



AGELOC Y-SPAN RESEARCH

PEER-REVIEWED STUDY: EFFECT ON GENE EXPRESSION IN MULTIPLE TISSUES

The peer-reviewed study results summarized below were published in the journal [Nutrients](#) in 2020. The study provides further validation of the science behind ageLOC Y-Span—Nu Skin’s most advanced anti-aging supplement developed to deliver a wide range of systemic youth preservation benefits.

BACKGROUND

People want to live young and live well, so strategies to lessen the negative effects of aging are important. One well-established method of healthy aging, related to caloric intake, has been shown in scientific research to have favorable outcomes on health. However, it is difficult for humans to maintain caloric restriction for extended periods of time. Therefore, our research has focused on identifying ingredients that provide similar effects on gene expression as this method of healthy aging.

We used a proprietary gene expression screening tool to filter through a library of potential ingredients as we developed ageLOC Y-Span. Certain ingredients showed positive impacts in one tissue but had little effect in another tissue. Our screening method indicated that aging at the genetic level is different from one tissue to another and that there is no single ingredient that mimics the benefits of healthy aging in all tissues. Therefore, we hypothesized that a blend of ingredients would be most successful at providing similar gene expression of healthy aging at a systemic level, and this study demonstrated not only positive gene expression changes in several tissues with the supplement, but also positive outcomes.

METHODS

In our gene expression screenings of individual ingredients, we identified a blend of ingredients shown to have favorable results. We then tested this formula for its impact on gene expression in several tissues including the brain (cerebral cortex), skeletal muscle, and heart. The objective of this study was to determine if this formula would mimic aspects of healthy aging in various tissues in the body.

We used mice in this study because it was important to examine critical tissues like the brain and heart. Mice were equally divided into three groups (n=7). The first group—typical aging—represented typical aging with no anti-aging intervention. The second group—healthy aging—represented aging with a well-established healthy aging intervention. The third group—“ageLOC Y-Span”—represented typical aging with ageLOC Y-Span supplementation.

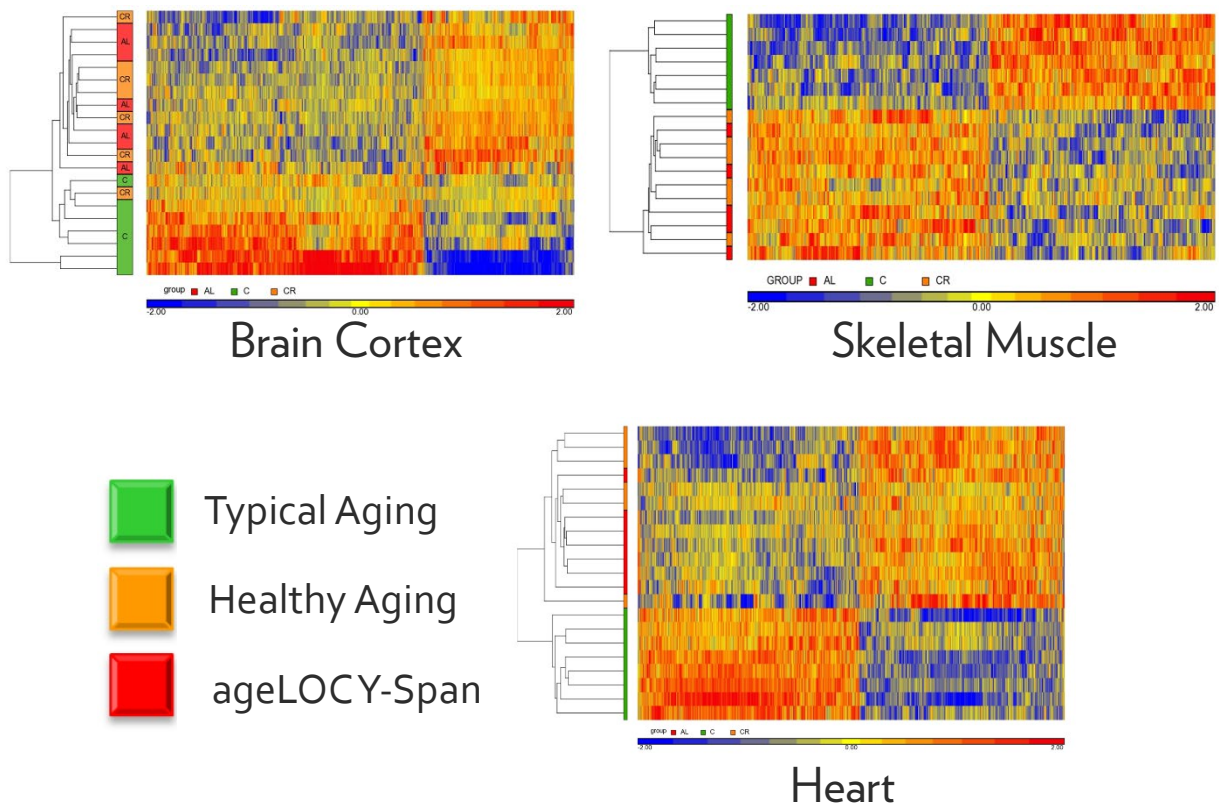
We used microarrays (gene chips) to measure gene expression in three important tissues (brain, skeletal muscle, and heart). We conducted further analysis using principal component analysis (PCA) to compare the expression patterns of the different groups as well as specific subnetworks/pathways and master regulators (important genes that influence many other genes).

RESULTS

HEATMAPS

We used software to analyze gene expression data; this software clustered similar patterns of gene expression together, as represented by the heatmaps below. For each heatmap, the colors in the left-hand column denote which group each row belongs to. As shown below, the Typical Aging rows (green) clustered together, whereas the Healthy Aging (orange) and ageLOC Y-Span groups (red) were interspersed and nearly indistinguishable.

In the brain cortex, skeletal muscle, and heart, the gene expression profiles of typical aging are distinctly different from those of healthy aging and ageLOC Y-Span, whereas the healthy aging and ageLOC Y-Span groups had similar gene expression patterns. In other words, ageLOC Y-Span mimics the intervention of healthy aging.



SUBNETWORK ANALYSIS AND OUTCOMES

We evaluated specific biological and functional networks and compared responses by groups. A subnetwork is a group of genes connected structurally or functionally to one common pathway or function. Using the genes that were identified in the differential analysis, we identified several subnetworks in each tissue analyzed. Each subnetwork has various biological processes; for specific details on these processes, please see the full paper, referenced at the bottom of this article. The subnetwork analysis provided insights into genes that impact a wide range of processes in certain

tissues. From the subnetwork analysis, genes tended to change in the same direction (whether upregulated or downregulated) in both the healthy aging and ageLOC Y-Span groups and were distinct from the typical aging group, even though the groups were the same age.

SUMMARY

Our major finding was that a blend of ingredients comprising an innovative nutritional formula induces gene expression changes in multiple tissues, like those induced by a well-established intervention of healthy aging. The results indicate that the benefits are achieved from the total blend of ingredients—not simply the contribution of one or two individual ingredients.

DISCLAIMER: This study was conducted in mice, not humans. The findings in this scientific study are not product claims; rather, they serve to further validate the science behind ageLOC Y-Span. For approved product claims consult official marketing materials.

(Mar 2020)

Reference:

Serna, E.; Mastaloudis, A.; Martorell, P.; Wood, S.M.; Hester, S.N.; Bartlett, M.; Prolla, T.A.; Viña, J. A Novel Micronutrient Blend Mimics Calorie Restriction Transcriptomics in Multiple Tissues of Mice and Increases Lifespan and Mobility in *C. elegans*. *Nutrients* 2020, 12, 486.

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