

## CHAPTER VI

### CONCLUSION

In conclusion, my present genetic study reveals that:

- Considerable genetic diversity exists in the ten common wild rice populations of four locations in Cambodia, although the diversity level varied among populations, which is most likely due to different conditions, under which the populations are grown and conserved.
- The degree of genetic differentiation among samples collected from Takeo province was higher ( $F_{ST} = 0.49$ ) than those from other three provinces which were very similar ( $F_{ST} = 0.30$  to  $0.32$ ). When compared for the whole population level, high degree of genetic differentiation among 10 common wild rice populations ( $F_{ST} = 0.39$ ).
- Cluster analysis showed relationship between geographic locations and genetic distance of common wild rice populations in the present study were separated into two major clusters by geographical locations. The first cluster consisted of three populations from Prey Veng province whereas the others included all populations from Phnom Penh, Kandal and Takao provinces which are close together and one population from Prey Veng was separated into another group.

- Significant contaminations from cultivated rice varieties to wild rice population were observed in most of the wild populations, which might impose a destructive effect on the genetic integrity among individuals rather than among populations.
- Morphological characters of F<sub>2</sub> populations between wild and cultivated rice were found, such as plant type, leaf sheath, stigma color, apiculus color, awn, awn color, and pericarp color were controlled by few major genes (1-3 genes) with complete dominant or complementary gene actions and plants segregated within the range of cultivated and wild rice parents in number of tillers per plant, days to flowering, seed length, and seed shape.
- Transgressive segregations were found in plant height, panicle length, number of branches panicle, number of spikelets panicle, seed fertility and the difference of segregating patterns between crosses was found in seed shattering. Therefore, the interspecific hybridization produced a large source of genetic variation and adaptation in segregation population. This will be useful in plant breeding program or the strategies development for protection against weedy rice infestation.