

STUDY OF GUT MICROBIOTA IN PATIENTS WITH DIFFERENT CLINICAL PRESENTATIONS OF ACNE VULGARIS

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Introduction

Acne vulgaris is a chronic inflammatory skin condition of the pilosebaceous units, affecting 80 to 90% of adolescents. It has been proposed that environmental factors, particularly the "Western-style" diet, play a part in the pathophysiology of acne. It has been proposed that environmental factors, particularly the "Western-style" diet, play a part in the pathophysiology of acne. A few recent research that examined the link between the gut and acne discovered notable changes in the microbiome of acne patients compared to healthy controls. Given the crucial involvement of mTORC1 in the etiology of acne and its influences on the composition of the intestinal microbiota, this offers a link for the gut microbiota to affect acne pathophysiology.

Aim of the work

The aim of this work was to study gut microbiota in patients with different clinical presentations of acne vulgaris.

Patients and Methods

A total of patients were divided into two groups. The case group consisted of 30 acne patients with different grades of severity presented to the outpatient clinic at the Dermatology department in Alexandria Main University Hospital, and the control group consisted of 30 healthy participants.

Results

Table (1): Comparison between the two studied groups according to different types of Bacteria:

	Cases, N = 30	Control, N = 30	p-value
Bacteroides			<0.001*
Range	6.28E-03 - 9.69E-02	1.33E-03 - 5.46E-01	
Mean ± SD	4.93E-02 ± 2.37E-02	2.08E-01 ± 1.67E-01	
Median (IQR)	5.24E-02 (3.37E-02, 6.70E-02)	1.56E-01 (7.60E-02, 2.98E-01)	
Bacteroidetes			0.29
Range	2.92E-02 - 1.05E+00	2.15E-03 - 8.72E-01	
Mean ± SD	3.83E-01 ± 2.25E-01	3.14E-01 ± 2.71E-01	
Median (IQR)	3.53E-01	2.90E-01	
	(2.27E-01, 4.85E-01)	(8.00E-02, 5.39E-01)	
Bifidobacterium			<0.001*
Range	1.15E-05 - 1.50E-03	1.06E-03 - 9.15E-01	
Mean ± SD	3.80E-04 ± 3.97E-04	1.85E-01 ± 2.75E-01	
Median (IQR)	2.02E-04	3.55E-02	
	(1.02E-04, 4.91E-04)	(1.56E-02, 2.99E-01)	
Firmicutes			0.21
Range	1.14E-01 - 7.98E-01	8.38E-02 - 9.57E-01	
Mean ± SD	4.23E-01 ± 1.93E-01	4.93E-01 ± 2.36E-01	
Median (IQR)	3.76E-01	4.18E-01	
	(2.94E-01, 5.48E-01)	(3.36E-01, 7.10E-01)	
Lactobacilli			<0.001*
Range	6.83E-05 - 6.07E-02	5.99E-04 - 7.00E-01	
Mean ± SD	1.53E-02 ± 2.14E-02	1.33E-01 ± 1.71E-01	
Median (IQR)	4.44E-03	7.78E-02	
	(1.00E-03, 2.08E-02)	(8.56E-03, 1.67E-01)	
Prevotella			0.044*
Range	1.72E-05 - 8.04E-01	1.42E-04 - 8.24E-01	
Mean ± SD	6.25E-02 ± 1.73E-01	1.46E-01 ± 2.50E-01	
Median (IQR)	8.17E-03 (3.36E-04, 3.05E-02)	1.42E-02 (5.39E-03, 1.06E-01)	
Wilcoxon rank sum test; Wilcoxon rank sum exact test			

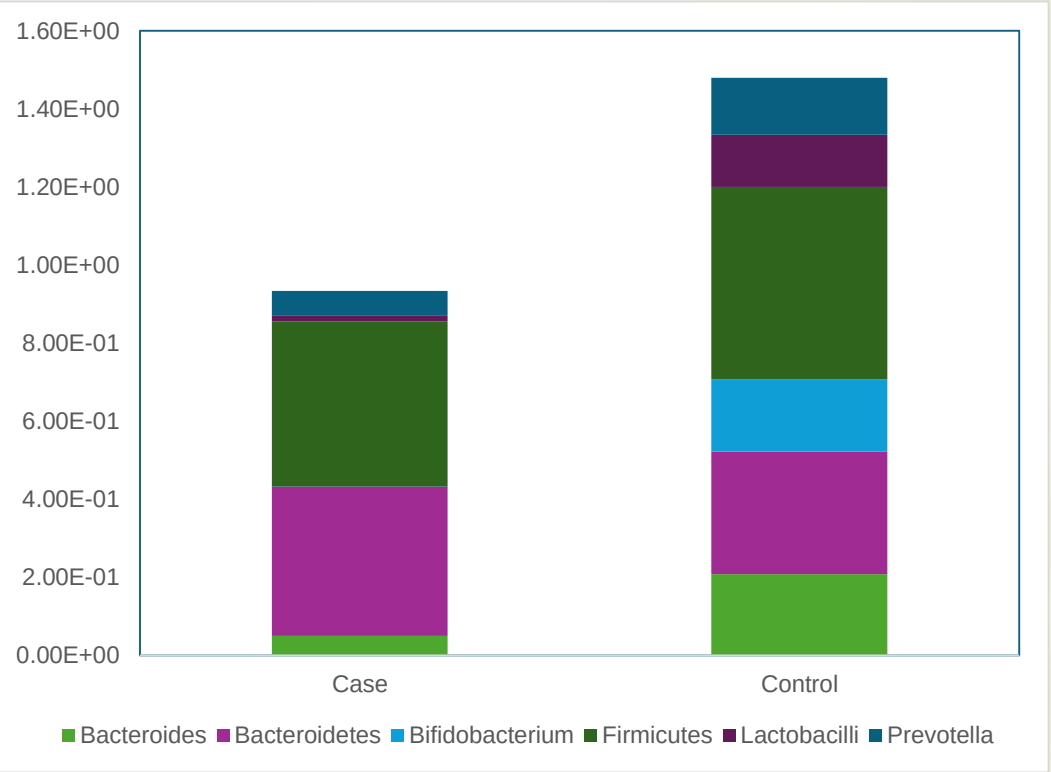


Figure (1): GUT microbiome profile for Cases and control

Conclusion

Growing knowledge of the role of gut microbiomes in acne vulgaris may aid in the creation of innovative treatments for this difficult ailment. Our data showed notable changes in the microbiome of acne patients in particular Bacteroides, Bifidobacterium, Lactobacilli, and Prevotella, compared to healthy controls, highlighting the significant link between the gut microbiomes and acne vulgaris, relatively irrespective of the acne severity and acne duration. It is crucial to preserve the gut microbiome balance to decrease the chance of acne vulgaris development.