CHAPTER 4

General Discussion

Weedy rice (*O. sativa* f *spontanea*) is one of the most noxious weeds due to its highly adaptive advantage under crop management, resulting in its' success as a weed in terms survival and distribution. The adaptive advantage is resulted from population genetic structure and dynamics (Loveless and Hamrick, 1984) under the influence of evolutionary processes (Postlethwalt, 2009). Gene flow and other ecological conditions drive genetic changes and distribution allele frequency, resulting in changed pattern of genetic variation and population structure, as seen in weedy rice populations from Thailand's main rice growing region, over the years.

Population of weedy rice in Thailand was strongly structured by crop rice in each region and changed their population genetic structure and dynamics by time. In spatial term, weedy rice populations collected from three rice production areas in each growing season has spatially differentiated patterns among regions by genetic differentiation and population structure analysis. This is clearly reflected by weedy rice populations from different regions showed the high level of genetic differentiation and were structured base on their cultivated rice varieties popular in each region, modern varieties (CNT1, SPR1, PTT1 and PSL2) which were common in the Central Plain and the Lower North while the Northeast commonly planted improved traditional varieties (KDML105, RD15 and RD6). This result suggested that weedy rice in the present study resulted from independent hybridization between native common wild rice and cultivated rice varieties popular each region (Niruntrayakul, 2007; Pusadee, 2009). Pusadee (2009) also found similarly result that the population structure of weedy rice in Thailand were differentiated by its crop rice varieties.

Commonly, the main cause of population structure and genetic differentiation among weedy rice populations from different region can be associated with migration or gene flow (Ellstrand *et al.*, 1999). The introgression of crop alleles from different companion crop rice varieties may contributed to the differentiation of weedy rice populations at different regions although other factors such as selection and agronomic practices may also played their roles (Cao *et al.,* 2006). As a conspecific weed of crop rice, weedy rice individuals are commonly surrounded by densely populated crop in rice fields. Recurrent gene flow from different varieties of companion crop rice grown at different rice fields can enhance genetic differentiation among weedy rice populations by incorporating crop alleles from different varieties. Thus, weedy rice populations from different regions with high level of genetic differentiation in this study were strongly structured base on their companion crop rice varieties which were used to plant in each region (Pusadee, 2009).

In temporal term, the ongoing of gene flow from companion crop rice to weedy rice plays the significant role on the patterns of genetic diversity and population structure of weedy rice. The results from all analysis of weedy rice populations collected in different growing seasons had tended toward cultivated rice over the years. Weedy rice populations in 2005 were segregated forms between wild and cultivar both in phenotypes and genotypes (Niruntrayakul, 2007) that was the consequence of early hybrid stage of intercross between native common wild rice and companion crop rice in the sympatric habitats in a recent invasion (Langevin *et al.*, 1990). After few years, genetic variation and population structure of weedy rice in 2008 and 2009, respectively, had temporally changed over the years. Population structure was clustered based on their companion crop rice varieties and more closely relationship to cultivated rice by increasing the proportion of cultivar genotype (Pusadee, 2009). Genetic variation and genetic diversity of weedy rice populations had tended to decrease over the years lead to the convergence of homogeneity of weedy rice populations toward the crop rice (Ellstrand *et al.*, 1999). It reflected the outcome of the ongoing gene flow process between weedy rice and their companion crop rice resulting the rapidly loss of wild genotypes in later segregating populations (Cao *et al.*, 2006).

Commonly, weedy rice frequently co-exists with companion crop rice in sympatric rice fields, introgressed genes from companion crop rice can be easily taken in the gene pool of weedy rice by crop-to-weed gene flow (Ellstrand *et al.*, 1999). This process contributes the persistence and increase adaptation of weedy rice to the farmers' management. Under agronomic practices and farmers' selection, the subsequent accumulating continuous backcrossing of weedy rice to companion crop which different rice varieties contribute to similar of weedy rice to the companion crop rice (Cao *et al.*, 2006). Therefore, gene flow is the major process in the adaptive evolutionary dynamics of weedy rice populations when they are co-existed with their companion crop rice in the sympatric rice fields through intensive agronomic practices and farmers' selection. However, they were strongly some characters, produced more yield components and high seed shattering, for increasing their fitness and distribution.

In summary, results from this study shown that weedy rice with high adaptive evolution was under the ongoing and the combination of gene flow and ecological conditions; farmers' selections and agronomic practices, lead to the changing of their genetic diversity and population structure in both space and time. High genetic diversity and wide diversity in phenotypes of weedy rice were resulted from gene flow between common wild rice and cultivated rice lead to earlier stage of invasive weedy rice. Long term, the accumulating subsequent continuous backcrossing of weedy rice to companion crop rice through farmers' managements has influenced the decreasing of genetic diversity and genetic variation lead to the convergence of homogeneity toward the crop and was strongly structured of weedy rice populations based on its companion crop rice varieties. The resembling to companion crop rice of weedy rice populations in each region will complicate weedy rice manage and control in future and consequently threaten rice production. Therefore, the further studies are needed to develop effective methodologies for weed control and management for prevent weedy rice from extensive spreading and infestation across all rice production regions in Thailand.