IDENTIFICATION OF TISSUE-SPECIFIC GENE EXPRESSION PATTERNS AND EVALUATION OF INGREDIENTS

A study was recently published in the prestigious scientific journal Aging Cell *(2017)[1] by scientists at LifeGen Technologies and Nu Skin, demonstrating Nu Skin's commitment to research and innovation. The focus of this study was to identify healthy gene expression patterns in a variety of tissues and then use these patterns to screen ingredients that mimic healthy aging. This is a tremendous advancement because Nu Skin scientists can leverage this understanding to develop powerful, unique, and innovative nutritional formulations.*

Introduction

Though there has already been demand for products that alleviate the effects of aging and help improve quality of life, until now, there has not been an easy way to screen and identify the most powerful anti-aging ingredients. Furthermore, different ingredients may have different effects in various tissues. Therefore, Nu Skin and LifeGen scientists set out with a strategy to first identify a consistent gene expression pattern of "healthy aging" in a diverse set of animal strains and then use this screen to identify important ingredients to incorporate into their nutritional supplements.

LifeGen and Nu Skin scientists began with a strategy and understanding of a nutritional intervention (Caloric Restriction - CR) that consistently provides anti-aging benefits, yet they recognized that models might potentially lead them astray by only using one animal strain. Therefore, they leveraged their understanding by studying several mouse strains and focused on the consistencies in gene expression across strains to increase their confidence that their findings could be more accurately translated. This strategy is extremely innovative and useful to the scientific community.

Methods

Seven different strains of 8-week-old mice were assigned to either the healthy aging intervention (CR) or a control diet until the animals were 22 weeks of age. For each of the seven strains, tissues from eight control and eight healthy aging mice were examined, using whole genome gene expression analysis of four different tissues (brain, muscle, heart, and fat) for a total of 448 separate microarrays. Gene expression measurements were conducted using gene chip microarrays and genetic software followed by statistical analysis. The gene expression patterns were compared between the healthy aging group and the control diet group in all four tissues. Different compounds were then evaluated for their impact on expression of marker genes and were also evaluated for their ability to modulate previously characterized biomarkers of CR.

Results

Gene expression profiling of different tissues in the healthy aging group showed different gene expression patterns from normal aging. The majority of these changes varied by tissue and by strain; however, there was a subset of genes that consistently changed across multiple strains. These genes that had healthy aging effects across multiple strains were identified as biomarkers of aging. Additionally, some ingredients tested demonstrated significant gene expression changes that mimic biomarkers of aging seen in the healthy aging model but without reducing energy (calories).

Discussion

This research is significant because it is the first study to examine gene expression of multiple mouse strains and tissues in a single protocol focused on healthy aging. Focusing on gene expression changes that were similar across multiple strains of mice allows for the identification of major conserved trends instead of only strain-specific effects.

Testing gene expression in four types of tissues revealed a different gene expression pattern from aging or healthy aging. The limited similarities between the biomarkers identified in different tissues suggests that the effects of healthy aging vary widely among these tissues.

Following identification of gene expression biomarkers of healthy aging, the evaluation of the effects of different ingredients on gene expression was insightful. Some ingredients displayed significant changes that mimicked gene expression biomarkers of healthy aging while others did not. Also, some of the different compounds displayed tissue-specific healthy aging activity. Because of this varied activity, it appears that stronger effects on healthy aging could be achieved by combining different ingredients that mimic healthy aging in various tissues.

Conclusion

Interest in identifying ingredients that mimic healthy aging is continuing to grow. This study successfully identified patterns of gene expression in a healthy aging model in multiple mouse strains and important tissues. Additionally, the findings of this study demonstrate innovation with the identification of tissue-specific gene expression biomarkers of healthy aging which can be used to screen and identify formulations that mimic the effects of a healthy aging model.

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Reference:

[1]Barger JL, Vann JM, Cray NL, Pugh TD, Mastaloudis A, Hester SN, Wood SM, Newton MA, Weindruch R, Prolla TA. Identification of Tissue-Specific Transcriptional Markers of Caloric Restriction in the Mouse and their Use to Evaluate Caloric Restriction Mimetics. Aging Cell. 2017 Aug;16(4):750-760.