

**P007** The effective size of the Icelandic population inferred from unphased microsatellite markers and the prospects for LD mapping

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Characterizing the extent of linkage disequilibrium (LD) in the genome is a pre-requisite for association mapping studies. Patterns of LD also contain information about the past demography of populations. On this study we focus on the Icelandic population where LD was investigated in 12 regions of ~15 cM using regularly spaced microsatellite loci displaying high heterozygosity. In total 1753 individuals were genotyped for 179 markers. LD was estimated using a composite disequilibrium measure based on unphased data. LD decreases with distance in all 12 regions and can be detected over approximately 4 cM for the given sample size. Differences in the patterns of decrease of LD with distance among genomic regions were mostly due to two regions exhibiting respectively higher and lower proportions of pairs in LD than average within the first 4 cM. We pooled data from all regions except these two and summarized patterns of LD by computing the proportion of pairs of loci exhibiting significant LD (at the 5% level) as a function of distance. We compared observed patterns of LD with simulated datasets obtained under scenarios with varying demography and intensity of recombination. We show that unphased data allow to make inferences on scaled recombination rates from patterns of LD. Patterns of LD in Iceland suggest a genome-wide scaled recombination rate of  $\rho^* = 200$  [130-330] per cM (or an effective size of roughly 5000) in the low range of estimates recently reported in three populations using SNPs data from the HapMap project.