PSORIASIS

PROTEOMIC ANALYSIS AND QUANTIFICATION OF LYSINE CROTONYLATION IN PSORIATIC LESIONS

Wj Wang [(1)] - Q Zhen [(1)] - B Li [(1)] - J Wu [(1)] - Hy Ge [(1)] - Ld Sun [(1)]

The First Affiliated Hospital, Anhui Medical University, Department Of Dermatology, Hefei, China [(1)]

Background: Psoriasis is a chronic inflammatory disease with unelucidated pathogenesis. Several biomarkers of psoriasis have been identified by proteomic analysis. Lysine crotonylation of non-histone proteins is now proven to exist widely, while the functions in diseases have not been elucidated.

Objective: To explore the dynamic changes of whole proteome and lysine crotonylation between psoriatic and adjacent normal skin samples.

Materials and Methods: The whole proteome and quantitative lysine crotonylome analysis between 45 pairs of psoriatic and adjacent normal skin samples were performed using TMT labeling, lysine crotonylation affinity enrichment and high-resolution LC-MS/MS analysis. The differentially quantified proteins were further annotated with functional classification and enrichment analysis.

Results?A total of 3,686 and 3,008 proteins were identified and quantified in lesions, among which 166 and 358 proteins were up-regulated and down-regulated. Eighty-four percent of these differently regulated proteins exhibited same expression trends as an online RNA sequencing dataset for psoriasis, while 38 differently regulated proteins exhibited negative relationship with DNA methylation data of psoriatic lesions. Altogether, 2,703 and 2,081 lysine crotonylation sites in 934 and 690 proteins were identified and quantified. A hundred sites in 69 proteins and 76 sites in 47 proteins were up- and down-regulated, respectively. A total of 82.4% of the differentially regulated lysine crotonylation sites exhibited negative correlations with protein expressions. The differentially expressed proteins were enriched in immune response, PI3K-AKT signaling, ribosome and proteasome pathways.

Conclusions: our study showed that the expression of multiple proteins is changed in psoriasis, affecting several biological processes and pathways associated with this disease. Furthermore, analysis of the lysine crotonylation of non-histone proteins in psoriasis provided valuable insights into the pathogenesis of other common diseases.