



PIGMENTATION

## PROTEOMICS OF FACIAL MELASMA IN WOMEN

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**Background:** Despite the high prevalence of melasma, the pathophysiology and the stimuli involved in melanocytic hypertrophy as well as focal hypermelanogenesis are not yet fully understood.

**Objective:** To identify the differential expression of proteins in the skin with melasma and in the adjacent healthy adjacent in women.

**Methods:** Cross-sectional study, involving 20 women over the age of 18, who presented facial melasma and used no specific treatment for it in the last 30 days, except sunscreen. Two biopsies with 3-mm punch were performed in the face of each patient, one in a region with melasma and other in the nearest healthy skin area (40 segments). Samples were frozen in liquid nitrogen, macerated, digested in trypsin, and all the proteins extracted were submitted to mass spectrometry. The size of the effect was estimated by the ratio between proteins found in the topographies (melasma/perilesional).

**Results:** The mean age (standard deviation) of the patients was 42.8 (8.9) years, 45% were phototype IV and 25% worked under the Sun. Melasma starting age was 29.3 (7.5) years, 55% of the women reported a family history and 30% used contraceptive drugs. 256 proteins were identified in the sample. A significant differential expression was observed among the topographies for the 29 proteins (25 super-regulated and 4 sub-regulated). ACTG1, ALB, SERPINA1, HBD, ALDOA and FGG showed a simultaneous participation in different biological processes identified. Cellular transport phenomena, tissue rehabilitation, coagulation, and stress response share similar abundance patterns among the proteins identified.

**Conclusions:** When compared to the adjacent skin, differentially expressed proteins were identified in the melasma, being part of biological functions associated with glycolysis, glycogenesis, cell transport phenomena, hemostasis, coagulation, repair/healing, and response to external stimuli.

