer's disease (AD) has been proposed based on biomarker profiles of amyloid-β (A), tau (T) and neurodegeneration (N). In order to implement this ATN classification in prevention studies, we estimated the frequencies of ATN biomarker profiles in cerebrospinal fluid (CSF) of persons without dementia as a function of age, *APOE* genotype and clinical diagnosis. In addition, we examined their association with memory function.

Approach & Methodology

- 5306 participants were selected from the **Amyloid Biomarker Study**
- Participants were classified into 8 ATN biomarker profiles based on CSF amyloid-β42 (A), phosphorylated tau (T) and total tau (N):

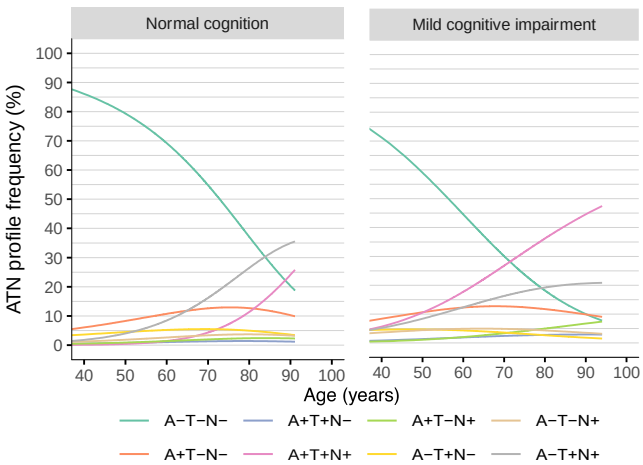
ATN profile	No.	Biomarker category
A-T-N-	1735	normal AD biomarkers
A+T-N- A+T+N- A+T+N+ A+T-N+	640 274 1187 204	Alzheimer continuum
A-T+N- A-T-N+ A-T+N+	310 293 663	non-AD pathological change

- Markov-Chain-Monte-Carlo generalized linear mixed models

Results

- Frequencies of the ATN biomarker profiles changed substantially with age (p<0.001; Figure 1), *APOE*-ε4 genotype (p<0.001; Figure 2) and clinical diagnosis (p<0.001).
- The biomarker profiles within the Alzheimer continuum category were associated with subtle memory dysfunction (p=0.002).

Figure 1. ATN biomarker profile frequencies according to age



Value of IMI collaboration

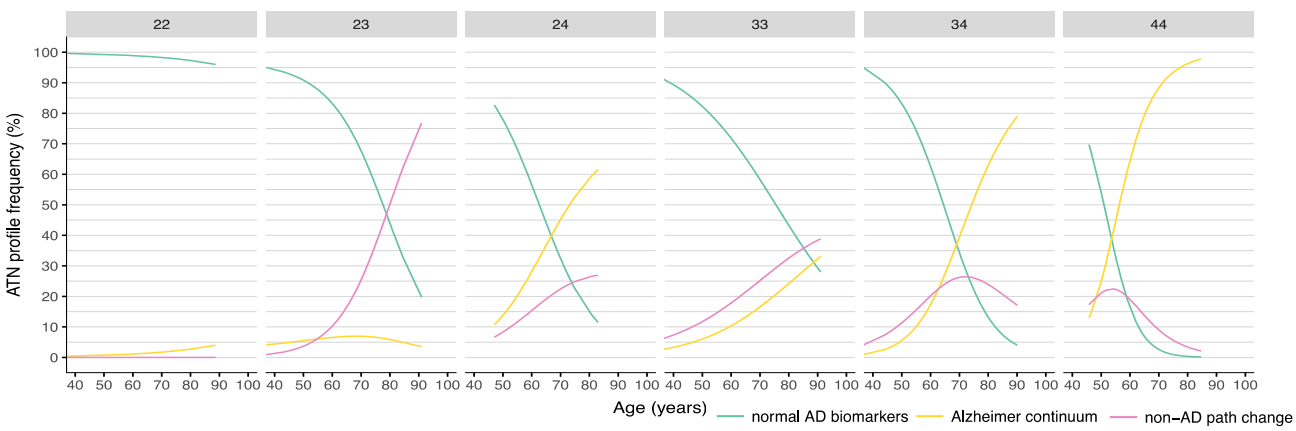
Many datasets were brought together through this collaboration resulting in a unique dataset including data of more than 75 centers worldwide.

Impact & take home message

- Pathology is almost inevitable at old age
- The presence of amyloid positivity seems important for the development of cognitive impairment

The ATN classification system may be useful to define AD subtypes thereby enabling a more specific approach to AD prevention.

Figure 2. ATN biomarker profile frequencies according to APOE genotype in participants with normal cognition



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