and GBP1. By inclusion into analysis of previously reported GWAS data, additional distinct interactions of gene modules, revealed by our analysis, with already reported genes could be elucidated.

To the best of our knowledge, this is the first study applying systems biology approach to identify shared molecular mechanisms between pemphigus and SLE diseases. This method could broaden our knowledge about pathogenesis of autoimmune diseases by identifying new possibly involved candidate genes, as well as improve our understanding of underlying genetic interactions and reveal new potential therapeutic targets.

P112 | Diet shifts the genetic association of multiple complex traits in outbred mice

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Genome-wide association and mapping studies identified a multitude of genetic variants associated with complex traits in humans and mice, thus conveying detailed insights into their genetic architecture. Yet, these genetic variations only partially account for the phenotypic variability. This missing heritability may be due to epistasis, rare variations and/or the environment. We here addressed the later, by exposing a large colony of outbred mice to different diets. Mice were fed control chow or western diet ad libidum, or were held at caloric restriction (n=350-400 mice per group). We show that complex phenotypes depend on both, genetic architecture and diet. Full-genome sequencing of parental mice and forward genomics allowed linking the associations to single genes. Considering diet as an interactive variable to determine the gene-phenotype association, leads to a considerable shift of the genetic association. Thus, gene-diet interactions explain a significant part of the missing heritability, which allows a more detailed understanding of complex traits.

P113 (OP06/04) | Mutations in three genes encoding proteins involved in hair shaft formation cause uncombable hair syndrome

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Uncombable hair syndrome (UHS), also known as "spun glass hair syndrome," "pili trianguli et canaliculi," or "cheveux incoiffables" is a rare anomaly of the hair shaft which occurs in children and improves with age. UHS is characterized by dry, frizzy, spangly and often fair hair that is resistant to being combed flat. Up to date both simplex and familial UHS cases with autosomal dominant as well as recessive inheritance have been reported. However, none of these cases were linked to a molecular genetic cause. Here, we report the identification of UHS causative mutations located in the three genes PADI3 (peptidylarginine deiminase 3), TGM3 (transglutaminase 3) and TCHH (trichohyalin) in a total of eleven children. All of these individuals carry homozygous or compound heterozygous mutations in one of these three genes, indicating an autosomal recessive inheritance pattern in the majority of UHS cases. The two enzymes PADI3 and TGM3, responsible for posttranslational protein modifications, and their target structural protein TCHH, are all involved in hair shaft formation. Elucidation of the molecular outcomes of the disease causing mutations by cell culture experiments and tridimensional protein models demonstrated clear differences in the structural organization and activity of mutant and wild-type proteins. Scanning electron microscopy observations revealed morphological alterations in hair coat of Padi3 knockout mice. All together, these findings elucidate the molecular genetic causes of UHS and shed light on its pathophysiology, and hair physiology in general.

HEALTH SERVICES RESEARCH

P114 | Urticaria Activity Score – Results of the available versions are comparable

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Background: The signs and symptoms of chronic spontaneous urticaria (CSU) strongly fluctuate from day to day and a biomarker for disease activity is still missing. Currently, the only widely accepted tool to determine disease activity in CSU is the patient-reported Urticaria Activity Score (UAS). The UAS daily documents wheal numbers and intensity of pruritus, usually over 7 consecutive days (UAS7). While