

Progressive loss of function Reduced survival capacity, increased morbidity and death probability

Mean life span: paleolithic middle age 1880 1900 nowadays	20 yr 30 yr 36 yr 46 yr (4% ≥ 65 anni) 80 (♂) - 84 (♀)	
people ≥ 65 yr	4% > 12% >20% pro	1900 1990 Djection to 2020
people ≥ 85 yr	10%	2000 (age range that is actively increasing)
Max life span	estimated 115-120 yr (on a genetic basis)	
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Late aging: populations characterized by long life span (Caucasus and Andes)

- A. genetic program
- **B.** errors and/or toxic metabolite accumulation
- (cf. accelerated metabolism and short life span in little animals)













Fig. 1. The figure is constructed according to data published by the Ministry of health, Labor, and Welfare (http://www.mhlw.go.jp/stf/houdou/0000097089.html).

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Demographic, phenotypic, and genetic characteristics of centenarians in Okinawa and Honshu, Japan: Part 2 Honshu, Japan

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The hallmarks of aging

Cell, 2013

Vital function





Aging and senescence (not synonyms)

Age chronologic biologic

Senescence

result of functional deficit

Cell types

germ

somatic

stem

No aging in cancer cells

Aging of extracellular components



Robbins and Cotran, VIII ed.

FIGURE 1–38B The role of telomeres and telomerase in replicative senescence of cells. A, Telomerase directs RNA template-dependent DNA synthesis, in which nucleotides are added to one strand at the end of a chromosome. The lagging strand is filled in by DNA polymerase. B, Telomere-telomerase hypothesis and proliferative capacity of cells. Telomere length is plotted against the number of cell divisions. Germ cells and stem cells both contain active telomerase, but only the germ cells have sufficient levels of the enzyme to stabilize telomere length completely. In normal somatic cells there is no telomerase activity, and telomeres progressively shorten with successive cell divisions until growth arrest. or senescence, occurs. Telomerase activation in cancer cells counteracts the telomere shortening that limits the proliferative capacity of normal somatic cells. (Modified and redrawn with permission from Holt SE, et

(Modified and redrawn with permission from Holt SE, et al: Refining the telomere-telomerase hypothesis of aging and cancer. Nat Biotechnol 14:836, 1996. Copyright 1996, Macmillan Magazines Limited.)



CHARACTERISTICS

non fatal processes	 ↓ sex hormone production ↓ efficiency of cell-mediated immunity arthritis/osis ostheoporosis asthenia presbyopia (↑ crystalline rigidity) cataract (crystalline opacity) hearing impairment systemic senile amyloidosis fibrosis cerebral amyloidosis
diseases	neoplasia late onset diabetes (type II) autoimmune phenomena liver cirrhosis Parkinson
other	incidents atherosclerosis hypertension CNS vaculopathies vascular nephropathies respiratory infections



Farnaz et al., 2016



Fig. 1. SIRT1 produces different outputs as a result of different stimuli. Activation of SIRT 1 to the brain causes an increase in the expression of the transcription factor FOXO 3A with antiaging properties. Besides an increase in NF transcription factor may explain, among others, the neuroprotective properties of SIRT1. SIRT1 protects pancreatic cells and muscle cells against stress-induced apoptosis by increasing activity of the forkhead protein FOXO1. In the liver, SIRT1 deacetylases the coactivator PGC-1 α , thereby increasing the expression of genes for gluconeogenesis. In the muscles, the effect of SIRT1 on FOXO1 increases mitochondrial biogenesis and insulin secretion (Camins et al., 2010).



Figure 2. Hypothetical mode of action of resveratrol and spermidine as autophagy inducers. While resveratrol functions as an activator of the deacetylase Sirtuin 1, spermidine inhibits one or several histone acetylases. Therefore, both resveratrol and spermidine are expected to favor protein hypoacetylation. However, the autophagy-relevant substrates whose deacetylation is induced by resveratrol and spermidine are not fully characterized and it is even not known if they are completely distinct, partially overlapping or identical (Morselli et al., 2009).

INFLAMMAGING







Di Benedetto et al., 2017



Blunting effects on hormonal stress system (HPA axis), on sympathetic nervous system and on immune system

Reduction of peripheral CRP levels and decrease in incidence of cardiovascular, metabolic and infectious diseases





Increase in numbers of circulating Tregs and reduction of pro-inflammatory monocytes and macrophages expressing toll-like receptors





Reduction of adipocytes; switch from M1- to M2macrophages; from activated to regulatory T cells and from release of pro-inflammatory to anti-inflammatory adipokines accordingly



Contracting muscles produce myokines, which induce metabolic effects, glucose homeostasis, affect expression of BDNF synthesis and produce strong anti-inflammatory effects





Physical activity, running, physical exercise



PATHOLOGICAL AGING

Early aging syndromes

- Progeria (Hutchinson-Guilford) early death due to cardiac and cerebrovascular diseases

- Werner syndrome early telomer shortening, altered Homologous Recombination Repair (HRR)

- **Down syndrome** trisomia cr. 21 (neurodegenerative lesions and other deficits)
- Alzheimer disease (neurodegenerative lesions)



FIGURE 1–37 Finite population doublings of primary human fibroblasts derived from a newborn, a 100-year-old person, and a 20-year-old patient with Werner syndrome. The ability of cells to grow to a confluent monolayer decreases with increasing population-doubling levels.

(From Dice JF: Cellular and molecular mechanisms of aging. Physiol Rev 73:150, 1993.)



Taking its toll. As a teenager (left) this Japanese American looked normal, but by age 48, the effects of Werner's syndrome were readily apparent. [Image credit: William and Wilkens Publishing Inc.]



of chromosome 21 (Hsa21), which is trisomic in Down syndrome. Effector genes on the triplicated Hsa21 act on downstream target genes, mostly on other chromosomes, both by acute transcriptional effects and via epigenetic effects, including alterations in DNA methylation that can propagate to daughter cells in growing and self-renewing tissues, to produce biological phenotypes. DS-DM: Differential CpG methylation.



Fig. 1. Increased lipid peroxidation product HNE leads to neurotoxic effects in Down syndrome brain. Trisomy of chromosome 21 in Down syndrome (DS) brain is associated with the overexpression of a number of proteins among which are amyloid precursor protein (APP) and superoxide dismutase 1 (SOD1). Overexpression of APP and SOD1 is considered to be associated with an increased production of amyloid beta-peptide (A β) and superoxide anion (O₂⁻⁻), respectively. Furthermore, increased A β levels are able to promote mitochondrial damage and thus to sustain a further elevation of O₂⁻⁻ levels. These events are associated with an increase of both reactive oxygen species (ROS) and reactive nitrogen species (RNS), known to promote proteins and lipids peroxidation. Among the LPO products, 4-hydroxy-2-nonenal (HNE) is known to bind proteins, thus modifying protein structure and promoting proteins impairment. Proteins found to be HNE-modified in DS brain are associated with reduced: (I) autophagy; (II) unfolded protein response (UPS); (III) glucose metabolism; (IV) antioxidant defense and (V) neuronal trafficking. All these events contribute to sustain a further increase of ROS/RNS, thus amplifying a vicious cycle. In addition, HNE modifications would promote proteins aggregation, which, because the observed defects in autophagy and UPS, are less cleared from neurons. Increased protein aggregation like in the case of A β and SOD1, also represent an additional stimulus sustaining ROS/RNS production.



Fig. 1. Multifunctional role of DYRK1A. The central role of DYRK1A in controlling various physiological processes is outlined using the cartoon above.

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Fig. 2. The DYRK family and DYRK1A structure. (A) Domain architecture of DYRK kinases. DH domain characteristic to DYRK family is given using *red* (*gray* in the print version) *rectangles*. The PEST region is shown using *red* (*gray* in the print version) *hexagons*. *Red* (*gray* in the print version) *oval*, *cylinder*, and *pentagons* show histidine-rich region, serine/threonine-rich region, and nuclear localization sequences, respectively. (B) Overall structure of DYRK1A catalytic domain with N-terminal lobe shown in *orange* (*gray* in the print version). The C-terminal lobe is given in *green* (*dark gray* in the print version) while the DYRK-specific insert region is given in *purple* (*gray* in the print version). (C) A representative figure showing DYRK1A bound to ATP-mimetic small molecule inhibitor in the ATP-binding site in the hinge region of DYRK1A between N and C lobes. The P loop closing over the inhibitor is also shown in the figure along with activation segment α C helix.



Fig. 4. Role of DYRK1A in tau hyperphosphorylation and neuronal diseases. In tauopathies, there is a reduction in the ability to bind microtubules and promote microtubule assembly. Hyperphosphorylated Tau by DYRK1A and DYRK1A-primed GSK β contribute toward destabilized microtubule network, impaired axonal transport, results in neurofibrillary tangle (NFT) formation and eventually neuronal death. *Tau spheres* are given as *yellow* (*white* in the print version) *sticks* and the phosphorylation is shown using *small purple* (*dark gray* in the print version). Microtubule is shown using *cyan* (*white* in the print version) and *blue* (*dark gray* in the print version) *spheres*.

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