

Aug. 11: Aging (Kim)

150 SNPs predict likelihood to live 100 yrs

Scienceexpress

Report

Genetic Signatures of Exceptional Longevity in Humans

Paola Sebastiani,^{1*} Nadia Solovieff,¹ Annibale Puca,² Stephen W. Hartley,¹ Efthymia Melista,³ Stacy Andersen,⁴ Daniel A. Dworkis,³ Jemma B. Wilk,⁵ Richard H. Myers,⁵ Martin H. Steinberg,⁶ Monty Montano,³ Clinton T. Baldwin,^{6,7} Thomas T. Perls^{4*}

¹Department of Biostatistics, Boston University School of Public Health, Boston, MA 02118, USA. ²IRCCS Multimedica, Milano, Italy; Istituto di Tecnologie Biomediche, Consiglio Nazionale delle Ricerche, Segrate, 20122, Italy. ³Department of Medicine, Boston University School of Medicine, Boston, MA 02118, USA. ⁴Section of Geriatrics, Department of Medicine, Boston University School of Medicine and Boston Medical Center, Boston, MA 02118, USA. ⁵Department of Neurology, Boston University School of Medicine, Boston, MA 02118, USA. ⁶Departments of Medicine and Pediatrics, Boston University School of Medicine and Boston Medical Center, Boston, MA 02118, USA. ⁷Center for Human Genetics, Boston University School of Medicine, Boston, MA 02118, USA.

*To whom correspondence should be addressed. E-mail: sebas@bu.edu (P.S.); thperls@bu.edu (T.H.P.)

Healthy aging is thought to reflect the combined influence of environmental factors (lifestyle choices) and genetic factors. To explore the genetic contribution, we undertook a genome-wide association study of exceptional longevity (EL) in 1055 centenarians and 1267 controls. Using these data, we built a genetic model that includes 150 single nucleotide polymorphisms (SNPs) and found that it could predict EL with 77% accuracy in an independent set of centenarians and controls. Further in-silico analysis

Based upon the hypothesis that exceptionally old individuals are carriers of multiple genetic variants that influence human lifespan (4), we conducted a genome-wide association study (GWAS) of centenarians. Centenarians are a model of healthy aging, as the onset of disability in these individuals is generally delayed until they are well into their mid-nineties (5, 6). We studied 801 unrelated subjects enrolled in the New England Centenarian Study (NECS) and 926 genetically matched controls. NECS subjects were

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- For course credit
- Need 1-2 volunteers
- Write app. to look up 150 SNPs and calculate longevity score.
- Write commentary on how the app. works.
- Present to class on Aug. 11
- Contact Stuart Kim stuartkm@stanford.edu

Class picture

- Aug. 4 class picture
- Aug. 11 sign class picture

Student volunteers

- Stanford Medicine. Contact "Ruthann Richter"
<richter1@stanford.edu>
- Possibly SF Chronicle later on.