Abstract

Introduction : Drought is an important climatic phenomenon, which is the second most severe constraint to maize production in developing countries, after low soil fertility. Maize (Zea mays L.) is particularly sensitive to water stress at re productive stages, and breeding to improve drought tolerance has been a challenge. When drought occurs just before or during flowering, it results in delayed silking and a consequent increase in the length of anthesis-silking interval (ASI). Selection for a reduced ASI has shown correlated response to improved grain yields under drought. However, conventional selection has been limited by the difficulty of managing uniform experimental conditions to eliminate environmental effects and their possible interactions with the genotype. Objectives : Simple sequence repeat (SSR) molecular markers were used to identify genomic regions responsible f or the expression of ASI in F2 population derived from a cross of drought susceptible and tolerant landraces using bulked segregant analysis (BSA). Methodology : An F 2 population of 203 individuals was developed from a cross between drought susceptible (KCB) and drought tolerant (GBK032357) maize landraces. The population was screened under drought to categorize into drought tolerant and drought susceptible phenotypes. Based on the BSA procedure, the DNA from 10 most drought tolerant and 10 most drought susceptible F 2 plants based on ASI values were used to make DNA pools. These DNA pools and DNA from parents were assayed at 109 loci. Results: A confirmation of polymorphic candidate markers on these 20 individuals 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. The candidate QTLs accounted for about 65% of the observed variation f or 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 implied pleiotropism between loci for ASI and FFT, KN and GY. Conclusion and application of results : The four candidate markers (p-umc2189, p-bnlg1179 and p-bnlg1014 and p-umc1542) identified in this study may be useful in developing molecular marker assisted selection (MAS) strategies to transfer drought tolerance traits into the elite varieties. The use of MAS will significantly expedite the breeding process by reducing length

of the selection cycles required in conventional breeding. However, the candidate QTLs should be validated in other environments to establish their stability.