MALASSEZIA OVERGROWTH : a promising new 3D skin model



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Protein secretion (fold to control)

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Malassezia furfur is a lipophilic natural cutaneous yeast, generally located in hyperseborrheic regions of the body, like face and neck. In case of dysbiosis, *M. furfur* is related to pityriasis versicolor or seborrheic dermatitis on the body skin. On human scalp, Malassezia overgrowth is however responsible for dandruff.

To allow new studies on the efficacy of innovative antifungal actives, StratiCELL has overcame the challenging colonization of reconstructed epidermis by living *M. furfur*, as a model of Malassezia infection. This new *in vitro* model displays a huge reactivity of the tissue, as observed by the expression of inflammatory, immunity and skin barrier biomarkers.

Description	Replicates the colonization of skin by Malassezia furfur.			
Skin mode	RHE-MF: Reconstructed Human Epidermis (RHE) topically colonized by Malassezia furfur.			
Positive reference	Ketokonazole (KTZ)			
Endpoint	1. Growth of <i>M. furfur</i> on RHE by C.F.U. (Colony Forming Units) counting.	PAS LY	3. Morph and Tran Control	
	M. furfur M. furfur + KTZ O hour 72 hours	lynoit		4. Skin response to <i>M. furfur</i> colonization by quantification of biomarkers (ELISA).
	2. Skin response to <i>M. furfur</i> colonization by gene expression (RT-qPCR) : individual TaqMan probes or 93 genes TaqMan Low Density Array (TLDA – "Skin Response to Microorganisms").	Hingeren Signaling Others Inflartin Allocation of the 93 transcripts detacted in the TLDA "Skin Response to Microorganisms"	Barrier Cell John	HBD-2 IL-8

info@StratiCELL.com +32 (0)81 72 85 82 www.StratiCELL.com