025 Analysis of the related factors that leading to the resistance of topical treatment for bullous pemphigoid patients
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Based on clinical and laboratory data, we analyzed the related factors leading to the resistance of topical treatment for BP patients. Totally, 64 BP patients were enrolled in the study, and divided into two groups according to different methods of treatment. One of the groups contained 22 patients that showed effective to topical treatment. Another group contained 42 patients, who got more than 3 new blisters in the continuous 3 days during 4 weeks of the topical treatment, which showed resistant to topical treatment. The types of lesions, the BPDAI (Bullous Pemphigoid Disease Area Index score, Bullous Pemphigoid Disease Area Index), the concentration of albumin, eosinophil counts, the titer of anti-BP180 and anti-BP230lgE of the two groups were analyzed by GraphPad Prism’s software, and Mann Whitney inspection methods were used for statistical analysis. The results of analysis will be helped to select the proper treatments for different BP patients. The results showed that the main lesion type of the group that showed effective to topical treatment was dermatitis herpetiformis (63.6%) which was the majority of the patients that resistant to topical treatment. The BPDAI, EOS counts, the concentration of total IgE, the titer of anti-BP180 lgE, anti-BP230 lgE and anti-BP230 lgE were significantly higher in the group of patients that effective to topical treatment (P < 0.05). There’s no difference of the concentration of albumin and the titer of anti-BP180 lgE between the two groups. So according to our study, in addition to BPDAI and anti-BP180 lgE titer, we can also select appropriate treatment for BP patients according to their lesion type, peripheral eosinophil counts, the concentration of total IgE, and the titer of anti-BP230 lgE.

026 Study on detection of IgM and IgG of the anti-42000 protein from egg nucleus antibodies in SLE patients’ sera with Dot immunogold filtration assay
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SLE (systemic lupus erythematosus) is a systemic autoimmune disease which attacks the skin. Based on the data from our laboratory, we studied the histocompatibility antigen presentation and anti-virus activity (OAS1, MX1, BANF1, CANX and AP1S1). Protein-protein interaction analysis of DEPs identified 68 interactions involving 49 different proteins (KRT5, KRT27, KRT75, KRT76 and H2AFY2), whereas it stimulated processes involved with metabolism (GALT, H6PD, EXOSC4 and EXOSC6) and keratinocyte differentiation revealed that hyperthermia inhibited multiple processes related to energy and nucleic acid metabolism (295.62 and 30.05), and 65 downregulated). K-means clustering and GO-BP enrichment analysis of the DEPs showed that the type of erythema with blister (63%) was the major type of the patients that resistant to topical treatment. The BPDAI, EOS counts, the concentration of total IgE, the titer of anti-BP180 IgG, anti-BP230 IgG and anti-BP180 lgE were significantly higher in the group of patients that effective to topical treatment (P < 0.05). Based on clinical and laboratory data, we analyzed the related factors leading to the resistance of topical treatment for BP patients. Totally, 64 BP patients were enrolled in the study, and divided into two groups according to different methods of treatment. One of the groups contained 22 patients that showed effective to topical treatment. Another group contained 42 patients, who got more than 3 new blisters in the continuous 3 days during 4 weeks of the topical treatment, which showed resistant to topical treatment. The types of lesions, the BPDAI (Bullous Pemphigoid Disease Area Index score, Bullous Pemphigoid Disease Area Index), the concentration of albumin, eosinophil counts, the titer of anti-BP180 and anti-BP230lgE of the two groups were analyzed by GraphPad Prism’s software, and Mann Whitney inspection methods were used for statistical analysis. The results of analysis will be helped to select the proper treatments for different BP patients. The results showed that the main lesion type of the group that showed effective to topical treatment was dermatitis herpetiformis (63.6%) which was the majority of the patients that resistant to topical treatment. The BPDAI, EOS counts, the concentration of total IgE, the titer of anti-BP180 lgE, anti-BP230 lgE and anti-BP230 lgE were significantly higher in the group of patients that effective to topical treatment (P < 0.05). There’s no difference of the concentration of albumin and the titer of anti-BP180 lgE between the two groups. So according to our study, in addition to BPDAI and anti-BP180 lgE titer, we can also select appropriate treatment for BP patients according to their lesion type, peripheral eosinophil counts, the concentration of total IgE, and the titer of anti-BP230 lgE.

027 Global proteomics and bioinformatic analysis of hyperthermia-induced differential protein expression in condyloma acuminata
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Hyperthermia has proved successful in treating cutaneous human papillomavirus infectious diseases such as plantar wart and condyloma acuminata (CA). Moreover, this treatment provides improved therapeutic efficacy in these conditions as compared with conventional therapies. In order to achieve a better understanding of the mechanisms of hyperthermia against HPV-infected diseases, we applied a global proteomic investigation (iTRAQ) in CA tissues in response to ex vivo 44 °C hyperthermia (isothermal water bath). Compared to 37 °C counterparts, a total of 102 differentially expressed proteins (DEPs), with fold change greater than 1.2 or less than 0.833, p-value < 0.05) were identified in 44 °C groups (37 upregulated and 65 downregulated). K-means clustering and GO-BP enrichment analysis of the DEPs revealed that hyperthermia induced soluble protein expression related to energy and nucleic acid metabolism (GALT, H6PD, EXOSC4 and EXOSC6), as well as keratinocyte differentiation (KRT5, KRT27, KRT75, KRT76 and H2AF2/2), whereas it stimulated processes involved with antigen presentation and anti-virus activity (OAS1, MX1, BANF1, CANX and AP1S1). Protein-protein interaction analysis of DEPs identified 68 interactions involving 49 different proteins (consisting of 2 major modules), whose GO-BP enrichment analysis results revealed similar pattern as those of k-means clustering of the overall proteomic changes. These results demonstrated that hyperthermia induces anti-viral activities whereas it inhibits metabolism and keratinocyte differentiation, which substantiate some of our speculations on the mechanisms of hyperthermia therapy and provide additional insights into some specific pathways through which local hyperthermia alters HPV infection.

028 Comprehensive assessment of T cell receptor β repertoire in Stevens–Johnson syndrome/Toxic Epidermal Necrolysis patients using high-throughput sequencing
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Stevens–Johnson syndrome (SJS) /toxic epidermal necrolysis (TEN) are life-threatening severe cutaneous adverse drug reactions characterized by widespread epidermal necrosis. Recent studies have indicated that SJS/TEN is a specific immune reaction regulated by T cells. Certain drug serves as foreign antigens that are presented by major histocompatibility complex (MHC) and recognized by T cell receptors (TCRs), inducing adaptive immune responses. However, few studies have performed detailed characterization of TCR repertoire in SJS/TEN. Furthermore, the TCR repertoire diversity of these patients showed certain associations with the clinical severity of disease. Similar predominant clonotypes, shared-usage TRBV/TRBJ subtypes and combinations thereof were observed among different subjects with the same causative agent. Our observations provide enhanced understanding of the role of T lymphocytes in the pathogenesis of SJS/TEN and enumerate potential therapeutic targets.

029 JAK inhibitors prevent and reverse vitiligo in mice, but do not eliminate established autoreactive T cells in the skin
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Vitiligo is an autoimmune disease in which autoreactive, cytotoxic CD8+ T cells destroy the pigment-producing melanocytes, resulting in disfiguring, well-defined white patches on the skin. The IL10/IL10R pathway is required for the immune privilege of the skin and melanocytes. IL10 is produced by keratinocytes and regulates the polarization of M1 macrophages into M2 and regulatory T cells. In the current study, we set our objective to test the effects of JAK inhibitors in a model of vitiligo, which is the hallmark of multiple cell types and cytokines in the skin. We found that JAK inhibitors were able to reduce the number of CD8+ T cells in the epidermis and dermal compartments. These results suggest that the use of JAK inhibitors in the treatment of vitiligo is a promising therapeutic approach.

030 Single-cell transcriptomic level reconstruction of human psoriatic skin
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Psoriasis is an immune-mediated chronic inflammatory skin disease involving cell-to-cell communications within the lesional skin. Although psoriatic skin contains a highly increased number of cells with great heterogeneity, population diversity and single-cell level transcriptomic expression within psoriatic plaques harbored an additional population of CD69+ βF1+ cells expressing high level of multiple heat shock proteins, REL, JUN, and FOS, but negligible expression of checkpoint molecules. Population of CR2+ migratory dendritic cells and CD14+CD68+ macrophages were also distinctly segregated between normal and psoriatic skins. Thus, our data provide a comprehensive catalogue of whole cell populations in the inflamed human skin which expanded our knowledge of cellular diversity in psoriasis.