Xenohormetic, hormetic & cytostatic selective forces drive the evolution of longevity regulation mechanisms within ecosystems

Michelle Burstein

Concordia University, Montréal, Canada



Aging can be delayed by ...

Single-gene mutations in a limited number of "master" genes regulating longevity

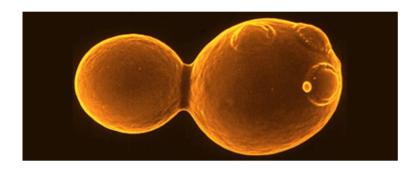
Caloric restriction (CR) or dietary restriction (DR)

Anti-aging compounds:

Resveratrol (yeast, worms, flies, mice)
 Spermidine (yeast, worms, flies, human immune cells)
 Rapamycin (yeast, mice)
 Caffeine (yeast)

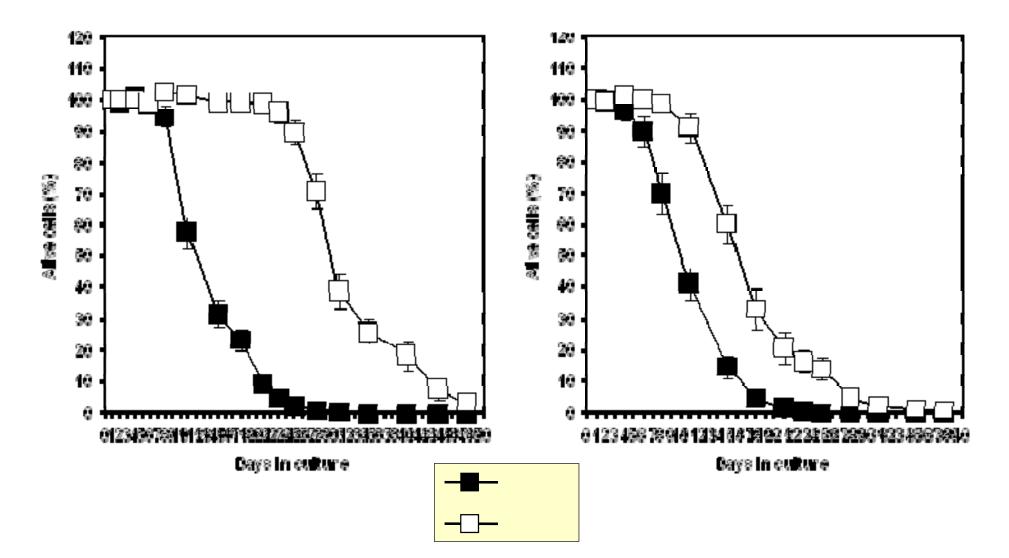
Longevity signaling pathways & their modulation by dietary & pharmacological interventions are <u>evolutionarily conserved</u>

Thus ...

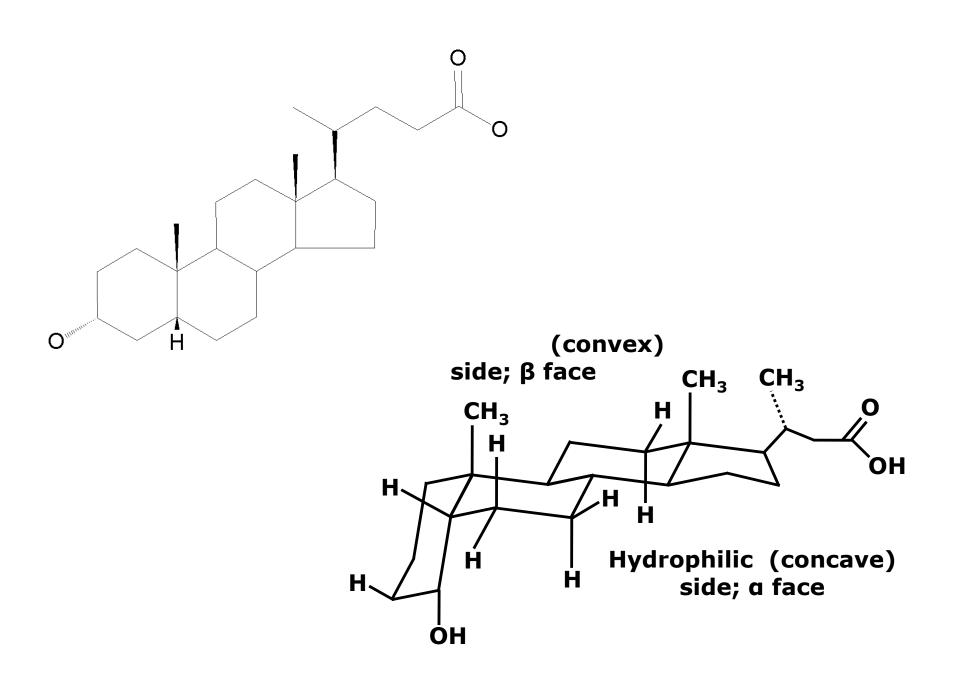


The baker's yeast is a <u>valuable model</u> for unveiling mechanisms of cellular aging in multicellular eukaryotes We identified <u>24 novel compounds</u> that greatly extend yeast longevity & belong to <u>5 chemical groups</u>

All these compounds are structurally & functionally <u>distinct</u> <u>from currently known anti-aging</u> <u>compounds</u>, namely resveratrol, spermidine, rapamycin & caffeine Lithocholic acid (LCA) is one of these anti-aging compounds extending yeast chronological life span under <u>caloric restriction</u> (CR) conditions to a <u>higher degree</u> than that under non-CR conditions

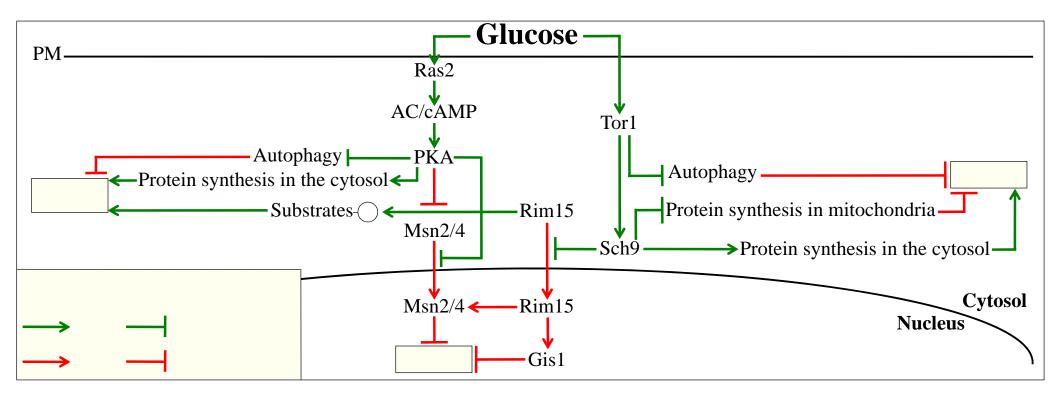


Lithocholic acid (LCA)



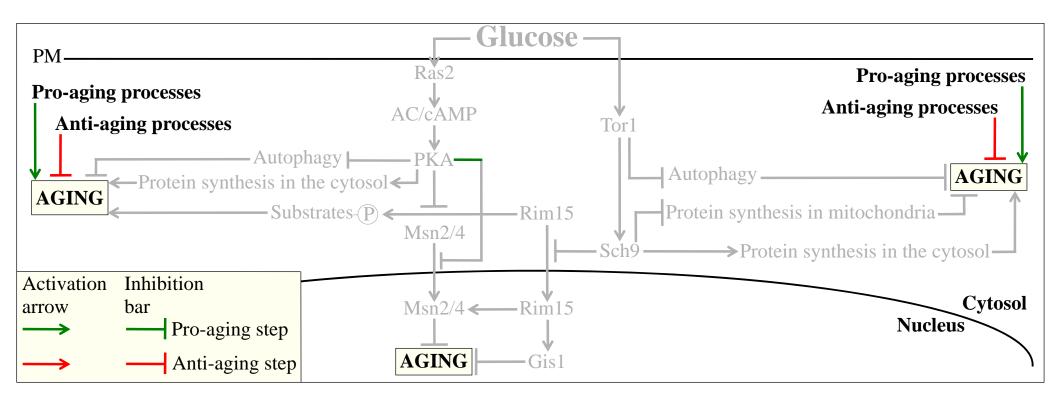
□ The TOR & cAMP/PKA longevity signaling pathways are "<u>adaptable</u>" by nature ...

They regulate longevity <u>only in response to certain</u> <u>changes</u> in the organismal & intracellular nutrient & energy status (*e.g.*, <u>calorie availability</u>)

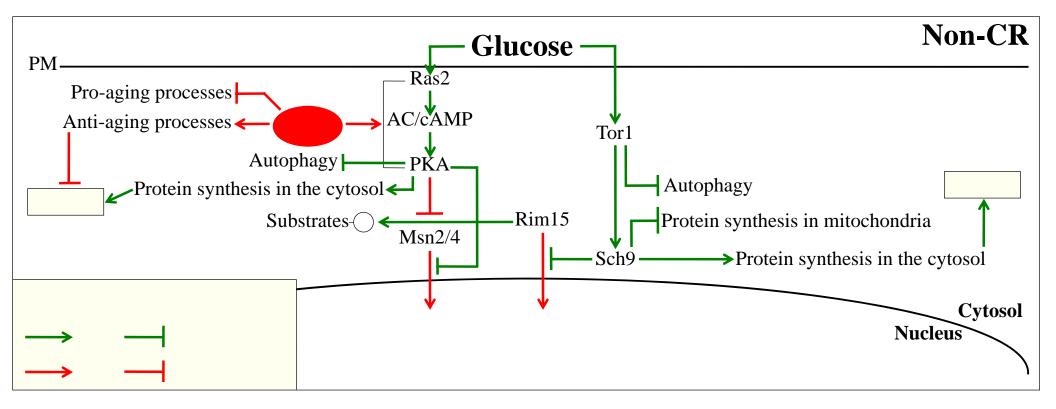


However, we found that some longevity regulation pathways are "<u>constitutive</u>" or "<u>housekeeping</u>" by nature …

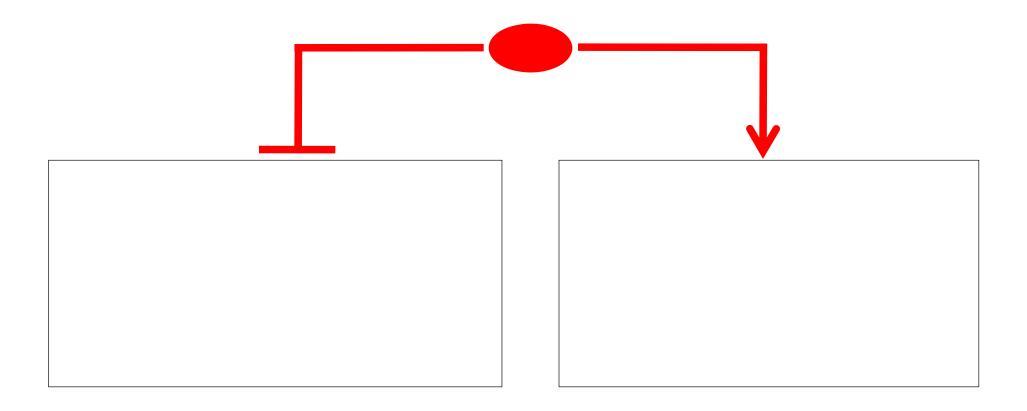
They regulate longevity <u>irrespective</u> of the organismal & intracellular nutrient & energy status & do <u>not</u> overlap with the adaptable pathways



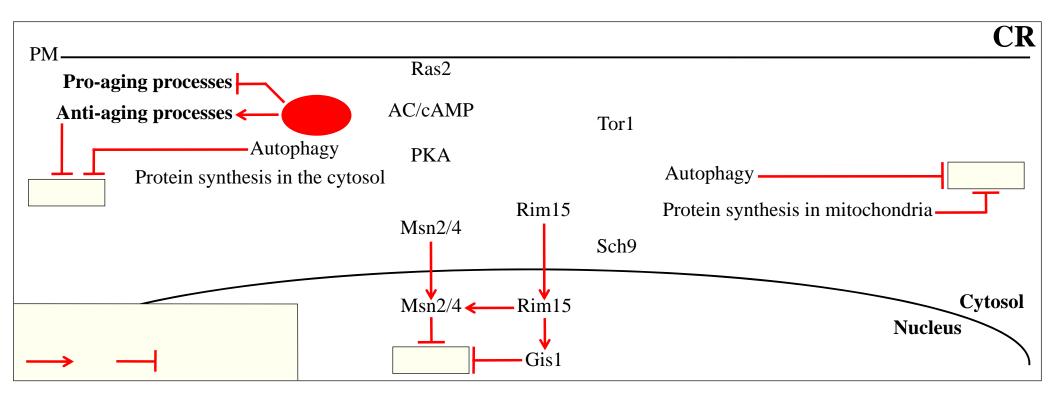
Under non-CR conditions, LCA targets "<u>housekeeping</u>" longevity assurance processes <u>& the "adaptable</u>" cAMP/PKA longevity pathway



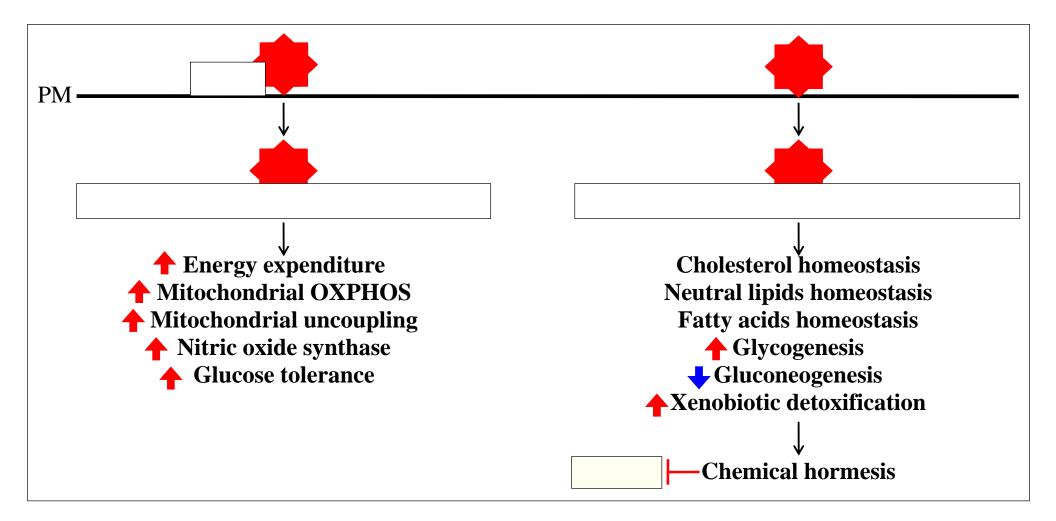
We found that LCA modulates <u>the following</u> "<u>housekeeping</u>" longevity assurance processes



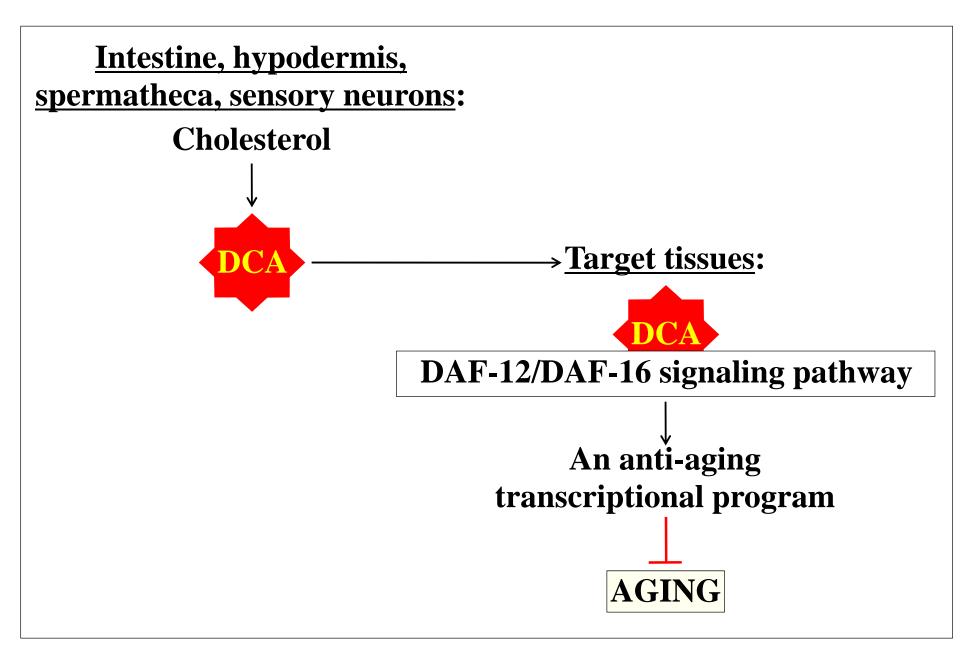
Under CR conditions, LCA targets <u>only</u> <u>housekeeping</u> longevity assurance processes



Bile acids (BA) are beneficial to health & longevity in <u>mammals</u>



Bile acid-like dafachronic acids (DCA) extend longevity in worms



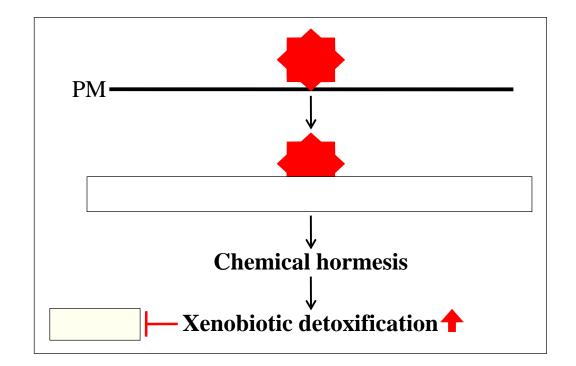
Important observations:

The levels of bile acids are <u>elevated</u> in the <u>long-lived</u> Ghrhr^{lit/lit} mice

Cholic acid, a bile acid, administered to food of wild-type mice <u>activates</u> transcription of <u>numerous xenobiotic</u> <u>detoxification genes</u> Therefore, it has been proposed that ...

By promoting chemical hormesis in mammals, bile acids - mildly toxic molecules with detergentlike properties - may extend their longevity by

acting as endobiotic regulators of aging

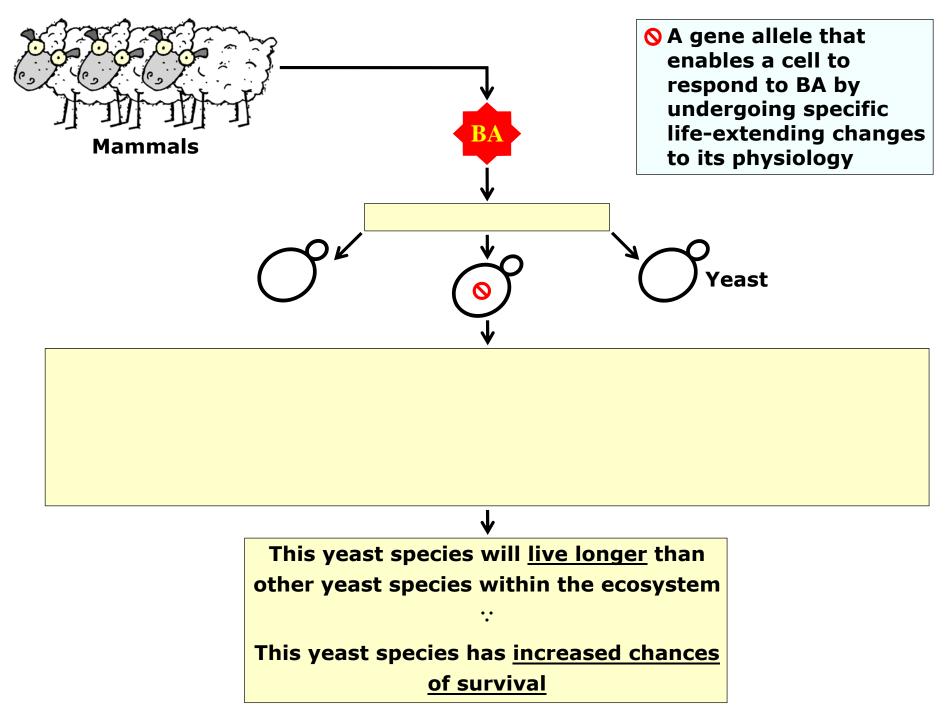


Importantly ...

Yeast do <u>not</u> synthesize LCA or any other bile acid found in mammals

Therefore, we hypothesize that ... Bile acids released into the environment by mammals may act as <u>interspecies chemical signals extending</u> <u>yeast longevity within ecosystems</u>

In our hypothesis ...



In our hypothesis ...

Bile acids released into the environment by mammals <u>extend longevity of yeast species &</u> <u>other organisms that can sense these compounds</u>

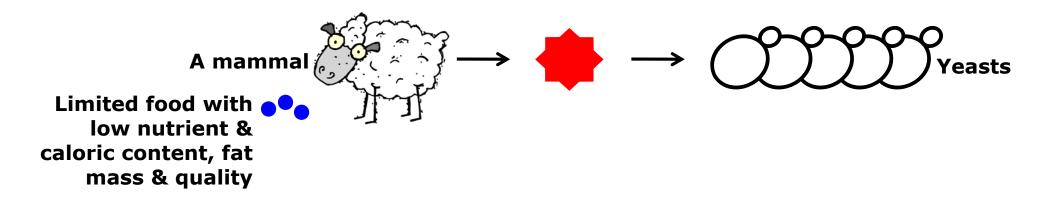
Thereby ...

Increasing their chances of survival & creating selective force aimed @ maintaining the ability of organisms composing the ecosystem to respond to bile acids by undergoing specific life-extending changes to their physiology

In our hypothesis ...

The evolution of longevity regulation mechanisms in yeast species & other organisms composing an ecosystem is driven by their ability to undergo specific lifeextending physiological changes in response to bile acids & other mildly toxic, hormetic compounds that are permanently or transiently released to the ecosystem by mammals

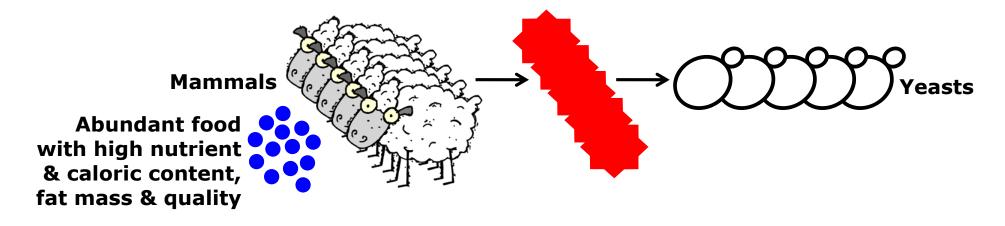
Yeast are <u>permanently</u> exposed to BA due to their fecal loss by mammals



Thus, in yeast exposed to BA released by mammals, BA modulate <u>HOUSEKEEPING</u> longevity assurance pathways that ...

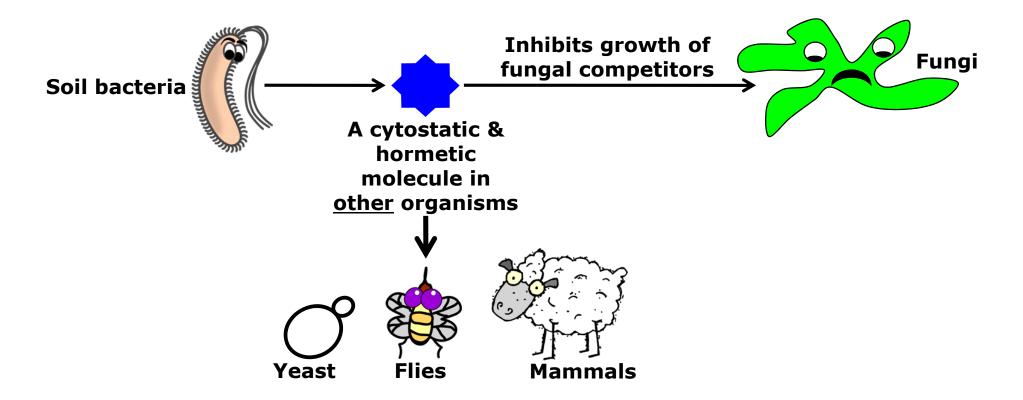
- Regulate yeast longevity <u>irrespective</u> of the number of mammals or their food supply
- Do <u>not</u> overlap with the <u>adaptable</u> TOR and cAMP/PKA longevity pathways

The quantity of BA released into the environment by mammals <u>could vary</u> due to changes in the density of mammalian population & abundance of food & its quality



- Thus, in addition to the ability of yeast to respond to the <u>permanently available</u> exogenous pool of BA by modulating <u>housekeeping</u> longevity pathways ...
- Yeast may have also evolved the ability to sense the <u>environmental status-dependent variations of BA</u> abundance by modulating the <u>ADAPTABLE</u> TOR & <u>cAMP/PKA longevity pathways</u>

Another anti-aging compound, called <u>rapamycin (RAP)</u>, may also act as an <u>interspecies chemical signal</u> modulating longevity at the ecosystemic level

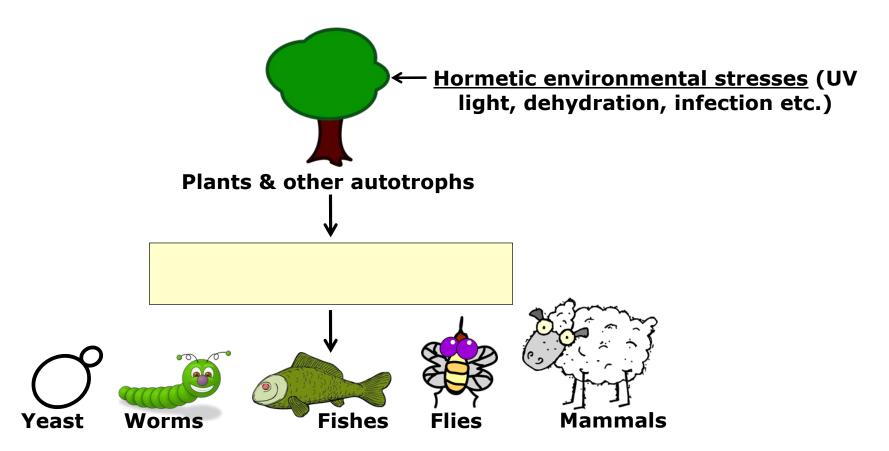


RAP extends longevity in yeast, fruit flies & mice by <u>inhibiting TOR</u>, a nutrient-sensory protein kinase that operates as a master negative regulator of the key <u>adaptable</u> longevity pathway

Therefore, we hypothesize that ...

The ability of yeast, fruit flies & mice to sense RAP produced by soil bacteria & then to respond by undergoing certain life-extending changes to their physiology may increase their chances of survival, thereby creating selective force for maintaining such ability

"Xenohormetic" hypothesis (Howitz & Sinclair)

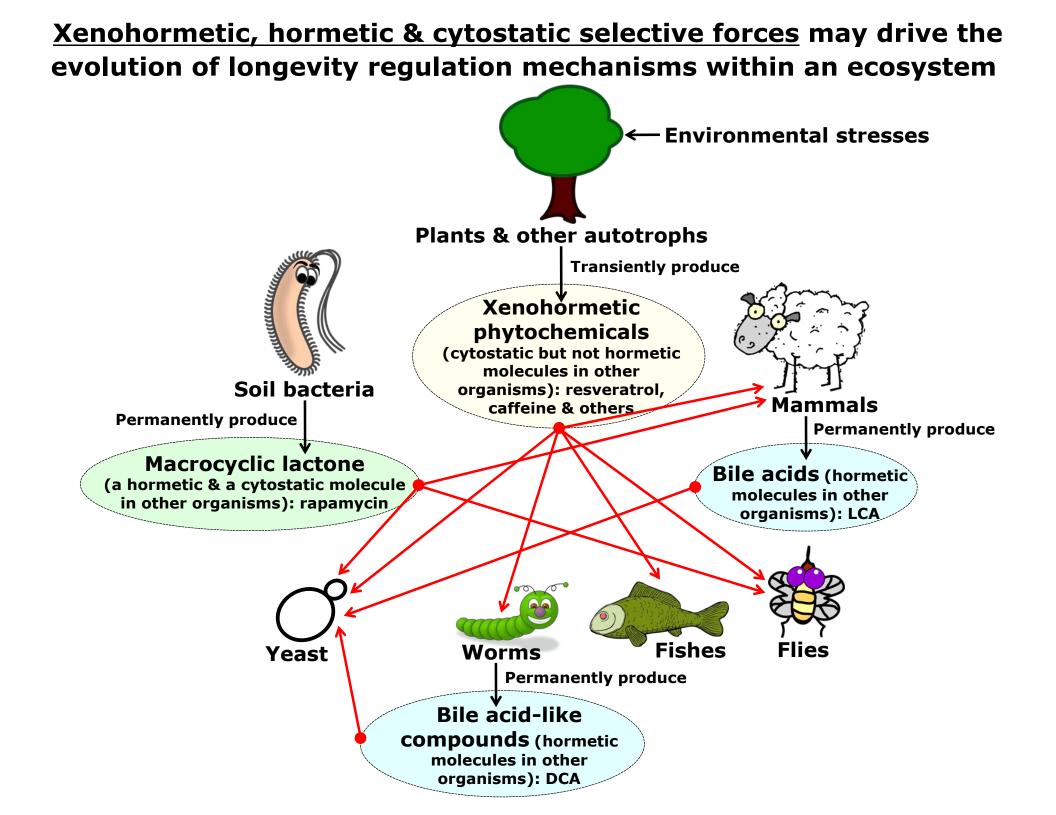


Extend longevity of yeast, worms, fishes, flies & mammals by:

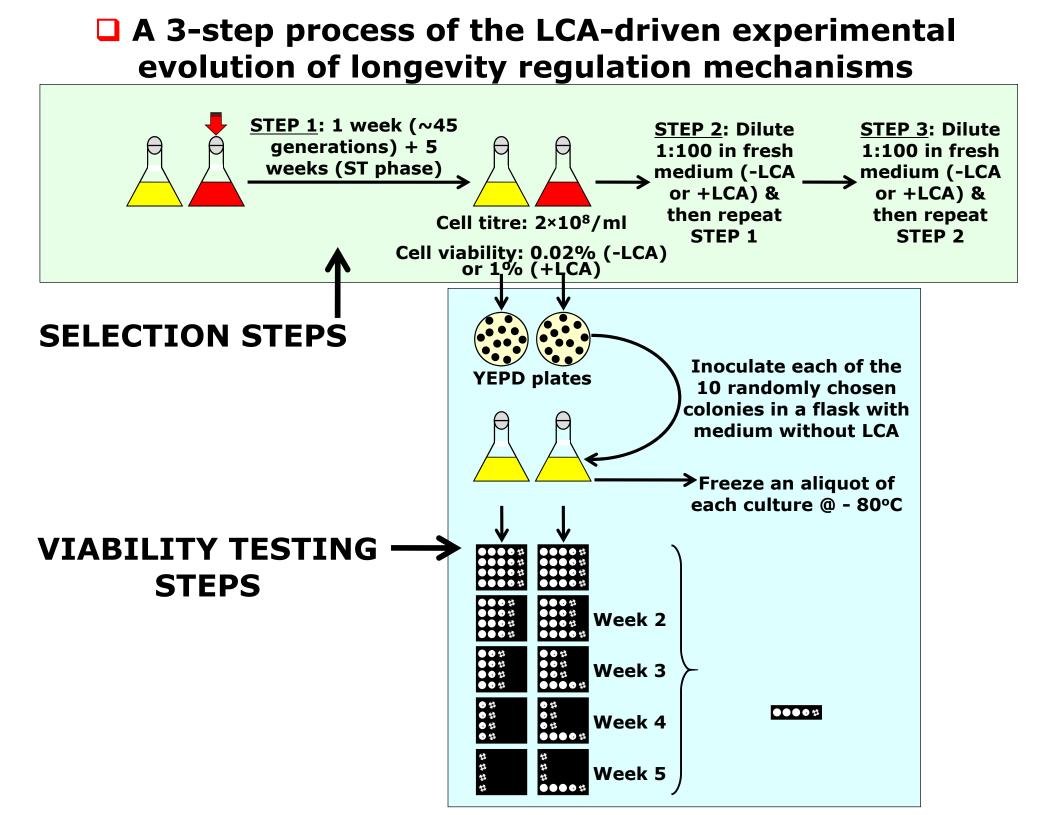
Modulating the key enzymes of <u>stress-response pathways</u> governing longevity-related processes

Inhibiting the pro-aging TOR signaling pathway (*i.e.*, exhibiting a cytostatic effect)

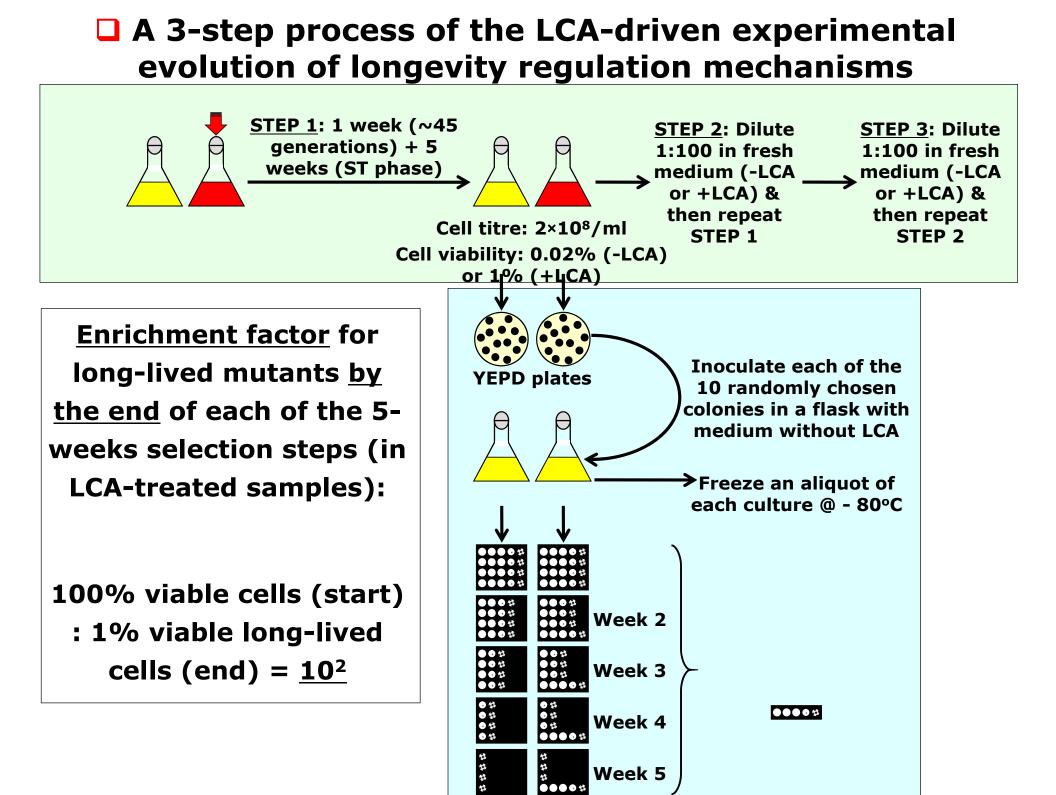
We propose a unified hypothesis of the xenohormetic, hormetic & cytostatic selective forces driving the evolution of longevity regulation mechanisms @ the ecosystemic level

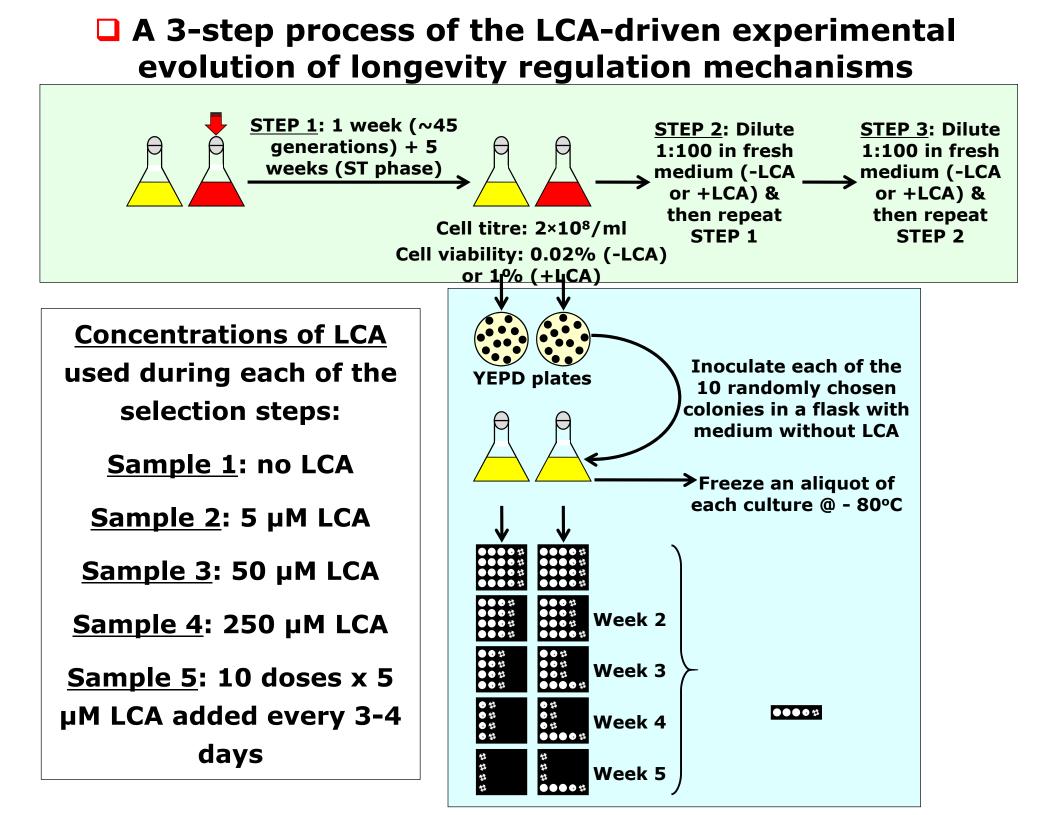


To test the validity of our hypothesis of the xenohormetic, hormetic & cytostatic selective forces driving the evolution of longevity regulation mechanisms within an ecosystem, we carried out the LCA-driven multistep selection of long-lived yeast species

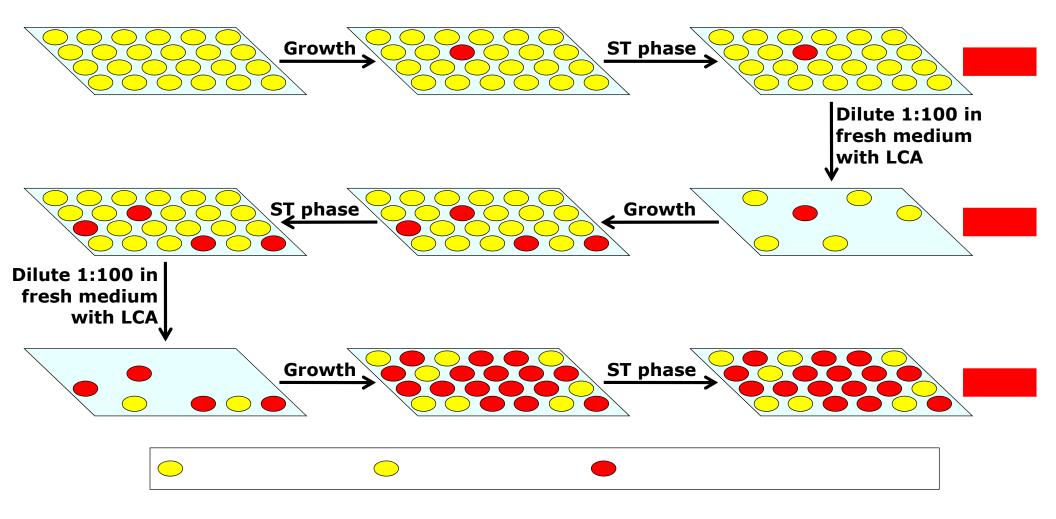


A 3-step process of the LCA-driven experimental evolution of longevity regulation mechanisms STEP 1: 1 week (~45 **STEP 2: Dilute STEP 3: Dilute** generations) + 5 1:100 in fresh 1:100 in fresh weeks (ST phase) 、medium (-LCA medium (-LCA or +LCA) & or +LCA) & then repeat then repeat Cell titre: 2×10⁸/ml STEP 1 STEP 2 Cell viability: 0.02% (-LCA) or 1% (+LCA) The number of cell Inoculate each of the generations in each of **YEPD** plates **10** randomly chosen colonies in a flask with the selection steps medium without LCA prior to entry into a ➤Freeze an aliquot of non-proliferative state each culture @ - 80°C (*i.e.*, stationary phase [ST] of senescence): Week 2 (2 x 10⁸ cells/ml) : Week 3 ●●●● t ● t ● t $(10^5 \text{ cells/ml}) = 2,000$ Week 4 ~ 45 generations ☆ ☆ ◆●●●●↓ Week 5

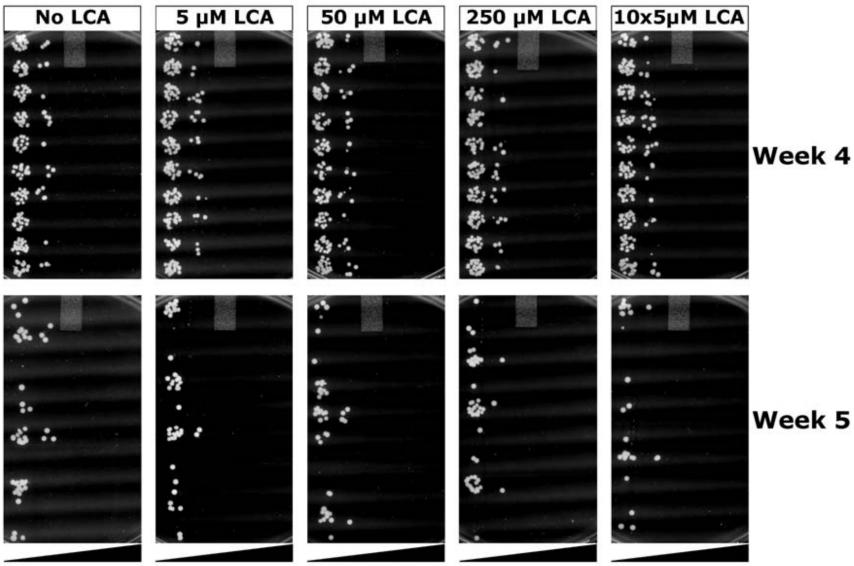




The fraction of long-lived mutants in a population of yeast is <u>increased</u> by the end of each of the 3 steps of the LCA-driven experimental evolution



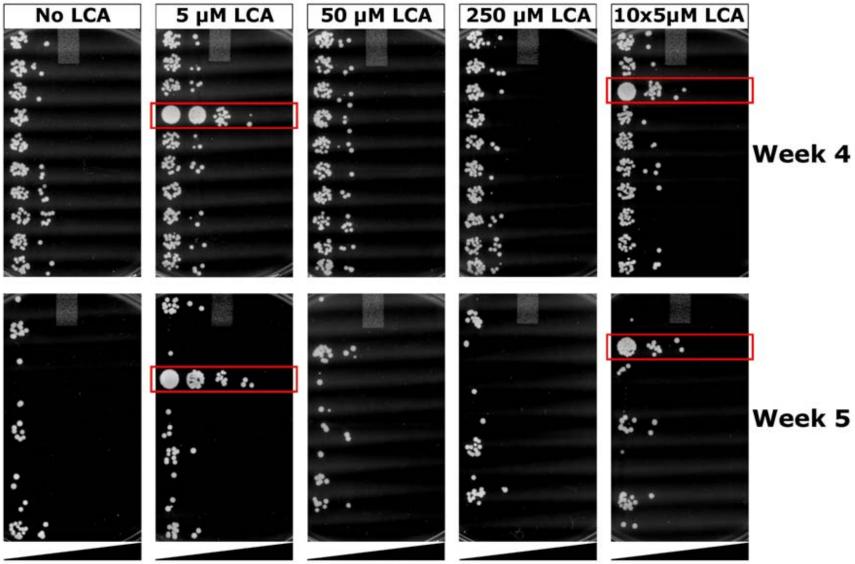
The 1st step of the LA-driven experimental evolution of longevity regulation mechanisms in yeast



Serial dilutions



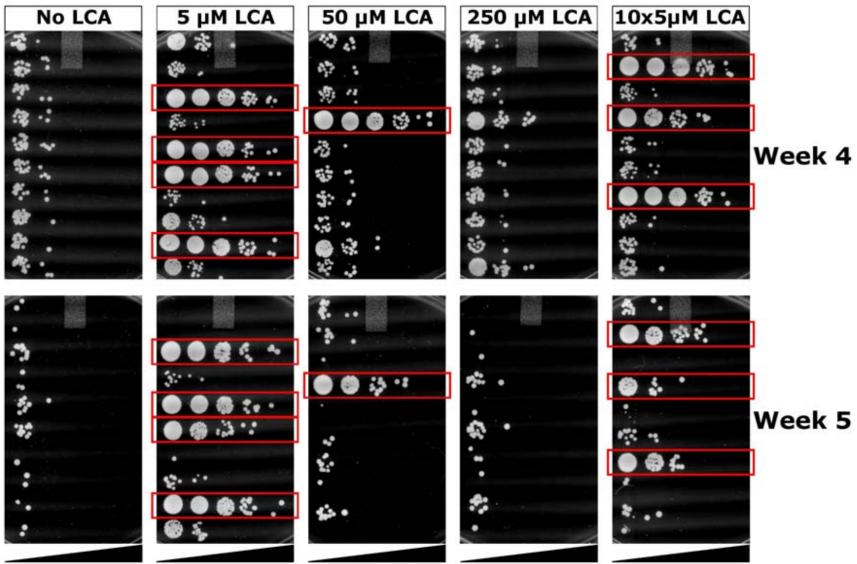
□ The 2nd step of the LA-driven experimental evolution of longevity regulation mechanisms in yeast



Serial dilutions



□ The 3rd step of the LA-driven experimental evolution of longevity regulation mechanisms in yeast



Serial dilutions



Conclusions:

A long-term exposure of wild-type yeast to LCA under laboratory conditions results in <u>selection of yeast species</u> <u>that live longer in the absence of LCA than their ancestor</u>

The order of different LCA concentrations ranked by the efficiency with which they cause the appearance of long-lived species (frequencies of such appearance are shown):

<u>5 μM LCA</u> (~ 4 x 10⁸/generation) > <u>10 doses x 5 μM LCA</u>
 (~ 3 x 10⁸/generation) > <u>50 μM LCA</u> (~ 1 x 10⁸/generation)
 <u>250 μM LCA</u> (no long-lived species found)

Because the lowest used concentration of LCA results in the highest frequency of long-lived species appearance, it is <u>unlikely</u> that the life-extending mutations they carry are due to <u>mutagenic action of LCA</u> **Future perspectives:**

What genes are affected by mutations responsible for the extended longevity of selected long-lived yeast species?

How these mutations influence the "housekeeping" longevityrelated processes modulated by LCA in chronologically aging yeast?

Do these mutations affect the growth rate of yeast in media with or without LCA?

Will selected long-lived yeast species be able to <u>maintain their</u> <u>ability to live longer</u> than wild-type yeast if they undergo several successive passages in medium without LCA? [Is there <u>selective</u> <u>pressure</u> aimed at maintaining of an "optimal" rather than a "maximal" chronological life span of yeast?]

If mixed with an equal number of wild-type yeast cells, will selected long-lived yeast species <u>out-grow and/or out-live</u> them in medium without LCA <u>or the opposite will happen</u>?

Acknowledgements

