

O10 ASSOCIATION BETWEEN IL23R, ATG16L1, IRGM AND NOD2 SUSCEPTIBILITY GENES AND SUBPHENOTYPES ON A LARGE COHORT OF IBD PATIENTS

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The aim of the study was to determine the genotype/phenotype correlations for 3 newly reported susceptibility genes on IL23R, ATG16L1 and IRGM genes as well as for the main NOD2 CD associated SNPs in a large cohort of IBD patients with detailed records on disease subphenotypes. 1028 IBD patients (788CD, 192UC, 48IC) have been genotyped for IL23R, ATG16L1 and IRGM SNPs (rs11209026, rs2241180, rs13361189) and for the 3 main NOD2 variants and correlations between genotypes and phenotypes were searched for. The association of ATG16L1 and NOD2 SNPs with CD but not with UC or IC was confirmed ($p=0.21$, $p=0.001$, respectively). NOD2 rare variants were associated with an earlier age of CD onset ($p=0.001$) and with an ileal involvement ($p=0.001$). On CD patients, ATG16L1 at risk allele was associated with a penetrating behavior ($p=0.27$) whereas the protective alleles of ATG16L1 and IRGM were associated with an inflammatory behavior ($p=0.09$ and $p=0.3$ respectively). The IL23R at risk allele was associated with a familial history of IBD ($p=0.2$). No interactions between the analyzed variants were found. NOD2 SNPs are confirmed to be strongly associated with an ileal location and a young age of CD onset while the newly reported IBD genes -IL23R, ATG16L1 and IRGM are only modestly associated with CD clinical presentation.