

Association mapping for aluminum tolerance in candidate regions of the Alt_{SB} locus in sorghum

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Keywords: linkage disequilibrium, aluminum tolerance, association mapping, Alt_{SB} , sorghum bicolor

The toxicity caused by aluminum (Al) is one of the most limiting factors for crop growth and development on acid soils. Genetic studies revealed that allelic variation at the Alt_{SB} locus accounts for nearly 80% of the phenotypic variation for the trait, even though other loci controlling Al tolerance in sorghum do exist. Recently, high-resolution mapping allowed for the identification of a 24.6kbp region comprising the Alt_{SB} locus, which was completely sequenced among the parental lines of a mapping population derived from the Al tolerant and sensitive standards, SC283 and BR007B, respectively, revealing candidate polymorphisms for quantitative trait nucleotides (QTNs). These polymorphisms were assessed in 254 sorghum accessions representative of a wide range of sorghum genetic diversity. Five traits related to the Al tolerance response were also characterized in the association panel. Population structure and familial relatedness were assessed with 38 simple sequence repeat (SSR) loci randomly distributed across the sorghum genome. Linkage disequilibrium (LD) was estimated for all pair-wise combinations of polymorphisms within the 24.6kpb region where Alt_{SB} is located. Association mapping was performed using a mixed linear model that accounts for multiple levels of relatedness for appropriate Type I error control. LD in the target region decayed to values close to zero within 5000pb. Highly significant associations were detected between polymorphisms in the Alt_{SB} region and different phenotypic traits. An important role in Al tolerance is played by a polymorphism located in the second intron of the Alt_{SB} gene, which had a major contribution to the overall tolerance index obtained by Principal Component Analysis, explaining 10.8% of the variation. In addition, a low frequency allele at this locus discriminates 8 out of the 14 highly Al tolerant accessions in the complete association panel, make this SNP a promising candidate for developing tag markers for marker-assisted selection, which can be used for allele mining in diverse sorghum germplasm.

Financial Support: FAPEMIG, CNPq, CAPES, McKnight Foundation-CCRP Project and the Generation Challenge Programme.