

Maize Genome Structure, Linkage Disequilibrium and Genetic Association Mapping.

Antoni Rafalski, Stephan Brunner, Kelly Palaisa, Christine Hainey, Stan Luck, Mark Jung, Maureen Dolan, Oscar (Howie) Smith and Scott Tingey
DuPont Crop Genetics, Wilmington, DE, USA, and Pioneer Hi-Bred International,
Johnston, IA (USA).

Genetic mapping of simple or complex (quantitative) traits is usually carried out in biparental mapping population developed specifically for this purpose. Recently, a lot of interest has been generated by an alternative approach, genetic association mapping. This approach explores the statistical relationship between the alleles or haplotypes present in pre-existing collections of germplasm and the traits of interest. This method may be applied to specific genes (candidate-gene based association mapping) and to the whole genome (whole genome scan). The choice between these alternatives depends on several factors, including the extent of linkage disequilibrium in the maize populations used for genetic association mapping. We show that the amount of LD is very dependent nature of the population used, and varies widely across the genome. Recently, DNA sequence level comparison of maize inbred lines at the bronze locus (H. Dooner and collaborators) demonstrated that two maize alleles could differ in their gene complement and in the content on non-genic insertions and deletions. We have now extended these studies to other loci. The presence of extensive allelic non-homologies has a significant impact on recombinational properties of the genome, and on the distribution of linkage disequilibrium in populations. The impact of these factors on genetic association mapping, and on breeding strategies, will be discussed.