IFSCC 35TH CONGRESS FRANCE_CANNES 15-18 SEPT 25

THE FUTURE IS SCIENCE

IFSCC2025-1330

How Genomic Analysis Can Guide the Development of a Cosmetic Formulation

Ferial Fanian[1]*, Shannel Curic[1], Laurent Peno-Mazzarino[2], Rania Bakour[1], Elian Lati[2]

[1] FILLMED Laboratories, Paris | [2] Laboratoires BIO-EC

INTRODUCTION

Cosmetic science is now leveraging genomic technologies such as microarrays to understand the biological effects of formulations and to design targeted, effective skin care solutions. This study investigates the transcriptomic impact of a cosmetic complex using ex vivo human skin.

Microelements, including [Si] Silicium Oligo-Catalyst, contribute to the maintenance of the extracellular matrix by supporting collagen organization and tissue integrity. Combined with Hyaluronic Acid, which ensures hydration and cellular signaling, the Si-Hyal complex synergistically promotes skin regeneration and barrier restoration.

MATERIALS & METHODS

STUDY DESIGN

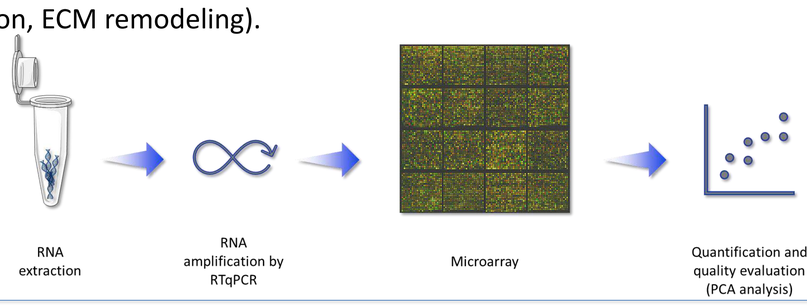
A total of **21 human skin explants** were maintained in survival culture conditions (37 °C, 5% CO_2) and treated topically on days 0, 1, 2, 3, 6, and 7. Product applications were performed from Day 0 (D0) to Day 7 (D7)

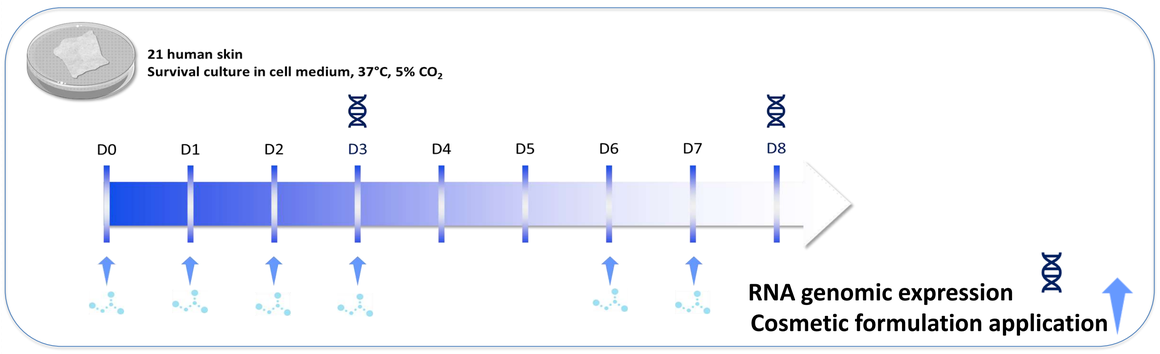
TESTED FORMULATION

The tested cosmetic complex, Si-Hyal®, combines Hyaluronic Acid with [Si] Silicium Oligo-Catalyst, providing synergistic effects on hydration, extracellular matrix organization, and skin regeneration.

TRANSCRIPTOMIC ANALYSIS

RNA was extracted from *ex vivo* human skin samples (treated vs. control). Gene expression profiling was performed by microarray analysis, followed by normalization and bioinformatic analysis. Significantly modulated genes (fold change ≥1.5, $p < 0.05$) were identified and classified into skin-related biological pathways (keratinization, adhesion, inflammation, ECM remodeling).





RESULTS

Transcriptomic profiling revealed a **time-dependent modulation** of gene expression in response to the cosmetic complex. A total of **122 genes were differentially expressed at Day 3** (65 upregulated, 57 downregulated), while **105 genes were modulated at Day 8** (40 upregulated, 65 downregulated) (Figure 1-a). Notably, only 8 genes were commonly regulated at both timepoints, supporting a **biphasic transcriptional response (figure 1-b)**

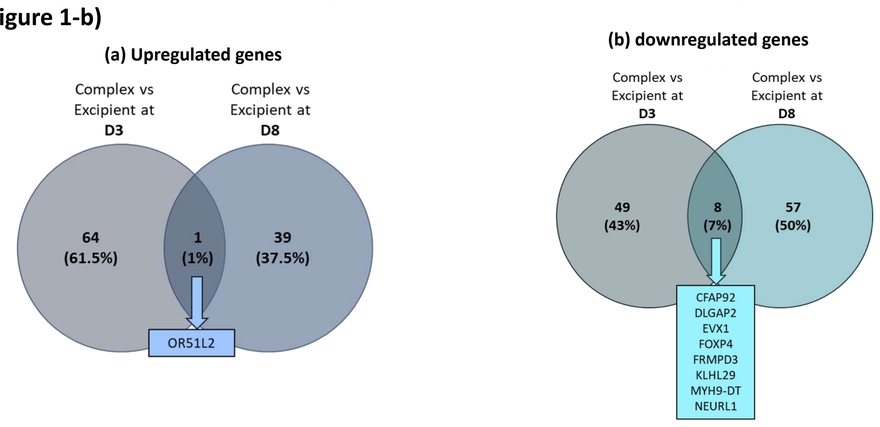


Figure 1. Venn diagrams: genes modulated by the complex at D3 and D8

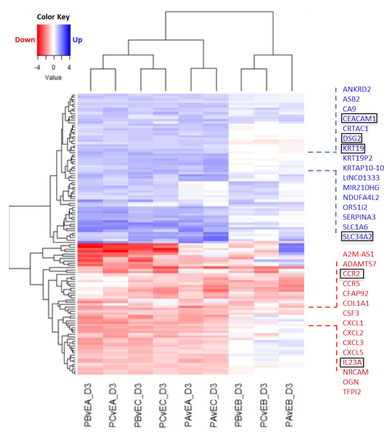


Figure 2. Heatmap of Differentially Expressed Genes at Day 3

The heatmap shows the global transcriptomic modulation induced by Si-Hyal® treatment in human skin explants at Day 3 . Clear clustering was observed between treated and control samples, indicating distinct gene expression profiles. Genes upregulated (blue) are mainly associated with keratinization, cell adhesion, and extracellular matrix reinforcement, while downregulated genes (red) are linked to inflammatory pathways. This pattern demonstrates the dual activity of the complex, enhancing skin barrier and structural functions while reducing pro-inflammatory responses.

Si-Hyal® application induced specific transcriptomic changes across skin layers. In the epidermis, keratinization-related genes (KRT16, KRT19, DSG2) and **cell adhesion genes** (CEACAM1, CEACAM5) were **upregulated**, supporting epidermal renewal and **barrier reinforcement**. In the basal layer, DLL1 and CA9 (**Vit D pathway**) showed increased expression, suggesting **improved differentiation and pH regulation**. Conversely, in the dermis, **inflammatory markers** (ARG1, IL23A, CCR2) were downregulated, indicating **reduced inflammatory responses**. Together, these modulations highlight the dual effect of Si-Hyal®: stimulation of epidermal regeneration and attenuation of inflammation

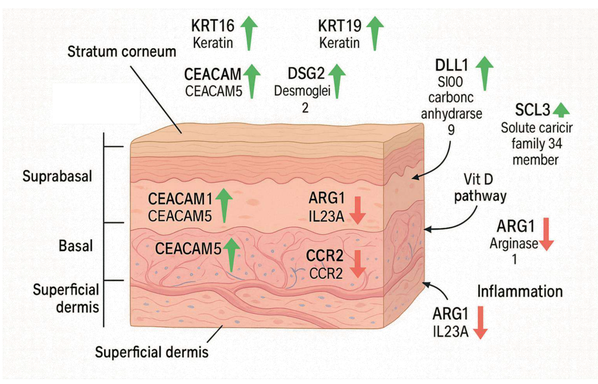


Figure 3. Modulated gene expression upon Si-Hyal application

CONCLUSION

- This study highlights the potential effects of a cosmetic product on the transcriptomics profile. Considering the correlation of some of these genes with cellular function and morphology, this evolution could affect the cell activity and structure.
- Stimulates epidermal and dermal regeneration
- Further studies should evaluate the correlation between this evolution and clinical results.
- These findings support the development of next-generation, individualized science-backed cosmetic products.

REFERENCES

1. Zouboulis, C.C. & Makrantonaki, E. Clinical aspects and molecular diagnostics of skin aging. Clin Dermatol. 2011;29(1):3–14
2. Zou, Z. et al. A Single-Cell Transcriptomic Atlas of Human Skin Aging. *Dev Cell.* 2021;56(3):383–397.e8.
3. Glass, D. et al. Gene expression changes with age in skin, adipose tissue, blood and brain. *Genome Biol.* 2013;14(7):R75.
4. Naciff, J.M. et al. Transcriptional profiling efficacy to define biological activity similarity for cosmetic ingredients' safety assessment. *Front Toxicol.* 2022;4:1082222.
5. Nadra, K. et al. A hyaluronic acid-based filler reduces lipolysis in human mature adipocytes. *J Cosmet Dermatol.* 2021;20(5):1474–1482.
6. Marionnet, C. et al. Modulation of gene expression induced in human epidermis by environmental stress in vivo. *J Invest Dermatol.* 2003;121(6):1447–1458.

FILLMED LABORATOIRES

IFSCC

SOCIÉTÉ FRANÇAISE DE COSMÉTOLOGIE