

Genome patterns of common dna variations in three human populations

[Science](#), [Genetics](#)



The article “ Whole-Genome Patterns of Common DNA Variations in Three Human Populations” provides detailed and examination of core individual differences in DNA sequences. The authors pay attention to genetic basis of human variability stressing that it is variability that identify differences in DNA sequences. The article touches the following issues: a dense SNP map; common SNPs in three populations; natural selection between populations; structure of common populations; LD and functional elements, etc.

Further, the interesting moment is analyzing the impact of genetic variations on humanhealth. They conducted their examination in more than 70 ancestries in Asian, American and African countries. The researchers revealed that linkage disequilibrium is the main reason of genetic variations. It means that functional genomic elements are correlated with particular regions of linkage imbalance. Then the authors proceed to identifying the role of common genome variations and their impact of human traits, ancestries and populations.

71 unrelated individual were chosen for investigation: 23 African Americans, 24 Europeans and 24 Asians. The metrics were scored: call rate, observed genotype clusters, and consistency with Hardy Weinberg equilibrium. Actually, these tests are considered very effective because they ensure quality control. During investigation, researchers revealed more than 112 million individual genotypes, whereas the missing data accounts only 5%. Most of SNPs are found to be high-quality genotypes with polymorphic structure.

Further, 94% of African Americans' SNPs have two alleles, whereas only 84% of Europeans and Americans' SNPs have two alleles. After reading the paper, two questions appear on the agenda: 1. What methods are the most effecting in analyzing phenotypic differences and DNA variations? 2. What are particular effects of genome variations on human psyche? References Hinds D. , Stuve L. , Nilsen G. B. , Halperi, E. , Eskin E. , Ballinger D. , Frazer K. , & Cox, D. (2005, February 18). Whole-Genome Patterns of Common DNA Variations in Three Human Populations. *Science*, 307, 1072-1079.