New insights in vitiligo pathogenesis: Transcriptomic approaches

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Vitiligo is an acquired autoimmune disease with complex pathogenesis involving the interaction of genetic factors, metabolic factors linked to cellular oxidative stress, melanocyte adhesion defects, and innate/adaptive immunity. In vitiligo, melanocytes are more sensitive to oxidative stress, leading to the increased expression of DAMPs such as HSP70i. Altered expression of epithelial adhesion molecules, such as DDR1 and E-cadherin, facilitates damage to melanocytes and exposure of antigens that favor autoimmunity. Activation of the type 1-IFN pathway induces activation of CD8+ cells against melanocytes, which is facilitated by regulatory T-cell dysfunction. Multiple translational research have greatly improved our understandings about the pathogenesis of vitiligo. In the initial development of vitiligo, increasing number of studies have investigated the mitochondrial dysfunction and metabolic impairment in epidermal cells in vitiligo patients. Regarding the immunologic aspects of progression of vitiligo, IFN-γ–CXCL10–CXCR3 signaling axis has been implicated in the pathogenesis of vitiligo. The scRNA-sequencing analyses revealed the signatures of increased antigen presentation through MHC-1, loss of immunotolerance cytokines such as TGF-β and IL-10, and changes in T cell profiles including altered Treg functions. Furthermore, IL-15 and Th2 cytokines mediated by JAK/STAT pathway have been also implicated as important pathogenic cytokines in vitiligo. Here, I would like to introduce above advances made in vitiligo research based on recent literature review.