Mosaic NLRP3 Mutations Underlying Urticaria

Urticaria is a common feature that results from multiple etiologies, including NLRP3-associated autoinflammatory disease. Assrawi et al. identified two distinct mosaic mutations in the key inflammasome protein NLRP3 in two unrelated elderly patients with late-onset chronic urticaria accompanied by systemic inflammation. These gain-of-function mutations resulted in increased inflammasome activation and secretion of IL-1β, and treatment of these patients with the IL-1β antagonist anakinra resulted in complete remission of symptoms. These patients exhibited disease that was refractory to standard anti-inflammatory treatments for decades. Identification of the underlying etiology with next-generation sequencing techniques led to an effective treatment strategy in these patients. See page 791.

Myeloid Cells Link Psoriasis and Cardiovascular Disease

It is now well known that psoriasis is associated with increased cardiovascular risk beyond that associated with typical cardiovascular risk factors. Myeloid cells were found to be associated with noncalcified coronary burden (NCB) in psoriasis, and increased monocyte counts were found to be associated with increased cardiovascular disease. In a prospective cohort study of 81 patients with psoriasis, Teague et al. reported that classical monocytes, but not nonclassical or intermediate monocytes, are associated with both psoriasis disease severity and NCB. Absolute myeloid cell number was also associated with disease severity and bone marrow granulopoiesis. These findings suggest that cells of myeloid origin provide a link between psoriasis and cardiovascular disease and that they may play a critical role in atherosclerosis. See page 785.

Assessment of the Interpretability of the QOLHEQ

The Quality of Life in Hand Eczema Questionnaire (QOLHEQ), which measures impairment of health-related quality of life in patients with hand eczema, has been validated in Germany and Japan, as well as in a cross-cultural study in six countries. Oosterhaven et al. sought to determine the interpretability of these scores in 294 adult patients after 1–3 days and after 4–12 weeks. Analysis of the smallest detectable change and preferred minimally important change offered insight into the interpretability of the QOLHEQ. Results from this study and previous validation studies support the use of the QOLHEQ for patient-reported outcomes for hand eczema and suggests incorporation of this measure into a core outcome set for hand eczema. See page 928.

Novel SNPs Identified in Amelanotic Melanoma

Gibbs et al. assessed 47 SNPs in putative melanoma risk loci in patients with amelanotic melanoma (AM). Principal component analysis revealed that SNPs in IRF4 (rs12203592*T) and CCND1 (rs1485993*C) were associated with AM in individuals of European descent. The IRF4 SNP association, but not the CCND1 SNP association, was partially attenuated after adjustment for phenotypic confounders. These findings indicate that IRF4 and CCND1 genotypes may influence AM development and support further functional investigations into the pathogenesis of AM, which is often diagnosed at an advanced stage. See page 918.

Distinct Microbiomes in HS

Microorganisms have been implicated in the debilitating inflammatory skin disease hidradenitis suppurativa (HS), and treatment of HS with broad-spectrum antibiotics is common. Naik et al. examined the skin bacterial communities in 12 adults with HS and matched healthy volunteers. Increased bacterial diversity at sites of disease predilection was noted in subjects with HS compared with healthy volunteers. Increased disease severity was associated with increasing bacterial community perturbations, and an association between anaerobe abundance and disease severity was also detected. The conclusion that skin microbial communities in HS are distinct, diverse, and divergent from those in healthy skin will inform future investigations on the pathogenesis of HS. See page 922.