QTL Analysis in Multiple Sorghum [Sorghum bicolor (L.) Moench]
Mapping Populations to Dissect the Genetic Control of Drought Tolerance Related Traits

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Introduction
Drought tolerance is a complex quantitative trait with complicated phenotype that affects many developmental stages in plants. The level of tolerance of sorghum to various drought conditions is coordinated by the action of different drought-responsive genes in relation with other stress components (Li et al., 2003). The identification of genetic factors involved in plant responses to drought stress provides ground to improve drought tolerance in crops (Kebede et al., 2001). QTL mapping using biparental mapping population has been useful in identifying and localizing important genomic regions controlling quantitative traits in a wide range of species (Tanckley et al., 1989). It has become a routine approach for genetic studies of complex traits in plants (Li et al., 2003; Holland, 2007).

To date, majority of the QTL mapping studies were based on QTL linkage mapping using single bi-parental mapping populations. Genetic mapping using single bi-parental populations are effective in detecting QTL but suffer from low resolution and limited allelic diversity. Because only two parents are involved in population development, QTL from single bi-parental population can only be assumed to be relevant to the cross and environment(s) in which they were mapped. However, drought tolerance is a very complex trait and any single bi-parental population is unlikely to segregate for all genetic loci influencing it. Hence, the use of multiple mapping population would help to detect population specific and consistent QTLs that would be candidates for marker-assisted transfer of drought tolerance related traits. Therefore, the present study was initiated with the following objectives:

Objectives
- To map QTLs associated with drought tolerance and grain yield related traits and verify their consistency across the three populations

Materials and Methods
Three mapping populations derived from 76T1-23 x Baji, Meco-1 x Birmash and 76T1-23 x Birmash crosses were used for this study. Each population consisted of 207 F2-derived F3 lines (F2:3 lines). The female parents (Meco-1 and 76T1-23) are early maturing varieties while as the male parents (Baji and Birmash) are high-yielding and late maturing. The parental lines were crossed to produce an F1 that was selfed to produce the subsequent F2 and F2:3 progenies using single seed descent.

The F2:3 progenies were evaluated under two moisture stress environments (Kobo and Meiso), during 2016/17 cropping season using an alpha lattice design with two replications. Five plants per plot were randomly taken for recording morphological data related to drought tolerance and grain yield.

Theory and Methods
Genotyping was done using genotyping by sequencing (GBS) approach at UGA. The genotypic and phenotypic data were used to map QTLs associated with drought tolerance and analysis was done using R software (version 5.6). Identified QTLs in the individual populations were projected on the consensus linkage maps for meta-QTL analysis. Meta QTL was declared only when it was common to all the three populations or when one region harbored an elevated number of QTL derived from a minimum of two populations (Danan et al., 2011).

Results
Genotypes were significantly different in their response to drought stress. Some progenies showed promising grain yield performance compared to their parents and the standard check. These genotypes appear well suited for further drought stress adaptation breeding.

A total of 2,643 SNPs were assembled from all the three individual populations, of which 1,774 SNPs were unique among the three populations (Fig 3). All the SNPs from the three populations were finally integrated to make a single saturated composite linkage map (Fig 1).

Conclusion
The bi-parental populations were effective in producing good number of promising lines for grain yield and drought tolerance related traits. We also identified large number of QTLs controlling drought tolerance related traits in sorghum. Therefore, QTLs associated with the traits will provide an important tool towards the development of MAS program in sorghum breeding.

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