SKIN MICROBIOME AND ACNE VULGARIS: *STAPHYLOCOCCUS*, A NEW ACTOR IN ACNE

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INTRODUCTION

Acne is a chronic inflammatory disease targeting the pilosebaceous follicle. *Propionibacterium acnes (P. acnes)*, the sebaceous gland and follicular keratinocytes play a role in the development of acne. Together they induce inflammation in the follicle by activating the innate immunity. For several years, the role of *Staphylococcus*, another bacterium genus, has been discussed in the development of acne. However, to date its role has never been demonstrated. The objective of this study was to investigate the characteristics of the microbiome on unaffected skin and acne lesions (comedone and papulo-pustular lesions) and to determine changes after applying either erythromycin 4% or a dermocosmetic containing lipohydroxy acid, salicylic acid, linoleic acid, niacinamide, piroctone-olamine, a ceramide and Thermal Spring Water for 28 days.

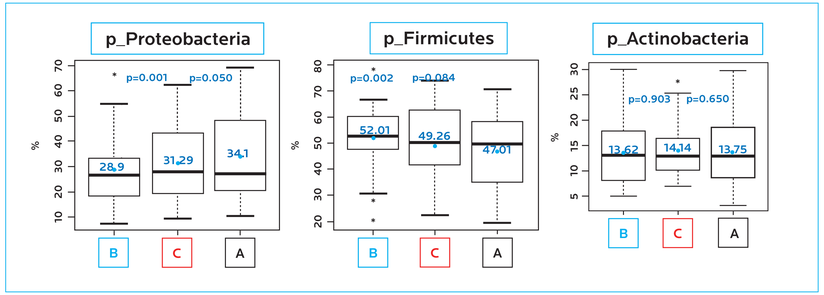
METHODS

This single-centre controlled, randomized, double blinded, intra-individual study was conducted in 55 subjects with mild to moderate acne (GEA Grading)[(1)] before and after treatment either with a dermocosmetic formulation or a topical antibiotic. Microbiota were collected with swabs at D0 and D28, under axenic conditions from 3 sites (comedones, papulo-pustular lesions and unaffected or clinically healthy looking skin) and characterised using a high-throughput sequencing approach that targets a portion of the 16S rRNA bacterial gene[(2)].

RESULTS

An overabundance of Proteobacteria and Firmicutes and an underrepresentation of Actinobacteria on the skin surface of subjects with acne were observed. Moreover, Proteobacteria were less abundant in areas with comedones and papulo-pustular lesions than in unaffected skin areas (29% vs 34% - p=0.001 and 31% vs 34% - p=0.05) while Firmicutes were more abundant in zones with comedones (52% vs 47% - p=0.002). No difference for Actinobacteria was evidenced.

Main bacterial Phyla on the skin surface of the 3 sampled areas (comedones (B), papulo-pustules (C) and healthy skin (A)) at D0 (n=26)



Staphylococci were more abundant on the surface of comedones and papulo-pustular lesions (p=0.004 and p=0.003 respectively) compared to unaffected skin. *Propionibacteria* represented less than 2% of the bacteria characterised.

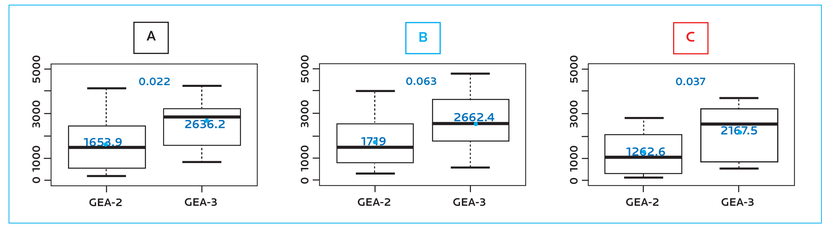
Main bacterial phyla and genus in percentage at the skin surface of the 3 sampled areas (comedones, papulo-pustular and unaffected skin) at D0 (n=26)

		Area		
PHYLUM	GENUS	Comedones (%)	Papulo-pustular (%)	Unaffected skin (%)
Actinobacteria		13,61	14,15	13,75
	Propionibacterium	1,04	1,20	1,36
	Corynebacterium	7,93	8,54	7,71
	Other Actinobacteria	4,64	4,40	4,69
Firmicutes		52,01*	49,27	47,01
	Staphylococcus	33,87*	34*	26,85
	Other Firmicutes	18,14	15,27	20,16
Proteobacteria		28,90*	31,30*	34,10
Bacteroidetes		4,16	3,78	3,73
Fusobacteria		0,73	0,84	0,64
Other		0,58	0,67	0,76

*p<0.05 versus unaffected skin

In all 3 sampled areas, *Staphylococci* proportions increased with the acne severity (p<0.05 between GEA-2 and GEA-3).

***Staphylococcus* genus at the skin surface of 3 sampled areas (comedones (B), papulo-pustules (C) and healthy skin (A)) in GEA-2 (n=16) and GEA-3 (n=10) at D0**



After one month of treatment, erythromycin was mainly effective on Actinobacteria while the dermocosmetic was effective on both Actinobacteria and *Staphylococcus*.

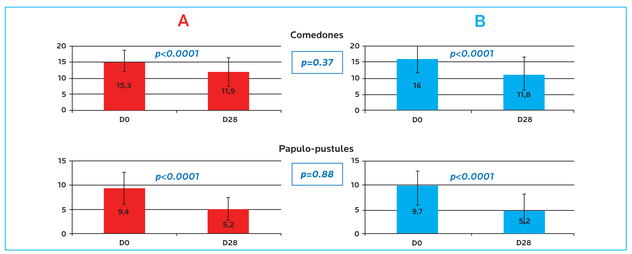
Main bacterial phyla and genus in percentage at the skin surface of the 3 sampled areas (comedones, papulo-pustular and unaffected skin) for the hemi-face receiving Erythromycin 4% or the dermocosmetic after (Day 28) treatment (n=26)

		Day 28 - Erythromycin			Day 28 - Dermocosmetic		
PHYLUM	GENUS	Comedones (%)	Papulo-pustular (%)	Unaffected zone (%)	Comedones (%)	Papulo-pustular (%)	Unaffected zone (%)
Actinobacteria		11,89*	11,09	11,98	11,56	10,87*	11,25
	Propionibacterium	0,82**	0,82	1,22	0,64	0,76	1,06
	Corynebacterium	5,87*	5,72	5,88	7,37	5,27*	4,95**
	Other Actinobacteria	5,20	4,56	4,89	3,56	4,84	5,25
Firmicutes		49,43	43,79	45,80	44,55	47,11	46,40
	Staphylococcus	27,04	24,53**	24,91	19,96*	26,24**	23,52
	Other Firmicutes	22,39	19,30	20,91	24,60	20,89	22,92
Proteobacteria		30,54	36,32	37,15	35,60	33,19	33,95
Bacteroidetes		5,21	4,87	3,61	5,11	5,52	5,32
Fusobacteria		0,62	0,49	0,38	0,65	0,81	0,51
Other		2,27*	3,28*	1,01	2,48**	2,45	2,41**

*p<0.05 versus Day 0, **p<0.1 versus Day 0

In addition, a significant reduction of both comedones and papulo-pustular lesions with no significant difference between the products was observed.

Reduction of the number of papulo-pustular lesions and comedones on both hemi-faces after 28 days of treatment with either erythromycin (A) or the dermocosmetic (B) (n=26, values are expressed in mean±SD)



CONCLUSION

The study showed that in subjects with acne, the bacterial diversity is similar on the surface of unaffected skin as well as on comedones and papulo-pustular lesions. Before and after treatment with either a topical antibiotic or a dermocosmetic, *Staphylococci* remained the predominant genus of the superficial skin microbiota of acne lesions as well as of the unaffected skin.

REFERENCES

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2. Caporaso JG, Lauber CL, Walters WA et al. Global patterns of 16S rRNA diversity at a depth of millions of sequences per sample. *Proc Natl Acad Sci USA*, 2011: **108 Suppl 1**: 4516-4522

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