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Towards a gene expression biomarker set for human biological age

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Summary

We have previously described a statistical model capable of distinguishing young (age<65yrs) from old (age≥75yrs) individuals. Here we studied the performance of a modified model in three populations and determined whether individuals predicted to be biologically younger than their chronological age had biochemical and functional measures consistent with a younger biological age. Those with 'younger' gene expression patterns demonstrated higher muscle strength and serum albumin, and lower interleukin-6 and blood urea concentrations relative to 'biologically older' individuals (odds ratios 1.05, 1.13, 0.61, 0.98; $p=3.2\times10^{-2}$, 2.7×10^{-4}, 1.1×10^{-2}, 2.6×10^{-2} respectively). We conclude that our expression signature of age is robust across three populations and may have utility for estimation of biological age.

Keywords

Biological aging; mRNA expression; cell senescence; predictive model

Although the importance of a healthy and active lifestyle in promoting good health during aging is well understood (van den Brandt 2011), the physiological processes that influence

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biological rather than chronological aging are unclear. Identification of biomarkers for biological aging could provide a key insight into the heterogeneity of age-related decline in function, but has been an evasive goal. Recently, gene expression analysis has shown promise as a new tool to measure physiological age and identify a physical marker of aging (Weindruch *et al*. 2002). We previously carried out a transcriptome-wide gene expression analysis in human peripheral blood leukocyte samples, to determine which transcripts were most associated with advancing age in the InCHIANTI study, a large well-characterized population-representative cohort aged 30 to 104 years (Ferrucci *et al.* 2000). We found that large-scale differences in transcript expression levels occurred for only a small, focused set of genes, and that using the expression levels of only 6 of these (*LRRN3, CD27, GRAP, CCR6, VAMP5* and *CD248)*, we could distinguish between younger (age <65) and older subjects (age≥75) with high accuracy (Harries *et al.* 2011).

In this new study, we aimed to validate a modified InCHIANTI marker set in two independent cohorts and test whether expression marker based prediction of age in the original InCHIANTI data could identify people who were 'biologically younger' than their chronological age. To validate our marker set, we used blood leukocyte samples from the Exeter-10000 study (http://www.peninsulacrf.org/node/155) and isolated lymphocyte derived Affymetrix expression array data from the San Antonio Family Heart Study (SAFHS) (Goring *et al.* 2007). Cohort characteristics are given in supplementary table 1 online. Expression data on five of the six original transcripts were available in all three populations (*LRRN3, GRAP, CCR6, VAMP5* and *CD27*). Three of these (*LRRN3*, *CCR6* and *CD27*) were significantly associated with age by quantitative real-time PCR in n=95 samples from the Exeter 10000 population and five were significantly associated with age ($p<0.05$) in SAFHS data (n=1,238) (supplementary table 2 online). Using the expression levels of these 5 transcripts in fitted multivariable logistic regression models distinguishing younger (age<65) from older (age≥75) and subjects in the InCHIANTI and SAFHS cohorts produced Receiver Operating Characteristic (ROC) curves with Area Under the Curve (AUC) values of 94% and 87% respectively (supplementary figure S1). We were unable to fit a ROC curve with these age cut-offs in the Exeter 10000 data, since only 3 individuals in this sample were aged >75, although a curve with cut-offs of ≥60 versus <60 was feasible. To assess the validity of applying these amended cut-offs of ≥60 versus <60 in the Exeter 10000 data, we first fitted ROC curves using these modified cut points in the two larger populations. We found that the choice of age cut-off had little effect, with ROC curves with Area Under the Curve (AUC) values of 92% and 82% being obtained in InCHIANTI and SAFHS cohorts respectively (supplementary figure 2). Applying the modified cut-off in the Exeter 10000 data, we obtained an AUC value of 73% (supplementary figure 2). This suggests that our five transcript expression panel is robust across populations, despite differences in cohort characteristics, white cell subsets, sample handing and analytical approach, and that the model is robust across two different age categories.

To compare biological and chronological age in the InCHIANTI respondents, we used a linear regression model to estimate each individual's age based on the five expression transcript intensities, with continuous age as the outcome. 134 individuals were classified as 'biologically younger' if, in a regression model of the five transcripts, their predicted age

was >8.5 years younger than their actual chronological age (corresponding to 20% of the sample). To explore associations with clinical markers of aging we included only those aged >=65yrs, as clinical ageing markers such as the Short Physical Performance Battery (SPPB) are validated mainly in such older groups (Guralnik *et al.* 1994; Freire *et al.* 2012). This group was then analyzed for biomarkers of biological aging including C-reactive protein (CRP), Short Physical Performance Battery (SPPB) scores, muscle strength, interleukin-6 (IL-6) serum levels, systolic blood pressure, hematocrit, serum albumin and blood urea level, which are known physiological markers of aging (Studenski *et al.* 2003; Nakamura & Miyao 2007).

We determined that 4 of these 8 parameters (IL-6, muscle strength, blood urea and serum albumin) displayed a statistically significant difference between the biologically young outliers (n=134) and the rest of the cohort ≥65yrs (n=430) (Odds Ratios: 0.61, 1.05, 0.98, 1.13; p-values: 1.1×10^{-2}, 3.2×10^{-2}, 2.6×10^{-2}, 2.7×10^{-4} respectively) (figure 1, table 1). Muscle strength decreases with age and predicts mobility disability in older adults (Bean *et al.* 2003), accordingly muscle strength was significantly higher in the 'biologically young' group. IL-6 is an inflammatory marker (Cesari *et al.* 2004) and serum concentrations rise with advancing age: significantly lower levels of IL-6 were found in the 'biological young' group. Individuals who were predicted to be younger than their actual age demonstrated higher serum albumin and lower blood urea nitrogen levels. Serum albumin decreases with age (Liu *et al.* 2012) and is associated with increased morbidity, mortality, and disability in older people (Baumgartner *et al.* 1996). In particular, low blood albumin is associated with reduced muscle mass and may be indicative of sarcopenia in elderly individuals (Visser *et al.* 2005). Blood urea nitrogen levels increase with age (Aono *et al.* 1994) and may represent reduced kidney function. The lower levels in 'biologically young' individuals may indicate better renal performance. Systolic blood pressure, SPPB scores, CRP and hematocrit did not differ significantly between the 'biologically young' and the remaining population, but this is probably due to the increased variability of these parameters and a lack of statistical power. These data indicate that individuals who have gene expression signatures characteristic of a younger age group also have some biochemical or functional features consistent with a younger age and we conclude that our bi-class discriminative model may therefore be capable of estimating biological, rather than chronological age, and may hold utility in the future to predict individuals who may age badly.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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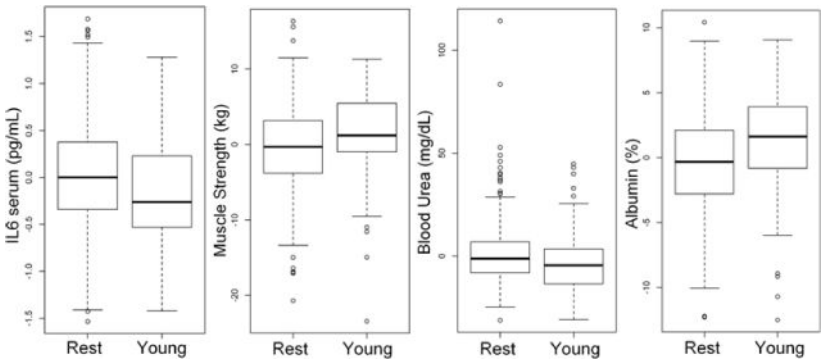

Figure 1. Functional and physiological parameters in 'biologically younger' respondants

This figure shows the distribution of four aging biomarkers in respondants with five transcript regression-predicted ages >8.5 years younger than their chronological age, versus the remainder of the study population.