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Oral Communication

KERATINOCYTE & SKIN PHYSIOLOGY

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Effect of a moisturizing active ingredient on the expression of barrier function and epidermal hydration-related genes

Skin moisturizing, and particularly that of the stratum corneum, is ensured by structural components (mainly within the cornified layer) and by water transport regulation. A mix composed of Xylityl glucoside, anhydroxylitol and Xylitol (XG) is a moisturizing active ingredient, which efficacy has been clinically proven. XG is also able to increase both the production of glycosaminoglycanes (which are considered as “water reservoirs” in the dermis) in normal human fibroblasts (in vitro) and that of ceramides in the epidermis (ex vivo). The aim of this study was thus to further investigate its regulation properties on the genes or proteins involved in skin barrier function and hydration. Reconstructed epidermis (REp), composed of normal human keratinocytes (NHK), were topically treated with a XG containing-formulation (vs. placebo-treated REp). This study was carried out by qRT-PCR analysis using low density TaqMan (StraticellTM). Pathway analysis of XG-induced gene regulations was performed with the GeneSpring® software (Agilent). Protein investigations were performed in parallel by western-blot against aquaporin (AQP)-3 and by anti-hyaluronic acid (HA) or anti-chondroitin sulfate (CS) ELISA on XG-treated NHK and/or normal human fibroblasts (NHF) (vs. untreated cells). XG, when topically applied on REp, was able to increase the level of expression of differentiation-and barrier function- related genes in comparison with placebo-treated REp. XG targets included genes encoding proteins involved in keratinocyte-keratinocyte junctions (claudins, AQP-3…), enzymes or structural components of the cornified layer (transglutaminases; loricrin…), and epidermal differentiation (involucrin, kallikreins…), most of them belonging to the epidermal differentiation complex 1q21. Moreover, XG induced an increase in the protein expression of AQP-3, CS and HA in NHK and/or in NHF. In conclusion, XG is able to regulate the structural components and the metabolic regulators involved in epidermal differentiation and skin moisturisation, at both gene and protein levels. Further protein confirmations will be required to confirm this newly identified mode of action.