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"Application of Multi-Omics Technologies in Cosmetics and Supporting Personalized Skincare Solutions"

Xiaoming Xu[1]，Xinhang LI[1]，Hao LI[1]，Peipei Li[1]，Yangyang Fang[1]，Zihui Wang[1]，Shiqiang Zhu[1]，Huiliang Li[1]

[1]Zhejiang EastGarden Beauty Group Co., Ltd., Hangzhou 310000, China

1. Introduction

Recently, the trend of applying multi-omics technologies has shifted toward the cosmetics field[1]. Multi-omics refers to the comprehensive analysis of various "omes," including the genome, transcriptome, proteome, and metabolome, to capture a global snapshot of biological functions. The cosmetic industry continually seeks to innovate and personalize products to meet consumer demands. multi-omics technologies have emerged as powerful tools to gain a holistic understanding of biological processes at a molecular level[2]. Multi-omics technologies can help predict processes such as signal transduction or target pathways, especially in areas where experimental methods are insufficient[3]. In cosmetics, these technologies offer insights into skin aging, sensitivity, pigmentation, and the microbiome, helping to craft personalized solutions[1,5,6,7]. This article explores how multi-omics can transform the cosmetics industry by elucidating skin biology and facilitating the development of customized skincare.

2. Materials and Methods

2.1 Sample Collection

Skin samples were collected from volunteers representing diverse demographics, ensuring a range of skin types and conditions. Samples included skin swabs, biopsies, and surface lipid collections.

2.2 Genomics Analysis

Whole-genome sequencing was performed to identify genetic variations associated with skin type, sensitivity, and response to ingredients. Bioinformatics tools were used to analyze Single Nucleotide Polymorphisms (SNPs) and other genetic markers.

2.3 Transcriptomics

Transcriptomics is an important approach for studying cell phenotypes and functions，as well as the emerging field of spatial transcriptomics. RNA sequencing (RNA-Seq) was conducted to profile gene expression in different skin conditions, providing insights into the molecular basis of skin health and disease. Spatial transcriptomics can be categorised into three major methods: in situ hybridisation, in which the tissue is labelled by predesigned probes; in situ sequencing, in which transcripts are amplified in the tissue, labelled by fluorescent nucleotides and detected by imaging; and next-generation sequencing-based methods, which

label all acquired transcripts with spatial barcodes that can map their appropriate locations within the tissue[4].

2.4 Proteomics

Mass spectrometry was used to analyze the protein composition of skin samples, identifying biomarkers relevant to skin hydration, elasticity, and barrier function. MS-based proteomic approaches have significantly contributed to our understanding of skin pathophysiology.

2.5 Metabolomics

Gas Chromatography-Mass Spectrometry (GC-MS)、Liquid Chromatography-Mass Spectrometry (LC-MS) identified metabolites involved in skin metabolism, aging, and oxidative stress. And Using 2bRAD technology, microbiome sequencing was performed to accurately characterize low-biomass microbiomes at species-level resolution, analyzing the facial skin microbiota of the ensitive skin and non- ensitive skin groups.

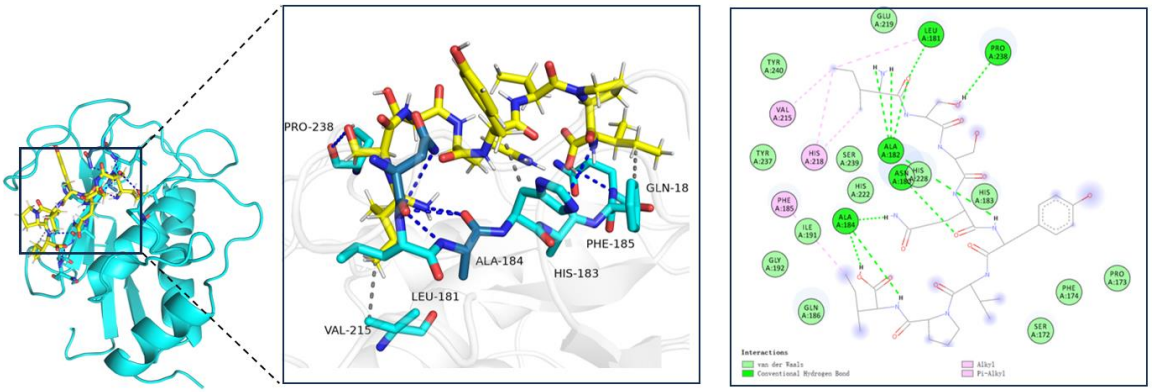
3. Results

The integration of omics data revealed distinct molecular signatures associated with different skin types and conditions. Genomic data identified key SNPs linked to pigmentation and sensitivity. Transcriptomic analysis illuminated gene pathways involved in hydration and aging. Proteomic profiling highlighted proteins crucial for maintaining skin barrier integrity. Metabolomic studies revealed variations in lipid profiles correlating with age and environmental exposure. The use of transcriptomics to investigate the potential mechanisms and biological pathways underlying the anti-aging effects of naringenin on photoaging induced by ultraviolet B (UVB) and naturally aged skin was reported by Zhao-Qing Shen et al. The title of the article is《Hesperetin activates CISD2 to attenuate senescence in human keratinocytes from an older person and rejuvenates naturally aged skin in mice》[5].Through microbiome analysis, streptococcus can significantly influence the expression levels of the inflammatory factor IL-8 in keratinocytes[6], and dermabacter hominis and chryseobacterium was firstly reported with a significantly increase in SS, and the S.capitis, as well as M.luteus, but not S.aureus, may be associated with skin inflammation, was reported by Yi-na LU et al. And we employed molecular docking techniques to predict the binding targets of our proprietary lotus peptide. The results demonstrated strong binding affinities with key targets including MMP-1 (Matrix Metalloproteinase-1), COL4A1 (Collagen Type IV Alpha 1), and Elastin, suggesting potential anti-aging mechanisms through these pathways. Subsequent in vitro experiments will be conducted to functionally validate the efficacy of these target interactions.

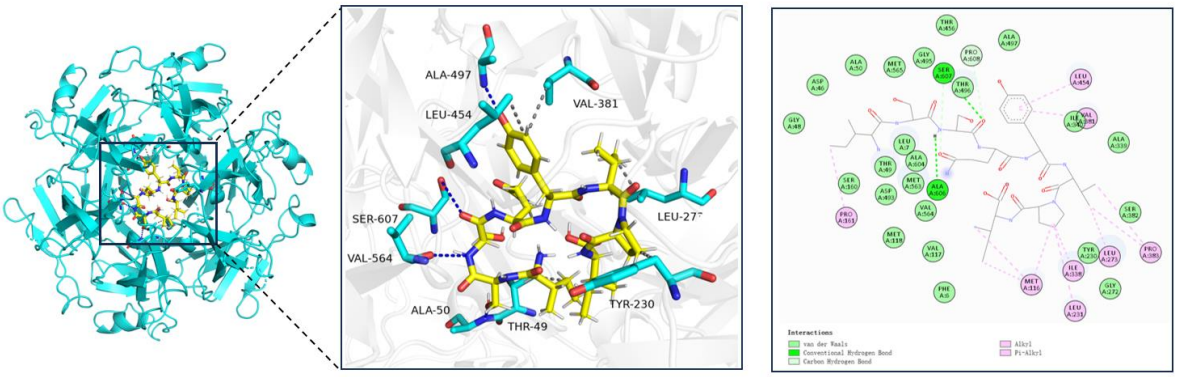
3.1. Figures & Tables

Table 1. Molecular docking was utilized to predict the binding affinity between lotus-derived peptides and anti-wrinkle-associated targets

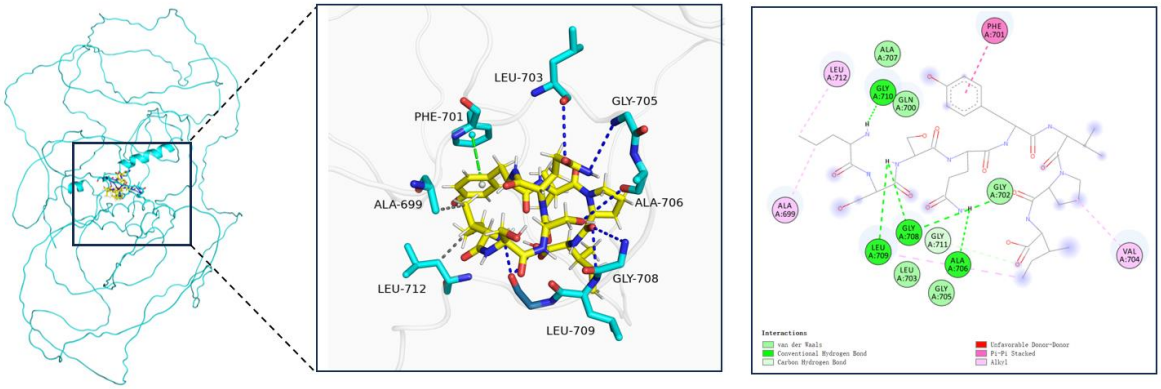
Target	MMP-1	COL4A1	Elastin
Molecular docking binding affinity	-6.442	-7.617	-5.017



(a)MMP-1



(b)COL4A1



(c)Elastin

Figure 1. This figure illustrates the molecular docking of lotus peptide:(a) Binding to the MMP-1 target, (b) Binding to the COL4A1 target, and (c) Binding to the Elastin target.

4. Discussion

The use of multi-omics technologies in cosmetics provides unprecedented insights into individual skin biology. This knowledge facilitates the development of targeted skincare solutions that address specific consumer needs, such as anti-aging, hydration, and sensitivity. Personalized products not only improve efficacy but also enhance consumer satisfaction and loyalty. However, challenges such as data integration, cost, and ethical considerations regarding genetic data must be addressed to fully harness the potential of multi-omics in cosmetics.

5. Conclusion

Multi-omics technologies represent a powerful approach to revolutionize the cosmetics industry through personalized skincare solutions. By understanding the complex interplay of genetic, transcriptomic, proteomic, and metabolomic factors, this approach may further enable the identification of novel critical targets within intricate regulatory networks, there by establishing technical barriers and product differentiation through proprietary target-based innovations. The companies can develop products tailored to individual skin needs. As these technologies become more accessible, their application in cosmetics is likely to expand, paving the way for a new era of precision skincare.

This research article highlights the transformative potential of multi-omics technologies in advancing cosmetic science and catering to consumer demands for personalized products. Future studies focusing on integrating these technologies will further enhance their impact and utilization in the industry.

6.References

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