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DEEP GENOME -WIDE CHARACTERIZATION OF RECOMBINANT NEAR-ISOGENIC LINES FOR HETEROTIC QTL IN MAIZE

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In a previous study on a maize (*Zea mays* L.) population of Recombinant Inbred Lines (RILs) derived from B73 x H99, we detected several Quantitative Trait Loci (QTL) for agronomic traits and with a high dominance ratio (heterotic QTL). Then, to gain a better insight on the effects of such QTL, we developed two pairs of near-isogenic lines (NILs) for QTL at bin 3.05, two pairs of NILs for QTL at bin 4.10 and one pair for QTL at bin 10.03. For each pair, the two NILs should contrast for the parental genotypes at the corresponding QTL region (NIL-BB and NIL-HH if homozygous either for the QTL allele provided by B73 or by H99, respectively), while should share in homozygosity the rest of the genome for the alleles provided by both parents. This work was conducted on these five pairs of NILs to characterize them at about 50,000 genome-wide distributed SNPs by the Illumina MaizeSNP50 Genotyping Bead Chip platform.

After general data quality check, 14,937 (34.9%) of the 42,776 good quality SNPs were found polymorphic for the parental alleles. The observed low residual heterozygosity in NILs (average 0.93%) confirmed the success of the inbreeding program employed for QTL introgression. The proportion of SNPs in homozygous state for the B73 allele in NILs ranged from 28.5% (NIL4.10_R55-B) to 51.3% (NIL3.05_R8-B), with an average of 39.4%. Plotting the pattern of inherited genotypes and identity-by-state (IBS) values of single SNPs against their chromosome position allowed to precisely map all recombination blocks in NILs as well as to identify all genomic regions harbouring different genotypes between NILs within the same pair. This analysis confirmed that the selected QTL regions were successfully introgressed as expected in all NILs. Moreover, the dense and genome-wide SNP coverage allowed us to identify undesired chromosomal regions unexpectedly segregating between NILs belonging to the same pair, which had gone undetected by all previous analyses. A NIL-F2 segregating population derived from one of the NIL pairs (4.10_R55) for fine mapping purposes is currently being scored by selected SSR markers in order to include and evaluate the effect of allele substitutions at all segregating regions on the phenotypic values previously associated with the introgressed QTL only.