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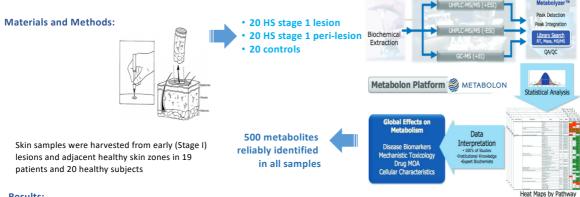
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Metabolic alterations in Hurley stage 1 Hidradenitis Suppurativa

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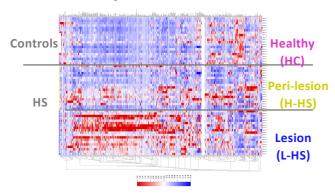
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Introduction: HS pathophysiology is only partially understood. Previous metagenomic studies have identified distinctive anaerobic flora in HS skin, whose expansion correlate with lesion severity. Targeted antibiotic combinations are efficient in treating HS. Dysregulated immune responses have also been identified. In this study, we conducted the first metabolomic analysis of HS skin to gain insights into potential mechanisms linking cutaneous dysbiosis with dysregulated immune responses and HS pathophysiology.



Results:

A metabolomic signature associated with HS lesions:

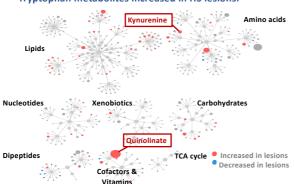


Our analysis detected a total of 500 metabolites, which distributed differently among skin samples from HC, and from H-HS and L-HS

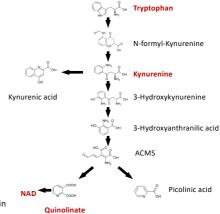
2 (10 %) Healthy control Lesional Skin Peri-lesional Skin

Principal component analysis clearly discriminated the metabolomes of L-HS and HC skin, while H-HS showed an intermediate signature.

Tryptophan metabolites increased in HS lesions:



At a 5% FDR, 228 metabolites were differently modulated between H-HS and L-HS skin, among which 214 were significantly augmented in lesions. The most up-regulated metabolite in L-HS skin was quinolinate (more than **10 000** times higher in L- HS lesions than in HC)



H-HS

Discussion and conclusion:

It has been reported that Tryptophan metabolism can modulate immune response (Harden et al; J Allergy Clin Immunol. 2016). It seems to play a role in Inflammatory Bowel Diseases (Agus et al; Cell Host Microbe. 2018.)

This study suggests Tryptophan metabolism has a key role in HS. It thus highlights a new potential pathway in HS and could help us to move forward in the comprehension of HS pathophysiology.







