

Abstract

This study was aiming to improve food security in Kenya through the development of a drought tolerant sorghum variety by the introgression of stay green QTLs. Marker-assisted backcross breeding was utilized to transfer stay-green QTLs from the Ethiopian donor parental line E36-1 into a Kenyan farmer-preferred variety, Ochuti as the recurrent parental line. E36-1 has 3 stay green QTLs located at three linkage groups of sorghum genome (SBI-01, SBI-07 and SBI-10). Five foreground markers flanking stay green QTLs at linkage groups SBI-07 and SBI-10 that were polymorphic between the two parental genotypes were used to identify true F1 individuals. Only two of the possible three QTLs namely, SBI-07 and SBI-10 were identified as having been transferred into three individual genotypes. This is because no polymorphic markers flanking stay-green QTL at linkage group SBI-01 was available for this particular study. The identified F1 genotypes were used as the female parents in the generation of 128 BC1F1 individuals. About 25% of the BC1F1 progenies that were genotyped had at least one QTL introgressed. Thirty polymorphic SSR markers were used to select 20 BC1F1 individuals that had a higher proportion of recurrent parent genome. These were backcrossed to recurrent parent to generate 157 BC2F1 family lines. These were screened with the five foreground SSR markers where 45 individuals were confirmed to be having among them single and double introgressions of stay-green QTL(s). This study shows that, marker-assisted backcrossing can successfully and accurately transfer genomic regions contributing to the stay green trait into Kenyan sorghum prone to drought. This was possible with the availability of polymorphic co-dominant markers like SSRs.