Acne Vulgaris and the Facial Cutaneous Microbiome: A Cross-Sectional Pilot Study from the Annual Twins Day Festival

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Synopsis

Acne Vulgaris

Inflammatory dermatosis of the pilosebaceous unit[1] driven by:

- Follicular Hyperkeratinization
- Hyper-/Dys-seborrhea
- *Cutibacterium acnes* colonization
- Inflammation

Other intrinsic and extrinsic factors may affect acne severity including epidermal barrier dysfunctions[2], high glycemic index diet[3], and dysbiosis within the superficial and follicular microbiome[4].

Facial Cutaneous Microbiome

Superficial facial and truncal cutaneous microbiome are dominated by[5]:

- *Staphylococci* spp. (e.g. *S. epidermidis*): >27% of bacterial organisms
- *Propionibacterium* (including *Cutibacterium acnes*): <2%

Physiologically-healthy follicular microbiome[6] is more homogenous:

- *C. acnes* comprises 89-94% of the bacterial population, functioning as a commensal organism in healthy skin.

Additional microbes include

- *Malassezia* spp.
- Bacteriophages (including strains that specifically target *C. acnes*)

Acne & Dysbiosis

Studies suggest pre-existing and treatment-associated transepidermal water loss (TEWL) may pathogenically alter the cutaneous microbiome.[7,8]

Additional factors that may instigate cutaneous dysbiosis include:

- age and physiologic changes associated with puberty[9]
- Colonization with virulent *C. acnes* phylotypes (e.g., IA1)[6]
- Elimination of commensal microbes with broad spectrum antibiotics[10]

Objectives

1. To determine correlations between the facial cutaneous microbiome and the presence and severity of acne vulgaris.
2. To use questionnaire and survey data to identify potential environmental factors that may alter the facial cutaneous microbiome.

Methods

Cross-sectional, IRB-approved study during a Pre-COVID-19 Twins Day Festival. Participants with and without acne were assessed by a board-certified dermatologist and completed a questionnaire regarding

- Demographics, exercise, and environmental factors (e.g., pet ownership)
- history of acne, acne treatment, and skin care regimen

Demographic analysis was performed using R. P-values were calculated based on t.test for pairwise comparisons or X^2 test for multiple categories comparisons.

Microbiome Assessment & Analysis

Superficial facial swabs of the forehead and malar cheeks were collected on-site. Microbiome data were collected and analyzed for 16S sequences clustered into Operational Taxonomic Units (OTUs) using the UPARSE algorithm. OTUs were mapped to an optimized version of the SILVA and UNITE Databases.

Analysis was performed using R. Custom script was used to identify trends in taxa abundance, α-diversity, and β-diversity. Significance of categorical variables was determined using the non-parametric Mann-Whitney U test and/or the Kruskal-Wallis test. Ordination method was based on principal coordinates analysis (PCoA) followed by Monte Carlo permutation test for p-value estimation. Differential abundance was calculated using DESeq2. P-values were adjusted for multiple comparisons with Benjamini-Hochberg FDR correction.

Results

Table 1. Participants' Characteristics: Acne v. Control

	Acne (N = 158)	Control (N = 64)	p-value
IGA – n (%)			
Mild	71 (53.0)	-	
Moderate	50 (37.3)	-	
Severe	13 (9.7)	-	
Truncal Acne – n(%)	61 (38.6)		
Age – mean (SD)	18.3 (6.0)	23.35 (10.7)	<.001
Female Gender – n (%)	123 (77.8)	47 (73.4)	.236
BMI – mean (SD)	22.8 (4.9)	25.5 (6.9)	0.002
Fitzpatrick Score – mean (SD)	3.01 (0.9)	3.00 (1.1)	.930
Pets Now – n (%)	115 (72.8)	40 (62.5)	0.066
Exercise/Week – mean (SD)	2.3 (1.7)	3.6 (2.2)	<.001
Strenuous Exercise/Week – mean (SD)	1.6 (1.5)	1.8 (1.7)	0.321

Table 2. Current use of Over the Counter and Prescription Topical and Systemic Agents

	Acne (n = 158)	Control (n = 64)	p-value
Topical Products			
Over the Counter, n(%)	8 (5.1)	0 (0)	.336
Benzoyl Peroxide, n(%)	54 (34.2)	3 (4.7)	<.001
Prescription Topicals, n(%)	36 (22.8)	3 (4.7)	<.001
Systemic Treatments			
Oral Contraceptive, n(%)	32 (20.3)	12 (18.8)	.401
Systemic Antibiotics, n(%)	17 (10.8)	0 (0.0)	0.003
Isotretinoin, n(%)	4 (2.5)	0 (0)	.100
General Skin Care			
Moisturizer, n(%)	88 (55.7)	34 (53.1)	.363
Cleanser, n(%)	115 (72.3)	40 (62.3)	.065
Sunscreen, n(%)	120 (75.9)	39 (60.9)	.012

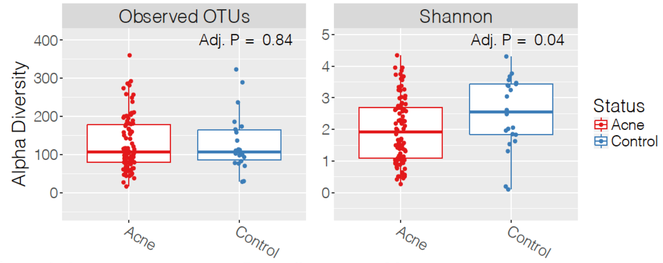

Figure 1. Alpha diversity in the Facial Cutaneous Microbiome

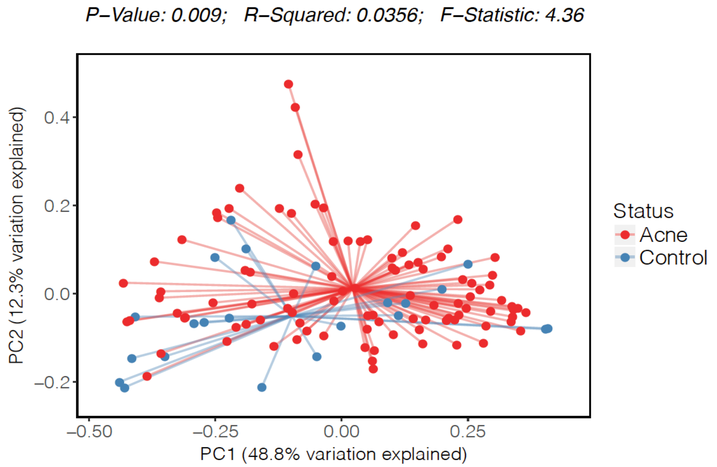

Figure 2. Beta diversity in the Facial Cutaneous Microbiome

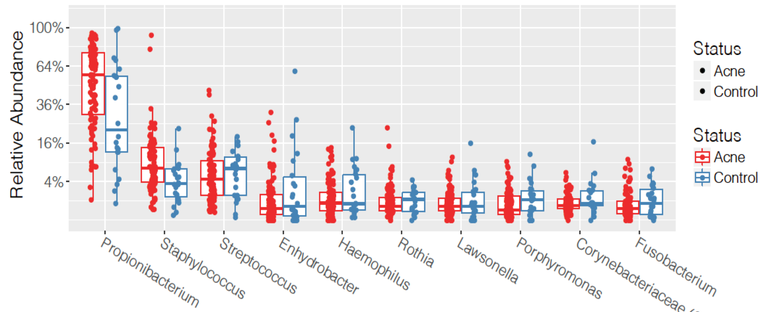

Figure 3. Differential Abundances of Bacterial Genera

Results & Conclusions

1. Demographically, participants with acne:
   - Had mild-moderate acne (>90%)
   - Were younger (p<.001) with a lower BMI (p=.002)
   - Exercised less frequency (p<.001)
2. Participants with acne were significantly more likely to have used
   - Benzoyl peroxide (p<.001)
   - Other prescription topicals (p<.001)
   - Systemic antibiotics (p=.003)
   - Sunscreen (p=.012)
3. Significant difference in Shannon diversity index (p=.04) suggests decreased diversity in participants with acne than control
4. Significant difference in β-diversity suggests a significant (p=.009) difference in composition of bacteria between participants with acne and control
5. Individuals with acne trended towards having increased relative abundance of *Propionibacterium spp.* and *Staphylococcus spp.*.

Environmental factors, including acne therapy, UV exposure, and sweat may (indiscriminately and preferentially) alter the relative abundances and lead to decreased microbial diversity. Further studies are needed, especially of the follicular microbiome and C. acnes phylotypes, to study the role of dysbiosis in acne pathogenesis.

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