CHRD 2021: Abstract & Poster Submission Form

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Research Category:

- ◉ Basic Science
- ○ Clinical
- ○ Community Health / Policy

What was your role in the project?

- ☐ Design
- ☑ Perform Experiments
- ☑ Analyze Data
- ☑ Write Abstract
- ☐

Presenter Status:

- ○ Undergraduate Students
- ◉ Masters Student
- ○ PhD Student
- ○ Post-Doctoral Fellows
- ○ Residents
- ○ Non-Trainee

Title

Epigenetic age acceleration can predict frailty in postmenopausal women

Background

Epigenetic age (eAge) measures biological aging, the rate of physiological and metabolic dysregulation over time, by using specific changes in DNA methylation (DNAm). Frailty is a decreased ability to cope with imposed life stressors, and the leading cause of mortality in postmenopausal women.

Objective

Determine the relationship between eAge and frailty.

Methods

Whole blood from 56 postmenopausal women (64 ± 5.97 years) participating in the WARMHearts study (REBH2019:063) was used for DNAm characterization with the Illumina EPIC microarray. WARMHearts Frailty Index was used to determine frailty status. Epigenetic age acceleration (eAgeAccel) was calculated from the standardized residual of eAge from the DNAmPhenoAge clock regressed on chronological age. Cell type deconvolution with IDOL predicted differential distribution of white blood cells.

Results

DNAmPhenoAge had a correlation of 0.712 ($p < 0.00001$) with chronological age. The 29 participants with a positive eAgeAccel were 43% more frail than the 27 negative eAgeAccel participants ($p = 0.0332$). However, no significant differences in eAgeAccel were found in comparing the 28 frail with the 28 non-frail/robust participants ($p = 0.0807$). Cell type deconvolution estimated a 13% increase in neutrophils with frailty ($p = 0.0002$), while CD8T ($p = 0.0154$) and NK cells ($p = 0.0482$) decreased by 37% and 24%, respectively. No significant effects were observed for CD4T cells ($p = 0.0833$), monocytes ($p = 0.1214$), or B cells ($p = 0.1923$).

Conclusion

Our data demonstrate that epigenetic age acceleration is a better predictor of frailty than vice versa. Frailty is also associated with more neutrophils, and less CD8T and NK cells. An ongoing epigenetic wide association study is being conducted to determine further differences in DNAm that occur with frailty. Future experiments will also help establish a mechanistic link between eAgeAccel and frailty status.

Authors

- For each author, please click "**[+] Add Item**" and provide the author's information

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