In Vitro Granulysin Assay to Evaluate Causality in Severe Cutaneous Adverse Drug Reactions

In vitro assays that identify the causative agents in cutaneous adverse drug reactions (cADRs), which are often caused by first-line antiepileptic drugs, are desirable because accurate and timely diagnosis is critical for removing the culprits, avoiding re-exposure, and identifying safe alternative treatments. Chu et al. described an in vitro T-lymphocyte activation test (LAT) to evaluate drug causality in cADRs. This assay measured three biomarkers, including granulysin, which has been implicated in epidermal detachment in cADRs, including in Stevens–Johnson syndrome and toxic epidermal necrolysis. This granulysin-based LAT was highly sensitive and specific for identifying carbamazepine and phenytoin as causative agents in cADRs. It may prove to be useful for preventing cADRs or for providing expedited treatment options for these adverse reactions. See page 1461.

Correlation between Atopic Dermatitis Severity and Staphylococcal Hemolysis

Staphylococcus aureus levels increase on the skin during atopic dermatitis (AD) flares, but a relationship between disease severity and toxin genotype has not been detected. In a single-site pilot study comprising 30 patients with AD and controls, Gurnee et al. found a significant increase in hemolytic activity of staphylococcal isolates from patients with mild AD compared with the activity in those from patients with moderate and severe AD. Patients with severe disease had the highest levels of staphylococci in affected areas, whereas patients with mild and moderate disease had bacterial loads similar to those of the controls, in agreement with the notion that bacterial load does not correlate with disease severity. These insights support additional inquiry into the contribution of individual staphylococcal isolates to AD severity. See page 1588.

Altered Skin Bacteria in Cutaneous T-Cell Lymphoma

Although viruses have been suggested to mediate T-cell transformation in cutaneous T-cell lymphoma (CTCL), viruses are not consistently detected in patient skin or blood. Harkins et al. utilized shotgun metagenomic sequencing to evaluate the skin microbiome in patients with mycosis fungoides (MF) and Sézary syndrome to characterize microbial involvement. Relative abundances of eukaryotic viruses and fungal communities were low in the skin microbiome of patients with CTCL, and these were not significantly different from those in healthy controls. However, bacterial communities exhibited shifts to higher relative abundances of Corynebacterium species and to lower relative abundances of Cutibacterium species in patients with CTCL, suggesting that bacterial shifts may be related to disease stage and CTCL pathogenesis. See page 1604.