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Identification of genetic risk loci associated with Hodgkin's lymphoma

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Hodgkin's lymphoma (HL) is a rare disease with an age standardized incidence rate of 2-3 cases per 100,000 in the European Union, accounting for approximately 30% of all malignant lymphomas. To identify novel genetic loci associated with susceptibility to classical Hodgkin's lymphoma (cHL), statistical methods were applied to a genetic case-control study. The study population comprised 1,001 cases and 1,226 controls, all of them genotyped for 730,525 markers. To further investigate the association between variants and disease risk, a meta-analysis was performed using the German data and a previous reported GWAS from the UK, which after quality control analysis consisted of 589 cHL cases and 5,199 controls, all individuals with information available for 504,374 SNPs. Promising variants were followed up in three independent replication sets, one from Germany, which comprised 951 cHL cases and 1248 controls, and two from the UK, one with 1,071 cases and 1,288 controls and the other one with 953 cases and 565 controls. In total, 21 SNPs were chose for follow up. Two novel associations were identified: rs3806624 mapping to 3p24.1 (P = 1.73 x 10-16, odds ratio (OR) = 0.79) and rs7745098 mapping to 6q23.3 (P = 2.77 x 10-8, OR=1.17). The SNP rs3806624 is located 5' to the EOMES gene in a putative response element affecting the binding of the p53 gene. The SNP rs7745098 is located in the intergenic region between the HBS1L and MYB, a region that has been shown to play substantial role in hematopoiesis. These findings provide further insight into the genetic and biological basis of the predisposition to cHL.