GENETICS AND GENODERMATOSES

ASSOCIATION ANALYSIS WITHIN MHC REGION OF PSORIASIS VULGARIS ABOUT FAMILY HISTORY

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Background: Psoriasis vulgaris(PsV) is a common and recurrent chronic inflammatory skin disease, there is a distinct genetic predisposition about this disease. Although many genetic studies on major histocompatibility complex(MHC) have been carried out about psoriasis, but the effects of the genetic architecture in MHC region with respect to family history have yet to be elucidated.

Objectives: We attempt to investigate the genetic variants within the MHC egion that differentiate patients with a family history from patients with no family history .

Materials and Methods: We conducted analysis by directly sequencing the whole MHC region to investigate independent associations, totally 8744 patients and 9906 healthy individuals were involved.

Results: HLA-C*06:02 and HLA-C*07:04 were identified both significant in two case-control groups(family history versus control and nonfamily history versus control respectively), and C*06:02 was the most significant risk (P =1.00 × 10−352, OR=12.49; P=1.00×10-687,OR=13.20;respectively),followed by C*07:04(P =6.87 × 10−13,OR=3.56; P=1.40×10-33,OR=4.05,respectively).Further,when we compared family history group with nonfamily history group, two protective loci MICA*49(P=1.57×10-4,OR=0.53) and amino acid 51 in gene VARS(P=1.76×10-4,OR=0.84) were identified, they were distinguish markers between case-only groups.

Conclusions: We validated two alleles HLA-C*06:02,HLA-C*07:04 in case-control group, the result is consistent with our previous study in Chinese PsV patients. We find distinguish genetic markers MICA*49 and amino acid 51 in gene VARS in the MHC region that differentiates family history group from nonfamily history.