

Unravelling the enigma of the complex relationship between aging, senescence, molecular biomarkers and sex/gender influences: a roadmap of open questions

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Senescence is a crucial hallmark of aging

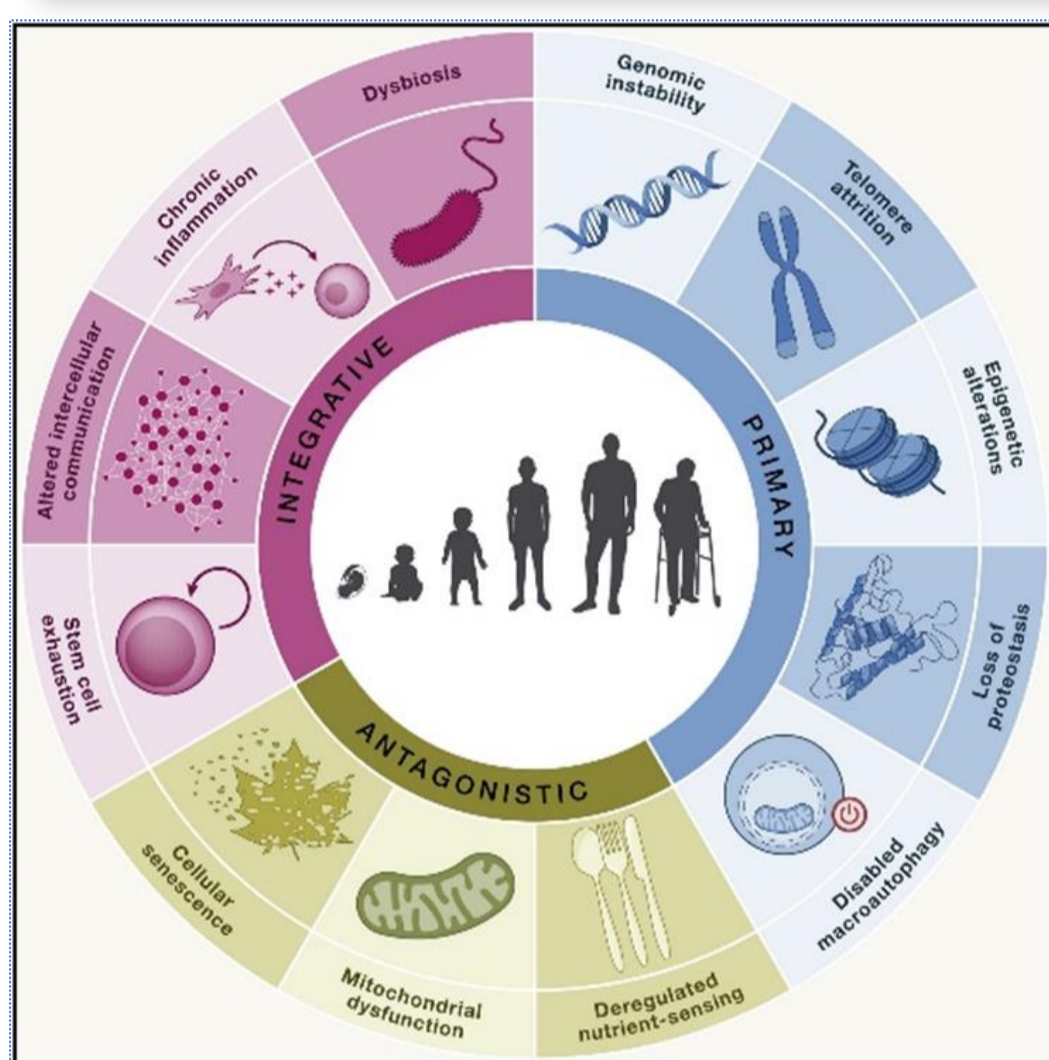


Figure 1 [López-Otín C. et al. (2023)]

Aging involves a myriad of molecular changes at the cellular, tissue, and systemic levels. In 2023, López-Otín et al¹ proposed **12 hallmarks of aging** grouped into three categories: **primary**, **antagonistic**, and **integrative** (Figure 1). All the hallmarks are **strongly interconnected** among each other.

Senescence, a hallmark of aging, is defined as the **stable arrest of cell cycle associated with a distinctive phenotype**. Cells stop to proliferate but remain viable and apoptosis-resistant and develop a pro-inflammatory **Senescence Associated Secretory Phenotype (SASP)**. Cellular senescence is induced in response to multiple intrinsic and extrinsic *stimuli*, as well as to developmental signals². The accumulation of senescent cells during lifetime is one of the leading causes of aging (Figure 2).

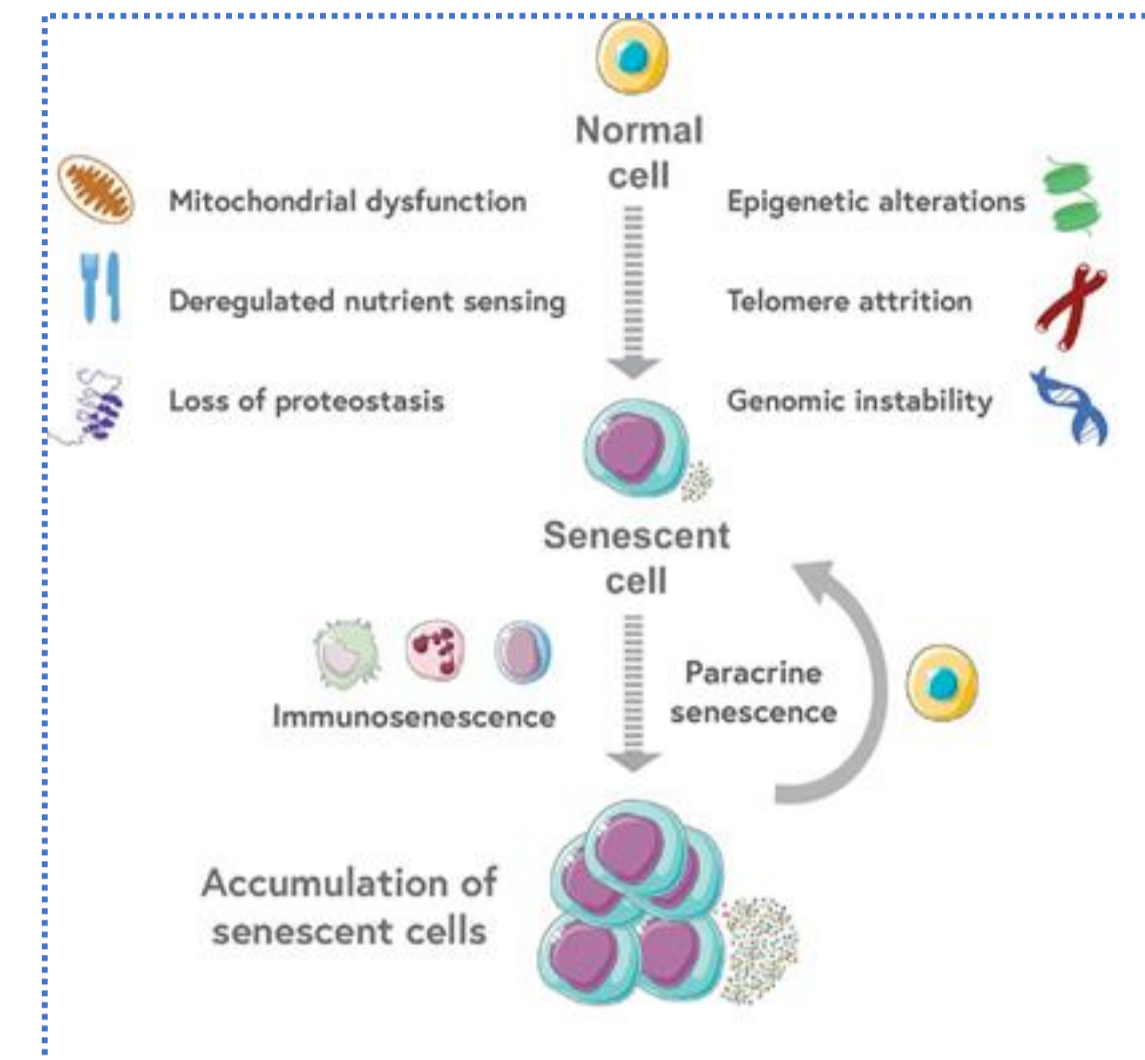


Figure 2 [Borghesan M. et al (2020)]

Are there common and universal molecular signatures of aging and senescence?

Phenotypes of senescent cells are remarkably variable, plastic and heterogeneous. The **most widely used senescence markers** include (i) an increased expression of cell cycle inhibitors **p16^{INK4a} (CDKN1A)** and **p21^{CIP1} (CDKN2A)**, (ii) an increased activity of the senescence-associated **β-galactosidase (SA-βgal)** enzyme and (iii) a decreased expression of the nuclear protein **Lamin B1**. However, **none of these markers** represent an invariable and universal indicator of senescence³.

To identify reliable molecular biomarkers for tracking the aging process and cellular senescence, the **Aging atlas** and the **Atlas of cellular senescence** have been developed, including data from multiple cell types and tissues exposed to various conditions and analyzed with different experimental approaches⁴⁻⁶.

GenAge⁴
307 human genes

Aging Atlas⁵
358 human genes

Cellular Senescence Network⁶
127 human genes

Taking into account the human genes provided by the three atlas, a **molecular signature of 445 human genes** can be considered **relevant for the aging and senescence contributing to numerous signaling pathways** such as: longevity regulating pathway; GnRH signaling pathway; insulin/IGF1/IGF1R signaling axis; PI3K/AKT/mTORC1 network; Ras-MEK-ERK; NF-kappa B, JAK-STAT; P53 signaling; TNF signaling; cytokines signaling; pathway in cancer; response to oxidative stress; lipid and atherosclerosis; DNA damage.

Does sex/gender play a role in aging and age-related diseases?

Sex refers to the **different biological and physiological properties of male and female cells, tissues and organisms**, such as **reproductive organs, chromosomes, hormones and metabolism**. Biological sex is a factor in many conditions including aging, neurodegenerative disease and cancer^{7,8}. Data indicate that females sex is more susceptible to DNA damage and senescence onset⁸. **Gender** is a **multifaceted and dynamic concept** that refers to psycho-socio-cultural factors involving self-identity, social interactions, behaviors, expressions, roles and norms, relations, and power. Many **age-related disease** show **sex-specific patterns**⁸ and data show a remarkable **gender difference in life expectancy and mortality**⁹.

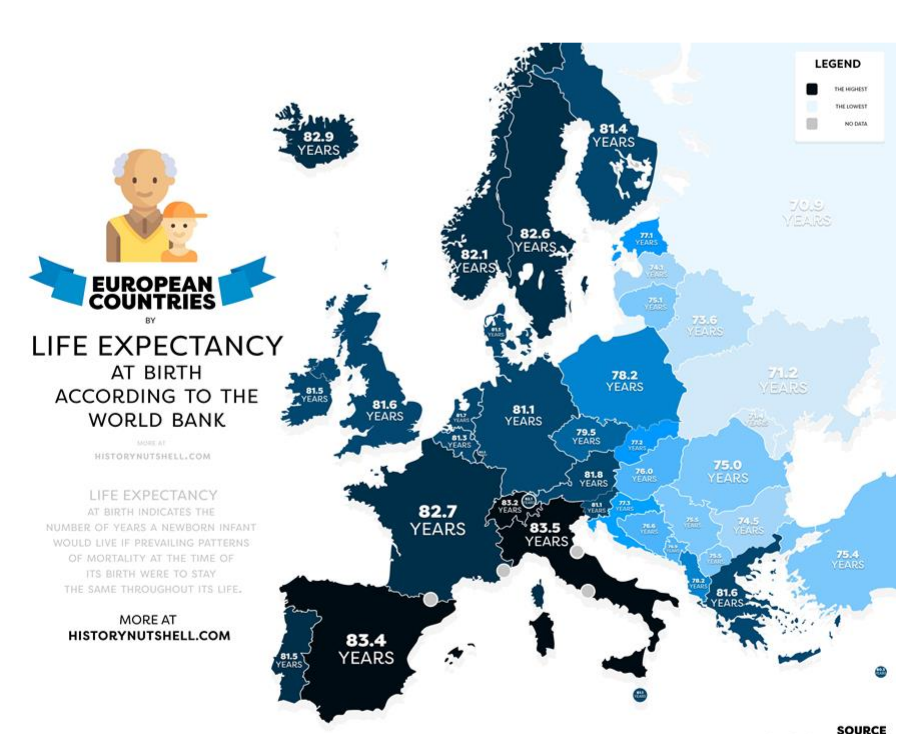


Figure 3

According to the **World bank** the **life expectancy at birth** across central **European countries** ranges from 75- to 83- yrs, with a mean value of 83.5- yrs in Italy (Figure 3). **Women have a longer life expectancy than men**, and this disparity may underline the proposed influence of sex on the aging process⁷⁻⁹. The primary causes of death in high-income countries include **1. ischemic heart disease 2. stroke 3. chronic obstructive pulmonary diseases 4. Alzheimer's disease (AD) and dementia 5. diabetes mellitus and 6. cancers**. Notably, all these pathologies show differences in incidence, prevalence, diagnosis, prognosis and treatment between **women** (Figure 4a) and **men** (Figure 4b).

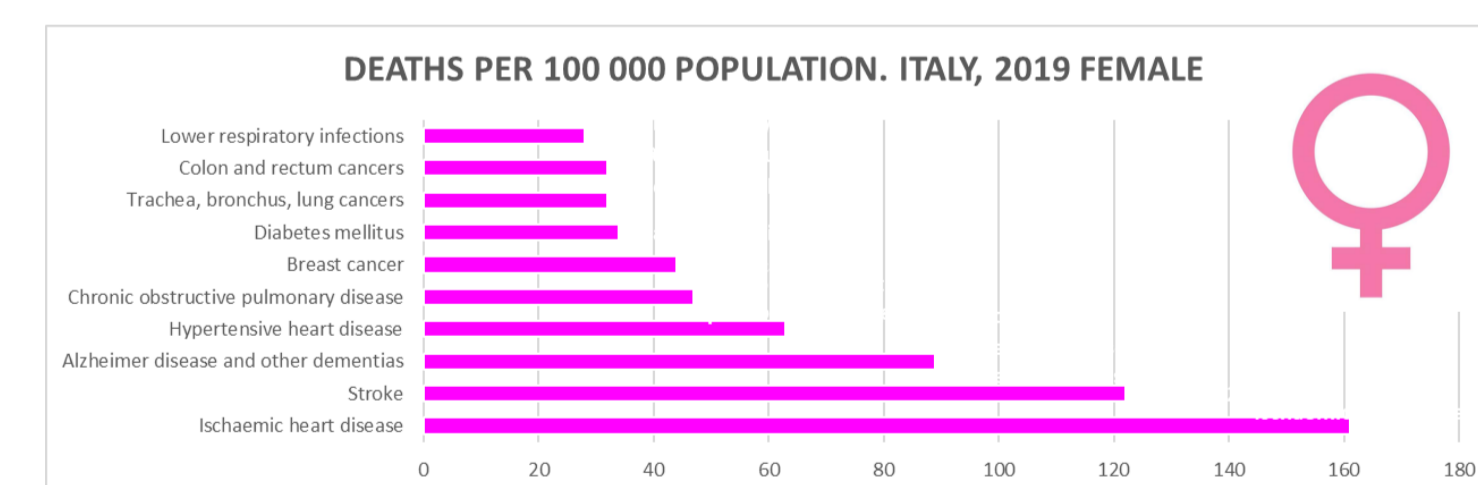


Figure 4a

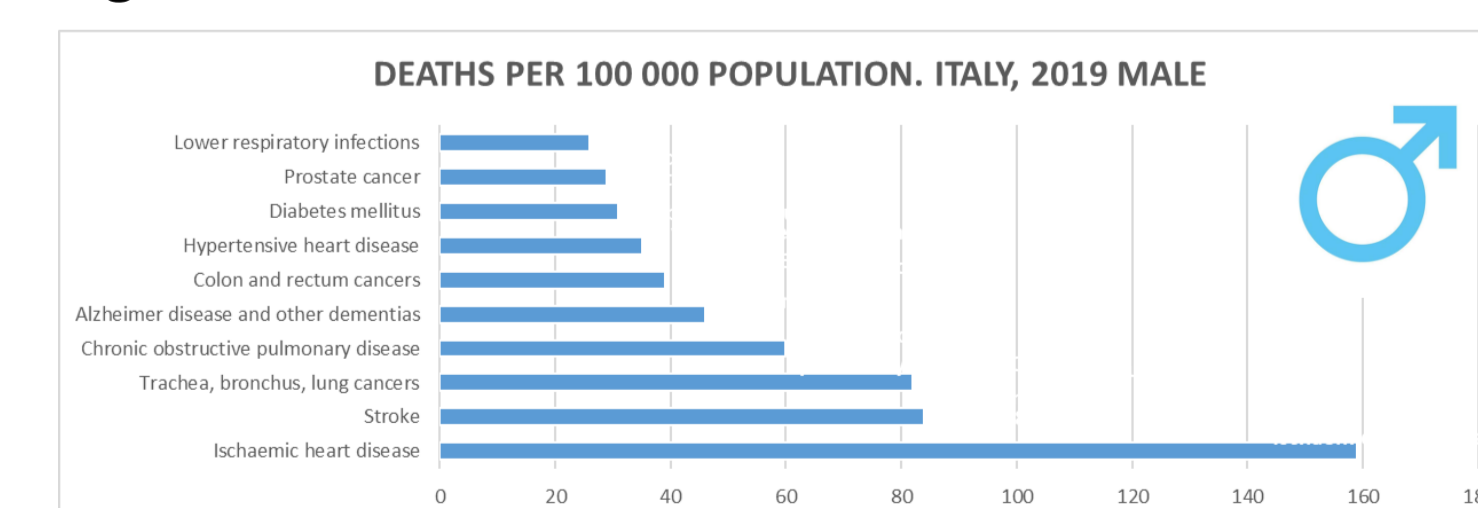


Figure 4b

An agenda for the future

The influence of biological sex and gender on aging adds a level of intricacy that warrants further investigation. Advancing in gender-specific medicine is crucial to help the understanding of molecular mechanisms of aging, with the final aim of reducing disparities in prevention, care, and treatment of age-related diseases across all gender.



<p>Bibliography</p> <ol style="list-style-type: none"> López-Otín C. et al. (2023). PMID: 36599349 Borghesan M. et al (2020). PMID: 32800659 Reimann M. et al. (2024). PMID: 38385946 Tacutu R. et al. (2018). PMID: 29121237 Aging Atlas Consortium (2021). PMID: 33119753 Saul D. et al. (2022). PMID: 35974106 	<p>Webography</p> <ul style="list-style-type: none"> GenAge [last update 2021.03.11] GenAge Database Statistics (senescence.info) Aging Atlas [last update 2023.10.01] https://ngdc.cncb.ac.cn/aging/index Cellular Senescence Network [Last updates 2024.02.20] https://sennetconsortium.org/ World Bank [accessed 2023.03.20] https://data.worldbank.org WHO, Mortality and global health estimates (who.int). [accessed 2024.03.20] 	<p>Contact</p> <p>Cristina Battaglia Email: cristina.battaglia@unimi.it</p> <p>Financial support The project is supported by PSR2022 (University of Milan)</p>
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