

## TABLE OF CONTENTS

	<b>Page</b>
<b>Acknowledgements</b>	iii
<b>Abstract (English)</b>	v
<b>Abstract (Thai)</b>	xiii
<b>List of Tables</b>	xxv
<b>List of Figures</b>	xxxii
<b>Introduction</b>	1
<b>Chapter 1 Literature review</b>	4
<b>1.1 <i>Oryza</i> genus</b>	4
<b>1.2 <i>Oryza sativa</i> primary gene pool</b>	5
1.2.1 Common wild rice	5
<i>Perennial and Annual</i>	6
1.2.2 Weedy rice	7
<i>Origin of weedy rice</i>	7
<i>Adaptation-crop mimicry</i>	8
1.2.3 Cultivated rice	8
<i>Landraces variety</i>	9
<b>1.3 Rice ecosystem</b>	10
1.3.1 Irrigation	10
1.3.2 Rainfed-lowland	10
1.3.3 Upland	11

1.3.4	Floodprone	11
-------	------------	----

<b>Rice ecosystem in Thailand</b>	11
-----------------------------------	----

1) Upland rice	11
----------------	----

2) Mountain wetland rice	11
--------------------------	----

3) Irrigated rice	11
-------------------	----

4) Lowland rain-fed rice	11
--------------------------	----

5) Deep water and floating rice	12
---------------------------------	----

6) Dry season rice	12
--------------------	----

<b>1.4 Evolution of <i>Oryza sativa</i></b>	12
---	----

1.4.1	Domestication process	12
-------	-----------------------	----

1.4.2	Wild-weed-crop complex	13
-------	------------------------	----

1.4.3	Landraces populations	14
-------	-----------------------	----

1.4.4	Genetic diversity	15
-------	-------------------	----

1.4.4.1	Common wild rice	15
---------	------------------	----

1.4.4.2	Cultivated rice	16
---------	-----------------	----

<b>1.5 Evolutionary forces on crop population structure</b>	17
---	----

1.5.1	Plant population genetic structure	18
-------	------------------------------------	----

1.5.2	Spatial variation	18
-------	-------------------	----

<i>Isolation by distance</i>	19
------------------------------	----

1.5.3	Temporal variation	19
-------	--------------------	----

1.5.4	Selection	20
-------	-----------	----

1.5.5	Gene flow/Migration/seed flow	21
-------	-------------------------------	----

1.5.6	Genetic bottleneck	22
-------	--------------------	----

<b>1.6 Farmers' managements of socials' role</b>	23
<i>Seed system/Seed exchange/Seed flow</i>	24
<b>Chapter 2 Genetic diversity and population structure of <i>Oryza sativa</i></b>	
<b>primary gene pool in Thailand</b>	25
<b>2.1 Introduction</b>	25
<b>2.2 Material and Methods</b>	28
2.2.1 Genetic materials	28
2.2.2 DNA analysis	35
<u><i>Microsatellite markers analysis</i></u>	35
2.2.3 Data analysis	37
<u><i>Genetic diversity analysis</i></u>	37
<u><i>Genetic structure analysis</i></u>	37
<u><i>Population structure analysis</i></u>	37
<u><i>Genetic diversity and population structure of wild, cultivated, and weedy rice in Thailand</i></u>	39
<u><i>Tracing of widespread invasive weedy rice in various areas in Thailand</i></u>	40
<b>2.3 Results</b>	42
<u><i>Population genetic structure of common wild rice (<i>Oryza rufipogon</i> Griff.)</i></u>	42
<u><i>Allele diversity</i></u>	42
<u><i>Genetic diversity</i></u>	47
<u><i>Genetic structure</i></u>	47

<i>Analysis of Molecular Variance (AMOVA)</i>	47
<u><i>Population structure</i></u>	54
<i>Population genetic structure of cultivated rice (Oryza sativa L.)</i>	60
<u><i>Allele diversity</i></u>	60
<u><i>Genetic diversity</i></u>	62
<u><i>Population structure</i></u>	63
<i>Population genetic structure of weedy rice (Oryza sativa f</i>	
<i>spontanea)</i>	69
<u><i>Allele diversity</i></u>	69
<u><i>Genetic diversity</i></u>	71
<u><i>Genetic structure</i></u>	72
<i>Analysis of Molecular Variance (AMOVA)</i>	72
<u><i>Population structure</i></u>	75
<i>Genetic structure and relationship among wild, cultivated and</i>	
<i>weedy rice</i>	79
<u><i>Genetic diversity</i></u>	79
<u><i>Population structure</i></u>	83
<i>Evidence of widespread invasive weedy rice in various areas in</i>	90
<i>Thailand</i>	
2.4 Discussion	95
<b>Chapter 3 Genetic diversity and population structure of a landrace of</b>	
<b>Thai rice (<i>Oryza sativa</i>)</b>	106
<b>3.1 Introduction</b>	106

<b>3.2 Materials and Methods</b>	110
3.2.1 Sample collections	110
3.2.2 Microsatellite analysis	113
3.2.3 Data analysis	113
<b>3.3 Results</b>	115
3.3.1 Genetic diversity within farmer's fields	115
3.3.2 Genetic diversity within and among villages	120
3.3.3 Population genetic structure	120
3.3.4 Cluster analysis and Isolation by distance	124
<b>3.4 Discussion</b>	128
<b>Chapter 4 Dynamics of genetic diversity of landraces rice under farmers' managements based on seed exchange network approach in Northern Thailand</b>	134
<b>4.1 Introduction</b>	134
<b>4.2 Materials and Methods</b>	137
4.2.1 Rice varieties	137
4.2.2 Construction of seed exchange network	140
Bue Chomee seed exchange networks	144
Muey Nawng seed exchange networks	145
4.2.3 Pattern of seed exchange network analysis	146
4.2.4 Genetic diversity analysis	147
DNA extraction and microsatellite analysis	147

Data analysis	147
<b>4.3 Results</b>	150
4.3.1 Pattern of seed exchange network	150
4.3.1.1 Pattern of seed received	150
4.3.1.2 Pattern of seed provided	152
4.3.1.3 Pattern of seed exchange based on ethnic groups	154
4.3.1.4 Rule of seed received from older farmers	156
4.3.2 Genetic diversity and population structure	160
4.3.2.1 Allele diversity	160
4.3.2.2 Genetic diversity	164
4.3.2.3 Population genetic structure	167
4.3.3 Factors influenced genetic diversity	174
4.3.3.1 Farmers' age	174
4.3.3.2 Number of year grown	177
4.3.3.3 Ethnic group	180
4.3.3.4 Selection methods	180
<b>4.4 Discussion</b>	183
<b>Chapter 5 General Discussion</b>	188
<b>References</b>	193
<b>Appendix</b>	212
<b>Curriculum vitae</b>	246

## LIST OF TABLES

<b>Table</b>	<b>Page</b>
<b>2.2.1</b> Common wild rice accession, location and habitat in this study	29
<b>2.2.2</b> Location and description of weedy rice populations	31
<b>2.2.3</b> Name, type, pedigree description and year released of cultivated rice in the present study	33
<b>2.2.4</b> Typical characteristic description of common wild rice for life-history trait type classification according to Wongtamee (2008)	34
<b>2.2.5</b> Microsatellite markers in the present study	36
<b>2.2.6</b> Popular cultivated rice varieties, weedy rice and common wild rice populations in each rice growing region	41
<b>2.3.1</b> Distribution of 42 common wild rice populations from 4 regions determined by life-history traits, habitat type, and water conditions	44
<b>2.3.2</b> Allele diversity of 42 common wild rice populations collected from Upper north (UP), Lower-north (LN), Central (CT) and Northeast (NE) using 12 SSR markers	45
<b>2.3.3</b> Allele diversity of common wild rice for 2 life-history trait types	46
<b>2.3.4</b> Genetic parameters of 42 common wild rice populations collected from Upper north (UN), Lower-north (LN), Central (CT) and Northeast (NE) based on 12 SSR markers	50

<b>2.3.5</b>	Summary of genetic parameters of 42 common wild rice populations based on geographical regions using 12 SSR loci	51
<b>2.3.6</b>	Summary of genetic parameters of 42 common wild rice populations based on life history traits using 12 SSR loci	51
<b>2.3.7</b>	Analysis of molecular variance (AMOVA) among populations and regions for 420 individual of 42 common wild rice populations on 12 SSR loci	52
<b>2.3.8</b>	Analysis of molecular variance (AMOVA) among populations and life-history types for 420 individual of 42 common wild rice populations on 12 SSR loci	52
<b>2.3.9</b>	Pairwise genetic differentiation ( $F_{ST}$ ) within and between common wild rice collected from 4 regions and 2 different life-history traits	52
<b>2.3.10</b>	Pairwise genetic differentiation ( $F_{ST}$ ) between common wild rice collected from Upper north (UP), Lower north (LN), Central (CT) and Northeast (NE, P-perennial, A- annual)	53
<b>2.3.11</b>	Proportion of estimated assigned populations ( $Q$ ) of 42 common wild rice populations ( $K=2$ )	57
<b>2.3.12</b>	Allelic richness of 37 Thai cultivated rice varieties	61
<b>2.3.13</b>	Genetic parameters of 37 Thai cultivated rice varieties based on 12 SSR markers	63
<b>2.3.14</b>	Analysis of molecular variance (AMOVA) among varieties, between and within rice groups for 370 individuals of 37 cultivated varieties on 12 SSR loci	63



<b>2.3.15</b>	Proportion of estimate assigned populations ( $Q$ ) of 37 cultivated rice populations ( $K=3$ )	66
<b>2.3.16</b>	Allele diversity of 12 weedy rice populations collected from Lower-north (LN), Central (CT) and Northeast (NE) using 12 SSR markers	70
<b>2.3.17</b>	Genetic parameters of 12 weedy rice populations collected from Lower-north (LN), Central (CT) and Northeast (NE) based on 12 SSR markers	73
<b>2.3.18</b>	Summary of genetic parameters of weedy rice collected from 3 geographical regions based on 12 SSR loci	73
<b>2.3.19</b>	Analysis of molecular variance (AMOVA) among populations and 3 regions for 120 individuals of 12 weedy rice populations on 12 SSR loci	74
<b>2.3.20</b>	Pairwise of genetic differentiation ( $F_{ST}$ ) within and between 3 regions of weedy rice	74
<b>2.3.21</b>	Proportion of estimated assign populations ( $Q$ ) of 12 weedy rice populations ( $K=2$ )	76
<b>2.3.22</b>	Summary of allele diversity of 42 common wild rice populations , 37 cultivated varieties and 12 weedy rice populations using 12 SSR markers	81
<b>2.3.23</b>	Summary of genetic parameters of common wild rice, weedy rice, and cultivated rice based on 12 SSR markers	81
<b>2.3.24</b>	Analysis of molecular variance (AMOVA) for among and within 3 rice groups; common wild rice, cultivated rice and weedy rice on 12 SSR loci	82

<b>2.3.25</b>	Average pairwise genetic differentiation ( $F_{ST}$ ) within and between 3 rice groups	82
<b>2.3.26</b>	Inferences of cultivated, weedy and common wild rice populations to each inferred population ( $K=5$ )	87
<b>2.3.27</b>	Inferences the admixed ancestors of weedy rice populations to cultivated gene pools ( $K=3$ ) and common wild rice gene pools ( $K=2$ )	94
<b>3.2.1</b>	Locations and sample sizes for 13 populations, representing 13 villages of <i>Bue Chomee</i> local rice variety in Chiang Mai (CM) and Mae Hong Son (MHS) province northern Thailand	111
<b>3.3.1</b>	Number of alleles per locus and per population	117
<b>3.3.2</b>	Estimates genetic diversity per locus and per field using an unbiased estimator (Nei's 1973)	118
<b>3.3.3</b>	Genetic parameters of <i>Bue Chomee</i> landrace from 33 fields and 4 elite rice varieties (*)	119
<b>3.3.4</b>	Population structure and genetic diversity of <i>Bue Chomee</i> among 13 villages	122
<b>3.3.5</b>	Analysis of molecular variance (AMOVA) for 525 individual plants from 33 fields in 13 villages	123
<b>3.3.6</b>	Pairwise genetic differentiation ( $F_{ST}$ ) among 13 villages	123
<b>4.2.1</b>	Location, farmers' accession, sample sizes and general information of farmers in Bue Chomee seed exchange network	142
<b>4.2.2</b>	Location, farmers' accession, sample sizes and general information of farmers in Muey Nawng seed exchange network	143

<b>4.2.3</b>	Microsatellite markers in seed exchange network study	149
<b>4.2.4</b>	Polymerase chain reaction condition in seed exchange network study	149
<b>4.3.1</b>	Patterns of seed received of Bue Chomee and Muey Nawng rice varieties	151
<b>4.3.2</b>	Relationship between rice varieties and seed provided patterns by relatives	153
<b>4.3.6</b>	Relationship between ethnic group and seed exchange patterns for Muey Nawng	155
<b>4.3.7</b>	Relationship between rice varieties and pattern of seed received from older farmers	159
<b>4.3.8</b>	Number of allele (A) of Bue Chomee seed exchange networks	162
<b>4.3.9</b>	Number of allele (A) of Muey Nawng seed exchange networks	163
<b>4.3.10</b>	Genetic diversity per locus per seed lot of Bue Chomee seed exchange networks	165
<b>4.3.11</b>	Genetic diversity per locus per seed lot of Muey Nawng seed exchange networks	166
<b>4.3.12</b>	Genetic parameters of 4 seed exchange networks of Bue Chomee variety collected from 3 villages based on 6 microsatellite loci	168
<b>4.3.13</b>	Genetic differentiation ( $F_{ST}$ ) between and among four Bue Chomee seed exchange networks	170
<b>4.3.14</b>	Genetic parameters of 2 seed exchange networks of Muey Nawng variety from 2 villages based on 6 microsatellite loci	172

<b>4.3.15</b>	Distribution of genetic diversity related to farmers' age of Bue Chomee rice variety	175
<b>4.3.16</b>	Distribution of genetic diversity related to farmers' age of Muey Nawng rice variety	176
<b>4.3.17</b>	Distribution of genetic diversity and no. of year farmers grown Bue Chomee variety	178
<b>4.3.18</b>	Distribution of genetic diversity and no. of year farmers grown Muey Nawng variety	179
<b>4.3.19</b>	Distribution of genetic diversity (h) of farmers' seed lots relate to ethnic groups and selection methods of Bue Chomee	181
<b>4.3.20</b>	Distribution genetic diversity (h) of farmers' seed lots related to ethnic groups and selection methods of Muey Nawng	181

## LIST OF FIGURES

<b>Figure</b>	<b>Page</b>
<b>2.3.1</b> Location of common wild rice sampling in Thailand of the present study	30
<b>2.3.2</b> Location of weedy rice sampling in Thailand of the present study	32
<b>2.3.3</b> Distribution of observed heterozygosity ( $H_o$ ) of annual and perennial type of common wild rice	51
<b>2.3.4</b> Population assignment of 42 common wild rice populations in natural habitat collected from 4 regions of Thailand reveal $K=2$ . Each bar represent each common wild rice population consisted of 10 individuals. Different colors represent different inferred populations; Red-Annual type; Green-Perennial type	56
<b>2.3.5</b> Distribution of 420 individuals of 42 wild rice populations. Different color represent 2 clusters referred to the assignment obtained from STRUCTURE; Red - Annual type and Green – Perennial type, formed by the principle coordinate analysis (PCA) on the basis of 12 microsatellite markers	58
<b>2.3.6</b> Cluster analysis using NJ method based on C.S. Chord (1967) genetic distance among 42 common wild rice populations in Thailand	59

- 2.3.7** Population assignment of 37 cultivated rice varieties reveal  $K=3$ . Each bar represent each population consisted of 10 individuals. Different colors represent different inferred populations, referred to different  $K$  65
- 2.3.8** Distribution of 37 cultivated Thai rice varieties. Different colors represent 3 clusters referred to the assignment obtained from STRUCTURE; Blue - Cr1 gene pool (modern varieties), Green - Cr2 gene pool (improved traditional varieties), Red - Cr3 gene pool (improved traditional varieties and modern varieties) formed by the principal coordinate analysis (PCA) on the basis of 12 microsatellite markers 67
- 2.3.9** Cluster analysis using NJ method based on C.S. Chord (1967) genetic distance among 37 cultivated rice varieties derived from 12 SSR loci 68
- 2.3.10** Population assignment of 12 weedy rice varieties reveal  $K=2$ . Each bar represent each population consisted of 10 individuals. Different colors represent different inferred populations, referred to different  $K$  76
- 2.3.11** Distribution of 120 individuals of 12 weedy rice populations. Different color represent 2 clusters referred to the assignment obtained from STRUCTURE: Red-weedy rice collected from modern variety (MV) cultivation fields and Green-weedy rice populations collected from improved traditional variety (ITV) cultivation fields, formed by the principle coordinate analysis (PCA) on the basis of 12 microsatellite markers 77

- 2.3.12** Cluster analysis using NJ method based on C.S. Chord (1967) genetic distance among 42 common wild rice populations in Thailand 78
- 2.3.13** Population assignment of cultivated, weed, and wild populations illustrated that weedy rice genotypes were the mixture of cultivated rice (K=3; Pink, Green and Blue) and common wild rice (K=2; Red and Yellow). Each bar represent each population consisted of 10 individuals. Different colors represent different inferred populations 86
- 2.3.14** Distribution of *Oryza sativa* complex including, 42 common wild rice populations, 12 weedy rice populations and 11 cultivated varieties, different color represent different groups: Blue – common wild rice perennial type; Red – common wild rice annual type; Orange – weedy rice; Green-cultivated rice, formed by the principle coordinate analysis on the basis of 12 microsatellite markers 88
- 2.3.15** Cluster analysis using NJ method based on C.S. Chord (1967) genetic distance among 37 cultivated rice varieties (Green), 12 weedy rice populations (Orange) and 42 common wild rice populations (Blue and Red) in Thailand constructed based on 12 microsatellite loci 89
- 2.3.16** Distribution of 10 cultivated rice varieties and 120 individuals of 12 weedy rice populations, different color represent different rice group: Green-popular cultivated rice, Blue - Lower north, Orange - Central and Purple- North-east formed by the principle coordinate analysis on the basis of 12 microsatellite markers 92

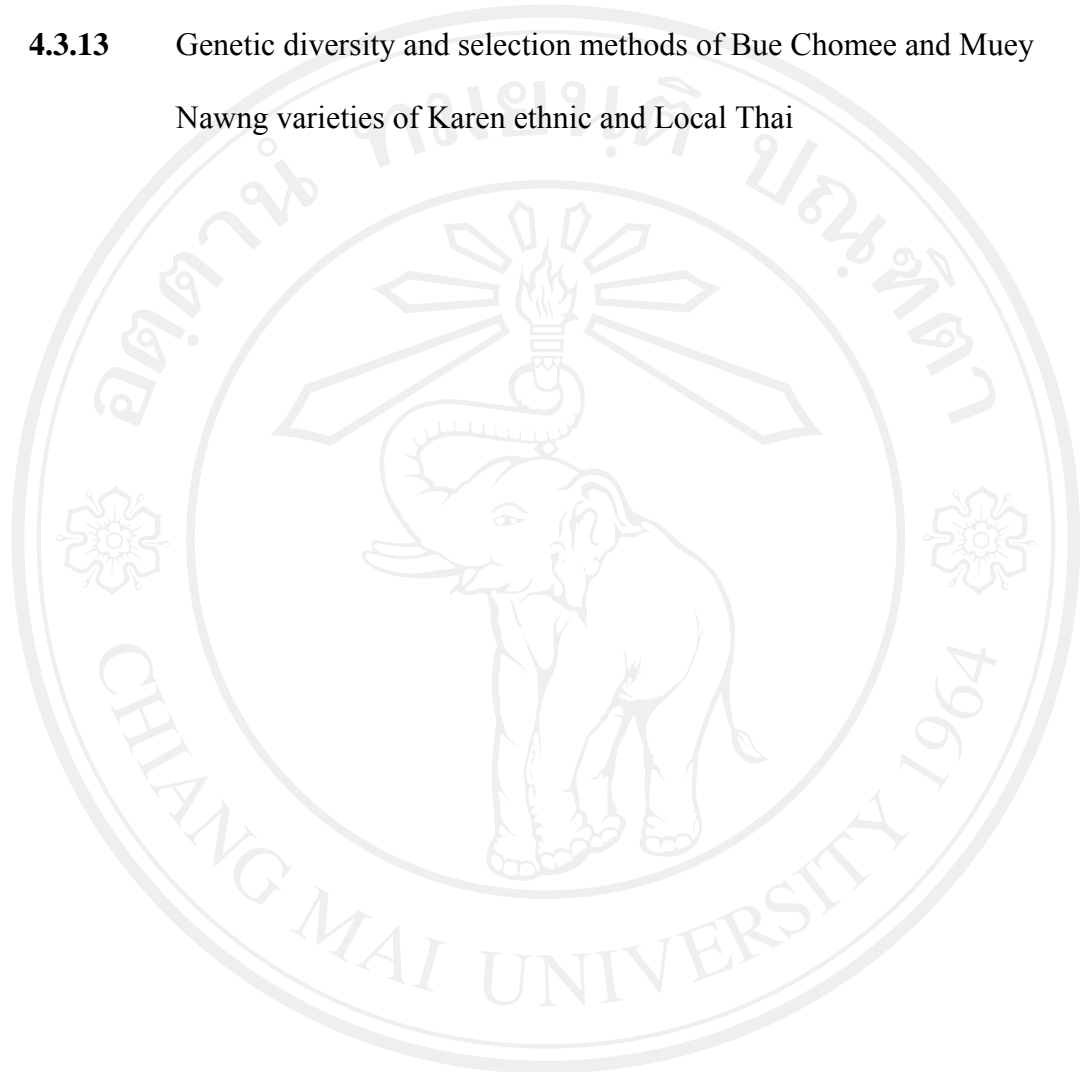
<b>2.3.17</b>	Population assignment of cultivated, weed, and wild populations illustrated that weedy rice genotypes were the mixture of cultivated rice (K=3; Yellow, Pink and Blue) and common wild rice (K=2; Red and Green). Each bar represent each population consisted of 10 individuals. Different colors represent different inferred populations	93
<b>3.2.1</b>	Sampling locations of 33 subpopulations of <i>Bue Chomee</i> local rice ( <i>Oryza sativa</i> L.) variety from 13 villages, 8 districts in Chiang Mai (CM) and Mae Hong Son (MHS) province, northern Thailand	112
<b>3.3.2</b>	Dendrogram based on C.S. Chord (1967) genetic distance clustering by UPGMA methods showing genetic relationship among 33 seed lots of <i>Bue Chomee</i> from 13 villages and 4 elite rice varieties (KDML105, RD6, CNT1 and SPR1)	125
<b>3.3.3</b>	Dendrogram constructed based on C.S. chords (1967) genetic distance showed genetic relation among 13 Bue Chomee populations from 13 villages in 8 districts indicated by different color in 2 mountainous provinces Northern Thailand and elite rice varieties	126
<b>3.3.4</b>	A Mantel's test for correlation between C.S. chords (1967) genetic distance and geographic distance (km) showed high correlation, $r=0.599$ $p<0.0058$ from 100000 randomizations	127
<b>4.2.1</b>	Location of Bue Chomee seed exchange network collection in 3 villages in Mae Wang, Chiang Mai	138



- 4.2.2** Location of Muey Nawng seed exchange network collection in 2 villages in Mae Cham, Chiang Mai 139
- 4.2.3** Bue Chomee seed exchange networks diagram from (a) Huai-ecang village with BC1, (b) Huai-khao-leep village with BC2, and (c) Huai-yen village with BC3 and BC4 networks. The direction of the arrow indicated the direction of seeds provided from source to sink while those without arrow were classed as seed lots outside the network within each village 144
- 4.2.4** Muey Nawng seed exchange networks diagram from (a) Sam-sob village with MN1 and (b) Mae-ming village with MN2 networks. The direction of the arrow indicated the direction of seeds provided from source to sink while those without arrow were classed as seed lots outside the network within each village 145
- 4.3.1** Seed received pattern of (a) Bue Chomee from 3 villages in Chiang Mai and (b) Muey Nawng from 2 villages in Chiang Mai 151
- 4.3.2** Seed provided pattern of (a) Bue Chomee from 3 villages in Chiang Mai and (b) Muey Nawng from 2 villages in Chiang Mai 153
- 4.3.3** Seed exchange pattern of (a) Karen ethnic group of Bue Chomee, (b) Muey Nawng and (c) Local Thai of Muey Nawng 155
- 4.3.4** Diagram of Bue Chomee seed exchange network represent the age of each farmer within the network in the parenthesis of network BC1, BC2, BC3 and BC4. The center or source of the network was represented by the *italic* characters with (\*). Number in the parentheses is the age of each farmer 157

- 4.3.5** Diagram of Muey Nawng seed exchange network represent the age of each farmer in the parenthesis of network MN1 and MN2. The center or source of the network was represented by the *italic* characters with (\*). Number in the parentheses is the age of each farmer 158
- 4.3.6** Pattern seed received from older or younger farmers of; (a) Bue Chomee and Muey Nawng local rice varieties and (b) Karen of Bue Chomee (BC), Karen of Muey Nawng (MN) and Local Thai of Muey Nawng (MN) 159
- 4.3.7** Diagram of Bue Chomee seed exchange network represent genetic diversity (h) of each farmer of network BC1, BC2, BC3 and BC4. Number in the parentheses is genetic diversity of each farmer. Farmers BC30 passed away 171
- 4.3.8** Diagram of Muey Nawng seed exchange network represent genetic diversity (h) of each farmer of network MN1 and MN2. Number in the parentheses is genetic diversity of each farmer. Farmer MN27 passed away 173
- 4.3.9** Relationship between genetic diversity and farmer's age of Bue Chomee with  $r=0.07$  175
- 4.3.10** Relationship between genetic diversity and farmer's age of Muey Nawng with  $r=0.145$  176
- 4.3.11** Relationship between genetic diversity and number of year grown Bue Chomee rice variety ( $r= -0.042$ ) 178

<b>4.3.12</b>	Relationship between genetic diversity and number of year grown Muey Nawng rice variety ( $r=-0.498^*$ )	179
<b>4.3.13</b>	Genetic diversity and selection methods of Bue Chomee and Muey Nawng varieties of Karen ethnic and Local Thai	182



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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