Skin Tape Stripping Effective for Skin Barrier Analysis

The pathophysiology of atopic dermatitis is commonly studied using skin biopsies, which are invasive and refused by many patients, including children. Kim and colleagues reported that, in a side-by-side comparison with skin biopsy samples, skin tape stripping is a reliable method for assessing epidermal differentiation marker expression in the stratum corneum and the upper granular layer of the epidermis. This noninvasive and inexpensive method may allow for expanded cohorts of subjects, including children and infants, in studies for lipid, protein, and RNA analysis. In addition, serial skin tape stripping is likely to be tolerated and useful for clinical evaluation of skin barrier function in response to therapy. See page 2387.

Transcriptome Changes Induced by Glucocorticoid Treatment

Topical glucocorticoids (GCs) are frequently prescribed for inflammatory and hyperproliferative skin diseases. The molecular signatures of action of GCs and their receptors (GRs) in skin have not been reported. Lili and colleagues examined the GC/GR-induced human skin transcriptome using high-resolution RNA sequencing and integrative network biology approaches. In addition to confirmatory results of anti-inflammatory, metabolic, and atrophic effects of GC, these studies revealed that GRs function as regulators of transcription in skin via effects on cell receptors and regulatory noncoding RNAs, as well as via direct transcriptional control of numerous transcription factors. These findings shed light on the molecular signature of GCs and also provide insights into the development of novel therapies that may circumvent the adverse effects of GC treatment. See page 2281.

Genetic Landscape of Basosquamous Carcinoma

Basosquamous carcinomas (BSCs), which comprise 1.2–2.7% of skin carcinomas, are aggressive skin tumors that feature histopathologic characteristics of both basal cell carcinoma (BCC) and squamous cell carcinoma (SCC). BSC origin and genetic etiology remain controversial. Chiang and colleagues reported underlying PTCH and SMO mutations in BSCs, suggesting that Hedgehog signaling drives BSC similar to BCC. Principal component analysis indicated that BSC has greater genetic similarity to BCC than to SCC, supporting the concept that BSCs are derived from BCCs. Identification of frequent mutations in the gene encoding chromatin remodeling factor ARID1A in BSCs highlights a potential bifurcation event in which ARID1A mutations promote SCC driver mutations and squamatization, leading to BSC development from BCCs. These findings have implications for BSC treatment with SMO and PARP inhibitors. See page 2263.

Insertion/Deletions Implicated in Psoriasis

Previous genome-wide studies have identified more than 100 psoriasis-associated susceptibility genes based on single nucleotide polymorphism (SNP) analysis, but these loci only account for a small percentage of psoriasis heritability. As insertion/deletions (InDels) are the second most common gene variation after SNPs, Zhen and colleagues assessed the presence of InDels in 1,326 genes in more than 30,000 Chinese Han patients with psoriasis and controls. These analyses uncovered 29 unreported InDels, including 12 common, 9 low-frequency, and 8 rare InDels in 25 susceptibility genes that collectively account for an additional 1.29% of the heritability of this disease. Expansion of these studies to the whole genome level is important to fully elucidate the heritability of psoriasis and other complex diseases. See page 2302.

B-Cell Receptor Mutations Predict Resistance in Primary Cutaneous Diffuse Large B-Cell Lymphoma Leg-Type

To delineate mutations that may predict therapeutic responses and survival, Ducharme and colleagues compared the mutational status of 14 patients with primary cutaneous diffuse large B-cell lymphoma leg-type (PCLB-LT) and a durable therapeutic response to rituximab and polychemotherapy with that of 18 patients with refractory or relapsing PCLB-LT. The presence of mutations in B-cell receptor (BCR) signaling genes CD79A/B or CARD11 was associated with therapeutic resistance as well as with reduced progression-free and specific survival. Information about BCR mutations in patients may therefore inform selection of targeted therapies for PCLB-LT, minimizing resistance and disease relapse. See page 2334.