CHAPTER 6
CONCLUSION

Mungbean resistance to Cercospora leaf spot (CLS) and powdery mildew (PM) can be developed through marker-assisted selection in breeding programs. The use of 160 SSR and EST-SSR molecular markers for identification of polymorphisms between parents demonstrated that 27 (16.9%) and 23 (14.4%) SSR and EST-SSR markers were found to be distinct and clearly polymorphic between KING and SUPER5, and H3 and SUPER5, respectively. Among these polymorphic markers, six markers were associated with traits related to domestication, i.e., 100-seed weight, pod length, length of the internodes, primary leaf width, hypocotyl plus epicotyl length, and number of twists along the length of the dehiscence pod when kept at room temperature. The BC$_2$F$_1$ progenies selected through the polymorphic markers showed the highest RPG recovery of 94.7% and 97.8% in KING and H3 populations, respectively, were further used to produce BC$_3$F$_1$ seeds. This study found that background selection using SSR and EST-SSR markers can be used to accelerate backcrossing. Furthermore, we used marker-assisted selection (MAS) for pyramiding the CLS and PM resistance genes into the recurrent parents. Six markers linked to CLS and PM resistance genes, including ISSR I16274, VrTAF5_Indel, ISSR (I85420), ISSR-RGA (I42PL222), ISSR-RGA (I27R565), and VrMLO12_Indel3 markers, were used for foreground selection in every generations of both populations for transferring the triple resistance genes (2 PM resistance genes and one CLS resistance gene) into KING and H3, while 50 polymorphic markers were used for background selection.

Moreover, the detached leaf assay for CLS evaluation in the laboratory were used to confirm the resistant progenies, as well as PM evaluation under field conditions. When compared to their parents and check cv. CN72, the selected BC$_2$F$_1$ progenies with high RPG recovery showed the resistant response to CLS and moderately resistant response to PM. When assessing PM resistance genes in a KING × SUPER5 population, the pyramided BC$_2$F$_1$ progenies with marker combinations linked to both PM resistance genes including I85420 + I42PL222, and I27R565 were more resistant to PM than KING, check cv. CN72, and BC$_2$F$_1$ progenies with only one or no
PM resistance gene. In addition, we observed that most of pyramided progenies exhibited some agronomic traits similar or superior to KING, especially yield per plant. These results suggest that we can effectively transfer triple resistance genes into KING and H3 through MAS. Using this technique, we can reduce the number of generations of backcrossing, thereby saving more time and cost than conventional breeding. Moreover, these pyramided BC progenies can be further used to develop new resistant mungbean varieties in the future.