Multi-omics Analyses Reveal Bacteria and Catalase Associate with Keloid Disease

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BACKGROUND:
The pathology of keloid and especially the roles of bacteria on it were not well understood.

METHODS:
In this study, multi-omics analyses including microbiome, metaproteomics, metabolomic and single-cell transcriptome were used to explore the roles of bacteria on keloid disease.

RESULTS:
We found that the types of bacteria are significantly different between keloid and healthy skin. The 16S rRNA sequencing and metaproteomics showed that more catalase (CAT) negative bacteria, Clostridium and Roseburia existed in keloid compared with the adjacent healthy skin. In addition, protein mass spectrometry shows that CAT is one of the differentially expressed proteins (DEPs). Overexpression of CAT inhibited the proliferation, migration and invasion of keloid fibroblasts, and these characteristics were opposite when CAT was knocked down. Furthermore, the cell-derived xenograft (CDX) model showed that Clostridium butyricum promote the growth of patient's keloid fibroblasts in vivo, while CAT positive bacteria Bacillus subtilis inhibited it. Single-cell RNA sequencing verified that oxidative stress was up-regulated and CAT was down-regulated in mesenchymal-like fibroblasts of keloid.

CONCLUSION:
In conclusion, our findings suggest that bacteria and CAT contribute to keloid disease.