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System biology approaches in atopic dermatistis

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Atopic dermatitis field is undergoing a translational revolution lately with active development of novel topical and systemic therapeutics. In psoriasis a system biology approach was instrumental in defining biomarkers of disease and therapeutic response as well as predictors of successful response to treatment. We have lately defined a unified atopic dermatitis phenotype using a meta-analysis approach that highlighted key features and biomarkers of atopic dermatitis. This meta-analysis derived transcriptome (MADAD) identified wide lipid abnormalities and for the first time *in vivo*, correlated Th2 immune activation with down-regulation of key epidermal lipids, emphasizing the role of cytokines on the barrier disruption in AD. MADAD is now applied to evaluate changes with different investigational treatments, allowing us to evaluate drug effect at the transcriptomic level not only on the AD phenotype but also the effect on suppressing specific pathways. Since many aspects of atopic dermatitis are constantly evaluated in various mouse models, we also seek to see how well the commonly used mouse models of atopic dermatitis compare with the human MADAD AD phenotype at the transcriptomic level and which mouse model if any captures the hallmark pathways of AD better.

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Evaluating serum levels of hypersensitive C-reactive protein in patients with vitiligo

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CRP is an acute phase protein secreted in the blood stream by the liver in response to inflammatory cytokines such as IL6 and several other systemic inflammation biomarkers. Since inflammatory and immune factors have a key role in the pathogenesis of vitiligo, we aimed to assess the relationship between the serum level of hs-CRP (as a marker for systemic inflammation) and the pathogenesis of vitiligo. In this case-control study, we enrolled patients with vitiligo who had referred to our Dermatology Department. The patients were divided into two groups: Those with type A vitiligo (generalized, n=30) and those with type B vitiligo (segmental, n=30). Moreover, 30 people who had the inclusion criteria and did not have vitiligo were selected among those referring to the clinic as the control group and matched with the other two groups. The serum hs-CRP levels were checked for all the patients in the three groups and compared. The serum level of hs-CRP was 4.76±1.31 mg/l in patients with type A vitiligo, 3.71±1.03 in those with type B vitiligo and 3.01±1.08 in those in the control group. The mean serum hs-CRP level was significantly higher in patients with type A compared with those with type B and the control group ($P<0.001$). However, in patients with type B and the control groups, no significant difference was seen in this regard ($P=0.053$). We found an association between hs-CRP and generalized vitiligo. This association could imply that hs-CRP could intensify the severity of vitiligo.

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