Aging is the time-dependent functional decline of an organism at all levels, from nanoscopic to the whole person; it results in vulnerability to perturbation and increased risk of death. This complex process lies at the intersection of genetics, biology, and the environment.

There are seven factors, highly inter twined processes that define aging.

* Adaptation to stress:
  + Bridge continuum from psychological to molecular stresses
  + Differentiate hormesis from toxic stress
  + Better align human and animal studies
* Epigenetics:
  + Biomarker development: chronologic vs. biologic aging
  + Link age-related environmental inputs to epigenetic signatures
  + Test small molecules that regulate enzymes controlling epigenetic events
* Inflammation:
  + Differentiate adaptive and maladaptive inflammatory responses
  + Define age-related inflammatory sources and their systemic effects
  + Determine how obesity and metabolic dysfunction alter inflammation with age
* Macromolecular damage:
  + Generate systems-level understanding of the types of macromolecular damage and their roles in chronic disease states
  + Understand how stochastic damage influences the variability of aging events
* Metabolism:
  + Define role of signal transduction pathways linked to metabolism in the aging process
  + Understand contribution of circadian clocks to aging and metabolism
  + Connect metabolic dysfunction with tissue-specific decline in aging

There is not surprise to anyone that Aging is a complex process, and because of the highly interconnectivity of the factors, hard to understand.

One of the most striking effects of age is the involuntary loss of muscle mass, strength, and function, termed sarcopenia. From the time you are born to around the time you turn 30, your muscles grow larger and stronger. But at some point in your 30s, you start to lose muscle mass and function. No matter the lifestyle, everybody is going to loss between 3 to 8% of muscle mass per decade after age 30, and this rate of decline is even higher after the age of 60. Sarcopenia is associated with detrimental clinical outcomes, such as a reduced quality of life, frailty, an increased risk of falls, fractures, hospitalization, and mortality.

We mentioned that aging have a lot of factors attached to it, in the specific case of Sarcopenia we can include chronic inflammation, increased reactive oxidative species, and increased fibrosis of muscle, among others have been reported to contribute to development of sarcopenia by progressing muscle atrophy.

However, we know that the regeneration in adults of the muscle is possible through a process called myogenesis that start with muscle stem cells. The formation of new muscle fibers and repair of injured myofibres requires the differention of myogenic progenitors from satellite cells.

During the quinescence and activation of these cells, different sets of mirNAS are being expressed, suggesting the role of miRNAS in regulaton of saltellite cell homeostasis, and several miRNA have been shown to regulate miogenesis in adulthood.

Muscles express their own set of muscle-enriched mirnas known as myomirs: mir1, 206, 208, 133, 486, 499.

It had been several ways to approach Sarcopenia, some use small molecules like rapamycin, but this is only a preventive methodoly since it cannot regenerate muscle. There are also plenty of single gene approaches used, but being Sarcopenia a degenerative process due to aging, there are many pathways involved like autophagy or senesce that makes harder to isolate a single gene and see how it works. However, microRNA allows a cleaner approach, because we can know the target and escalate to more parts of the body.

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This places microRNA therapy as a good contestant against sarcopenia.

So… what is a miRNA?

miRNA are defined as 18 to 25 nucleotide single stranded RNAs (ssRNAs), which are produced from hairpin shaped precursors. They are conserved small non-coding RNAs that play an important role in the regulation of gene expression and participate in a variety of biological processes miRNAs have been found to regulate almost all cellular functions including cell proliferation, growth, differentiation and apoptosis, And as we mention, have been implicated in controlling the fate and behavior of stem cells

In Gita Shafiee et al, 2018, 41,715 DEG (19 downregulated and 41,696 upregulated) in men, and 3,015 DEGs (2,874 upregulated and 141 downregulated) in women in sarcopenia.

Target identification and validation is a pressing challenge, with many targets failing for efficacy reasons or showing poor association with the disease.

A single microRNA can be involved in thousands of gene expressions, each gene can be affected by several microRNA, each gene can be involved in several pathways and of course many genes are involved in each pathway. This creates a clear complex network, making the exporatory analysis impractical by manual methodologies. Not all potential miRNA are functionally relevant in a given cell. Thus, researches need to perform target analysis in the context of specific models

Fortunelly, since more than a couple decades, the computer techniques had been applied for biology discovery.