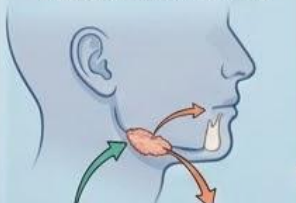


Rapamycin Stops Salivary Gland Aging in Primates

Jul 1, 2026 2:05 pm

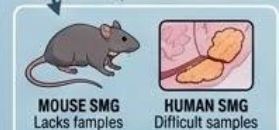
HOW THE COMMON MARMOSET MODEL REVEALS THAT RAPAMYCIN REVERSES AGE-RELATED DEGENERATION OF THE SUBMANDIBULAR GLAND

THE SUBMANDIBULAR GLAND (SMG) & XEROSTOMIA (DRY MOUTH)



HEALTHY SMG:
• Generates ~2/3 of resting saliva.
• Protects oral cavity, enamel, gums.

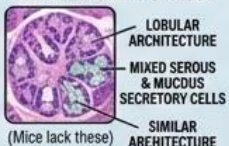
AGING & XEROSTOMIA:
• Chronic Dry Mouth affects ~50% over 65.
• Symptomatic management.
• Underlying biology underexplored.
• Mouse model fails due to differing architecture.



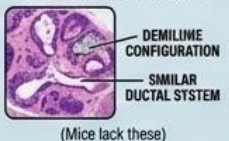
A SUPERIOR MODEL: COMMON MARMOSET (*CALLITHRIX JACCHUS*)



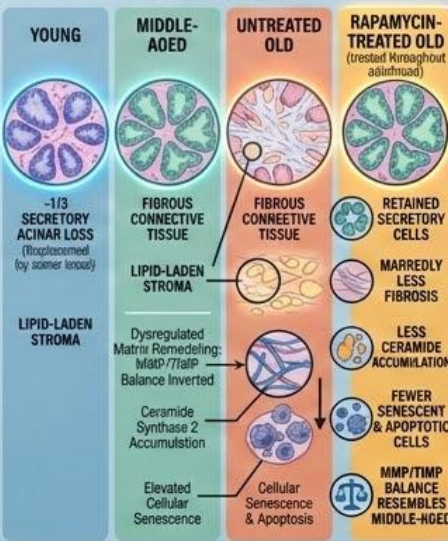
MARMOSET SMG HISTOLOGY



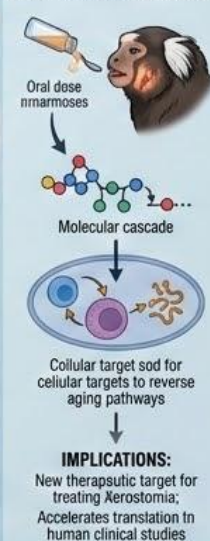
HUMAN SMG HISTOLOGY



AGE-RELATED DEGENERATION & RAPAMYCIN REVERSAL (MARMOSET SMG)



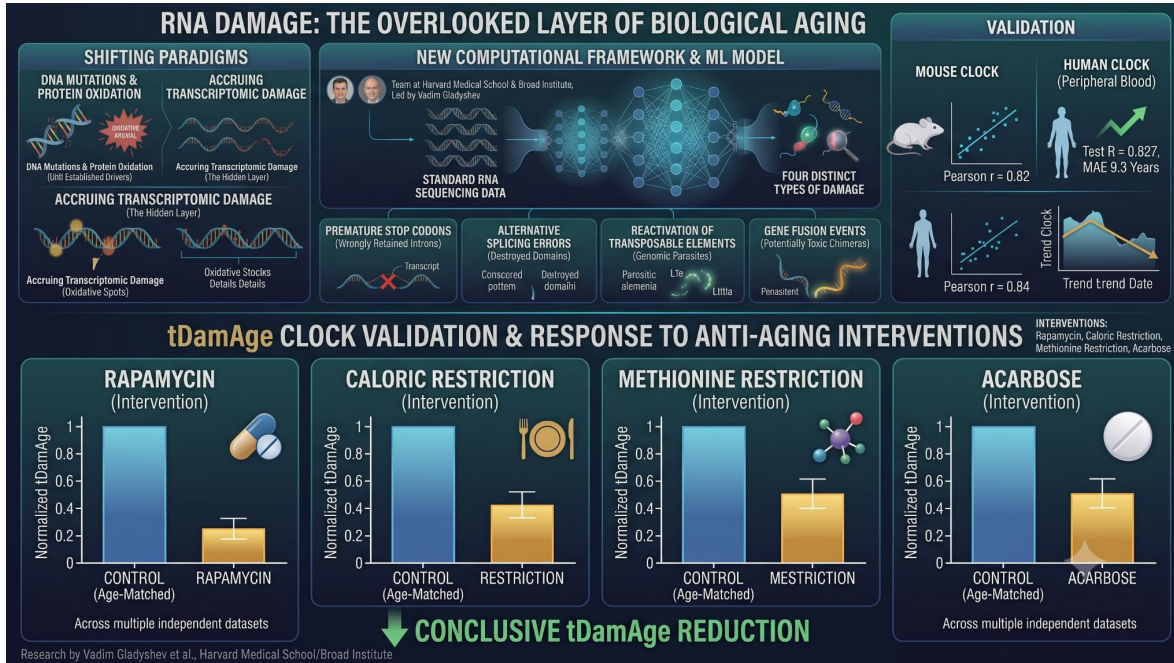
MECHANISTIC INSIGHT: HOW RAPAMYCIN WORKS



For the aging adult who takes rapamycin for longevity reasons, the practical implication is novel: the intervention may be offering protection against a dysbiosis—that triment—dry mouth, oral fragility, dysbiosis—that rarely appears on the target organ list but carries outsized consequences for long-term health.

This paper delivers the first primate-tissue evidence that rapamycin attenuates aging across the full suite of salivary gland hallmarks—acinar loss, fibrosis, matrix remodeling imbalance, lipid dysregulation, apoptosis, and senescence. The marmosets histological fidelity to human SMG architecture substantially strengthens translational credibility relative to any rodent dataset.

RNA Is Rotting as You Age, Harvard's New Damage Clock Measures it, and Rapamycin Helps Prevent it



KEY TAKEAWAYS

1. Multi-Damage Tracking

Extracts four concrete types of transcriptomic decay from standard RNA data.

2. tDamAge Validation

Highly accurate biological aging clock verified in both mouse and human cohorts.

3. Proven Interventions

Demonstrates robust damage reduction from Rapamycin and dietary restriction.

RNA Is Rotting as You Age, Harvard's New Damage Clock Measures it, and Rapamycin Helps Prevent it

A team at Harvard Medical School and the Broad Institute, led by Vadim Gladyshev, has now built a computational framework that extracts four distinct types of transcriptomic damage from standard RNA sequencing data. These are not soft correlations. The damage types are structurally concrete: premature stop codons generated when introns are wrongly retained in transcripts (producing truncated, non-functional proteins or triggering degradation); alternative splicing errors that physically destroy conserved protein domains; the reactivation of transposable elements — genomic parasites that are normally suppressed — across multiple repeat classes; and gene fusion events, where unrelated RNA strands are incorrectly joined into potentially toxic chimeric molecules. Each of these increases with age. All four damage types positively correlate with chronological age across the majority of human and mouse tissues tested.

