Genome-wide association study identifies a psoriasis susceptibility locus at TRAF3IP2.

Psoriasis is a multifactorial skin disease characterized by epidermal hyperproliferation and chronic inflammation, the most common form of which is psoriasis vulgaris (PsV). We present a genome-wide association analysis of 2,339,118 SNPs in 472 PsV cases and 1,146 controls from Germany, with follow-up of the 147 most significant SNPs in 2,746 PsV cases and 4,140 controls from three independent replication panels. We identified an association at TRAF3IP2 on 6q21 and genotyped two SNPs at this locus in two additional replication panels (the combined discovery and replication panels consisted of 6,487 cases and 8,037 controls; combined $P = 2.36 \times 10^{-15}$ for rs13210247 and combined $P = 1.24 \times 10^{-11}$ for rs33980500). About 15% of psoriasis cases develop psoriatic arthritis (PsA). A stratified analysis of our datasets including only PsA cases (1,922 cases compared to 8,037 controls, $P = 4.57 \times 10^{-12}$ for rs33980500) suggested that TRAF3IP2 represents a shared susceptibility for PsV and PsA. TRAF3IP2 encodes a protein involved in IL-17 signaling and which interacts with members of the Rel/NF-κB.
transcription factor family.

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