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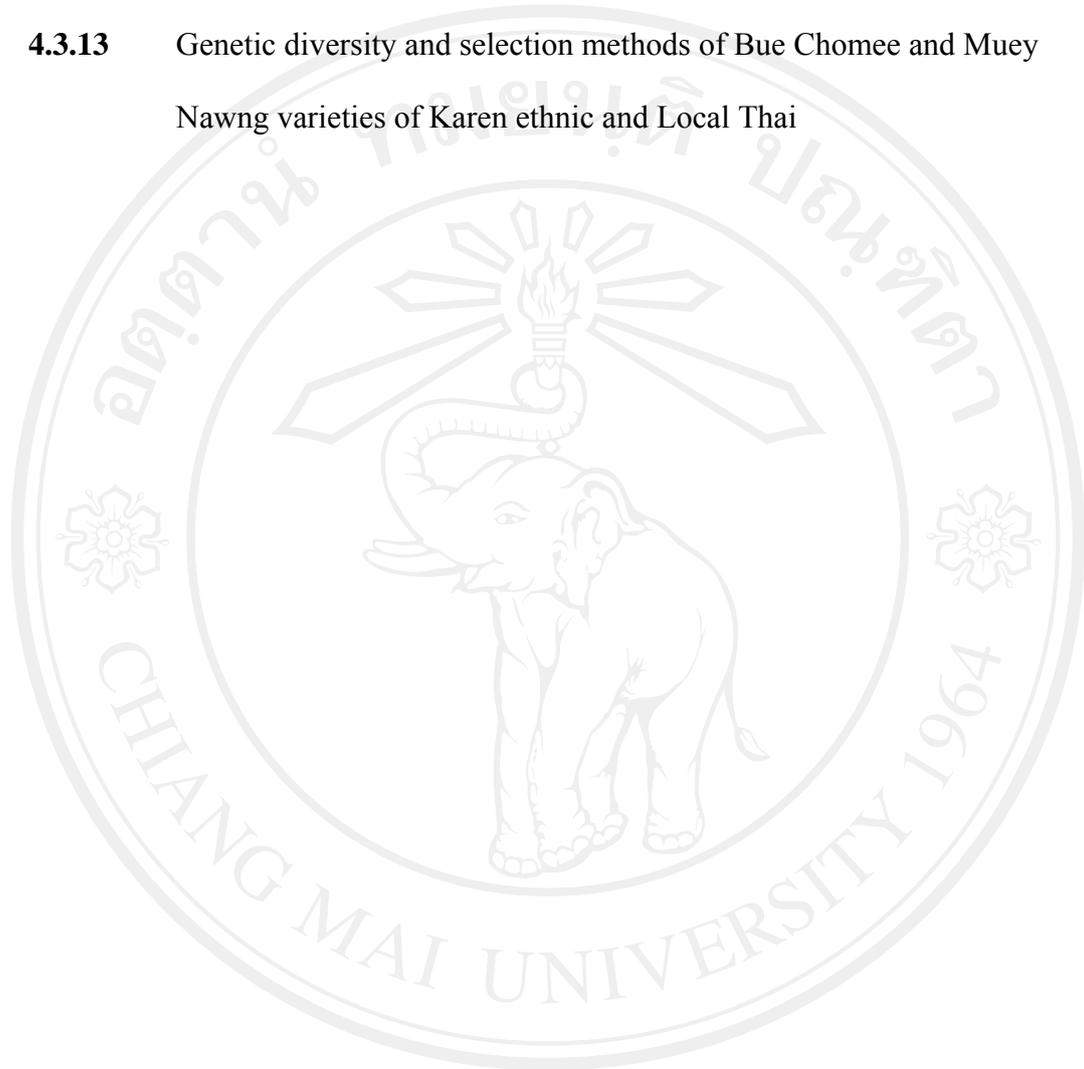
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INTRODUCTION

Rice (*Oryza sativa* L.), the major staple food crop feeds more than half of the world's population. As rice is important for world's food supply many aspects were investigated such as its origin, domestication process, and evolution genetics (Oka, 1988; Khush, 1997; Vaughan, 2008). Rice is placed in the genus *Oryza*, which consisted of two cultivated and twenty wild species. *Oryza sativa*, the Asian cultivated rice is grown worldwide whereas *O. glaberrima*, the African cultivated rice is grown on a limited scale in West Africa. Other 20 wild species are widely distributed in the tropics and subtropics, particularly in Asian countries (Khush, 1997). Thailand lies partly in the center of rice (*Oryza sativa*) diversity (Oka, 1988) and domestication (Londo *et al.*, 2006). Within the center of rice diversity and domestication area, *Oryza sativa* primary gene pool included cultivated rice (*O. sativa* L.), weedy rice (*O. sativa* f. *spontanea*) and wild ancestor (*O. rufipogon* Griff.) are still undergoing evolutionary changes (Chang, 1976).

Common wild rice (*O. rufipogon* Griff.), is widely distributed in the tropics and subtropics of Asia (Vaughan, 1994). As the ancestor of the Asian cultivated rice, *O. rufipogon* has been proven to be a valuable gene pool for rice genetic improvement and plays an important role in rice breeding in the future (Xiao *et al.*, 1998). Cultivated rice including elite varieties and landrace varieties, among those the landrace varieties are placed as the earliest form of cultivar and represent the first step in the domestication process (McCouch, 2004). Therefore, landrace varieties are

also maintain valuable genes passed from wild ancestor through evolutionary process for rice improvement.

Various evolutionary forces played an efficient role in population genetic structure of *O. sativa* gene pool. Knowledge of the genetic structure of populations is essential for understanding the evolutionary process of this gene pool. Dynamics of wild-weed-crop complex of *O. sativa* in the primary center of diversity is the ongoing process where hybridization between wild relative and domesticated that are growing in close proximity is not uncommon event (Ellstrand *et al.*, 1999). Gene flow between wild and domesticated crop is one of the expected evolutionary event that play the major role in the complex variation. Whereas dynamics of landraces rice populations was role by different forces such as selection, domestication, and farmers' managements.

Plant genetic resources are the basis of food security and sustainable agricultural development as they comprise diversity of genetic material contained in traditional varieties (landraces), modern cultivars, wild and weedy relatives of crop plants. Moreover, genetic diversity provides farmers and plant breeders with options to develop, through selection and breeding, new and more productive crops that are resistant to virulent pests and diseases, and adapted to changing environments. To getting better understanding of genetic variation and population structure of these germplasm which are essential for its conservation and sustainable use to meet the demand for future food security, distribution of genetic variation in population structure of each component within the *O. sativa* gene pool will be assessed and key evolutionary factors affected genetic structure will be determined.

Population structure of rice populations in Thailand were revealed based on microsatellite analysis presented in Chapter 2, Chapter 3 and Chapter 4. Chapter 2 illustrated population genetic structure of *Oryza sativa* complex which consisted of 3 components; common wild rice (*O. rufipogon* Griff.), pure line cultivated rice (*O. sativa* L.) and weedy rice (*O. sativa* f *spontanea*) in their ecosystems and determined the evolutionary processes those play an important role of the complex. Chapter 3 displayed population genetic structure of the intermediated stage rice during domestication process from common wild rice to elite cultivated rice, the landraces rice. Finally, Chapter 4 demonstrated what factors influenced population genetic structure of the landraces rice using seed exchange network approach.

The objectives of this study are as follows:

1. To assess genetic diversity and population structure of *Oryza sativa* primary gene pool in Thailand
2. To demonstrate what evolutionary forces play an important rule in dynamics of the complex of *Oryza sativa* primary gene pool in its ecosystem
3. To determine the origin of widespread weedy rice in various areas in Thailand
4. To assess genetic diversity and population structure of Thai landrace rice germplasm
5. To demonstrate how farmers' managements influenced genetic diversity and population structure of landraces rice germplasm