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Identification of molecular markers linked to drought tolerance using bulked segregant analysis in Kenyan maize (*zea mays* l) landraces

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EXTENDED ABSTRACT

Introduction: Drought is an important climatic phenomenon, which is the second most severe limitation to maize (*Zea mays* L.) production in developing countries, after low soil fertility. Maize is particularly sensitive to water stress at reproductive stages, and breeding to improve drought tolerance has been a challenge. When drought occurs just before or during the flowering period, it results in delayed silking and a consequent increase in the length of anthesis-silking interval (ASI) (Li *et al*., 2003). Selection for reduced ASI has shown correlated response to improved grain yields under drought (Banziger *et. al*., 2000). However, conventional selection has been limited by the difficulty in establishing uniform experimental conditions to eliminate environmental effects and their possible interactions with the genotype (Ribaut *et al.,* 2002; Campos *et al.,* 2004). The objectives of this study were: (i) to identify SSR polymorphisms for ASI between the parents and the F_2 population developed from selected Kenyan maize landraces; (ii) to determine correlations between morphological traits such as ASI, grain yield and SSR markers (iii) to estimate co-segregation of SSR candidate markers and ASI.

Methodology: An F_2 population of 203 individuals developed from a cross between drought susceptible (KCB) and drought tolerant (GBK032357) maize landraces was screened under drought to categorize into tolerant and susceptible groups. Based on the ASI values derived through the BSA procedure, the DNA from the 10 most drought tolerant and 10 most drought susceptible F_2 plants was used to make DNA pools. These DNA pools and DNA from parents were assayed at 109 loci using SSR primer pairs. Polymorphic candidate markers were then confirmed on the 20 individuals making up the bulks, alongside the parental DNA. Association between markers and quantitative traits in the F_2 individuals selected for the bulked segregant analysis was determined by regression analysis. A $p < 0.05$ value based on the F-test significance, was used as the threshold for considering the likely presence of a candidate QTL near a marker (Crouzillat *et al*., 2000).

Results: The investigation of polymorphic candidate markers on the 20 individuals used to make DNA bulks revealed four genomic regions associated with ASI. These were regions near markers *p-umc2189*, *p-bnlg1179* and *p-bnlg1014* on chromosome 1 and *p-umc1542* on chromosome 2. Together, the candidate QTLs accounted for about 65% of the observed variation for ASI. Significant phenotypic correlations among flowering parameters, grain yield and yield components were observed. Overlaps between the corresponding candidate QTLs were also observed. For instance, markers p-*umc2189* and *p-bnlg1014* showed significant association with female flowering time (FFT) whereas markers *p-bnlg1179* and *p-umc1542* showed significant association with both kernel number (KN) and grain yield (GY). This finding could imply pleiotropism between loci for ASI and FFT, KN and GY.
The candidate QTLs identified in the study may be useful in developing molecular marker assisted selection strategies to transfer drought tolerance traits from the local landraces into the elite varieties. However, the candidate markers as identified here need to

be screened in the entire F_2 population and further analysis be carried out to confirm and Map these QTLs. The candidate QTLs should also be tested in varied environments to establish their stability.

References

Banziger M, Edmeades GO, Beck D. and Bellon M, 2000. Breeding for Drought and Nitrogen Stress Tolerance in Maize: From Theory to Practice. Mexico DF CIMMYT.

Campos H, Copper M, Habben JE, Edmeades GO. and Schussler JR, 2004. Improving drought tolerance in maize: A view from industry. *Field Crops Res*. 90: 19-34.

Crouzillat D, Menard B, Mora A, Phillips W. and Petiard V, 2000. Quantitative trait analysis in *Theobroma cacao* using markers. Yield QTL detection and stability over 15 years. *Euphy*. 114: 13-23.

Li X, Li M. and Zhang S, 2003. Identification of quantitative trait loci for anthesis-silking interval and yield components under drought stress in maize. *Acta Bot. Sci*. 45(7): 852-857.

Ribaut JM, Banziger M, Bertran J, Jiang C, Edmeades G, Dreher K. and Hoisington H, 2002. Use of Molecular Markers in Plant Breeding: Drought Tolerance Improvement in Tropical Maize. In: Manjit S.K. (ed.). Quantitative Genetics, Genomics and Plant Breeding. Wallingford, UK: CABI Publishing pp 85-99.