Proceedings of the 56th Italian Society of Agricultural Genetics Annual Congress
Perugia, Italy – 17/20 September, 2012
ISBN **978-88-904570-1-2**

Poster Communication Abstract – 3.41

ASCERTAINMENT BIAS IN A SUBSET OF MAIZESNP50 ARRAY USED FOR GENETIC DIVERSITY ANALYSIS OF ELITE EUROPEAN MAIZE (*ZEA MAYS* L.) INBRED LINES

FRASCAROLI E.*, SCHRAG T.A.**, MELCHINGER A.E.**

*) Department of Agroenvironmental Sciences and Technologies, University of Bologna, Viale Fanin 44, 40127 Bologna (Italy)
**) Institute of Plant Breeding, Seed Science, Population Genetics, University of Hohenheim, 70593 Stuttgart (Germany)

SNP marker chip, AFLPs, SSRs, genetic diversity

Different marker systems can be utilized for assessing crop genomic diversity and performing marker assisted selection. Recent advances in high-throughput sequencing technologies have triggered a shift toward single nucleotide polymorphism (SNP) markers in many species, particularly for model organisms with substantial genomic resources. A systematic bias can be introduced if SNPs are ascertained in a small panel of genotypes and then used for characterizing a larger population (ascertainment bias). With the objective of evaluating a potential ascertainment bias of the Illumina MaizeSNP50 array with respect to elite European maize dent and flint inbred lines, we compared the genetic diversity among these materials based on amplified fragment length polymorphisms (AFLPs), simple sequence repeat (SSRs), SNPs of the MaizeSNP50 array (SNP-A) and two subsets of it, i.e., the Panzea (SNP-P) and the Syngenta markers (SNP-S). We evaluated the bias effects on major allele frequency, allele number, gene diversity, modified Roger´s distance (MRD) and on molecular variance (AMOVA). We revealed mild ascertainment bias in SNP-A, compared to AFLPs and SSRs. It affected especially European flint lines analyzed with markers SNP-S, specifically developed to maximize differences among North American dent germplasm. The bias, introduced primarily by SNP-S, affected all genetic parameters. However, the principal coordinate and Procrustes analyses for the different marker systems resulted in similar graphical representations of the structure in the dent and flint populations, thus it did not substantially alter the relative distances between inbred lines within groups. For these reasons we conclude that the SNP markers of the MaizeSNP50 array can be employed for breeding purposes in the investigated material. However, attention should be paid in case of comparisons between genotypes belonging to different heterotic groups. In this case, it is advisable to prefer a marker subset with potentially low ascertainment bias, like in our case the SNP-P marker set.