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Meta QTL (mQTL) Analysis Using Three Connected Mapping Populations in *Sorghum bicolor* for Drought Tolerance Related Traits

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dentifying Quantitative Trait Loci (QTL) of considerable effects that are expressed in diverse genetic backgrounds across different drought stress regions can significantly complement the conventional breeding efforts. The purpose of this study was therefore to map consistent QTL related to drought tolerance using three connected mapping populations of different genetic backgrounds.

Methodology and Theoretical Orientation: All QTL identified in the individual populations using CIM were projected on the consensus linkage maps using the chromosomal position, LOD score, confidence interval and proportion of phenotypic variance (R2) explained by each QTL. For each chromosome, meta-QTL analysis was used to estimate the numbers and positions of the mQTL. 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.

Findings: A total of 106 QTL were identified from the three individual population QTL analysis for all traits studied. All the 106 QTLs identified in individual populations were projected on the combined consensus map for Meta QTL analysis. The meta-analysis then reduced the total number of QTLs from106 to 16 mQTLs. As a result, 4 mQTL for grain yield per plant, two for days to maturity, one for days to flowering, two for leaf senescence and three for plant height were detected.

Conclusion and Significance: The final consensus map developed would allow us to map a larger number of markers than possible in any individual map and to obtain a more complete coverage of the sorghum genome. Therefore, the consensus map can be used as a reference resource for genetic studies in different genetic backgrounds and the QTL identified in this study could be used for marker assisted breeding programs in sorghum.