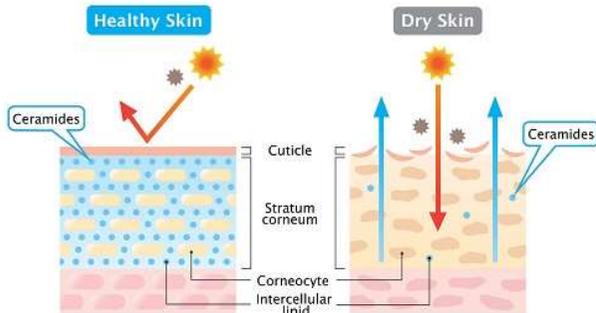


Ceramides are the main lipid constituent of the epidermal stratum corneum. Along with cholesterol and free fatty acids, ceramides play a major role in the integrity of the skin barrier function. In particular, **deficiency in long-chain ceramides results in various skin disorders** such as **atopic dermatitis, psoriasis or ichthyosis**. Reduction of ceramides in the stratum corneum is also observed in **environmentally-stressed, dry and aged skins**.



Dermo-cosmetic products able to improve the biological level of ceramides synthesis in the epidermis could help restoring the natural hydration and, to a larger extent, the barrier function of disordered skins.

The new barrier-altered 3D skin model designed by StratiCELL, provides relevant data on the **natural production of ceramides** to allow investigation and confirmation on the in vitro efficacy of promising dermo-cosmetic ingredient. Comparison to a positive reference compound is available for full objectivation.

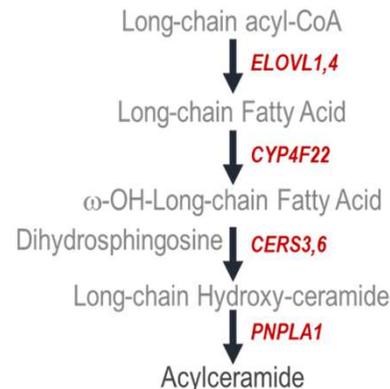
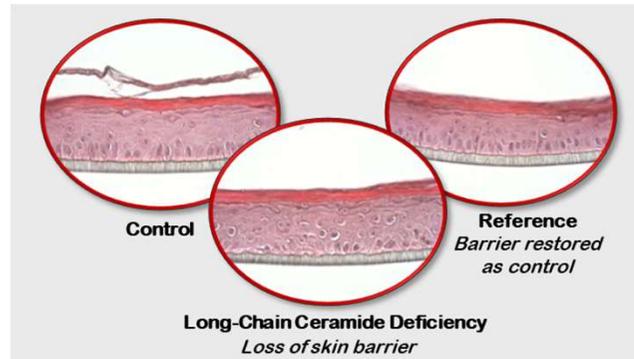
MODELS:

- *RHE-ΔCER*: reconstructed human epidermis deficient in long-chain CER synthesis
- *NHEKS-ΔCER* : primary human keratinocytes deficient in long-chain CER synthesis

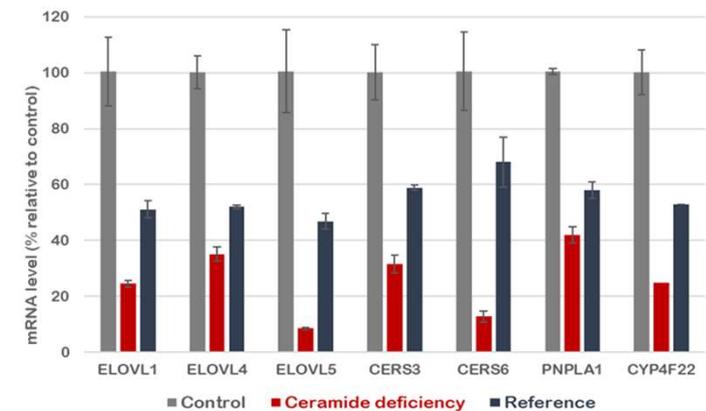
TESTS:

- RHE morphology
- Gene expression signature of CER synthesis by qRT-PCR
- Lucifer Yellow and Biotin dye diffusions (ongoing)
- Lipid content (ongoing)
- Positive reference available for full objectivation

RESULTS:

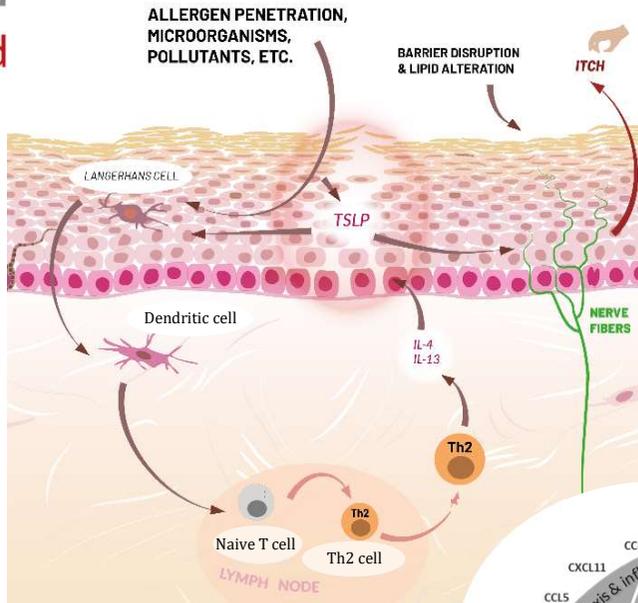


Gene expression signature of long-chain ceramide deficiency



Atopic eczema & barrier resilience in Th2-driven inflammation

Atopic eczema (AE) is a skin disorder driven by a Th2 inflammatory response associated with epidermal barrier defects. StratiCELL has developed skin models highly relevant to study barrier resilience, dyslipidemia, and inflammation, in atopic or sensitive skin conditions.



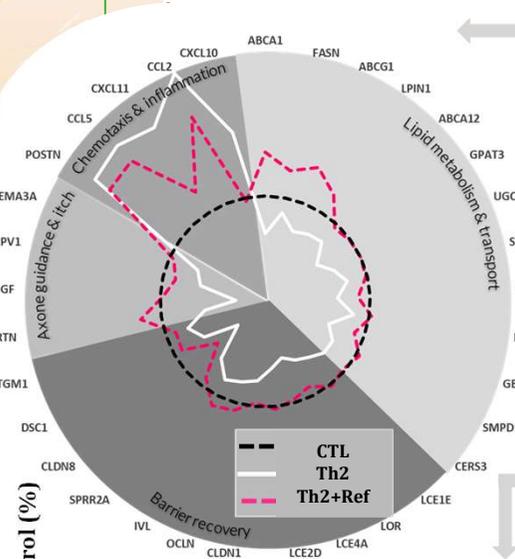
MODEL:

- RHE-Th2: reconstructed human epidermis treated with Th2 interleukins
- NHEK-Th2: primary human keratinocytes treated with Th2 interleukins
- Benchmark reference (Ref) : LXR agonist

TESTS:

- Gene expression levels by RT-qPCR, either of individual targets or using a TaqMan Low-Density Array to study simultaneously 96 key genes involved in typical AE features (e.g. FLG, ABCA12, CCL2, HAS3, CA2).
- Quantification of proteins by immunohistofluorescence (e.g. CA2, FLG, LOR, IVL).
- Spongiosis and morphological analysis by HE staining.
- Barrier function integrity using a biotin migration assay.

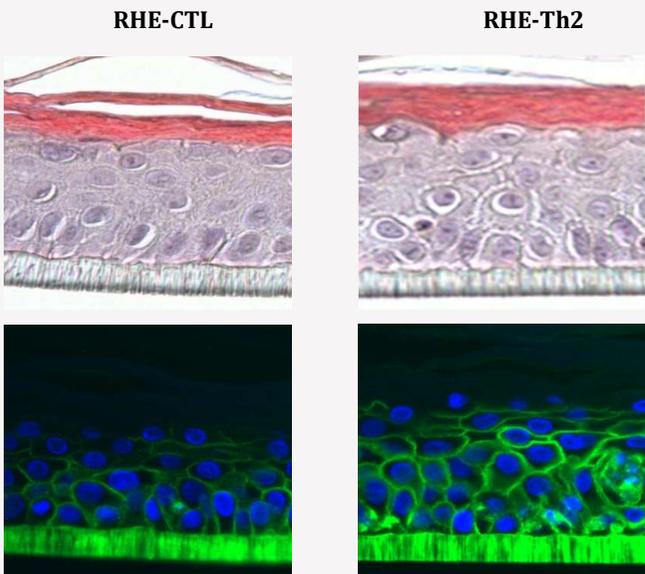
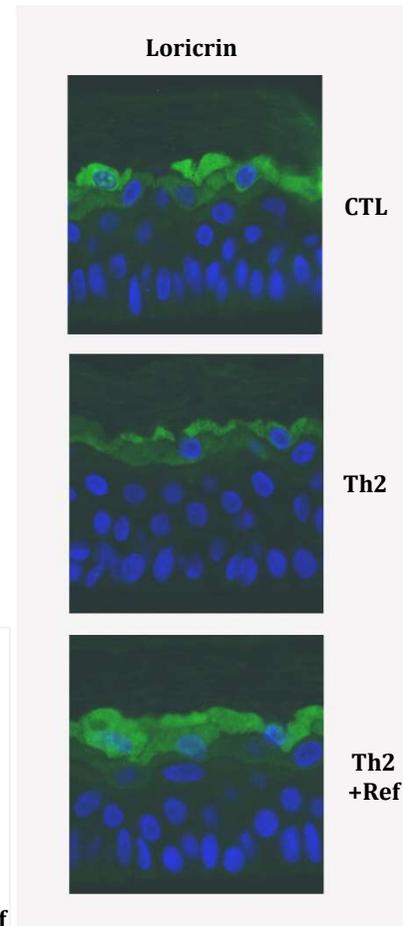
RESULTS:



Expression signature of main gene groups involved in chemotaxis, inflammation, barrier function, itch, and lipid metabolism. Black line represents the baseline expression levels in control tissues. White and pink lines represent Th2 stimulation and reference treated conditions respectively. Gene expression has been measured by RT-qPCR using customized TaqMan Low Density Arrays.

Representative Loricrin staining of control, Th2, and reference treated RHE (from top to bottom respectively)

mRNA expression levels evaluated by RT-qPCR using individual TaqMan assays. Expression levels are normalized through the $\Delta\Delta CT$ method and shown as percentages of the levels in the untreated control (mean + SD of triplicates). Student's t tests to Th2 condition: **, $p < 0.01$.



Representative Hematoxylin & Eosin (H&E, up) and biotin immunofluorescence (bottom) of RHE control (CTL, left) and Th2-treated (right) showing spongiosis (increased intercellular space) with destructuration (up, right) and weakened barrier function (bottom, right).

