A systematic literature review of the human skin microbiome in disease – a potential biomarker for dermatological drug development?

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INTRODUCTION

Changes or aberrations in the skin microbiome have been implicated in the pathophysiology of numerous skin diseases such as atopic dermatitis (AD) and acne vulgaris (AV). Consequently, skin microbiome-associated biomarkers may provide I) novel treatment targets for dermatological drug development programs II) novel options for drug profiling of new compounds targeting the skin mircobiome and III) objective data to support the mostly subjective clinical scores in clinical trials.

AIM

We aimed to provide a systematic review of studies that have investigated the use of the skin microbiome as a potential diagnostic, prognostic and therapeutic biomarker with emphasis on sample techniques and wet analysis methodology. To focus the review on illustrative examples we investigated 6 disorders with potential, i.e. atopic dermatitis (AD), seborrheic dermatitis (SD), acne vulgaris (AV), hidradenitis suppurativa (HS), psoriasis vulgaris (PV), chronic wounds/ulcers (CU).

METHODS

The 'Preferred Reporting Items for Systematic Reviews and Meta-analysis' (PRISMA) guidelines were followed. In collaboration with a trained librarian, a structured electronic literature search was composed. PubMed (incl. MEDLINE), Embase (OVID-version), Web of Science, Cochrane Library, CENTRAL, Academic Search Premier, and ScienceDirect were searched. Animal-only studies, reviews without original data, non-English studies, case studies and studies using culture based methods were excluded.

RESULTS

41 studies were included in the review

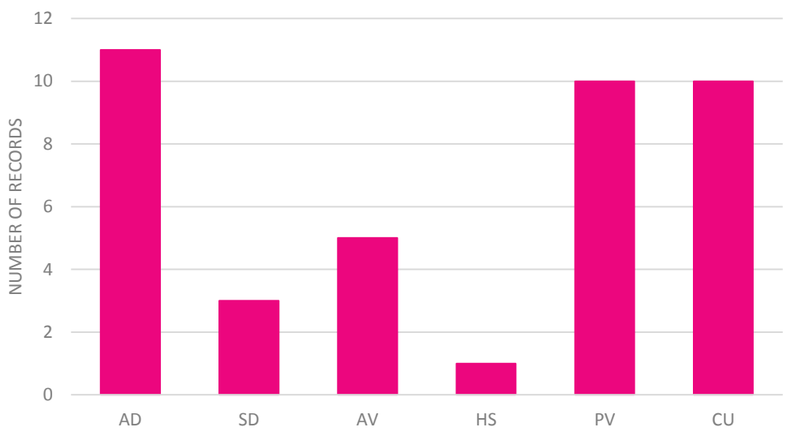

Figure 1. Number of studies investigating the skin microbiome in the selected skin diseases.

Key observations:

- Mainly case-control studies
- Wide variability in study design, poor standardization
- Small sample sizes (mostly patient populations N<30)
- Poor defined in- and exclusion criteria
- In some studies patients on active treatment during sampling
- Only 1-3 serial sampling per disease
- Multiple sampling methods
- Multiple analyzing methods
- Inconsistent findings SD, HS, PV and CU

Highlights AD:

- Correlation S. aureus abundance with disease severity (N=1).
- Taxonomic normalization and increased bacterial diversity in AD lesional skin following various treatments (N=4)

Highlights AV:

- Increased microbial diversity microbiome of acne patients, compared to healthy.
- Positive correlation Propionibacterium and acne severity grade (N=1)
- Propionibacterium decreased after treatment, together with an increase of microbial diversity

CONCLUSIONS

- No standardization for sampling and analysis yet
- Comparison of specific findings are problematic due to wide variability in study designs.
- Potentially useful for certain dermatological conditions, e.g. AV and AD to support drug development as complementary outcomes to clinical scores
- Further qualification and validation necessary to obtain
  - Robust, standardized methodology
  - Longitudinal microbiome datasets
  - Natural variability
  - Larger sample size for generalizability

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