ABSTRACT

MUHAMMAD AZRAI. Integression of opaque-2 Gene into Downy Mildew Resistance Lines, Utilizing Marker Assisted Selection (MAS) in Developing Hybrid Maize. Under advisory of HAJRIAL ASWIDINNOOR, MEMEN SURAHMAN, and JAJAH KOSWARA.

Quality protein maize (QPM) is one of the sources of plant protein that is necessary for human and monogastric livestock because the QPM contains opaque-2 mutant gene that expresses increased lysine and tryptophan in maize endosperm as compared to normal maize. One problem of QPM development in Indonesia is that all QPM collections were susceptible to downy mildews (DM). Application of marker-assisted selection (MAS) for introgression of the opaque-2 mutant gene to downy mildew resistance (DMR) elite lines faster developing of commercial QPM population or hybrids carrying DMR gene. The goals of this research were to generate QPM hybrid varieties having downy mildew resistance and high yield. The study consisted of four experiments. First: Estimate of genetic variance and genetic models to downy mildew resistance in maize. Each seven kinds of populations (P1, P2, F1, F2, BC1P1, BC1P2, and F3) from crosses CML161 x MR10 and CML161 x Nei9008 was developed then evaluated for DMR under artificial screening nursery using randomize bock design (RBD). The results of the experiment showed that DMR was controlled by quantitative genes and the level of its resistance was significantly played by gene action of additive and dominant. Complementary epitasis interaction and duplicate epitasis interaction observed for the cross of MR10 x CML161 and Nei9008 x CML161. Second: Introgression of o2 recessive mutant gene to downy mildew resistance maize lines with MAS-1 approach. Lines CML161, Nei9008 and 36 MR10, its progenies (BC1F1, BC2F1, BC3F1, BC3F2) were screened in the laboratory using specific markers umc1066 and phi057 with Partial MAS 1 method. The selected lines were evaluated for its performance using augmented design. There were 42 of Nei9008+o2 and 36 MR10+o2 lines and some lines showed higher yield potential compared to their original lines. Third: Selection and combining ability of lines containing homozygote recessive opaque2 gene for downy mildew resistance. Eight Nei9008+o2 lines, and eight MR10+o2 testers to DMR character having twice lysine and of tryptophan content compared to their backcross parental lines were screened. The lines were recombined to develop 64 single cross hybrids. Lines Nei9008+o2-11 and Nei9008+o2-71, and tester of MR10+o2-30 were identified have significant for general combining abilities and seven-cross combinations showed significance for specific combining abilities. Fourth: Evaluation of combining ability, yield potentials, yield components, and agronomy characters of lines and testers containing opaque-2 recessive homozygous gene. Genotype test consisted of eight lines, eight testers, hybrid crosses of lines x testers and four check varieties. The experiment was arranged in randomized block design, with two replications under lowland farm, Lapeccang (Bone) and upland farm, Bajeng (Gowa). Results showed that genotype x locations were significant for ears weight and yield characters. Line Nei9008+o2-09 and tester MR10+o2-31 were good combiner for yield and their hybrid gave highest yield and significantly different from all checks. Eight new hybrids of good and significant specific combining abilities for yield were selected. At the end, we identified three new QPM hybrids, having high yield potential, and resistant to downy mildew. The new QPM hybrids are Nei9008+o2-27//MR10+o2-13 (mean yield is 8.4 t/ha and DM infections is 2.2%), (Nei9008+o2-09// MR10+o2-26, (mean yield is 7.7 t/ha, and DM infections is 14.4%) and Nei9008+o2-27// MR10+o2-08 (mean yield is 7.4 t/ha and DM infections is 2.2%). The check varieties were three hybrid varieties and one open pollinated variety, with following performances: hybrid C7 (yield mean is 7.4 t/ha and DM infections is 48.7%), hybrid Bima 1 6.3 t/ha and 45%), hybrid Bima 1q (4.9 t/ha and 64.4%), and Srikandi Kuning-1 (5.3 t/ha and 100%), respectively.

Key words: maize, opaque-2 gene, downy mildew resistance, genetic analysis, combining ability.