CONCLUSION

The total of 50 monoconidial isolates collected from 5 districts of Savanakhet Province, Central Laos were identified into 3 groups by using pathotyping. The 8 weed isolates were grouped as one using similarity index of 65% while the 42 rice isolates were grouped into two using the same similarity index. Using similarity index of 70%, the rice isolates were grouped into three based on the isolates virulence pattern. The 22 rice isolates selected out of the 50, they were clustered into two groups at similarity index level of 45% and into three small groups at 62%. 3 isolates from 3 groups were chosen to screen RILs for the virulence pattern of the isolates.

Parental lines and test varieties screening using 22 isolates showed that resistance index of JHN, IR62266 and CT9993 were resistant to all isolates with RI value of 1 obtained for leaf blast screening and virulence testing of 32 rice varieties from Laos, Vietnam, Thailand and the Philippines against twenty-two blast isolates were classified into 3 groups, resistant, moderately resistant and susceptible. There were 13 test varieties resistant, 8 moderately resistant and 11 susceptible. From 22 blast isolates, 12 were virulent (55%) and 10 were not against the 32 test varieties. None of the Lao blast isolates were virulent on JHN and CT9993 and only two isolates infected IR64 and IR62266.

Five hundred and eighty-seven RILs from a cross between KDML105 and JHN were inoculated with three selected blast isolates. The disease severity index showed abnormal distribution. 71% of RILs were resistant to LPDR16, 75% were resistant to LPDR47 and only 52% were resistant to LPDR41. If the data were be classified into 2 groups, resistant and susceptible, the chi-square (X2) test revealed that 2 out of 3 sets of data had fitted a ratio of approximately 3:1 and one set fitted 1:1

ratio of resistant to susceptible population. The ratio of 3:1 was observed using LPDR16 and LPDR47 while ratio of 1:1 was observed using LPDR41.

To locate QTL on the chromosomes, linkage map construction using 16 SSR markers and QTL analysis revealed the presence of QTLs on chromosome1, 11 and 12. The peak of QTL on chromosome1 was close to RM319 marker. On chromosome 11 close to RM139 marker with high LOD value for three isolates (24.24, 58.63, 86.02) and the single coefficient of determination R^2 (39.96, 45.10, 58.06) with JHN being a sole contributor for all resistant alleles indicated the presence of polygenes on this chromosome. While resistant alleles on both chromosome1 and 11 were contributed by JHN, those on chromosome12 were contributed by JHN and KDML105. However, the peak for the highest LOD value being the detection of QTL on chromosome12 was found between OSR32 – RM179 with LOD value being 19.54 and resistant allele donated by KDML105.

Phenotypic reaction and analysis have supported those of the genetic analysis. Using NQTL analysis, the main effect was detected on chromosome11 between RM21 and RM224 using LPDR16 and LPDR41 with JHN as contributor of all resistant alleles. The minor effect was detected on chromosome1, 11 and 12 using LPDR47. Resistant alleles on chromosome1 and 11 were obtained from JHN while those on chromosome12 were obtained from KDML105. There were additive interactions between three QTLs on chromosome1, 11 and 12 with LPDR47 when JHN and KDML105 alleles were present, mean scores of disease severity were low ranging from 0.53 -3.82.