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**Assessment of Human Skin Gene Expression by Different Blends of Plant Extracts with Implications to Periorbital Skin Aging.**

[Namkoong J](https://www.ncbi.nlm.nih.gov/pubmed/?term=Namkoong%20J%5BAuthor%5D&cauthor=true&cauthor_uid=30373163)1, [Kern D](https://www.ncbi.nlm.nih.gov/pubmed/?term=Kern%20D%5BAuthor%5D&cauthor=true&cauthor_uid=30373163)2, [Knaggs HE](https://www.ncbi.nlm.nih.gov/pubmed/?term=Knaggs%20HE%5BAuthor%5D&cauthor=true&cauthor_uid=30373163)3.

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**Abstract**

Since the skin is the major protective barrier of the body, it is affected by intrinsic and extrinsic factors. Environmental influences such as ultraviolet (UV) irradiation, pollution or dry/cold air are involved in the generation of radical oxygen species (ROS) and impact skin aging and dermal health. Assessment of human skin gene expression and other biomarkers including epigenetic factors are used to evaluate the biological/molecular activities of key compounds in cosmetic formulas. The objective of this study was to quantify human gene expression when epidermal full-thickness skin equivalents were exposed to: (a) a mixture of betaine, pentylene glycol, *Saccharomyces cerevisiae* and *Rhodiola rosea* root extract (BlendE) for antioxidant, skin barrier function and oxidative stress (with hydrogen peroxide challenge); and (b) a mixture of *Narcissus tazetta* bulb extract and *Schisandra chinensis* fruit extract (BlendIP) for various biomarkers and microRNA analysis. For BlendE, several antioxidants, protective oxidative stress biomarkers and many skin barrier function parameters were significantly increased. When BlendE was evaluated, the negative impact of the hydrogen peroxide was significantly reduced for the matrix metalloproteinases (MMP 3 and MMP 12), the skin aging and oxidative stress biomarkers, namely FBN2, ANXA1 and HGF. When BlendIP was tested for cell proliferation and dermal structural components to enhance the integrity of the skin around the eyes: 8 growth factors, 7 signaling, 7 structural/barrier function and 7 oxidative stress biomarkers were significantly increased. Finally, when BlendIP was tested via real-time RT-PCR for microRNA expression: miR-146a, miR-22, miR155, miR16 and miR21 were all significantly increased over control levels. Therefore, human skin gene expression studies are important tools to assess active ingredient compounds such as plant extract blends to advance dermal hypotheses toward validating cosmetic formulations with botanical molecules.

**KEYWORDS:**

botanicals; gene expression; microRNA; oxidative stress; periorbital skin aging; skin equivalents

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