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Titel des Beitrags: Genome-wide association study of restless legs syndrome identifies common variants in three genomic regions.
Abstract: Restless legs syndrome (RLS) is a frequent neurological disorder characterized by an imperative urge to move the legs during night, unpleasant sensation in the lower limbs, disturbed sleep and increased cardiovascular morbidity. In a genome-wide association study we found highly significant associations between RLS and intronic variants in the homeobox gene MEIS1, the BTBD9 gene encoding a BTB(POZ) domain as well as variants in a third locus containing the genes encoding mitogen-activated protein kinase MAP2K5 and the transcription factor LBXCOR1 on chromosomes 2p, 6p and 15q, respectively. Two independent replications confirmed these association signals. Each genetic variant was associated with a more than 50% increase in risk for RLS, with the combined allelic variants conferring more than half of the risk. MEIS1 has been implicated in limb development, raising the possibility that RLS has components of a developmental disorder.
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