

NEUROPATHOLOGICAL BIOMARKERS – HRS PILOT RESULTS

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HRS | HEALTH AND
RETIREMENT
STUDY

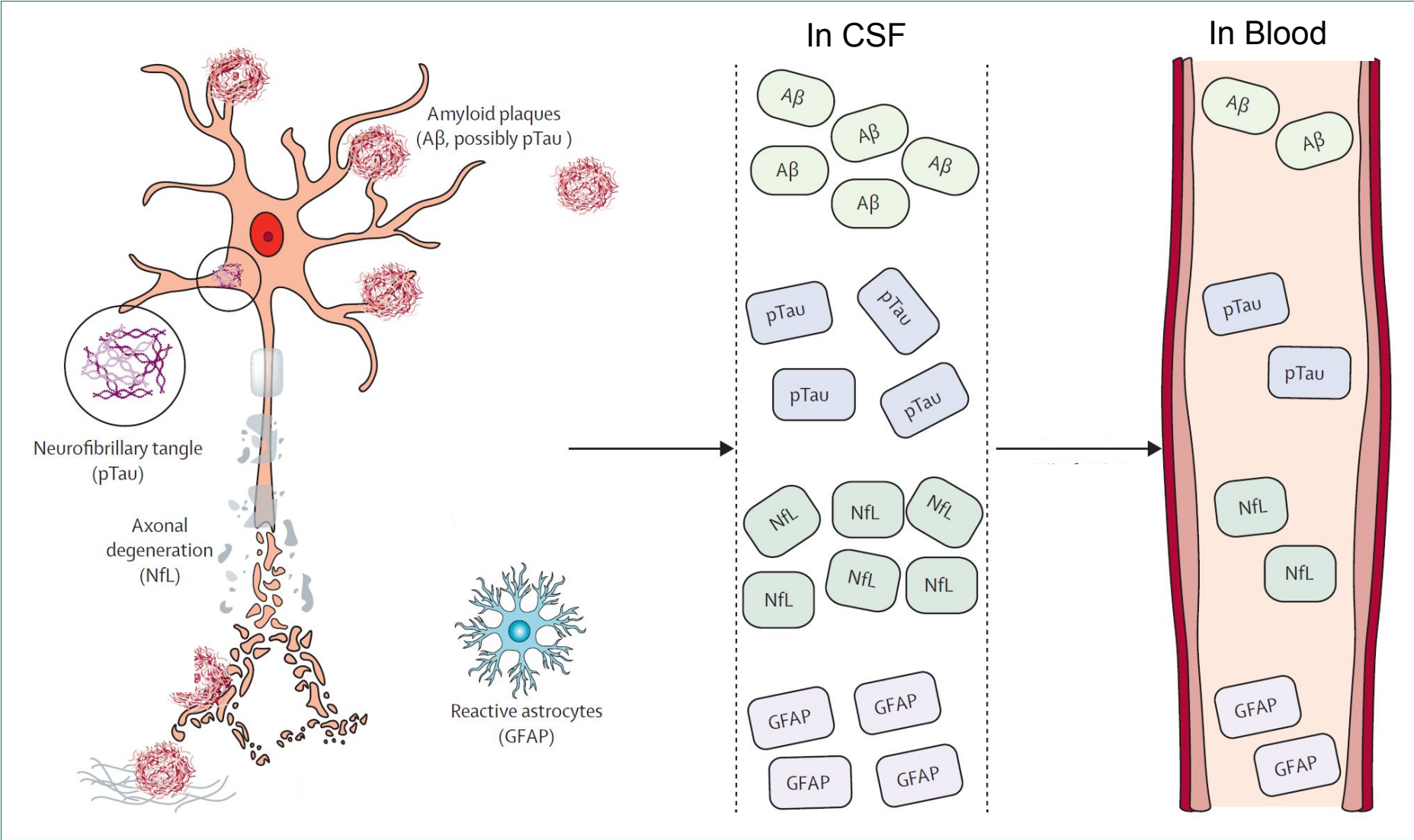
HCAP PILOT- GOALS

- *What was missing was replication of blood-based markers in representative population-based samples of older adults, including individuals from racial / ethnic minorities.*
- HRS conducted a pilot to test promising biomarkers of neurodegeneration.

Priorities:

- (1) highly reliable and replicable in blood (plasma/serum);
 - (2) have validated correlations with AD/ADRD neuropathology from cerebrospinal fluid (CSF) or autopsy measures;
 - (3) are found in higher concentrations in people with cognitive impairment and AD/ADRD;
- Final list based on consultation with dementia experts at the NIA Intramural Research Program

Pathological Mechanisms Involved in AD and Associated Biofluid Biomarkers



Adapted from *Teunissen et al., Lancet Neurol 2022; 21: 66–77*

HCAP PILOT ASSAYS

- A β 42/A β 40 ratio
- Phosphorylated Tau Protein 181 (pTau181)
- Neurofilament Light Chain (NfL)
- Glial Fibrillary Acidic Protein (GFAP)
- Olink Proteomics Neurology Panel

HCAP PILOT ASSAYS – RESULTS TO DATE

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HCAP PILOT – HRS SAMPLE

- HRS respondents over 50 years, n=4,214
- Sample overlaps with the HRS 2016 measures of DNA methylation, RNAseq, etc.
- Sample inclusive of the entire HCAP 2016 sample with venous blood (n=2,392)
- Cognitive tests included immediate and delayed word recall, serial 7s, and backward counting (total score range 0-27)
- Langa/Weir diagnostic algorithm
- 726 Black, 638 Hispanic, 153 Dementia (in 2016)

Correlations among neuropathological biomarkers (N=4,214)

| | AB42/40 Ratio | NfL | pTau-181 | GFAP |
|---------------|---------------|---------|-----------|---------------|
| AB42/40 Ratio | | -0.0027 | -0.0378* | 0.0007 |
| NfL | | | 0.2962*** | 0.4644** * |
| pTau-181 | | | | 0.2989** * |
| GFAP | | | | |

***p<.001; **p<.01; *p<.05

Regressions of each neuropathological biomarker on the HRS cognitive functioning score (n=4,214)

| | Total | | White | | Black | | Hispanic | |
|------------------------------------|---------------|------------------|---------------|------------------|--------------|--------------|--------------|--------------|
| Cognitive functioning score (0-27) | | | | | | | | |
| | b | p | B | p | b | p | b | p |
| AB42/40² | 0.04 | 0.094 | 0.06 | 0.042 | -0.09 | 0.382 | -0.09 | 0.333 |
| NfL | -0.02 | <.0001 | -0.02 | <.0001 | -0.01 | 0.012 | -0.01 | 0.003 |
| pTau-181 | -0.08 | 0.011 | -0.09 | 0.013 | -0.04 | 0.598 | -0.09 | 0.203 |
| GFAP | -0.005 | <.0001 | -0.005 | 0.0003 | -0.00 | 0.860 | -0.01 | 0.032 |

For regressions, we rescaled AB42/40 by multiplying 100
Adjusted for age, sex, batch

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| Combined model | | | | | | | | |
| AB42/40² | 0.04 | 0.158 | 0.05 | 0.067 | -0.10 | 0.320 | 0.12 | 0.221 |
| NfL | -0.02 | <.0001 | -0.02 | <.0001 | -0.01 | 0.010 | -0.01 | 0.017 |
| pTau-181 | -0.03 | 0.423 | -0.04 | 0.250 | -0.004 | 0.959 | -0.05 | 0.461 |
| GFAP | -0.003 | 0.026 | -0.002 | 0.088 | 0.001 | 0.548 | -0.01 | 0.132 |

For regressions, we rescaled AB42/40 by multiplying 100
Adjusted for age, sex, batch

Regressions of each neuropathological biomarker on predicted dementia (n=4,214)

| | Total | | White | | Black | | Hispanic | |
|----------------------------|-------------|--------------|-------------|---------------|-------|-------|----------|-------|
| Dementia | OR | p | OR | p | OR | p | OR | p |
| AB42/40² | 1.00 | 0.989 | 0.90 | 0.253 | 0.90 | 0.446 | 1.06 | 0.515 |
| NfL | 1.00 | 0.045 | 1.01 | 0.058 | 1.00 | 0.610 | 1.00 | 0.619 |
| pTau-181 | 1.02 | 0.425 | 1.06 | 0.047 | 1.00 | 0.994 | 0.84 | 0.230 |
| GFAP | 1.00 | 0.001 | 1.01 | 0.0002 | 1.00 | 0.937 | 1.00 | 0.691 |

For regressions, we rescaled AB42/40 by multiplying 100
Adjusted for age, sex, batch

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| GFAP | 1.00 | 0.001 | 1.01 | 0.0002 | 1.00 | 0.937 | 1.00 | 0.691 |
| Combined model | | | | | | | | |
| AB42/40² | 1.01 | 0.815 | 0.93 | 0.433 | 0.90 | 0.451 | 1.03 | 0.754 |
| NfL | 1.00 | 0.272 | 1.00 | 0.462 | 1.00 | 0.593 | 1.00 | 0.505 |
| pTau-181 | 1.01 | 0.746 | 1.05 | 0.151 | 1.00 | 0.892 | 0.83 | 0.249 |
| GFAP | 1.00 | 0.007 | 1.00 | 0.003 | 1.00 | 0.843 | 1.00 | 0.383 |

For regressions, we rescaled AB42/40 by multiplying 100
Adjusted for age, sex, batch

HCAP PILOT – LONGITUDINAL PREDICTION

- An additional 202 respondents convert to dementia between 2016 and 2020
- Mortality competing risk

| | By 2018 | By 2020 |
|--|----------------|----------------|
| No onset (from normal/CIND to normal/CIND) | 94.08% | 87.22% |
| New dementia (from normal/CIND to demented) | 2.01% | 3.17% |
| Death | 3.91% | 9.62% |

HCAP PILOT – LONGITUDINAL PREDICTION

Multinomial logistic regressions of Dementia/Death status in 2018, n=3923

| | Onset in 2018 (OR) | Death in 2 years (OR) |
|---------------------|--------------------|-----------------------|
| zNfL | 1.27** | 1.38*** |
| zGFAP | 1.17 | 0.96 |
| zAB42/40*100 | 1.01 | 0.91 |
| zpTau181 | 1.01 | 0.80** |

Multinomial logistic regressions of Dementia/Death status in 2020, n=3911

| | Onset in 2020 (OR) | Death in 4 years (OR) |
|---------------------|--------------------|-----------------------|
| zNfL | 1.56*** | 1.58*** |
| zGFAP | 1.06 | 0.97 |
| zAB42/40*100 | 1.10 | 0.74** |
| zpTau181 | 0.90 | 1.14** |

Age and gender controlled, ***p<.001, **p<.01, *p<.05

HCAP PILOT – SUMMARY

Summary:

- Markers are moderately correlated
- Results are not consistent across race/ethnic groups
- NfL promising across groups and prospectively
- The biomarker story is likely to be complex
 - Dementia is a “messy” phenotype
 - Individual markers may help distinguish between different types of dementias (e.g. A β required for AD)

THANK YOU!