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BACKGROUND:
The role of the balance between Staphylococcus aureus and commensal flora in the severity of atopic dermatitis (AD) lesions is not well understood.

OBJECTIVES:
To determine the structure of skin microbiome in patients with AD and its changes during an 18-day course of hydrotherapy and to assess the association between S. aureus and micro-organism colonisation, local skin condition and AD severity.

METHODS:
Three skin areas (xerotic, inflammatory and healthy) were identified in 25 moderate to severe AD patients for sampling before treatment, just after (day 1), and at day 10 and day 18. The structure of the bacterial community in the samples was assessed using a molecular biology approach based on 16S rRNA gene profiling. At each visit, AD severity was measured globally by the SCORAD index and at the lesional and healthy sampling sites.

RESULTS:
Clustering analysis of 296 samples showed two different bacterial community profiles: one with 2 peaks corresponding to S. aureus, the other displayed multiple peaks, identified as diversified microflora. At baseline, xerotic areas seemed to be less colonised by S. aureus than inflammatory areas. After 18 days of hydrotherapy, the number of lesional sites colonised by S. aureus (p<0.05) and the SCORAD index (p<0.00001) were significantly reduced, mainly in inflammatory and moist areas, promoting the emergence of a diversified microflora.
CONCLUSIONS:
We identified two bacterial community profiles corresponding to S. aureus and diversified microflora. The competitive balance between both profiles appears to be a key element associated with the severity of AD lesions.