

Research Article

Identification SSR Markers Linked to Resistance Against Maydis Leaf Blight in Maize Inbred Lines

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Abstract

Eight inbred lines were used to develop sixteen crosses and molecular SSR markers were also used to screen the plants of eight parental inbred lines and F₁ hybrids for resistance and susceptibility and to see the association of DNA marker with field studies. Eight parents were analyzed for polymorphism using 43 SSR primers all of the genotypes studied could evidently be distinguished with the combination of the SSRs used. The numbers of alleles confirm the wide genetic base of the maize varieties and the number of alleles at each locus ranged from 2 to 4. The overall size of PCR amplified products ranged from 105 bp (p-umc1380, p-bnlg1712, p-umc1020 and p-umc2158) to 230 (p-umc1086). The molecular size difference between the smallest and the largest allele at a SSR locus varied from 5 bp (p-bnlg1064) to 50 bp (p-bnlg1496). The size of PCR amplified product for individual primer and PIC values demonstrate the informativeness of the SSR loci and their potential to detect differences among the varieties based on their genetic relationships. The polymorphic information content (PIC) value ranged from 0.36 (p-umc1812) to 0.84 (p-phi085). The average PIC value provided sufficient discrimination to assess the genetic diversity for maydis leaf blight disease within the parental inbred lines. The SSR markers clearly distinguishes resistant and susceptible parents alongwith differences in F₁ crosses for resistance to maydis leaf blight disease and results indicated strong association between field results for inheritance of maydis leaf blight and SSR marker studied.

Key words: Diversity, maize, molecular markers, MLB, PIC value, SSR markers

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