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## ORIGINAL GENETIC DIVERSITY DISCOVERY COMPARING A SUGAR BEET ELITE PANEL WITH A PROGENY FROM (SUGAR BEET ELITE X EXOTIC) CROSS

**ABSTRACT**

Selection of stable varieties producing the highest amount of extractable sugar per hectare (ha), resistant to diseases and respecting environmental criteria is undoubtely the main target for sugar beet breeding. Introgressing exotic germplasm into breeding programmes can be a way to bring new interesting allelic diversity in breeding material.

Two sugar beet populations, an elite panel (2101 genotypes, phenotyped in 21 environments, genotyped with 629 SNPs) and (elite x exotic) progeny (187 genotypes, nine environments, genotyped with 303 SNPs), were compared for three traits: potassium quantity (K meq/100g), sodium quantity (Na meq/100g) and N-alpha-amino quantity (N meq/100g).

Genome-wide association studies (GWAS) were performed for each trait in each population with the multi-locus mixed model approach (MLMM) proposed by Segura et al. (2012). The eBIC parsimony criterion (Chen and Chen, 2008) was used to choose the MLMM model that explains best trait variability with the least SNPs. Then SNPs were merged into QTLs if they were located on the same chromosome and have linkage desequilibrium greater than a significance threshold, calculated for each population from corrected r2 (Mangin et al, 2012).

The number of selected SNPs was higher in the elite panel due to higher power of detection and larger diversity. Very close SNPs in both populations were found, e.g. a probably pleiotropic QTL for Na and N traits located at the middle of the chromosome 5. Differences in genetic architectures were also observed, as the SNP detected for Na in the second half of the 5th chromosome in the (elite x exotic) progeny for which there is not colocalized detected SNP in the elite panel for this trait. Moreover, some SNPs detected in the (elite x exotic) progeny showed a favorable effect of the exotic (i.e., the impurity quantity decreases with the presence of the exotic allele).

These results illustrate that the introgression of exotic alleles into elite germplasm is an interesting method to bring new useful variability in breeding material.

**References**

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