

FTO haplotyping underlines high obesity risk for European populations

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We analyzed the population specific haplotype profiles of the FTO gene genomic locus hotspot identified by Genome Wide Association Studies (GWAS) for the high obesity risk by scrutinizing eighteen 1000G populations from 4 continental groups. The hotspot is located in FTO gene intron 1 spanning around 40kb. We reconstructed the ancestral state of the locus, which comprised ‘healthy’ major allele found in all populations, and two minor ‘risky’ alleles, each one specific for African and European populations, correspondingly. The allele locus structure and frequency distribution underscores the high risk allele specifically for European population. South Asian populations take the second place on the ‘risky’ allele frequency, while East Asian populations have the minimal ratio of risky allele. African populations specific allele was only ‘partially’ risky, while the majority of GWAS SNPs were manifested by healthy alleles’. These observations corroborate the previous reports on the FTO locus implication in population specific manner as well as WHO BMI index population distribution. Thus, the conclusions presented imply FTO locus analyzed is rather a major genetic determinant of the genetic obesity risk from the GWAS SNPs set.