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Analysis of gut microbiome in patients with acne vulgaris

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Introduction: Acne vulgaris has long been postulated to feature a gastrointestinal mechanism. The human gut microbiota is a large microbial community, in which metabolites are shared among individual microorganisms. Recent studies demonstrate that various diseases are caused by certain component of bacteria in gut microbiome. The aim of this investigation is to evaluate the composition of gut microbiota of the patients who showed acne vulgaris.

Method: Ten healthy women with acne vulgaris (Score 4μ; Inflammatory lesions are more apparent: many comedones and papules/pustules, there may or may not be a few nodule-cystic lesions), ages between 20-25 were selected to evaluate the composition of gut microbiome. Ten healthy women without acne vulgaris (Score 0=Normal, clear skin with on evidence of acne vulgaris) ages between 20-25 were also evaluated as the control. Their fecal samples were collected and analyzed by deep sequencing of 16S ribosomal RNA by using gut microbiome detection kit (Mikinso Co. Ltd., Tokyo Japan). Those who had acne were treated by external use of antibiotics and other ointments such as benzoyl peroxide and adapalene to avoid any microbial substitution phenomenon by internal use.

Result: The present study showed significant increase in Firmicutes in patients with acne vulgaris with low ratio of Bacteroides to Firmicutes compared to the control (63±5%, $^*p<0.05$). Whereas, there was no significant difference in Actinobacteria and Proteobacteria between patients and control.

Discussion: Firmicutes is the bacteria that is known to decompose polysaccharides. Higher ratio of Bacteroides to Firmicutes has been linked to a healthier gut microbiota, since Bacteroides is involved to many of biosynthesis pathways such as B vitamins production. Further investigation is needed to show a casual association of acne vulgaris and Firmicutes.

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