

CHAPTER 5

General Discussion

Evolutionary dynamics were determined through population genetic structure analysis. The different population genetic structures reflected the consequences of different evolutionary processes (Tarnita *et al.*, 2009). The processes such as selection, mutation, drift, domestication bottleneck, gene flow, adaptation capacity, including social organization of human are subjected to shape genetic variation and population structure. As Thailand lies partly in the center of rice diversity and domestication, therefore, genetic variation of rice populations in Thailand is expected to be high and under the influence of evolutionary forces.

The complex of *Oryza sativa* primary gene pool in the natural ecosystem where gene flow among three components were revealed in Chapter 2, common wild rice (*O. rufipogon* Griff.), cultivated rice (*O. sativa* L.) and weedy form (*O. sativa* f *spontanea*), play the significant role on shaping genetic variation and population structure of the complex. Addition to gene flow, however, life-history traits, environmental conditions, and farmers' managements also influenced genetic diversity and population structure of rice gene pool. Forty-two common wild rice populations are highly diverse and structured base on life-history trait, perennial and annual types. Perennial type is more diverse than annual type due to the influence of habitat preference and mating system. For 37 pure line cultivated rice, highly total genetic diversity was due to broad genetic base of Thai cultivated rice and were

structured based on pedigree background; (1) modern varieties, (2) improved traditional varieties and (3) mixture of modern varieties and improved traditional varieties. The last component, weedy rice, illustrated various level of genetic variation within twelve populations and was structured base on it companion cultivated rice, modern varieties (CNT1 and SPR1) or improved traditional varieties (KDML105 and RD6).

Various level of genetic diversity within populations was the outcome of gene flow process among the three components of the complex in the area where they are co-existing. Low level of genetic variation was responded to the hybridization between weedy rice vs cultivated rice illustrated by high proportion of cultivated genetic constitution. While high level of genetic diversity might be due to low number of backcross to crop than the former one or these weedy rice were the early stage of invasive weedy rice or wild rice seed contamination in crop field. In addition, the widespread of weedy rice in various areas in Thailand also revealed the outcome of hybridization or gene flow between local common wild rice and local popular cultivated rice that existed in the same habitat. Therefore, evolutionary process that influenced the dynamics of population genetic structure of *Oryza sativa* primary gene pool clearly illustrated as hybridization or gene flow among the three components.

Genetic diversity and population structure of landrace rice was demonstrated in Chapter 3. Landrace Thai rice variety Bue Chomee was diverse and such variation was maintained within and among seed lots in traditional agricultural system. Unlikely to modern pure line cultivated rice of Chapter 2 those displayed no variation within varieties. Interestingly, genetic diversity of landrace rice Bue Chomee was

about 50% of its wild ancestor (*O. rufipogon* Griff.) as detected in Chapter 2. While others domesticated species maintain level of genetic diversity only 20% in average of their wild ancestors (Eyre-Walker *et al.*, 1998; Fugunaka *et al.*, 2005; Liu and Burke, 2006; and Hyten *et al.*, 2006). Bue Chomee was structure as genetic isolation by geographical distance suggested that seed lots of Bue Chomee within the same village and from the neighbor villages showed more genetic similarity than those from the remote villages. The outcome of such structure was assumed to be the consequence of farmers' managements especially the way farmers exchange their seed with the others. The present results consistent with Zeven (1999) that a key aspect of traditional agricultural systems throughout the world is the frequent exchange of seeds by farmers. In addition, the outcome of local adaptation of landrace rice also plays an influenced in isolation by distance structure. Because Bue Chomee is genetically diverse, and it is grown under variable environmental and agricultural conditions, Bue Chomee has the capacity of a dynamic system that can adapt to adverse conditions.

Finally, the results of Chapter 4 examined the consequence of farmers' managements on genetic diversity and population structure of landraces rice analysis based on seed exchange network approach as considered in Chapter 3. Genetic diversity, population structure, pattern of seed exchange and factors those may influenced genetic structure were analyzed in comparison between two landrace rice varieties, Bue Chomee and Muey Nawng. Different landrace rice varieties illustrated different levels of genetic diversity and population structure. Bue Chomee was diverse both within and among seed lots and genetic differentiation between nearby village was lower than the village with more distance. In addition, population structure of Bue Chomee was consistent with the pattern of seed exchange that most

farmers of Bue Chomee were exchange rice seed within village particular among relatives than with the farmers outside the village and non-relatives. The result of Bue Chomee variety in Chapter 4 was confirming the structure of isolation by distance presented in Chapter 3 that was the outcome of farmers' managements particularly on seed exchange system. While Muey Nawng illustrated lower level of genetic diversity and different population structure compared with Bue Chomee. Muey Nawng from the two villages represented two seed exchange networks revealed different levels of genetic diversity and different patterns of seed exchange within network. The differentiation between two Muey Nawng networks was responded mainly to different managements of different ethnic groups. The Karen seems to be maintaining higher levels of genetic diversity of landraces rice than lowland Thai farmers. Therefore, the differentiation of genetic diversity and population structure between Bue Chomee and Muey Nawng varieties were under the influence of different farmers' managements through seed exchange among farmers and social organization of the farmers.

In summary, rice in Thailand was under the continuous and the combination of evolutionary processes; farmers' management, seed exchange and gene flow, lead to the changing of genetic variation and population structure of the rice populations. The results of the present study elucidated that (1) genetic diversity and population structure of primary gene pool of *Oryza sativa* were influenced by the gene flow process, gene flow between common wild rice and cultivated rice lead to invasive weedy rice and subsequent continue hybridized with wild and cultivate rice resulting the increasing or decreasing of genetic variation of common wild rice, and weedy rice, (2) farmers' managements as social organization on local seed system

combination with the adaptation capability of landraces influenced genetic diversity and population structure of landraces rice. Therefore, understanding the dynamics of evolutionary forces those play the rules on genetic diversity and population structure of rice populations is an important issue to consider for conservation strategies, germplasm managements, and determination of ecological evolution aspect.

Conservation strategy of rice populations in the present study were considered for *ex situ* and *in situ* conservation implication. Firstly, populations those retained low level of genetic variation within population should be considered for *ex situ* conservation due to it's required less number of individuals with more number of populations. In addition, as common wild rice was separated into perennial and annual types and genetically differentiated thus both types should be sampling separately. Secondly, populations those maintain high level of genetic variation within population should be considered for *in situ* conservation to allow the populations adapt to the continually changing environments and evolve under the dynamics of evolutionary processes. In particular, as landrace rice populations were structured by geographical region, shaped by farmers' managements and well adapted to each local condition. Therefore, the suitable strategy for maintaining diversity as in the area is to reserve each of the populations observed on the farms from which they came and kept as large as possible both by space and time. Furthermore, the further studies are needed to focus on population genetic structure of functional genes involving adaptive phenotypes, which will provide new insights into the evolutionary dynamics of these rice populations.