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Molecular Genetic Characterization and Population Structure among Commercial F1 Maize Hybrids of Various Endosperm- and Eco-type

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[Introduction]

Maize (*Zea mays* L.) genetic diversity, which is larger than other crops, contains the huge genetic potential to be exploited. The purpose of this study was not only to build population genetic relationships among various types of maize but also to examine linkage disequilibrium patterns residing within it.

[Materials and Methods]

Genotypes of 119 commercial varieties and B73 were estimated using Illumina MaizeLD Beadchip with 3,047 single nucleotide polymorphic markers(SNPs).

[Results and Discussion]

Principal component analysis(PCA), model-based clustering, and phylogenetic tree divided the genotypes of varieties into three subgroups, and methods used here showed a highly consistent division pattern. Given distributions of different ecotypes into the same subgroups, there might be only a few genes involved in flowering. Based on results from both F_{st} and Nei's distance, field corn showed remote genetic distances from both sweet corn and waxy corn, which make their crosses become a suitable choice of parents for breeding populations. In Linkage Disequilibrium(LD) investigation, chromosome 5 had the longest LD decay distance, while chromosome 1 had the shortest LD decay distance. The frequency of $r^2 = 1$ increased with a higher window size. This can be proof of cause for spurious association in association studies. Haplotype blocks were searched at four loci related to flowering and starch biosynthesis. There was no haplotype group found near the *su1* locus, contradicting to *sh2* locus. This can indicate an absence of informative SNP, leading to the conclusion that the *su1* locus has a huge impact on fitness. The results reported herein are useful as decision-supporting information for breeders and as background knowledge for a better insight into the evolution of maize.

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