

Centro di Riferimento per l'Epidemiologia e la Prevenzione Oncologica in Piemonte

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La biologia delle diseguaglianze sociali legate all'invecchiamento.

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XLIII Convegno AIE 2019







Aging is the progressive decline in physiological ability and loss of function with advancing age:

<u>Chronological aging</u> is a measure of age in years and occurs at a constant rate in all individuals.

<u>Biological ageing</u> is due to the accumulation of damage at cellular level and it is determined by both environmental and genetic factors (*Adams, 2004*).



SEP and diseases

Socioeconomic differences in health could be understood as due to differential exposure: mediation role of traditional risk factors.



- Relative importance of traditional risk factors is different in different populations
- Differential exposure to traditional risk factors do not explain the increased risk of diseases.



SEP and biological aging





Biological ageing: A fundamental, biological link between socio-economic status and health?

Article in The European Journal of Public Health - October 2004







- Lifepath Funder European Union H2020
- Lifepath coordinator Paolo Vineis, Imperial College, London
- Lifepath Collaborators

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The biology of inequalities in health: the LIFEPATH project

Longitudinal and Life Course Studies 2017 Volume 8 Issue 4 Pp 417 – 439



Biological aging

Imperfect operation of maintenance mechanisms and the resultant accumulation of cellular damage.

The rate at which cellular damage accumulates is determined by the balance between damage and repair mechanisms.





Biomarkers of biological aging

Several biomarkers of biological aging have been proposed:

- Telomere length
- DNA methylation (epigenetic clock, epigenetic drift)
- Allostatic load

- ...

Telomere length



Telomeres are the protective nucleoprotein structures capping the ends of eukaryotic chromosomes.

Telomeres length can be decreased by aging for the increasing rounds of cell division, but also by biochemical environment.

The telomere shortening has important functional consequences: short telomeres lead to genomic instability and cellular senescence (i.e. short telomeres in leucocytes lead to the secretion of pro-inflammatory cytokines).



Telomere length

Author, Year (Reference No.)	Age Range, years	Sample Size(n)	Higher SES: Shorter TL	Higher SES: Longer TL	SM	D (95% CI)
Houben, 2011 (42)	73-91	192			0.035	(-0.316, 0.387)
Steptoe, 2011 (52)	53-76	221	_		0.350	(0.009, 0.691)
Zheng, 2010 (34) RPCI	43-69	328			-0.173	(-0.421, 0.076)
Honig, 2006 (40)	66-103	257		-	-0.018	(-0.265, 0.228)
Lee, 2011 (44)	18-90	257		-	0.203	(-0.042, 0.448)
Hou, 2009 (41)	21-79	272		_	0.250	(0.009, 0.491)
Mather, 2010 (45)—≥60	64-70	295			0.071	(-0.158, 0.299)
Nordfjall, 2009 (48)	25-74	310			0.150	(-0.074, 0.373)
Kananen, 2010 (43)	30-87	471	1 C		0.092	(-0.127, 0.310)
Mather, 2010 (45)—≥40	44-49	350			0.057	(-0.153, 0.266)
Shiels, 2011 (51)	35-64	382			0.102	(-0.099, 0.302)
Risques, 2010 (23)	65-69	615		-	0.143	(-0.032, 0.318)
Mirabello, 2009 (46)	55-74	760			0.097	(-0.046, 0.240)
Harris, 2010 (22)	68-70	1,048			-0.090	(-0.213, 0.032)
Chan, 2010 (35)	>64	2,566	-		0.005	(-0.073, 0.083)
Overall (Q=19.4, 12=28.0%, P=0.149)				>	0.060	(0.002, 0.118)
		1.00	-0.50 0.00	0.50	1.00	

Figure 3. Results from random-effects meta-analysis for the standardized mean difference (SMD) (i.e., effect size) between low and high education categories in the relation of socioeconomic status (SES) with telomere length (TL), ranked by weights applied in the analysis. Squares, SMDs for individual studies; diamond, overall SMD. Bars, 95% confidence interval (CI). (RPCI, Roswell Park Cancer Institute).

Epidemiol Rev 2013;35:98-111

Epigenetic clock



Epigenetic clock refers to specific CpG sites identified in specific DNA regions at which DNAm levels constantly increase (or decrease) during aging can be used to predict chronological age with high accuracy.

Three epigenetic clocks: Horvat, Hannum and Levine.

Epigenetic aging acceleration differences DNAm age and chronological age.





Epigenetic clock

Epigenetic aging acceleration has been associated with:

- Risk factors: obesity, poor physical activity, unhealthy diet, cumulative lifetime stress, infections.
- All causes mortality
- Diseases: cancer incidence, neurodegenerative disorders.

Age acceleration based on DNAm



Social adversity and epigenetic aging: a multi-cohort study on socioeconomic differences in peripheral blood DNA methylation

Giovanni Fiorito^{1,2}, Silvia Polidoro¹, Pierre-Antoine Dugué^{3,4}, Mika Kivimaki⁵, Erica Ponzi⁶, Giuseppe Matullo^{1,2}, Simonetta Guarrera^{1,2}, Manuela B. Assumma^{1,2}, Panagiotis Georgiadis⁷, Soterios A. Kyrtopoulos⁷, Vittorio Krogh⁸, Domenico Palli⁹, Salvatore Panico¹⁰, Carlotta Sacerdote¹¹, Rosario Tumino¹², Marc Chadeau-Hyam¹³, Silvia Stringhini¹⁴, Gianluca

SCIENTIFIC REPORTS | 7: 16266 | DOI:10.1038/s41598-017-16391-5





Epigenetic drift

Epigenetic drift represents the trend of increasing DNAm variability over time across the whole genome.

Age related genomic instability and chromatin deterioration lead to increased variability of genome-wide DNAm levels at older ages.

Teschendorff: differential DNAm variability

Gentilini: stochastic epimutations



Stochastic epimutations

The number of stochastic epimutations (SEMs) increases exponentially with age although there is high variability within individuals of the same age. Higher number of SEMs is associated with:

- risk factors such as cigarette smoking, alcohol intake and exposure to toxicants
- Hepatocellular carcinoma tumor staging





Stochastic epigenetic mutations



Socioeconomic position, lifestyle habits and biomarkers of epigenetic aging: a multi-cohort analysis

Giovanni Fiorito^{1,40}, Cathal McCrory^{2,40}, Oliver Robinson^{3,40}, Cristian Carmeli^{4,40}, Carolina Ochoa Rosales^{5,6,40}, Yan Zhang^{7,40}, Elena Colicino^{8,40}, Pierre-Antoine Dugué^{9,10,11,40}, Fanny Artaud^{12,40}, Gareth J McKay^{13,40}, Ayoung Jeong^{14,15,40}, Pashupati P Mishra^{16,40}, Therese H Nøst^{17,18,40}, Vittorio Krogh¹⁹, Salvatore Panico²⁰, Carlotta Sacerdote²¹, Rosario Tumino²², Domenico Palli²³, Giuseppe

Epimutations, SES and unhealthy lifestyle habits:
neta-analysis within
Lifepath cohorts.Low SES vs. High SESStudyNβ95% CIwd0.04(-0.63:0.55)0.44

Methods

logSEMs ~ f(age, sex, SES, lifestyle variables, technical covariates, cohort specific variables^{*}).

Random effect meta-analysis.



	-			
Study	Ν	β	95% CI	weigh
NAS	624	-0.04	(-0.63 ; 0.55)	0.49%
TERRE	174	0.25	(-0.27 ; 0.77)	0.63%
Skipogh 1	250	0.07	(-0.23 : 0.37)	1.84%
Young Finns	186	0.19	(-0.10 ; 0.47)	2.07%
EXPOsOMICS CVD	313	0.05	(-0.22 ; 0.31)	2.40%
Skipogh 2	451	0.13	(-0.11 ; 0.37)	2.85%
Rotterdam 2	730	0.17	(-0.06 ; 0.41)	2.92%
Rotterdam 1	720	0.05	(-0.17 ; 0.27)	3.36%
ESTHER 2	864	-0.02	2 (-0.24 ; 0.20)	3.38%
TILDA	490	0.04	(-0.18 ; 0.26)	3.42%
ESTHER 1	1,000	0.11	(-0.06 ; 0.28)	5.54%
EPIC Italy	1,803	0.01	(-0.14 ; 0.17)	6.45%
NICOLA	1,929	0.03	(-0.12 ; 0.19)	6.93%
AIRWAVE	1,127	0.04	(-0.06 ; 0.14)	13.92%
MCCS	2,817		(0.05 ; 0.21)	19.61%
KORA	1,727	0	(-0.07 ; 0.07)	24.18%
Summary	15,205	• 0.06	0.02 ; 0.10)	100%

Allostatic Load



McEwen and Stellar (1993): "wear and tear" on the body as a result of exposure to chronic stress.

Indexes constructed from biomarkers to assess the physiological deregulation of nervous, metabolic, immune, cardiovascular and endocrine system.



Allostatic Load







Robertson and Watts BMC Public Health (2016) 16:126

Allostatic Load







European Journal of Epidemiology (2018) 33:441-458

Conclusions

European Journal of Epidemiology https://doi.org/10.1007/s10654-019-00539-w

CORRESPONDENCE

Biography and biological capital

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Grazie dell'attenzione!

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Allostatic load and epigenetic clocks

Pearson correlations between age, epigenetic clocks and allostatic load

	Age	Horvath's clock	Hannum's clock	Levine's clock
Horvath's clock	0,74***			
Hannum's clock	0,74***	0,92***		
Levine's clock	0,85***	0,66***	0,65***	
Allostatic load	0,32***	0,26***	0,25***	0,38***

Mc Crory, 2019

*** p<0,001

Telomere length and epigenetic clocks

Telomere length and epigenetic clocks measures correlate close to zero Are they measuring different age related processes?



Pearson correlations between Hannum epigenetic clock and telomere lenght

Cohort	Ν	r (SE)	P-value
Wave 1	920	0.063 (0.03)	0.05
Wave 2	290	0.006 (0.06)	0.92
Wave 3	273	- 0.076 (0.03)	0.21

Marioni R, et al

International Journal of Epidemiology, 2016, 424–432





SEMs and Clocks



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