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Analysis of gut microbiome in patients with acne vulgaris

Naoko Hitosugi

Muse Dermatology and Pain Clinic, Japan

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 <4; 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. 10 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 faecal samples were collected and analyzed by deep sequencing of 16S ribosomal RNA by using gut microbiome detection kit (Mikins 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 were no significant difference in *Actinobacteria* and *Proteobacteria* between the patients and the control.

Discussion: *Firmicutes* is the bacteria that are 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*.

naoko1121daiya@gmail.com

Clinico-mycological pattern of nail infections in New Delhi

Ravinder Kaur, Charu Gupta, Deepthi Rawat and Ram Chander

Lady Hardinge Medical College, India

Onychomycosis is one of the most frequent conditions seen in dermatology clinics. The nail disease usually starts as a cosmetic concern progressing to have a major physical and psychological effect on the patients both in young and adults. The causative agent of onychomycosis can be dermatophyte, non-dermatophyte moulds (NDM), or yeasts. A mycological study of onychomycosis was undertaken in 550 patients from January 2016 to December 2016 in the Department of Microbiology, Lady Hardinge Medical College. The patients belonged to a wide range of age spectrum. Males were seen to be predominantly affected (53.5%), male to female ratio being 1.4:1. After clinical suspicion, nail clippings were sent for direct KOH microscopy and fungal culture. Direct microscopy of the nail clips in 20% KOH solution was positive in 183 (33.27%) and culture was positive in 396 (72%) cases. Non-dermatophyte moulds (NDM) were isolated in 232 (42.18%), yeasts in 91 (16.55%), dermatophytes in 52 cases (9.45%). Amongst the NDMs, *Aspergillus* spp. was the most prevalent species followed by *Alternaria* spp., *Cladosporium* spp., *Penicillium* spp. and *Fusarium* spp. There is a shift in the aetiology of onychomycosis from yeasts and dermatophytes to non-dermatophyte moulds (NDMs) in our study. Change in the causative aetiology of onychomycosis as well as the emergence of drug resistant fungi and consequent treatment failures make it mandatory for culture of the mycological agents to know the distribution and epidemiology of fungal agents of onychomycosis.

drkaur@hotmail.com