ESTABLISHING A SEEDLING SYSTEM FOR QTL ANALYSIS OF THE STAY-GREEN TRAIT IN SORGHUM

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Abstract
Sorghum ranks fifth in importance among other cereals in the world and is mostly grown as a source of food, fodder and biofuel. It is also one of the most drought resistant crops, thus very suitable for growth in arid and semi-arid areas. Exploitation of the drought adaptation mechanisms exhibited by sorghum is one approach for breeders to sustain food production in light of the deteriorating global warming situation. The stay-green trait is one such adaptation, by which plants continue grain filling even under post flowering drought stress, leading to higher yield, biomass and lodging resistance, compared to senescent counterparts. Our work aims at identifying new stay-green QTLs and characterizing the genes responsible for the trait in sorghum. 252 Recombinant inbred lines (RILs) were obtained from a cross between a stay-green parent, BTx623, and a non stay-green Japanese landrace, NOG. Using the parental lines, optimum growth conditions to be used in the study, were established. NOG and BTx623 were grown in a controlled growth chamber, under different soil nutrient concentrations, plant densities and time periods. Plants grown under a soil nutrient concentration of 15%, plant density of 10 plants per pot over a period of 24 days, exhibited a clear phenotypic difference between the parental lines without causing excessive damage to the plants. Hence this system was adopted to carry out the QTL analysis study involving 252 RILs. This study may prove to be a time saving approach towards identifying major QTLs for this stay-green trait, as it is done in a controlled growth chamber over a short period of time. Altogether, our results will contribute towards the fine mapping of QTLs and ultimately cloning of the genes responsible for the stay green-trait.

Key words: sorghum, RIL, stay-green trait, drought resistance, QTL analysis