CHAPTER V

DISCUSSION

From the survey, ten common wild rice populations were found. Most of them were scattered in man-made habitats such as abandoned and the edge of rice fields, or road-side ditches. Different life-history types were identified ranged from annual to perennial types. All plants showed characteristics of wild rice type such as open plant type, long awn, and black hull. However, most of them exhibited small anthers, purple stigma, and red awn, only two perennial populations (PV1 and PV2) had large anthers, three plants from PV1 and PV2 had white stigma and PV1 had white awn was found in all plants. Mixtures of plants with red awn and plants with white awn were found in four populations.

Results from DNA analysis showed that high genetic diversity, both within and between populations, were found for common wild rice in this study. When compared for the whole population level, high degree of genetic differentiation among 10 common wild rice populations ($F_{ST} = 0.39$) indicated that 39% of the total genetic variation was partitioned into among populations while 61% was the variation distributed within population. This finding was consistent with the results reported in cases of Thailand and Laos. High degree of genetic differentiations were found among common wild rice populations from north and central plain ($F_{ST} = 0.36$, Punyalue, 2005) and northeastern Thailand ($F_{ST} = 0.48$, Wongtamee, 2007). In the study of genetic differentiation of common wild rice in Laos, Kuroda (2004) reported that the F_{ST} was 0.467. And these values are consistent to the high genetic diversity

from South China based on previous allozyme and RAPD analyses (Xie 1999; Gao et al. 2000a).

Relationship between geographic locations and genetic distance of common wild rice populations was found in this study. The 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 (Figure 3.1). However, one population from Prey Veng was different from the other group. These results show that wild rice populations can be differentiated geographically; Prey Veng province is separated from Phnom Penh, Kandal and Takeo provinces by the Mekong River. However, as in case of PV1, anomalies in geographic differentiation can occur. This finding was consistent with result reported in case of wild rice in Laos, where the anomaly in geographic location and genetic differentiation was also found (Kuroda, 2004).

Relating to the high level of genetic differentiation of common wild rice, this may be due to restricted gene flow among remaining populations. However, the extent of gene flow between cultivated rice and wild rice may affect the integrity of population structure. If gene flow is extensive, there will be a tendency for all segregating alleles to be detected in populations within a common gene pool. Previous studies based on SSR alleles revealed that *O. sativa* membership was found in populations of *O. rufipogon*, in Laos (Kuroda, 2004). In the present study, the contamination of alleles from cultivated rice into wild rice populations were observed in most of the wild populations (Table 4.12). The highest proportion of cultivated allele's contamination was found in Prey Veng province (0.032-0.053), and slightly

lower in Phnom Penh plus Kandal (0.017-0.038) and Takeo was the lowest (0.011-0.036). Moreover, the results of the STRUCTURE program displayed K=2, wild and cultivated rice were split into different clusters (Figure 4.3). Gene flow between wild rice and cultivated rice was indicated by some wild rice plants, ranged from 1 to 7 plants in eight populations, contained proportion of cultivated rice signatures at 1-5%. No wild rice memberships were found in all cultivated rice samples. This suggests that the direction of the gene flow may occur from cultivated rice to wild populations. In addition, analysis of inbreeding coefficient and outcrossing rate also supported the direction of gene flow from cultivated rice to wild rice. Some common wild rice was partly outcrossing (f=0.8) while cultivated rice was complete inbreeding (f=1.0).

In general, out-crossing species maintain high genetic diversity within a population, whereas inbreeding species have higher genetic diversity among populations than within a population (Hamrick and Godt 1989). In this study, the inbreeding coefficient (F_{IS}) was found very high in all populations with Takeo (1.00), Phnom Penh (0.94) and Prey Veng (0.79). In addition, the overall out-crossing rate (t) calculated in this study was about 12%, which is nearly the same as the results reported in other studies about 20% (Song et al. 2003). The considerable out-crossing rate allows *O. rufipogon* to receive the genes of cultivated rice varieties through cross-pollination, given that the two species are grown sympatrically (Morishima et al. 1984) and high compatibility exists between *O. rufipogon* and *O. sativa* (Song et al. 2002, Nirutrayakul, 2008).
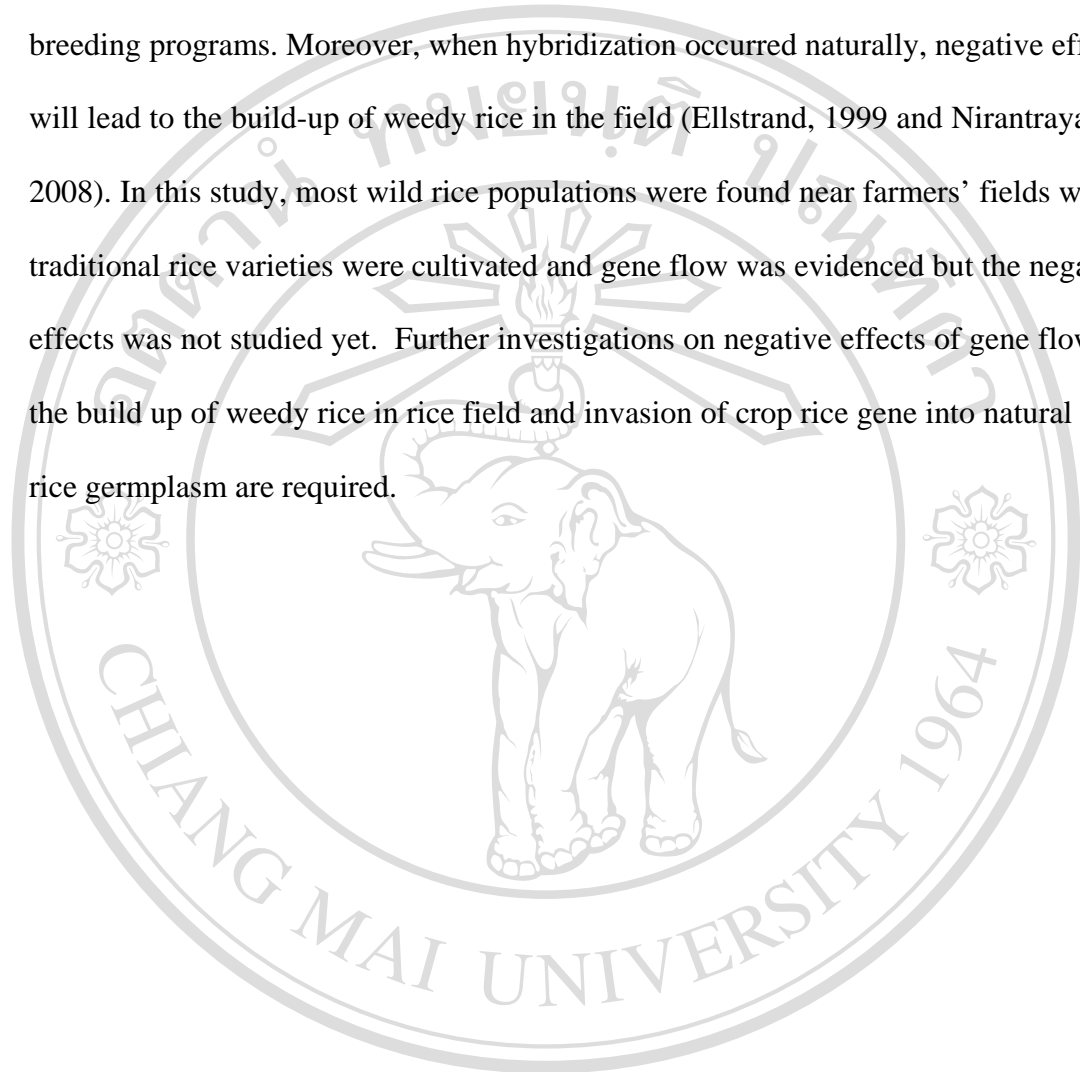
If interspecific hybridization between wild and cultivated rice did occur, hybrid populations would contained segregation on morphological and physiological characters with wild traits, such as awning and seed shattering dominated in the

population (Nirantrayakul, 2008). Two common wild rice populations showed noticeable morphological variations such as white stigmas and short awns, which are similar to cultivated rice varieties (Wongtamee 2007). These confirmed the introgression from cultivated rice into the wild rice, and consequently changed their genetic structure.

In F_2 populations, several morphological segregations have emerged. 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 and complementary gene actions. For physiological characters, some traits were segregated within the range of cultivated and wild rice parents including, number of tillers per plant, days to flowering, seed shattering, seed length, and seed shape. The difference of segregating patterns between crosses was found in seed shattering with offspring of cross with wild rice from Takeo province shattered their seed almost completely; while offspring of cross with wild rice from Kampong Thom province did not shatter all their seed (Figure 4.12).

Transgressive segregations of F_2 were found in plant height, panicle length, number of branches panicle, number of spikelets panicle, and seed fertility. Similar findings were reported, for example, Prommin (2007) studies segregation in F_2 generation of crosses between common wild rice (*O. rufipogon Griff.*) and cultivated rice (*Oryza sativa L.*), the transgressive segregation was found in number of tillers plant, culm length, heading date, panicle length, seeds width and seed length. Xiong et al (1999) also found that the segregating population derived from cultivated rice and wild rice parent possesses a number of desirable characteristics, such as tolerance to biotic and abiotic stresses. Therefore, the interspecific hybridization produced a large

source of genetic variation and adaptation in segregation population. Further studies should address these genetic bases of those characters in order to use these genes in breeding programs. Moreover, when hybridization occurred naturally, negative effects will lead to the build-up of weedy rice in the field (Ellstrand, 1999 and Nirantrayakul, 2008). In this study, most wild rice populations were found near farmers' fields where traditional rice varieties were cultivated and gene flow was evidenced but the negative effects was not studied yet. Further investigations on negative effects of gene flow on the build up of weedy rice in rice field and invasion of crop rice gene into natural wild rice germplasm are required.