

# **Biomarkers of Cognitive Decline in Perinatally-Infected Children with HIV**

David Bearden<sup>1,4</sup>, Alexander J Gill<sup>2</sup>, Paige L Williams<sup>3</sup>, Dennis L Kolson<sup>2</sup>, Laura Schankel<sup>4</sup>, Allison Agwu<sup>5</sup>, Russell B Van Dyke<sup>6</sup>, Steven D Douglas<sup>2,4</sup>, for the Pediatric HIV/AIDS Cohort Study (PHACS) network and the IMPAACT 219C study

# Background

Cognitive impairment is common in children with perinatally-acquired HIV (PHIV), but identifying children at high risk of cognitive decline has remained challenging. A combination of biomarkers and clinical characteristics may allow identification of children at high risk of developing cognitive impairment.

## **Methods**

- Data and plasma samples were obtained from PHIV youth on cART ages 6-16 participating in IMPAACT 219C.
- 13 biomarkers of immune activation and inflammation were measured in plasma using ELISA or multiplex assays at 2 timepoints spaced approximately 3 years appart.
- PHIV youth with neurocognitive decline (defined as sustained drop in full scale  $IQ \ge 15$  points during study follow-up) were compared to age-matched PHIV youth without decline (n=65 per group) in a case-control study.
- Factor analysis was utilized to derive a risk score utilizing a combination of clinical variables and biomarkers and ROC curve analysis was utilized

### Results

- In the univariate analysis, cases with cognitive decline had significantly higher levels of interferon-gamma, TNF-alpha and IL8 at time 1 and higher levels of CRP, TNFR1, and sCD163 at time 2 than did controls.
- Cases with cognitive decline had significantly greater increases in CD40 ligand, CRP, and sCD14 over time than did controls without decline.
- A Risk Score utilizing biomarkers and clinical characteristics had excellent performance characteristics for prediction of decline (AUC 0.81)

# **Subject Characteristics**

| Variable   | Controls (n=65)    | Cases (n=65)      | P-Value |  |  |  |
|--|--------------------|-------------------|---------|--|--|--|
| Age at timepoint 1   | 9.7 (7-12)         | 9.2 (8-11)        | 0.8     |  |  |  |
| Age at timepoint 2   | 12.2 (11-14)       | 12.2 (11-13)      | 1       |  |  |  |
| Black race   | 27 (42%)           | 29 (45%)          | 0.5     |  |  |  |
| Hispanic ethnicity   | 12 (18%)           | 28 (43%)          | 0.02*   |  |  |  |
| Male Sex   | 29 (44%)           | 29 (44%)          | 1       |  |  |  |
| Born in U.S.   | 60 (93%)           | 52 (80%)          | 0.03*   |  |  |  |
| Age at cART  | 6.8 (4.9-9.8)      | 7.3 (5-9.4)       | 0.66    |  |  |  |
| initiation   |                    |                   |         |  |  |  |
| Pre-cART viral   | 4591 (4299-13,000) | 7175 (655-46268)  | 0.7     |  |  |  |
| load   |                    |                   |         |  |  |  |
| Viral load time 1  | 400 (50-6340)      | 400 (239-6409)    | 0.5     |  |  |  |
| Viral load time 2  | 400 (50-1757)      | 1027 (400-10,033) | 0.006*  |  |  |  |
| CD4 timepoint 1  | 950 (572-1180)     | 737 (496-1052)    | 0.86    |  |  |  |
| CD4 timepoint 2  | 726 (515-1022)     | 655 (439-757)     | 0.03*   |  |  |  |
| Adherence time 1   | 100% (100-100)     | 100 (86-100)      | 0.002*  |  |  |  |
| Variables are reported as median and interquartile range or n (%). Variables with p values <0.05 are in bold and marked with * |                    |                   |         |  |  |  |

| Analyte  | Time 1        |                | Time 2        | Time 2         |                 | Change over time |  |
|--|---------------|----------------|---------------|----------------|-----------------|------------------|--|
|  | Beta          | <b>P-value</b> | Beta          | <b>P-value</b> | Beta            | P value          |  |
| hsCRP  | -0.68         | 0.34           | <b>1</b> .59  | 0.05*          | <b>↑</b> 5.3    | 0.04*            |  |
| Ifn-gamma  | <b>↑</b> 0.47 | 0.003*         | -0.017        | 0.88           | 1.6             | 0.54             |  |
| TNF-alpha  | <b>↑</b> 0.12 | 0.04*          | .04           | 0.36           | -1.03           | 0.19             |  |
| TNFR1  | 0.07          | 0.45           | <b>▲</b> 0.14 | 0.009*         | 439             | 0.21             |  |
| TNFR2  | 0.13          | 0.39           | 0.15          | 0.09           | 60              | 0.89             |  |
| sCD14  | -0.22         | 0.06           | 0.07          | 0.36           | <b>↑</b> 444920 | 0.05*            |  |
| sCD163   | 0.13          | 0.59           | <b>↑</b> 0.17 | 0.02*          | -33446          | 0.82             |  |
| IL1B   | 0.07          | 0.39           | 09            | 0.24           | 29              | 0.72             |  |
| IL6  | 0.02          | 0.83           | .07           | 0.44           | .39             | 0.53             |  |
| I18  | ▲0.38         | 0.01*          | -0.03         | 0.88           | -45             | 0.10             |  |
| Il10   | ₩*-0.28       | 0.002*         | 0.09          | 0.24           | -1.29           | 0.25             |  |
| sCD40L   | -0.15         | 0.43           | .22           | 0.07           | <b>↑</b> 546    | 0.04*            |  |
| Variables with p-values <0.05 are listed in bold and marked with * |               |                |               |                |                 |                  |  |

team

<sup>1</sup>University of Rochester School of Medicine, <sup>2</sup>University of Pennsylvania, Philadelphia, PA, <sup>3</sup>Harvard T.H. Chan School of Public Health, Boston, MA, <sup>4</sup>Children's Hospital of Philadelphia, <sup>5</sup>Johns Hopkins University, Baltimore, MD, <sup>6</sup>Tulane University, New Orleans, LA

# Univariate association between variables and cognitive decline

|   |                |         | <b>D</b> 2            |  |  |  |
|---|----------------|---------|-----------------------|--|--|--|
| Variable  | Odds Ratio     | P-value | <b>R</b> <sup>2</sup> |  |  |  |
| CRP (time 2)  | 2.5 (1.2-5.2)  | 0.01*   | 0.07                  |  |  |  |
| TNFR1 (time 2)  | 4.0 (1.3-12.0) | 0.01*   | 0.08                  |  |  |  |
| TNFR2 (time 2)  | 1.8 (0.9-3.7)  | 0.09    | 0.03                  |  |  |  |
| sCD163 (time 2)   | 2.3 (1.1-4.6)  | 0.02*   | 0.06                  |  |  |  |
| sCD14 (time 2)  | 1.6 (0.73-3.8) | 0.23    | 0.02                  |  |  |  |
| sCD40L (time 2)   | 2.3 (1.1-4.6)  | 0.02*   | 0.06                  |  |  |  |
| Biomarker Risk Score <sup>1</sup>   | 2 (1.4-2.8)    | <0.001* | 0.34                  |  |  |  |
| Detectable viral load   | 2.6 (1.1-5.5)  | 0.02*   | 0.07                  |  |  |  |
| CD4 count <200  | 4 (0.9- 18.9)  | 0.08    | 0.04                  |  |  |  |
| History of CDC class C  | 1.7 (0.67-4.4) | 0.26    | 0.02                  |  |  |  |
| diagnosis   |                |         |                       |  |  |  |
| Hispanic ethnicity  | 3.0 (1.3-6.7)  | 0.007*  | 0.09                  |  |  |  |
| Born outside U.S.   | 3.3 (1.1-10.0) | 0.04*   | 0.06                  |  |  |  |
| Caregiver education   | 3 (1.2-7.6)    | 0.02*   | 0.07                  |  |  |  |
| < 12 years  |                |         |                       |  |  |  |
| Clinical Risk Score <sup>2</sup>  | 1.9 (1.3-2.6)  | 0.001*  | 0.19                  |  |  |  |
| P values <0.05 are in bold and marked with a *. <sup>1</sup> The biomarker risk score was generated using a combination of listed   |                |         |                       |  |  |  |
| biomarkers weighted based on factor analytic loading. Clinical risk score was generated using a combination of all listed clinical variables weighted using Beta coefficients from a multivariable conditional logistic regression model. |                |         |                       |  |  |  |

## **Biomarkers in cases vs. controls**

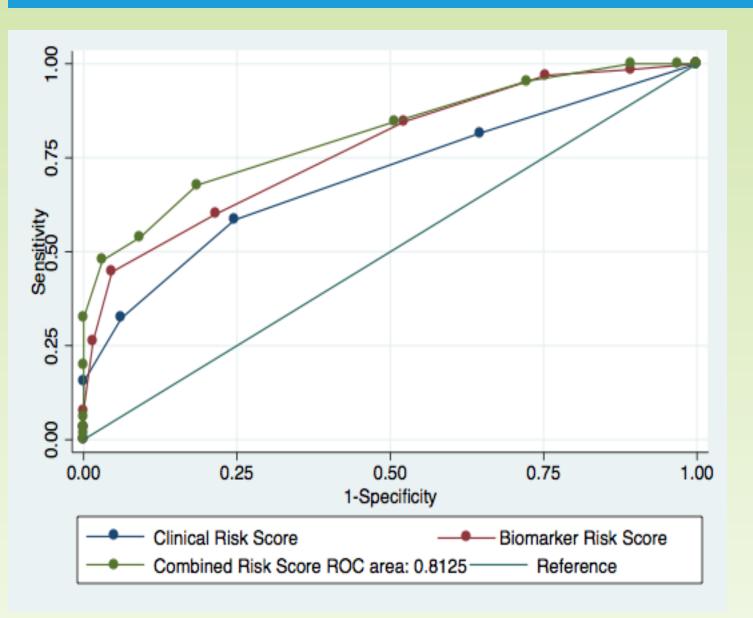


Figure 1: ROC curves comparing biomarker risk score, clinical risk score, and a combined score utilizing both biomarkers and clinical characteristics. AUC was significantly improved for combined score (AUC 0.81 vs. 0.77 vs. 0.70, p<0.001)

This study was funded by the IMPAACT Early Career Investigator Award

Overall support for the International Maternal Pediatric Adolescent AIDS Clinical Trials (IMPAACT) Network was provided by the National Institute of Allergy and Infectious Diseases (NIAID) of the National Institutes of Health (NIH) under Award Numbers UM1AI068632 (IMPAACT LOC), UM1AI068616 (IMPAACT SDMC) and UM1AI106716 (IMPAACT LC), with co-funding from the Eunice Kennedy Shriver National Institute of Child Health and Human Development (NICHD) and the National Institute of Mental Health (NIMH). The content is solely the responsibility of the authors and does not necessarily represent the official views of the NIH.

Prediction of decline combining biomarkers and clinical variables

## CONCLUSION

- These results show a significant association between inflammatory biomarkers and cognitive decline in children with HIV.
- Utilizing clinical characteristics and biomarkers may allow identification of children with HIV at high risk of decline
- Further studies are necessary to confirm these results in a prospective cohort
- Interventions to prevent cognitive impairment could utilize this risk score to target subjects at highest risk of decline.

Presented at CROI Seattle, 2/14/2017.