



AUTOIMMUNE BULLOUS DISEASES

EVALUATION OF CUTANEOUS, ORAL AND INTESTINAL MICROBIOTA IN PATIENTS AFFECTED BY PEMPHIGUS AND BULLOUS PEMPHIGOID: A PILOT STUDY

Luca Fania⁽¹⁾ - Giovanni Luca Scaglione⁽²⁾ - Elisa De Paolis⁽²⁾ - Maria De Bonis⁽²⁾ - Serena Messinese⁽³⁾ - Giovanni Di Zenzo⁽⁴⁾ - Stefania Lechiancole⁽⁵⁾ - Cinzia Mazzanti⁽³⁾ - Ettore Capoluongo⁽²⁾

Istituto Dermopatico Dell'immacolata-irccs, I Division, Rome, Italy⁽¹⁾ - Istituto Dermopatico Dell'immacolata-irccs, Advanced Diagnostic Unit, Genetic And Toxicology Laboratory, Rome, Italy⁽²⁾ - Istituto Dermopatico Dell'immacolata-irccs, I Division, Rome, Italy⁽³⁾ - Istituto Dermopatico Dell'immacolata-irccs, Laboratory Of Molecular And Cell Biology, Rome, Italy⁽⁴⁾ - Istituto Dermopatico Dell'immacolata-irccs, I Division, Rome, Italy⁽⁵⁾

Background: Recently, a significant alteration of the cutaneous microbiota (CM) have been demonstrated in bullous pemphigoid (BP) compared to healthy controls. Indeed, further studies specifically investigating the role of microbial population in patients affected by bullous diseases are still missing and no data are available regarding oral cavity (OM) and gut (GM) microbiota.

Objective: In this pilot study, we characterized the GM, OM and CM in patients affected by pemphigus vulgaris (PV) and BP to evaluate their potential impact in these dermatological disorders.

Methods: High-throughput sequencing of the V3-V4 hypervariable regions of 16S rRNA was used to compare the bacterial community composition of stool, skin and oral mucosae swabs in a cohort of patients with PV and BP. Dedicated bioinformatics software was used to collect taxonomical data, while a specific in-house pipeline was applied to aggregate and compare the dataset of these two disease groups.

Results: The analysis of the GM showed a concordance of the bacterial phyla in both PV and BP patients, with a prevalence of Firmicutes and Bacteroidetes. While evaluating CM data, Firmicutes phylum and Staphylococcus genus resulted as the most represented in both patients' groups. The phyla composition of oral mucosae was characterized by an increased diversity compared to gut and skin ones. Furthermore, in the oral mucosae of PV patients the Bacteroidetes phylum was significantly underrepresented in contrast with healthy controls.





Conclusion: Firmicutes phylum and Staphilococcus genus are the most represented in OM and CM in both PV and BP microbial populations. Moreover, the quantitative imbalance associated with the significant decrease of Bacteroidetes that we observed in the oral cavity of PV patients may be associated to disease typical fetor. To shed light on this peculiar feature in this rare disease further studies are still required.

