



MARKER-ASSISTED SELECTION FOR GENOME RECOVERING AND INTROGRESSION OF RESISTANCE TO MAIZE COMMON MOSAIC

Pinto, MO^{1*}; Souza, IRP¹; Carvalho, SGM²; Machado, LM²; Rafael, HA²; Gonçalves, IAM²; Barros, BA¹; Carneiro, NP¹

1 EMBRAPA CNPMS - Centro Nacional de Pesquisa Milho e Sorgo, Caixa Postal 151, CEP 35701-970, Sete Lagoas, MG. 2 Bolsista do CNPq – PIBIC. Centro Universitário de Sete Lagoas, MG.

*E-mail: marcos.deoliveira@embrapa.br

Keywords: Simple Sequence Repeats (SSR), *Zea mays* L., potyvirus, sugarcane mosaic virus (SCMV)

In Brazil, the “maize common mosaic”, caused by the potyvirus sugarcane mosaic virus (SCMV), is one of the most important viral diseases that affect the maize crop, reaching losses up to 50% in grain production. Breeding programs have focused attention to the introgression of resistance to SCMV in maize inbred lines that are used for hybrid production. Thus, in the present work, for the introgression of resistance to SCMV, we crossed a resistant inbred line, L520, with a susceptible one, L19, followed by recurrent backcrosses with the parent L19 for genome recovering. All the experiments were carried out at Embrapa Maize and Sorghum, located in Sete Lagoas, Minas Gerais, Brazil. Two hundred maize seedlings of the RC_1F_1 (L520xL19), at V3 stage, were inoculated four times, with weekly periodicity followed by three phenotypic evaluations. Seventy four SCMV resistant genotypes were evaluated for the parental genome recovering (L19) based on 18 polymorphic SSR markers distributed **throughout** the maize genome. The genotyping procedure was done in two steps, applying 9 SSR markers in each one. In the first genotyping step, the proportion of L19 genome recovering in the RC_1F_1 (L520xL19) population varied from 11,1% to 88,9%, with an average of 48,5%. For the second genotyping step, 55 individuals, with a greater proportion of the L19 genome recovered, were selected. Finally, using 18 polymorphic SSR markers, the proportion of the L19 genome recovering, within the selected 55 individuals from the RC_1F_1 (L520xL19) population, varied from 36,4% to 75%, with an average of 55,7%. Two genotypes, both with 75% of the recurrent parent (L19) genome, were selected to be used in the next backcrosses for the development of SCMV resistant inbred lines.

Financial support: Embrapa Maize and Sorghum