PSORIASIS

IDENTIFICATION OF GENETIC CONTRIBUTORS TO THE PROGRESSION FROM PSORIASIS TO PSORIATIC ARTHRITIS

Elena Campione [1] - Raffella Cascella [2] - Roberta Gaziano [3] - Sara Mazzilli [4] - Annamaria Mazzotta [5] - Claudia Strafella [6] - Virginia Garofalo [4] - Valerio Caputo [7] - Annunziata Dattola [4] - Arianna Zangrilli [4] - Daniele Marino [8] - Giuseppe Novelli [6] - Emiliano Giardina [9] - Luca Bianchi [10]

University Of Rome Tor Vergata, Department Of Systems Medicine, Rome, Italy [1] - University Of Rome Tor Vergata, Department Of Biomedicine And Prevention, Rome, Italy [2] - University Of Rome Tor Vergata, Department Of Experimental Medicine, Rome, Italy [3] - University Of Rome Tor Vergata, Department Of Systems Medicine, Division Of Dermatology, Rome, Italy [4] - San Camillo Forlanini Hospital, Uosd Dermatology, Rome, Italy [5] - University Of Rome Tor Vergata, Department Of Biomedicine And Prevention, Rome, Italy [6] - University Of Rome Tor Vergata, Derpartment Of Biomedicine And Prevention, Rome, Italy [7] - University Of Rome Tor Vergata, Department Of Dermatology, Rome, Italy [8] - University Of Rome, Department Of Biomedicine And Prevention, Rome, Italy [9] - University Of Rome Tor Vergata, Department Of Systems Medicnie, Rome, Italy [10]

Background: Psoriasis (Pso) and Psoriatic Arthritis (PsA) are characterized by environmental and genetic susceptibility factors. Psoriatic lesions localized on nails, scalp and intergluteal cleft are unfavorable signs, predictive of PsA evolution. Certain microbial and fungal species, including Candida Albicans, could trigger the exacerbation of skin and nail PsO, contributing to the progression towards PsA. These mechanisms may be explained by the presence of genetic factors which control the proper functioning of proteins involved in microbial recognition and skin maintenance and defense.

Objective: the study aimed to evaluate the severity of disease in a patients' cohort considering their peculiar phenotype, investigating the association of 120 genetic variants involved in skin integrity, microbial recognition, inflammasome pathway with the evolution from PsO to PsA.

Materials and Methods: 200 PsO patients presenting psoriatic lesions on nails, scalp and intergluteal cleft (in addition to other skin folds) have been recruited and were subjected to the assessment of PASI, pain VAS, NAPSI scores. The DNA samples were analyzed by Open-Array technology, biostatistical and bioinformatic analysis.

Results: the evaluation of the severity degree reported an average PASI score of 14 and a

PAIN VAS of 57, NAPSI 5, suggesting that the peculiar phenotype displayed by these patients may be associated with a severe disease phenotype. Genotyping analysis is still ongoing.

Conclusions: Our results pave the way for the identification of biomarkers which can be utilized for predictive and prognostic purposes. In particular, the progression from PsO to PsA may be explained by the complex interaction among genetic variants involved in skin integrity, microbial recognition, inflammasome pathway.