

CHAPTER 4

Dynamics of Genetic Diversity of Landraces Rice under Farmers' Managements based on Seed Exchange Network Approach in Northern Thailand

4.1 Introduction

As shown in Chapter 3, landrace rice maintained genetic variation within variety and was structured by geographic distribution, which was assumed to be the consequence of farmers' management. In addition to the farmers' management, several factors have been reported to influence genetic variation of landraces crop including natural selection, gene flow, migration or mutation. The present chapter will explore how farmers' management influences genetic diversity of landraces rice by focusing on the way farmers exchange their rice seed. The following questions are examined "How landraces maintain genetic variation within and between populations?" and "What factors play an influence on landraces genetic diversity?".

How landraces maintain genetic variation? Landraces tend to be well adapted to fluctuations in the environment due to its broad genetic base (McCouch, 2004). Different landraces differ in adaptation to soil type, time of seedling, date of maturity, height, nutritive value, use and other properties (Harlan, 1975). In addition, genetically diverse populations may also be resistant or tolerant to high levels of attack by pathogen disease and insect pest (Alvarez *et al.*, 2005). Therefore, many landraces species are required in traditional agricultural ecosystems throughout the

world. For example, Ceccarelli (1994) described several studies with barley that support the opinion that landrace varieties are superior in performance to modern varieties under low-yield conditions. In addition, under traditional agricultural systems, hundreds of fonio millet (*Digitaria* spp.) landraces were maintained and selected in local agriculture of West Africa (Adoukonou-Sagbadja *et al.*, 2007).

Population structure and genetic variation of crop landraces is shown to be influenced by various factors including selection, drift, migration, or mutation including farmers' management. In addition, most landraces of staple food crops have been maintained in traditional agricultural system (Javis *et al.*, 2008). Several studies illustrated that farmers' management plays a role in genetic variation of landraces including techniques such as selection for the next crop and farmers-to-farmers seed exchange systems (Alvarez *et al.*, 2005). Management of the seed system is a key process related to maintaining both local varieties and local crops' genetic diversity, in addition with the association of social role. Perales *et al.*, (2003) illustrated that different ethnolinguistic groups play different functions in shaping maize diversity in Central Mexico. Seed exchange systems found in local cropping systems for many crop species have been found to be embedded in with local culture and social systems (Sirabanchongkran *et al.*, 2004).

For this study, farmer to farmer seed exchange systems were examined and a network of exchange patterns among farmers was mapped for comparison to genetic data. A network approach is used to analyze genetic changes as the seed is exchanged from one farmer to the next and managed by farmers. This approach focuses on relationships that form the pathways through which diversity is maintained, shaped, or lost. Social relationships among farmers that may influence the seed flow include

marriage, immigration, work groups, friendships, etc. Therefore, the study will help understand factors that affect landraces crop populations in traditional agricultural systems, which needed for the success of conservation of genetic resource for the agriculture (Parales *et al.*, 2003).

Therefore, the present study aimed to:

- i) Map the patterns of seed exchange networks
- ii) Illustrate factors that influenced pattern of seed exchange networks in local villages of Northern Thailand
- iii) Evaluate genetic differentiation of rice germplasm within and between seed exchange networks
- iv) Demonstrate the influence of seed exchange and farmers' managements on genetic diversity of rice landraces
- v) Demonstrate factors that influence genetic diversity of the seed exchange network in local villages of Northern Thailand

4.2 Materials and Methods

4.2.1 Rice varieties

Bue Chomee

Bue Chomee (BC) is a popular traditional non-glutinous rice variety used by the Karen ethnic group who occupy the mid altitudes and adapted to upland paddy cultivation within medium to low altitudinal, 400-700 m. Bue Chomee is a variety grown by the Karen for many generations. The experiments were conducted in three Karen villages; Huai-e-cang, Huai-khao-leep and Huai-yen in Mae Wang district, Chiang Mai province (Figure 4.2.1).

Muey Nawng

Local Muey Nawng (MN) is a traditional glutinous rice variety consumed by lowland Thai who occupy the low altitude (<400 m). Muey Nawng is the most popular local rice variety in the area where rice gall midge damages rice production, especially in the Northern region. Recently, Muey Nawng was more widely cultivated by other ethnic groups, such as Karen, due to the widening infestation of rice gall midge at higher elevations, above 400 m., where Karen villages are predominant. The experiments were conducted in 2 villages; Sam-sob and Mae-ming in Mae Cham district, Chiang Mai province (Figure 4.2.2). Population of Sam-sob village is lowland Thai whereas population of Mae-Ming is Karen ethnic group.

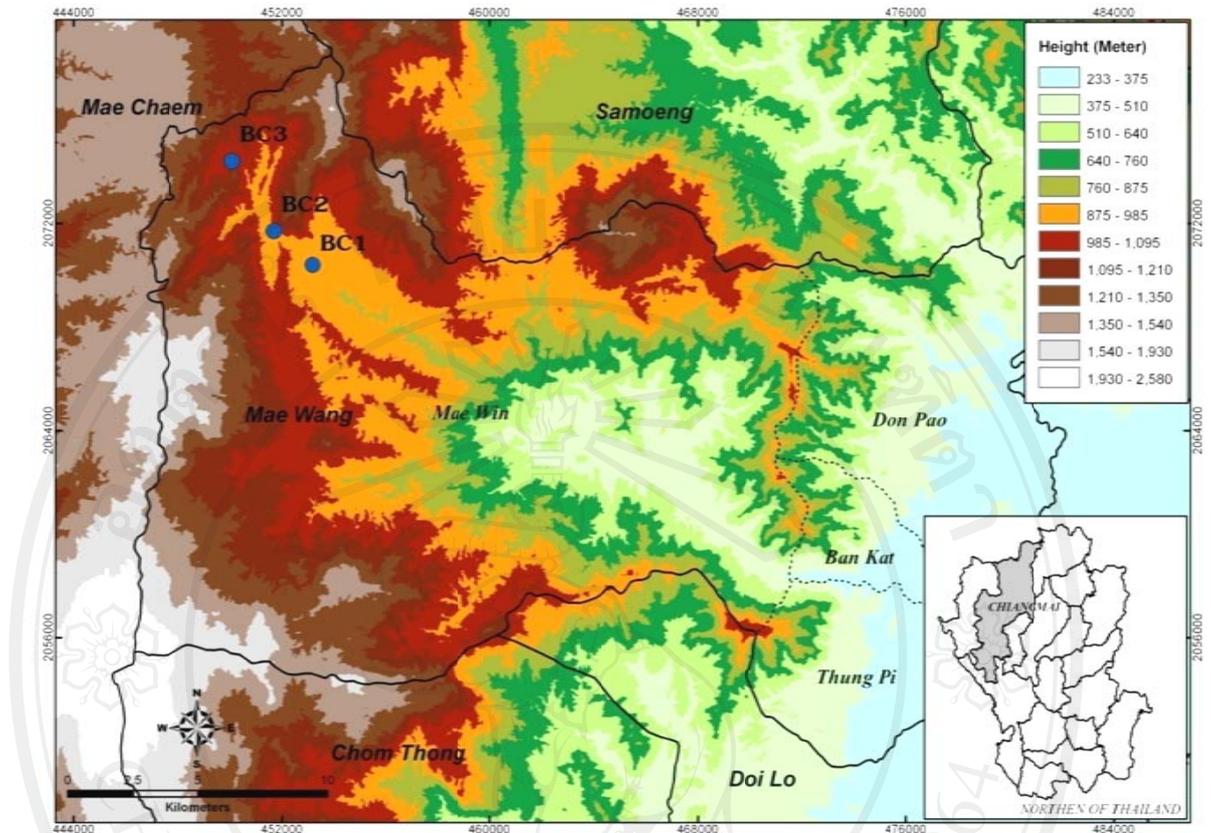


Figure 4.2.1 Location of Bue Chomee seed exchange network collection in 3 villages in Mae Wang, Chiang Mai

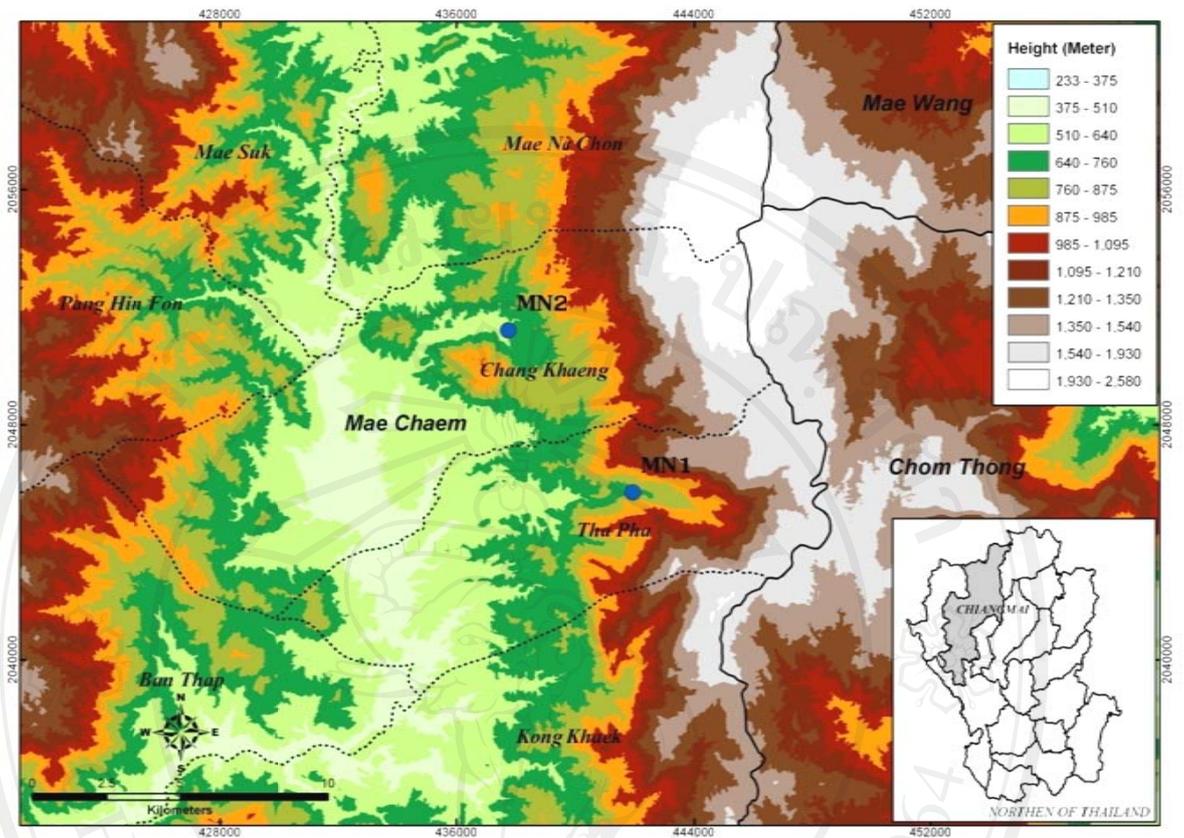


Figure 4.2.2 Location of Muey Nawng seed exchange network collection in 2 villages in Mae Cham, Chiang Mai

4.2.2 Construction of seed exchange network

Networks of seed exchange were constructed by interviewing with farmers in 2005 based on seed providing and seed receiving (the exchange data was collected in one year) information. Seed exchange in this study was defined as farmers' seed which were provided or received from one farmer to the next. The key questions for constructing the network are based on the following questions:

1. Who did you provided (sink) seeds to?
2. Who did you obtained (source) seeds from?

For each farmer, personal information such as age, gender and ethnic group were recorded. Seeds of each interviewed farmer were collected from his/her barn and represented as each seed lot. Each seed lot was designated by the variety name (BC and MN) following with the number identifies the network number for the first digit and the second digit was the farmer number who provided the seed, from his/her storage (see below for explanation). The direction of the arrows represented seed was provided from source to sink (Figure 4.2.3 and Figure 4.2.4).

Bue Chomee

Four seed exchange networks of Bue Chomee variety were constructed from three villages (Figure 4.2.3). The details of each network are as followed.

Network BC1 was constructed base on information from Huai-e-cang village consisted of 4 nodes represented 4 farmers (Figure 4.2.3 (a)). Farmer BC11 is the center of the network and acted as the seed source of the network. This center of the network, BC11, provided seeds to 3 farmers, BC12, BC13 and BC14.

Network BC2 was constructed base on information from Huai-khao-leep village consisted of 5 farmers (Figure 4.2.3 (b)) and showed similar pattern as

network BC1. Farmer BC21 is the center of the network and act as the seeds source of the network. The center of the network, BC21 provided seeds to 4 farmers, BC22, BC23, BC24 and BC25.

Network BC3 and network BC4 were constructed based on information from Huai-yen village (Figure 4.2.3 (c)). Network BC3 consisted of 5 farmers while farmer BC30 was pass away. BC32 act as the center of the network as he/she received seeds from BC31 and provided to 2 famers, BC33 and BC30.

Network BC4 consisted of 5 farmers (Figure 4.2.3 (c)). Farmer BC41 and BC44 were the key farmers of this network. Farmer BC41 provided seeds to 2 farmers, BC42 and BC44 while BC44 received seeds from 2 sources, BC41 and BC45, and then provided to BC43.

Muey Nawng

Two networks of Muey Nawng rice variety were constructed using the data collected in 2 villages (Figure 4.2.4). The details of each network are as followed.

Network MN1 was constructed base on information from Sam-sob village consisted of 10 farmers (Figure 4.2.4 (a)). Farmer MN11 is the center of the network and act as seeds source of the network by provided his/her seeds to 4 farmers; MN12, MN13, MN14 and MN17 represent 4 seed providing lines.

Network MN2 was constructed base on information from Mae-ming village consisted of 8 farmers (Figure 4.2.4 (b)). Farmer MN24 is the center of the network received seeds from 2 sources (MN20 and MN25) and provided to 2 sinks (MN21 and MN22).

Table 4.2.1 Location, farmer's accession, sample size and general information of farmers in Bue Chomee (BC) seed exchange network

Location	Farmer's accession	n	Age	Gender [†]	Ethnic group ^{††}	No. of year grown the variety [§]	Selection methods
Huai-e-cang village Mae wang district Chiang Mai province	Network BC1						
	BC11	20	60	F	K	>20	Selection of panicle before harvest
	BC12	20	26	F	K	5-10	Selection of panicle before harvest
	BC13	20	21	F	K	>10	Selection of seed and panicle before harvest
	BC14	20	23	M	K	>20	Selection of seed and panicle before harvest
	BC19*	20	34	M	K	>20	Selection of seeds before harvest
Huai-khao-leep village Mae wang district Chiang Mai province	Network BC2						
	BC21	20	59	M	K	>20	Selection of panicles before harvest
	BC22	20	39	M	K	2-5	Selection of seed and panicle after harvest
	BC23	20	50	M	K	>10	Selection of panicles before harvest
	BC24	20	25	M	K	2-5	Selection of panicles before harvest
	BC25	20	29	M	K	>10	Selection of seeds before harvest
	BC29*	20	30	M	K	>20	Selection of panicles before harvest
Huai-yen village Mae wang district Chiang Mai province	Network BC3						
	BC31	20	42	M	K	>20	Selection of panicles before harvest
	BC32	20	50	M	K	>20	Selection of seed after harvest
	BC33	20	40	M	K	>20	Selection of panicles and seed after harvest
	BC34	20	64	M	K	>20	Selection of panicles before harvest
	BC30	-	-	M	K	-	Selection of seeds before harvest
	Network BC4						
	BC41	20	65	M	K	>20	Selection of seeds before harvest
	BC42	20	46	M	K	>20	Selection of seeds before harvest
	BC43	20	35	M	K	>10	Selection of panicles before harvest
	BC44	13	60	M	K	>20	Selection of panicles before harvest
	BC45	20	56	M	K	>20	Selection of panicles before harvest
	BC349*	20	78	M	K	>20	Selection of seeds before harvest

* Farmers who are not included in the network set as out network

† F=Female, M=Male

†† LT=Lowland Thai, K=Karen

§ no. of year farmers grow the varieties

Table 4.2.2 Location, farmer's accession, sample size and general information of farmers in Muey Nawng (MN) seed exchange network

Location	Farmer's accession	n	Age	Gender [†]	Ethnic group ^{††}	No. of year grown the variety [§]	Selection methods
Sam-sob village Mea Cham district Chiang Mai province	Network MN1						
	MN11	20	66	F	LT	>20	Selection of panicle before harvest
	MN12	20	34	F	LT	10-20	Selection of seed and panicle before harvest
	MN13	20	45	M	LT	>20	Selection of seed and panicle after harvest
	MN14	20	49	M	LT	>20	Selection of seed and panicle after harvest
	MN15	20	68	F	LT	>20	No selection
	MN16	20	32	M	LT	>20	Selection of seed and panicle before harvest
	MN17	20	48	F	LT	>20	Selection of seed and panicle before harvest
	MN18	20	44	M	LT	>20	Selection of seed and panicle before harvest
	MN19	20	47	F	LT	>20	Selection of seed and panicle before harvest
	MN110	20	46	F	LT	>20	No selection
	MN119*	20	60	M	LT	>20	Selection of seed and panicle after harvest
Mae-ming village Mae Cham district Chiang Mai province	Network MN2						
	MN21	20	52	M	K	>10	Selection of seed and panicle before harvest
	MN22	20	70	M	K	5-10	Selection of seed and panicle after harvest
	MN23	20	39	M	K	>5	Selection of seed and panicle before harvest
	MN24	20	72	M	K	>20	Selection of seed and panicle before harvest
	MN25	20	75	M	K	>20	Selection of seed and panicle before harvest
	MN26	20	46	M	K	5-10	Selection of panicle before harvest
	MN27	20	-	M	K	-	-
	MN28	20	75	F	K	>20	Selection of panicle before harvest
	MN29	20	48	M	K	>20	Selection of seed and panicle before harvest
	MN229*	20	34	M	K	>20	Selection of seed and panicle before harvest

* Farmers who are not member of the network set as out network

[†] F=Female, M=Male

^{††} LT=Lowland Thai, K=Karen

[§] no. of year farmers grow the varieties (year)

Bue Chomee seed exchange networks

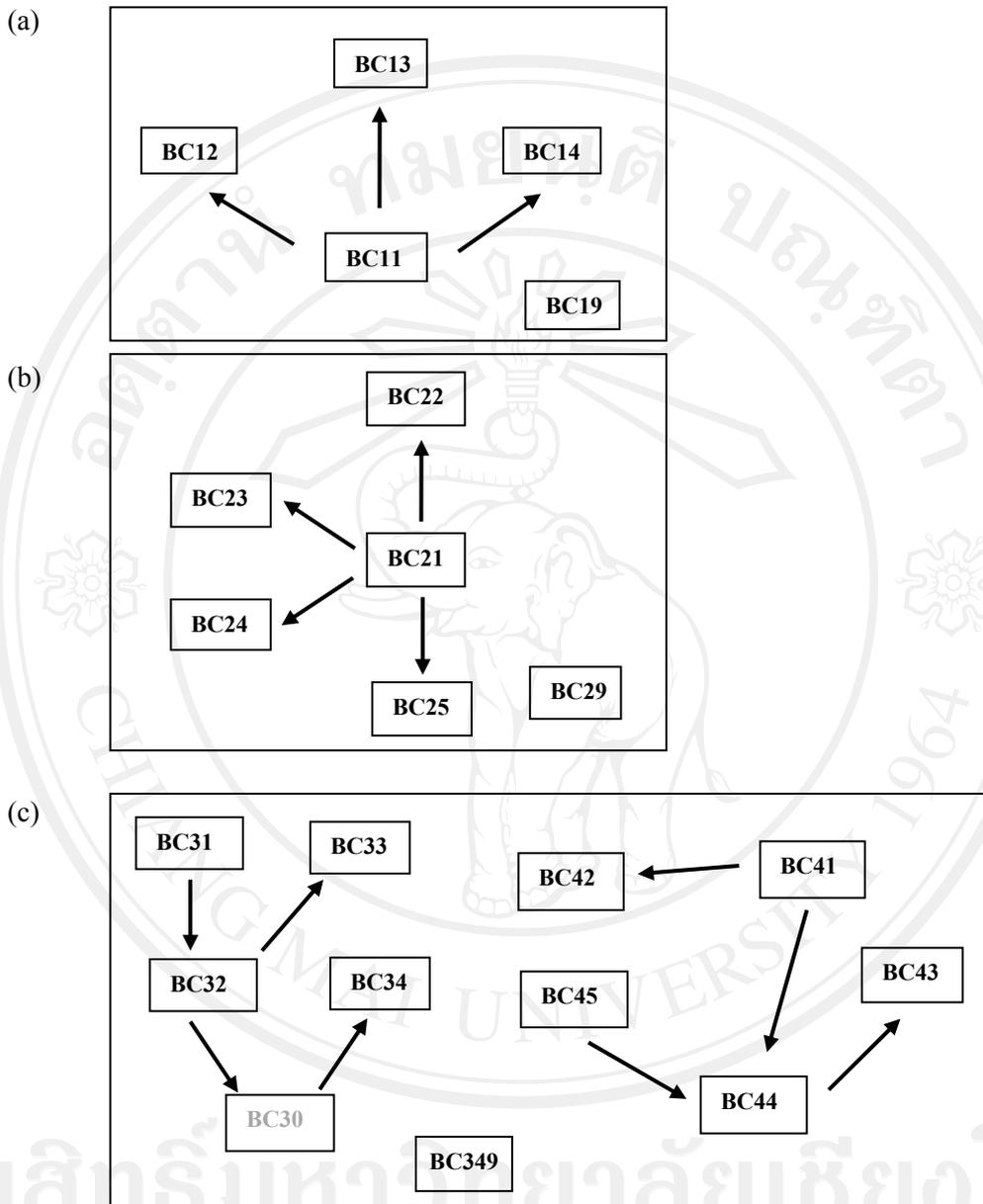


Figure 4.2.3 Bue Chomee seed exchange networks diagram from (a) Huai-e-cang village with BC1, (b) Huai-khao-leep village with BC2, and (c) Huai-yen village with BC3 and BC4 networks. The direction of the arrow indicated the direction of seeds provided from source to sink while those without arrow were classed as seed lots outside the network within each village.

Muey Nawng seed exchange networks

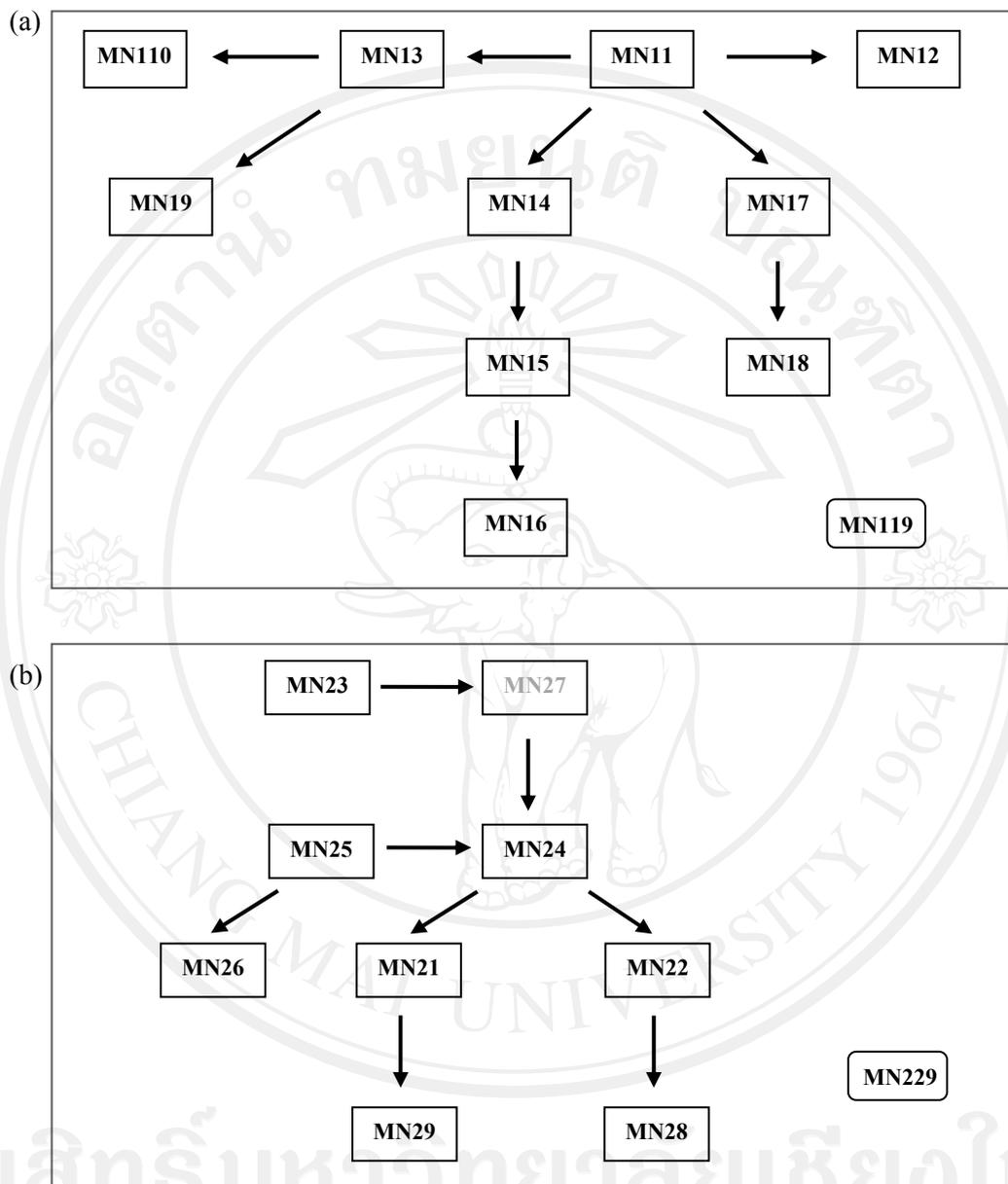


Figure 4.2.4 Muey Nawng seed exchange networks diagram from (a) Sam-sob village with MN1 and (b) Mae-ming village with MN2 networks. The direction of the arrow indicated the direction of seeds provided from source to sink while those without arrow were classed as seed lots outside the network within each village.

4.2.3 Pattern of seed exchange network analysis

Analysis the pattern of seeds exchange network lead to the answers of the following questions: what factors play a major role if farmers acquired new seeds stock?, and who should be the person that they preferred to ask for the new seeds stock? To answer the above questions the pattern of farmers' seeds exchange was assessed to correlate with social relationship between seeds provider (source) and seeds receiver (sink). As seeds exchange was defined as seeds were provided or received from one farmer to the next, therefore, pattern of seeds providing and seeds receiving were analyzed separately.

In addition, as social rule is believed to play a role on the pattern of seed exchange thus social relationship especially ethnic group of farmers were also observed. Farmers in the present study consisted of 2 ethnic groups, Karen and lowland Thai, farmers of Huai-e-cang (network BC1), Huai-khao-leep (network BC2), and Huai-yen (network BC3 and BC4) villages of Bue Chomee are all Karen. For Muey Nawng, farmers of Sam-sob (network MN1) are lowland Thai while farmers of Mae-ming (network MN2) are Karen.

Therefore, pattern of seeds exchange was considered to relate with social structure including;

- 1) Relationship between seed provider and seed receiver
- 2) Exchange within or outside the village
- 3) Ethnic group
- 4) Rule of seed provide from older farmers to younger farmers.

Contingency table for each pattern was constructed and the different between each structure was tested by Fisher exact test.

4.2.4 Genetic diversity analysis

DNA extraction and microsatellite analysis

Genetic diversity parameters of each seed lots within seed exchange network of Bue Chomee and Muey Nawng rice variety were assessed using microsatellite markers. Seeds those obtained from the farmers (Table 4.2.1 and Table 4.2.2) were sown and leaves of each individual plant were collected, 20 plants per seed lot. Leaves were silica-dried following the method described by Chase and Hill (1991). DNA was extracted by using modified CTAB method. A total of six microsatellite primer pairs that were randomly chosen, RM1, RM149, RM167, RM211, RM241 and RM253 (Table 4.2.3). Microsatellite polymorphism was analyzed by polymerase chain reaction as described in Table 4.2.4. Amplification of DNA was performed in 20 μ l reactions consisted of 20-50 ng DNA, 0.25 Mm of each dNTP, 0.2 μ M of each primers and 0.5 unit of Taq DNA polymerase (Invitrogen[®]). Amplified products were mixed with loading dye and were separated in 10% polyacrylamide gels by electrophoresis. Gels were stained with ethidium bromide and photographed under UV light.

Data analysis

Standard measures of genetic diversity were calculated the estimate of unbiased Nei's (1973) gene diversity (h) using POPGENE version 1.32 (Yeh et al., 1999) while number of allele (A), inbreeding coefficients (F_{IS}), within population gene diversity (H_S), total gene diversity (H_T), and degree of genetic differentiation (F_{ST}) were calculated using FSTAT version 2.9.3 (Goudet, 2001).

Wright's coefficient (F_{IS}) (Wright, 1990) was calculated according to the methods of Weir and Cockerham (1984). F_{IS} is the mean reduction in heterozygosity

of an individual due to non-random mating within a subpopulation. The significance of F_{IS} departures from zero was evaluated using permutation tests after standard Bonferroni corrections using the computer program FSTAT.

Then, genetic diversity was analyzed to correlate with four factors including;

- 1) Farmers' age,
- 2) Number of year grown,
- 3) Ethnic group
- 4) Selection methods that farmers used to select their seeds for the next season

Table 4.2.3 Microsatellite markers in seed exchange network study

Locus	Ch.	Primer sequence	T _m (°C)	No. of Alleles	Reference
RM1	1	F 5'-GCGAAAACACAATGCAAAA-3' R 5'-GCGTTGGTTGGACCTGAC-3'	55	13	Panaud et al., 1996
RM149	1	F 5'-GCTGACCAACGAACCTAGGCCG-3' R 5'-GTTGGAAGCCTTTCCTCGTAACACG-3'	55	11	Akagi et al., 1996
RM211	1	F 5'-CCGATCTCATCAACCAACTG-3' R 5'-CTTACGAGGATCTCAAAGG-3'	55	2	Chen et al., 1997
RM253	2	F 5'-TCCTTCAAGAGTGCAAAACC-3' R 5'-GCATTGTCATGTCGAAGCC-3'	67	3	Chen et al., 1997
RM167	2	F 5'-GATCCAGCGTGAGGAACACGT-3' R 5'-AGTCCGACCACAAGGTGCGTTGTC-3'	55	4	Wu et al., 1993
RM241	3	F 5'-GAGCCAAATAAGATCGCTGA-3' R 5'-TGCAAGCAGCAGATTTAGTG-3'	55	3	Chen et al., 1997

Table 4.2.4 Polymerase chain reaction condition in seed exchange network study

Step	Temperature (°C)	Time	No. of cycle
Denaturing	94	5 min	1
Denaturing	94	30 sec	40
Annealing	55 (67)	30 sec	
Extension	72	30 sec	
Extension	72	10 min	1

4.3 Results

4.3.1 *Pattern of seed exchange network*

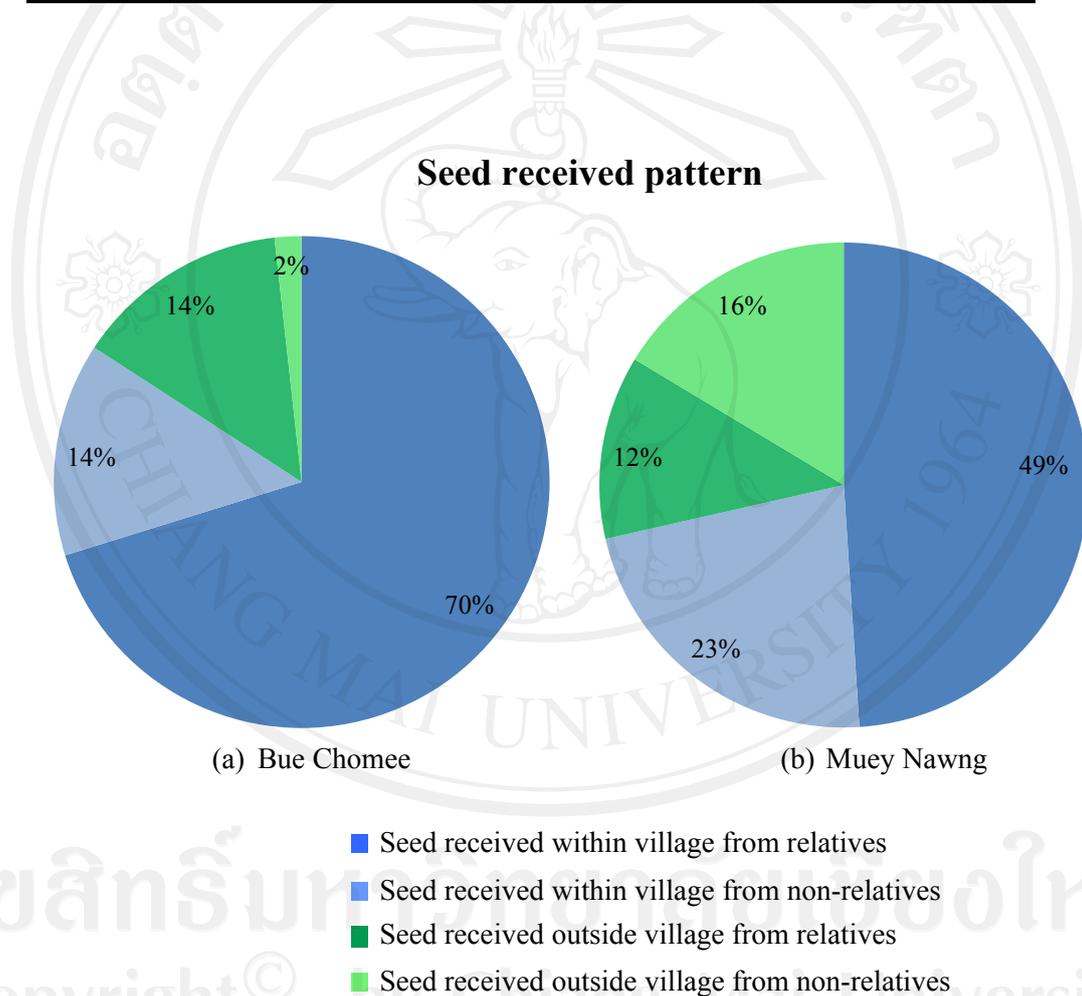
4.3.1.1 *Pattern of seed received*

Pattern of seeds received within or outside village and among relatives or non-relatives were observed (Table 4.3.1). When comparing between village and outside village seed source, both BC and MN seeds were received from within village more than outside village. For within villages, seeds of both BC and MN were also received from relatives more than non-relatives. However, different patterns ($P < 0.05$) between BC and MN were observed in seeds receiving outside the village, where most BC seed lots (8) were received from relatives, compared to only one from non-relatives. Those of MN were both from relatives and non-relatives, 6 and 8, respectively (Table 4.3.1).

Proportion of seed received between Bue Chomee and Muey Nawng were compared in Figure 4.3.1. Most of seeds were received from relatives within village with those of BC were much higher than MN, 70% compared with 40%, respectively. Similarly, proportion of seed received from non-relatives within village of Bue Chomee (23%) was also higher than Muey Nawng (14%). For seed received outside village, similar proportion of seed received from relatives was detected between Bue Chomee (14%) and Muey Nawng (12%) but Muey Nawng (16%) revealed higher proportion of seed received from non-relatives than Bue Chomee (2%).

Table 4.3.1 Patterns of seed received of Bue Chomee and Muey Nawng rice varieties

Varieties	Seed received pattern					
	Received within village		Received outside village			
	relatives	non-relatives	relatives	non-relatives	relatives	non-relatives
Bue Chomee	40	8	48	8	1	9
Muey Nawng	24	11	35	6	8	14
			P=0.185		P<0.05	
P=0.156						

**Figure 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.

4.3.1.2 *Pattern of seed provided*

Patterns of seed provided within village or outside village and among relatives or non-relatives between Bue Chomee and Muey Nawng were showed in Table 4.3.2. Similar patterns of seed provided within or outside village were detected in Bue Chomee and Muey Nawng ($P=0.098$). Farmers of Bue Chomee and Muey Nawng provided seed within village more than outside village. Considering seed provided within village or between village, patterns of seed provided between Bue Chomee and Muey Nawng were the same ($P=0.508$ and $P=1.00$).

Proportion of seed provided between Bue Chomee and Muey Nawng were illustrated in Figure 4.3.2. Most of Bue Chomee seeds (56%) were provided among relatives within village among relatives which were twice that of Muey Nawng (31%). For seed providing among non-relatives within village, the same proportion found for Bue Chomee (33%) and Muey Nawng (34%). For seed providing outside village, Bue Chomee revealed lower proportion of both provided to relatives or non-relatives (5% and 6%, respectively) compared with Muey Nawng (16% and 19%, respectively).

Table 4.3.2 Relationship between rice varieties and seed provided patterns by relatives

Varieties	Seed provided pattern					
	Provided within village			Provided outside village		
	relatives	non-relatives		relatives	non-relatives	
Bue Chomee	10	6	16	1	1	2
Muey Nawng	10	11	21	5	6	11
	P=0.508			P=1.00		
	P=0.098					

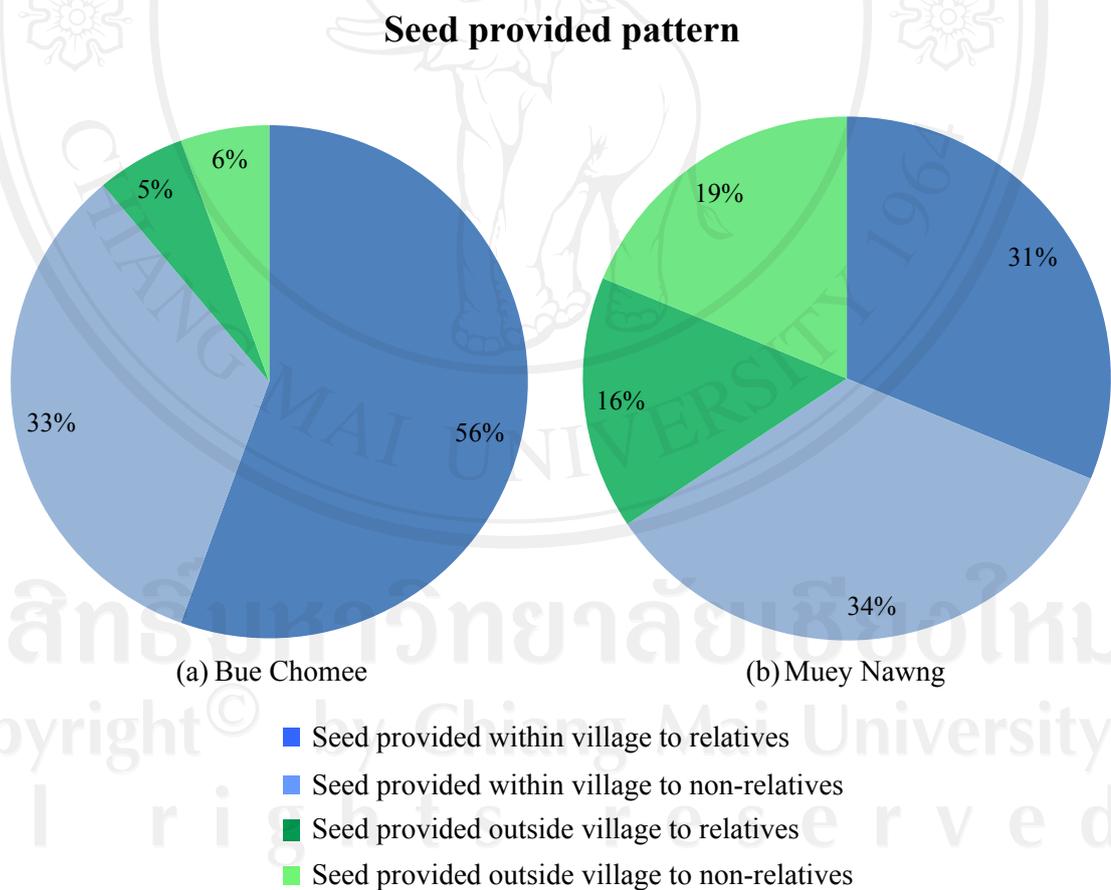


Figure 4.3.2 Seed provided pattern of (a) Bue Chomee from 3 villages in Chiang Mai and (b) Muey Nawng from 2 villages in Chiang Mai.

4.3.1.3 *Pattern of seed exchange based on ethnic groups*

Different ethnic group displayed different patterns of seed exchange among relatives or non-relatives and within or outside village (Table 4.3.3). Karen farmers who grew Muey Nawng tended to exchange among relatives than non-relatives while Lowland Thai exchanged equally ($P < 0.05$). Patterns of seed exchange within or outside village also differed among Karen and lowland Thai farmers of Muey Nawng ($P < 0.05$). Seed exchanges within village of Karen farmers were likely to exchange with farmers within than outside village but of the same for Lowland Thai farmers.

Proportion of farmers seed exchange pattern revealed in Figure 4.3.3 for (a) Karen of Bue Chomee, (b) Karen of Muey Nawng and (c) lowland Thai of Muey Nawng. Karen farmers of both Bue Chomee (66%) and Muey Nawng (56%) exchanged seed more with relatives within village than lowland Thai farmers (42%). In contrast, proportions of seed exchange with non-relatives within village were higher in Muey Nawng of both Karen (35%) and lowland Thai farmers (25%) than Karen of Bue Chomee (19%). For seed exchanged outside village, Karen farmers showed lower proportion of both with relatives and non-relatives of both Bue Chomee (12% and 3%) and Muey Nawng (2% and 7%) than lowland Thai farmers (11% and 22%).

Table 4.3.6 Relationship between ethnic group and seed exchange patterns for Muey Nawng

Muey Nawng	Seed exchange pattern			
	Relatives		Within-outside village pattern	
	relatives	non-relatives	within	outside
Karen (n=46)	35	11	39	7
Lowland Thai (n=50)	24	26	30	20
	P<0.05		P<0.05	

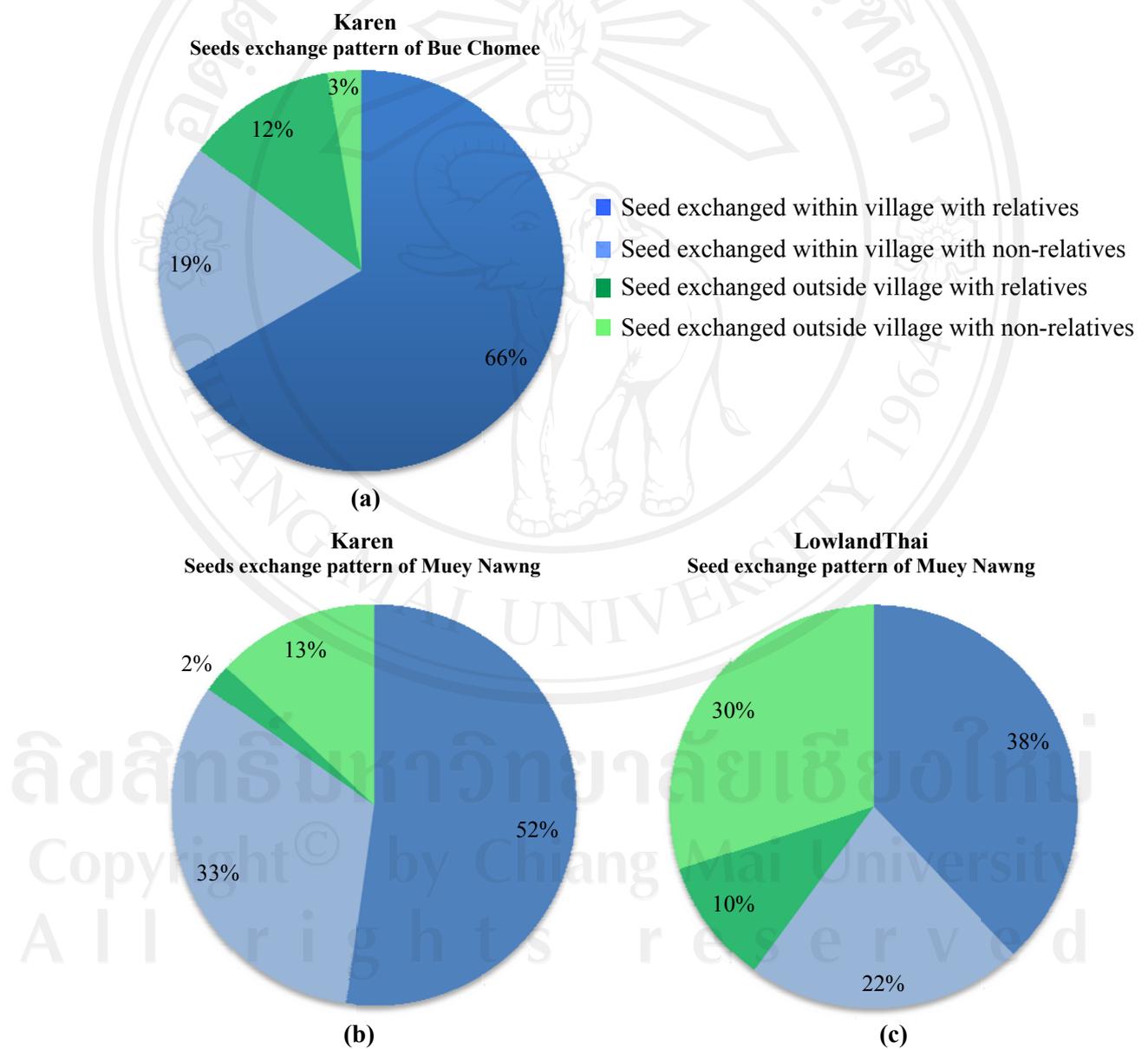


Figure 4.3.3 Seed exchange pattern of (a) Karen ethnic group of Bue Chomee, (b) Muey Nawng and (c) Lowland Thai of Muey Nawng.

4.3.1.4 Seed received from older farmers

Most centers of the network or source of the seeds of Bue Chomee variety (Figure 4.3.4) and Muey Nawng variety (Figure 4.3.5) were older farmers indicated by bold, and italic in the diagrams. Pattern of seed receiving was predominantly from the older farmers but not always the cases. However, patterns of seed received from older farmers were different between varieties ($P=0.185$, Table 4.3.7). Farmers of Bue Chomee were received more seeds from older farmers than younger farmers (Figure 4.3.6 a) while for Muey Nawng the frequencies of seed receiving from older farmer or younger farmer were the same. The influence of ethnic groups was shown in Figure 4.3.6 (b). Karen farmers of both Bue Chomee and Muey Nawng received new seed from older farmers while those of lowland Thai farmers of Muey Nawng were not differ between ages (Figure 4.3.6 b).

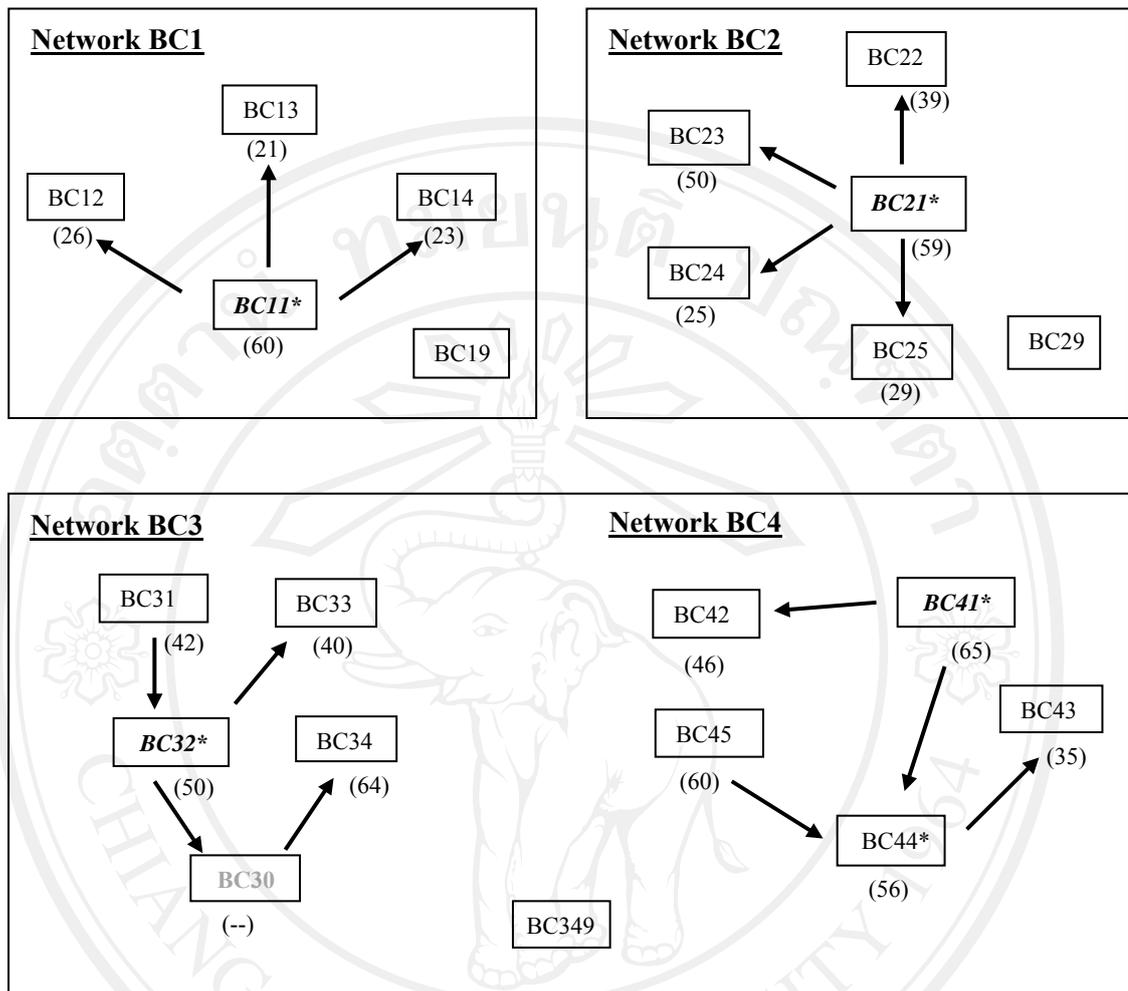


Figure 4.3.4 Diagram of Bue Chomee seed exchange network represent the age of each farmer within the network in the parenthesis of network BC1, BC2, BC3 and BC4. The center or source of the network was represented by the *italic* characters with (*). Number in the parentheses is the age of each farmer.

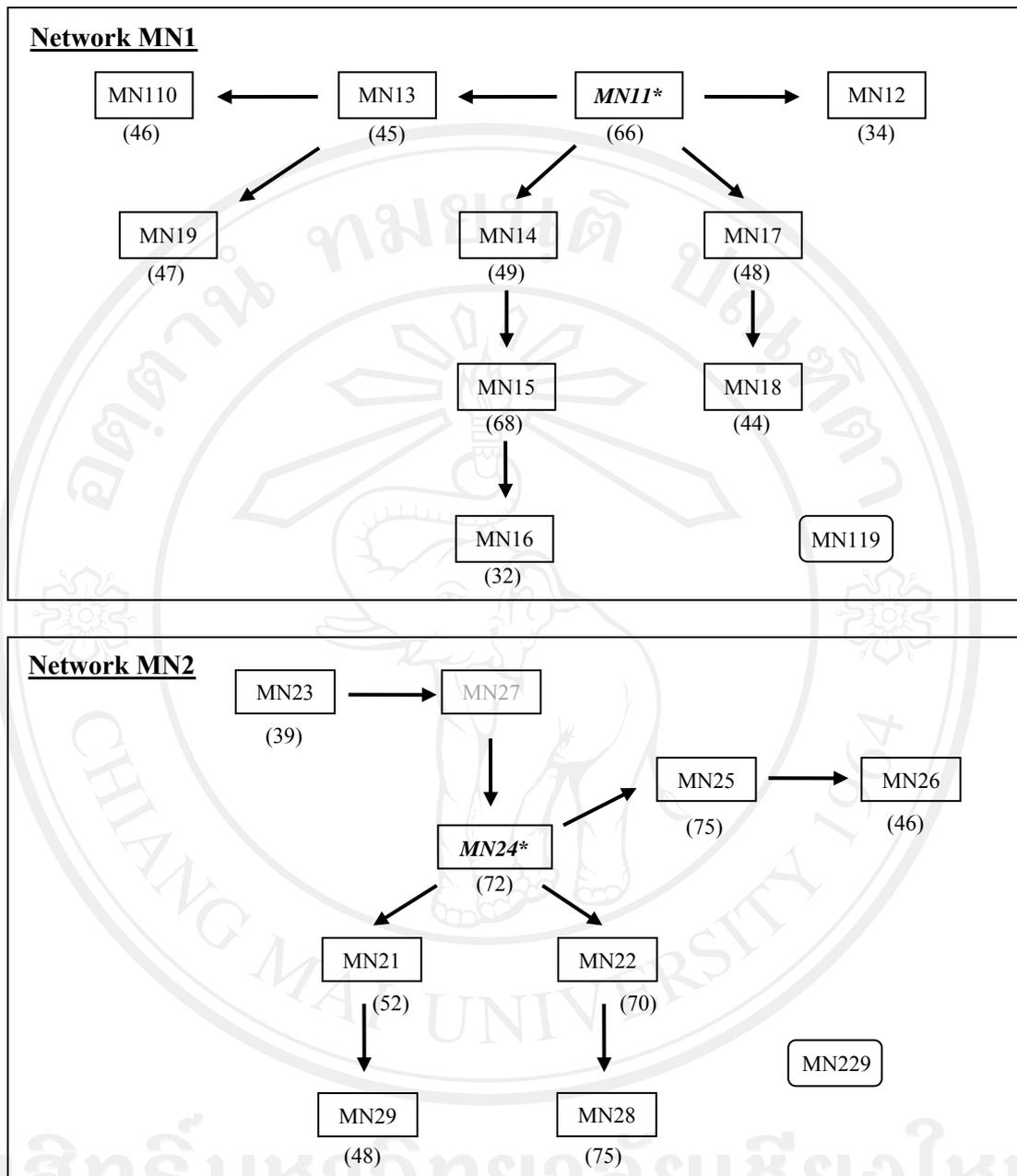


Figure 4.3.5 Diagram of Muey Nawng seed exchange network represent the age of each farmer in the parenthesis of network MN1 and MN2. The center or source of the network was represented by the *italic* characters with (*). Number in the parentheses is the age of each farmer.

Table 4.3.7 Relationship between rice varieties and pattern of seed received from older farmers

Varieties	Seed exchange pattern	
	From older	From younger
Bue Chomee (n=15)	13	2
Muey Nawng (n=16)	10	6

P=0.220

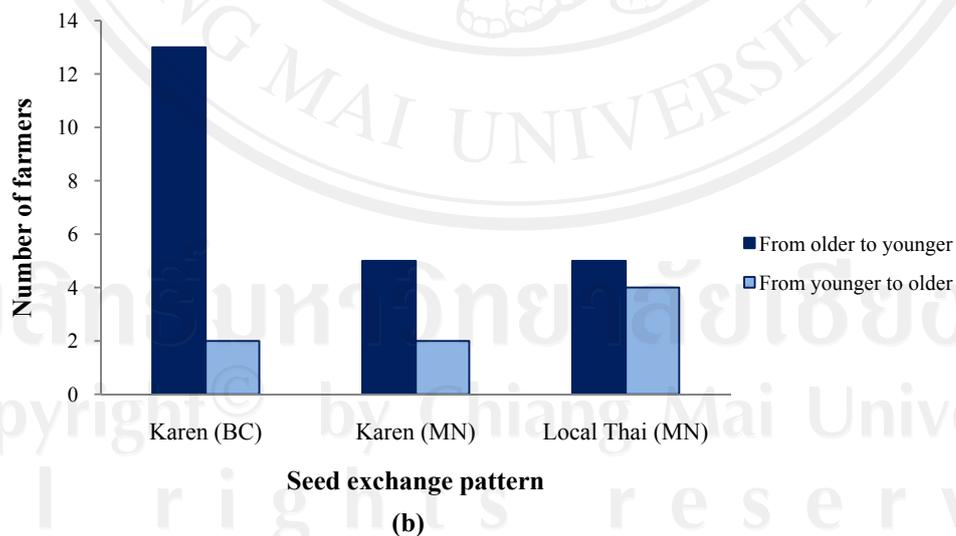
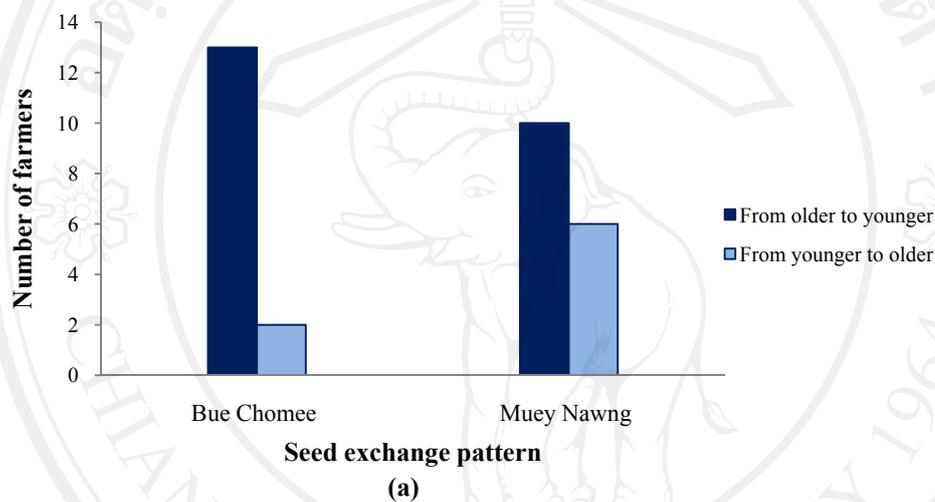


Figure 4.3.6 Pattern seed received from older or younger farmers of; (a) Bue Chomee and Muey Nawng local rice varieties and (b) Karen of Bue Chomee (BC), Karen of Muey Nawng (MN) and Lowland Thai of Muey Nawng (MN)

4.3.2 Genetic diversity and population structure

4.3.2.1 Allele diversity

Bue Chomee

Total of 36 alleles at 6 SSR loci with average 6 alleles per locus found in 4 networks of Bue Chomee. The most variable locus was RM1, 13 alleles, while RM211 was the lowest, 2 alleles. Different total number of alleles was found among seed lots and networks. The most diverse seed lots were BC45 and BC349 (16 alleles) while the lowest were BC11 and BC34 (8 alleles), average 12.3 alleles per seed lot. Among the networks, about 43 and 59 alleles (average 10.8 and 11.0 alleles per seed lot) were detected within the BC1 and BC3 networks, while those of the BC2 and BC4 networks were the same, 78 alleles with average of 13 alleles per seed lots. In addition, different patterns of allele diversity was found among network, network BC1 and BC2 were more diverse at RM1 locus, network BC4 was more diverse at locus RM149 while network BC3 was the lowest diverse at all 6 SSR loci (Table 4.3.8).

Muey Nawng

Total of 22 alleles at 6 SSR loci with average 3.5 alleles per locus found in 2 networks of Muey Nawng. The most variable locus were RM1 and RM149 (5 alleles) while the least was RM253 (2 alleles). Two Muey Nawng seed exchange networks revealed different levels of allele diversity. Different level of allele diversity at each seed lot was detected, highest in MN23 (17 alleles) and lowest in MN12, MN13, MN18 (7 alleles), average 10.9 alleles per seed lot. Among network, total no. of alleles at 6 SSR loci of MN1 and MN2 networks were 100 and 119 with average 9 and 13 alleles per network, respectively. The MN1 network had lower level of allele

diversity than MN2 at all 6 SSR loci, revealed by lower number of allele at least 4 loci of MN1 than MN2 (Table 4.3.9).



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Table 4.3.8 Number of alleles (A) of Bue Chomee (BC) seed exchange networks using six SSR markers

Accession No.	Number of allele (A)						Total	Average
	RM1	RM149	RM241	RM211	RM253	RM167		
Network BC1								
BC11	3	1	1	1	1	1	8	
BC12	5	1	2	1	1	1	11	
BC13	7	2	2	1	1	1	14	
BC14	5	3	2	1	1	1	13	
BC19*	5	2	2	1	2	1	13	
Total BC1	9	3	2	1	2	1	59	11.8
Network BC2								
BC21	5	2	2	1	2	1	13	
BC22	5	2	2	1	3	1	14	
BC23	5	2	2	2	1	1	13	
BC24	6	2	2	1	2	1	14	
BC25	4	1	2	2	2	1	12	
BC29*	4	1	2	2	2	1	12	
Total BC2	8	3	3	3	3	1	78	13
Network BC3								
BC31	4	1	2	1	1	1	10	
BC32	2	3	2	1	2	2	12	
BC33	3	3	2	1	2	2	13	
BC34	1	3	1	1	1	1	8	
Total BC3	8	7	3	1	2	3	43	10.8
Network BC4								
BC41	5	1	2	2	1	1	12	
BC42	1	4	1	1	2	1	10	
BC43	2	5	2	1	2	1	13	
BC44	2	3	2	1	2	1	11	
BC45	2	6	2	1	3	2	16	
BC349*	3	5	3	1	2	2	16	
Total BC4	7	9	3	2	3	3	78	13
Total BC	13	11	3	2	3	4	36	12.3

* seed lot outside the network within each the village

Table 4.3.9 Number of alleles (A) of Muey Nawng (MN) seed exchange networks using six SSR markers

Accession No.	Number of allele (A)						Total	Average
	RM1	RM149	RM241	RM211	RM253	RM167		
Network MN1								
MN11	2	1	1	1	1	2	8	
MN12	1	1	1	1	1	2	7	
MN13	1	1	1	1	1	2	7	
MN14	2	1	1	1	1	2	8	
MN15	3	1	1	1	2	2	10	
MN16	2	2	2	1	1	3	11	
MN17	2	1	1	1	1	2	8	
MN18	1	1	1	1	1	2	7	
MN19	2	4	2	1	2	4	15	
MN110	2	1	1	1	1	2	8	
MN119*	2	2	1	3	2	1	11	
Total MN1	3	4	2	1	2	4	100	9.09
Network MN2								
MN21	2	3	3	3	2	2	15	
MN22	2	2	2	3	1	3	13	
MN23	3	3	3	2	2	4	17	
MN24	1	1	1	2	2	3	10	
MN25	2	2	2	2	2	3	13	
MN26	3	3	2	2	2	3	15	
MN28	2	3	2	3	2	4	16	
MN29	2	2	2	2	2	3	13	
MN229*	2	1	1	1	1	1	7	
Total MN2	5	5	3	3	2	4	119	13.2
Total MN	5	5	3	3	2	4	22	10.9

* seed lot outside the network within each the village

4.3.2.2 Genetic diversity

Bue Chomee

Different levels and patterns of genetic diversity at each SSR locus was found among Bue Chomee seed lots and networks (Table 4.3.10). Within BC1, RM1 revealed similar values and pattern of gene diversity among seed lots but varied in the rest 3 loci while RM211 and RM167 showed no variation. For BC2, most seed lots showed various patterns and genetic variable in all 6 loci more in RM1 and RM241 while no variable was found in RM167. Network BC3 and BC4 displayed various patterns and variable gene diversity values varied in 5 SSR loci except no variation was observed in RM211 for BC3 network. Among networks, BC1 and BC2 networks revealed similar pattern of genetic variable loci. The highest variable locus was RM1 following with RM241 while RM167 was the least. Network BC3 and BC4 showed the highest variable in RM149 following with RM1 while less variable in RM211.

Muey Nawng

Different levels and patterns of genetic diversity at each SSR locus was found among Muey Nawng seed lots (Table 4.3.11). Both MN1 and MN2 networks had genetic variable in all 6 SSR loci. Most seed lots within network MN1 was less diverse than seed lots within network MN2 detected in all 6 loci. The highest variable locus in MN1 was RM241 and following with RM1 while RM253 is the least. High variation within each locus was detected in all seed lots of MN2 network. The most variable locus was RM241 with slightly lower in RM253 while RM1 was the least. Among network, high variable locus of MN1 was detected at locus RM241 (0.380) while high variable loci of MN2 were RM241 (0.431) and RM253 (0.392). The least divers locus of MN1 was RM211 (0.018) while RM1 (0.128) for MN2 network.

Table 4.3.10 Genetic diversity per locus per seed lot of Bue Chomee (BC) seed exchange networks

Accession No.	RM1	RM149	RM241	RM211	RM253	RM167
Network BC1						
BC11	0.518	0	0	0	0	0
BC12	0.621	0	0.479	0	0	0
BC13	0.758	0.100	0.505	0	0	0
BC14	0.758	0.195	0.479	0	0	0
BC19*	0.553	0.050	0.521	0	0.100	0
Average BC1	0.642	0.069	0.397	0	0.020	0
Network BC2						
BC21	0.553	0.189	0.521	0	0.100	0
BC22	0.189	0.100	0.505	0	0.195	0
BC23	0.500	0.100	0.505	0.189	0	0
BC24	0.484	0.050	0.479	0	0.189	0
BC25	0.389	0	0.479	0.100	0.189	0
BC29*	0.711	0	0.100	0.100	0.268	0
Average BC2	0.471	0.073	0.432	0.065	0.157	0
Network BC3						
BC31	0.658	0	0.395	0	0	0
BC32	0.100	0.542	0.100	0	0.505	0.100
BC33	0.279	0.195	0.229	0	0.189	0.268
BC34	0	0.358	0	0	0	0
Average BC3	0.259	0.274	0.181	0	0.174	0.092
Network BC4						
BC41	0.763	0	0.505	0.100	0	0
BC42	0	0.595	0	0	0.268	0
BC43	0.100	0.558	0.100	0	0.189	0
BC44	0.385	0.590	0.154	0	0.154	0
BC45	0.100	0.568	0.050	0	0.147	0.100
BC349*	0.489	0.442	0.353	0	0.268	0.268
Average BC4	0.306	0.459	0.194	0.017	0.171	0.061

* seed lot outside the network within each village

Table 4.3.11 Genetic diversity per locus per seed lot of Muey Nawng (MN) seed exchange networks

Accession No.	RM1	RM149	RM211	RM253	RM167	RM241
Network MN1						
MN11	0.100	0	0	0	0	0.521
MN12	0	0	0	0	0	0.442
MN13	0	0	0	0	0	0.395
MN14	0.100	0	0	0	0	0.337
MN15	0.358	0	0	0	0.100	0.442
MN16	0.268	0.100	0.100	0	0	0.416
MN17	0.100	0	0	0	0	0.395
MN18	0	0	0	0	0	0.479
MN19	0.189	0.284	0.100	0	0.337	0.489
MN110	0.100	0	0	0	0	0.268
MN119*	0.337	0.100	0	0.416	0.100	0
Average MN1	0.141	0.044	0.018	0.038	0.049	0.380
Network MN2						
MN21	0.100	0.353	0.279	0.484	0.521	0.526
MN22	0.100	0.100	0.189	0.574	0	0.484
MN23	0.353	0.542	0.353	0.521	0.337	0.742
MN24	0	0	0	0.505	0.100	0.353
MN25	0.100	0.100	0.100	0.268	0.229	0.426
MN26	0.195	0.195	0.100	0.395	0.395	0.563
MN28	0.100	0.195	0.268	0.595	0.189	0.363
MN29	0.100	0.100	0.100	0.189	0.303	0.426
MN219*	0.100	0	0	0	0	0
Average MN2	0.128	0.176	0.154	0.392	0.230	0.431

* seed lot outside the network within each the village

4.3.2.3 Population genetic structure

Bue Chomee

For individual seed lots, gene diversity (h) of sink seed lots differed from that of the source in each network (Figure 4.3.7). These included an increasing gene diversity in the sink seed lots in BC1 and variable with both increasing and decreasing in the other networks. Almost all seed lots had inbreeding coefficient (F) was 1, except four which F_{IS} between 0.845-0.964. Average pairwise genetic differentiation (F_{ST}) of seed lots within network of BC1 and BC2 were between 0.069-0.268, which were much lower than those of BC3 and BC4 networks (0.441-0.707) (Table 4.3.12)

At the network level, average genetic diversity (H_S) of BC2 (0.234) was the highest following with BC1 (0.188) and BC4 (0.181) while the least was BC3 (0.162). In contrast, total genetic diversity (H_T) of BC1 and BC2 networks were between 0.211-0.273, while higher level of total genetic diversity was detected in BC3 (0.557) following with BC4 network (0.377). Network BC1 and BC2 showed lower level of genetic differentiation within network (0.087-0.138) than network BC3 and BC4 (0.521-0.710), with the highest in BC3 network.

For overall Bue Chomee variety, average gene diversity (H_S) of =0.198, total gene diversity (H_T) of =0.468 with F_{ST} =0.308 were shown (Table 4.3.12). Pairwise genetic differentiation between networks were displayed in Table 4.3.18. The lowest pairwise F_{ST} was between BC1 and BC2 (0.044) following with between BC3 and BC4 (0.251) while between BC1 and BC4 was the highest (0.499) (Table 4.3.13).

Muey Nawng

For individual seed lots, gene diversity (h) of sink seed lots were increased and decreased from that of the source in both MN1 and MN2 networks (Figure 4.3.8). Genetic diversity of MN1 network were between 0.061-0.233 while MN2 network were between 0.017-0.475. Almost all seed lots had inbreeding coefficient (F) was 1, except three which F_{IS} were between 0.959-0.995. Average pairwise genetic differentiation (F_{ST}) of seed lots within network of MN1 were between 0.030-0.081, which were lower than those of MN2 networks (0.172-0.334) (Table 4.3.14).

At networks level, average genetic diversity (H_S) and total genetic diversity (H_T) of MN1 (0.107 and 0.108, respectively) was lower than those detected in network MN2 (0.281 and 0.417, respectively). Network MN1 showed about 5 times lower level of genetic differentiation within network (0.070) than those of MN2 (0.354).

For overall Muey Nawng variety, average gene diversity (H_S) of =0.175, total gene diversity (H_T) of =0.281 with F_{ST} =0.211 were shown (Table 4.3.14).

Table 4.3.12 Genetic parameters of 4 seed exchange networks of Bue Chomee variety collected from 3 villages based on 6 microsatellite loci.

Farmer's code	n	h	<i>F</i>	Average F_{ST}^{\dagger} within network	H_S	H_T	F_{ST}
Network BC1							
BC11	20	0.102	1	0.242			
BC12	20	0.173	1	0.128			
BC13	20	0.243	1	0.092			
BC14	20	0.233	1	0.069			
BC19*	20	0.234	0.964	0.172			
Total BC1	80				0.188	0.211	0.087
Network BC2							
BC21	20	0.259	1	0.101			
BC22	20	0.195	1	0.268			
BC23	20	0.227	1	0.128			
BC24	20	0.260	0.968	0.103			
BC25	20	0.235	1	0.176			
BC29*	20	0.150	1	0.235			
Total BC2	100				0.235	0.273	0.138
Network BC3							
BC31	20	0.169	1	0.656			
BC32	20	0.225	1	0.533			
BC33	20	0.193	0.957	0.659			
BC34	20	0.060	1	0.707			
Total BC3	80				0.162	0.557	0.710
Network BC4							
BC41	20	0.227	1	0.611			
BC42	20	0.144	1	0.488			
BC43	20	0.158	1	0.458			
BC44	13	0.214	1	0.441			
BC45	20	0.161	0.845	0.467			
BC349*	20	0.232	1	0.409			
Total BC4	93				0.181	0.377	0.521
Total 4 networks	353				0.198	0.468	0.308

[†] average pairwise F_{ST} with other seed lots within the network

* seed lot outside the network within each village

Nei's gene diversity (h), Inbreeding coefficient (*F*), Average gene diversity (H_S), Total gene diversity (H_T) and Genetic differentiation (F_{ST})

Table 4.3.13 Genetic differentiation (F_{ST}) between and among four Bue Chomee seed exchange networks

Network BC	Genetic differentiation (F_{ST})	
	Between	Among
Network BC1		
Network BC2	0.044	
Network BC3	0.428	
Network BC4	0.499	
Network BC2		
Network BC3	0.385	
Network BC4	0.444	
Network BC3		
Network BC4	0.251	
Network BC4		
Among 4 networks		0.308

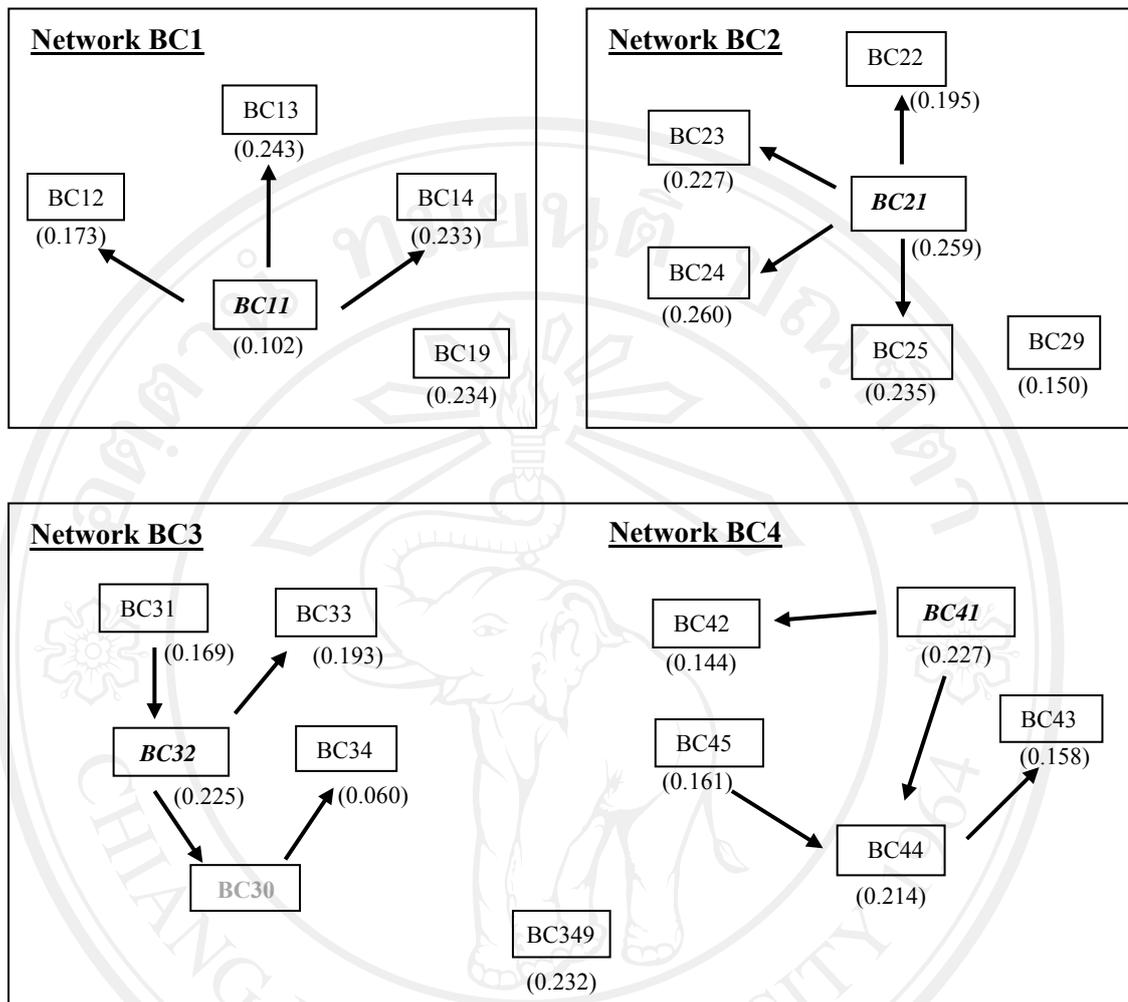


Figure 4.3.7 Diagram of Bue Chomee seed exchange network represent genetic diversity (h) of each farmer of network BC1, BC2, BC3 and BC4. Number in the parentheses is genetic diversity of each farmer. Farmers BC30 passed away.

Table 4.3.14 Genetic parameters of 2 seed exchange networks of Muey Nawng variety from 2 villages based on 6 microsatellite loci

Farmer's code	n	h	<i>F</i>	Average F_{ST}^{\dagger} within network	H_S	H_T	F_{ST}
Network MN1							
MN11	20	0.104	1	0.081			
MN12	20	0.074	1	0.039			
MN13	20	0.066	1	0.039			
MN14	20	0.073	1	0.040			
MN15	20	0.150	1	0.039			
MN16	20	0.147	1	0.042			
MN17	20	0.083	1	0.030			
MN18	20	0.080	1	0.048			
MN19	20	0.233	1	0.060			
MN110	20	0.061	1	0.062			
MN119*	20	0.159	1	0.464			
Total MN1	200				0.107	0.108	0.070
Network MN2							
MN21	20	0.377	1	0.240			
MN22	20	0.241	1	0.178			
MN23	20	0.475	1	0.172			
MN24	20	0.160	1	0.219			
MN25	20	0.204	0.959	0.257			
MN26	20	0.307	1	0.334			
MN28	20	0.285	1	0.297			
MN29	20	0.203	0.959	0.272			
MN229*	20	0.017	0.995	0.437			
Total MN2	160				0.281	0.417	0.354
Total 2 networks	400				0.175	0.281	0.211

[†] average pairwise F_{ST} with other seed lots within the network

* seed lot outside the network within each village

Nei's gene diversity (h), Inbreeding coefficient (*F*), Average gene diversity (H_S), Total gene diversity (H_T) and Genetic differentiation (F_{ST})

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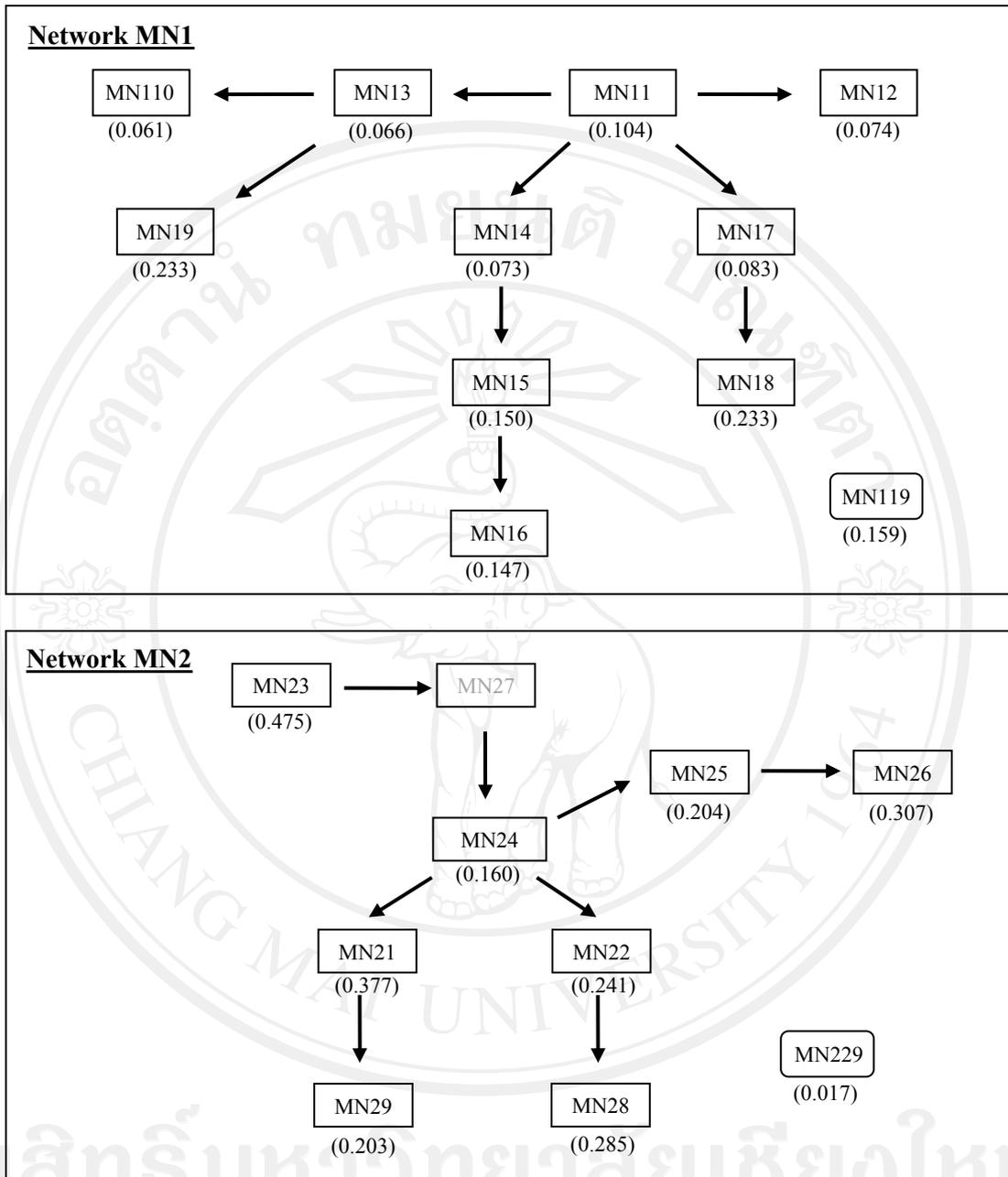


Figure 4.3.8 Diagram of Muey Nawng seed exchange network represent genetic diversity (h) of each farmer of network MN1 and MN2. Number in the parentheses is genetic diversity of each farmer. Farmer MN27 passed away.

4.3.3 Factors influenced genetic diversity

4.3.3.1 Farmers' age

Genetic diversity of each seed lot related to the owner (farmers) age are displayed in Table 4.3.15 and Table 4.3.16.

For Bue Chomee, ages of most farmers were evenly distributed within the ranges of <35, >35-55 and >55 year-old. While genetic diversity of each seed lot was mostly distributed between 0.2-0.3 (Table 4.3.15). There was no relationship between farmers' age and genetic diversity ($r=0.07$) (Figure 4.3.9).

For Muey Nawng, ages of most farmers were distributed within the ranges of >35-55 year-old. While genetic diversity of each seed lots were mostly distributed between 0-0.1 (Table 4.3.16). There was no correlation between genetic diversity of farmers' seed lots and the farmer' age ($r=0.145$) (Figure 4.3.10).

Table 4.3.15 Distribution of genetic diversity related to farmers' age of Bue Chomee rice variety

Gene diversity	Number of farmers				Total
	<35	>35 - 55	>55	unknown	
>0 - 0.1			1		1
>0.1 - 0.2	3	4	2		9
>0.2 - 0.3	5	2	4		11
>0.3 - 0.4					
>0.4 - 0.5					
>0.5 - 1.0					
Total	8	6	7		21

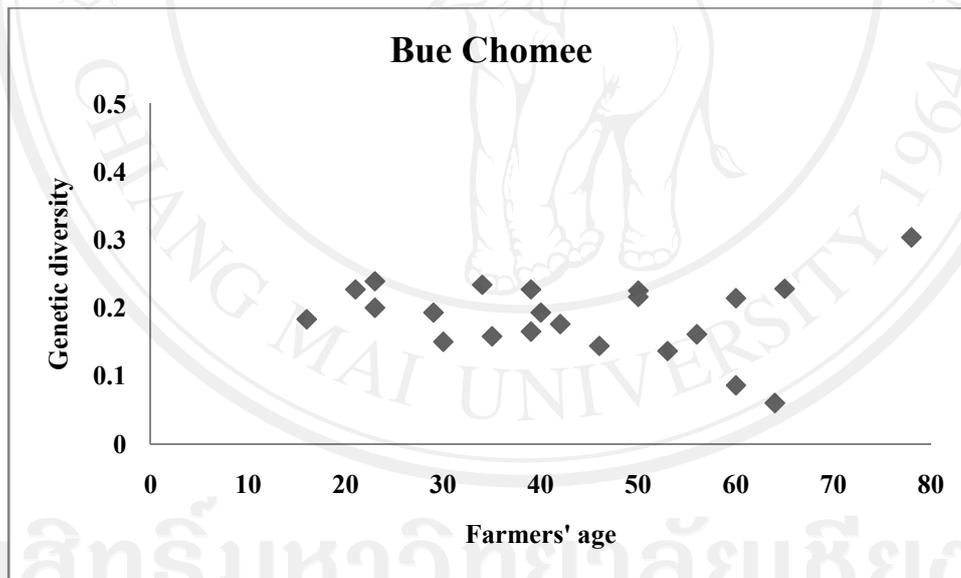


Figure 4.3.9 Relationship between genetic diversity and farmer's age of Bue Chomee with $r=0.070$.

Table 4.3.16 Distribution of genetic diversity related to farmers' age of Muey Nawng rice variety

Gene diversity	Number of farmers				Total
	<35	>35 – 55	>55	unknown	
>0 – 0.1	2	5			7
>0.1 – 0.2	1		3	1	5
>0.2 – 0.3		2	2	1	5
>0.3 – 0.4		1		1	2
>0.4 – 0.5		1			1
>0.5 – 1.0					
Total	3	9	5	3	20

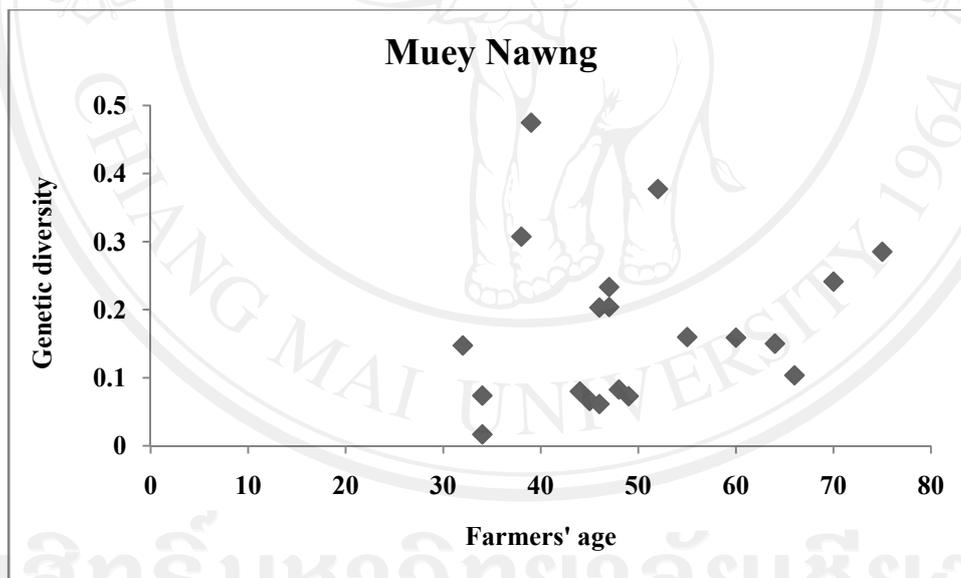


Figure 4.3.10 Relationship between genetic diversity and farmer's age of Muey Nawng with $r=0.145$.

4.3.3.2 Number of year grown

Bue Chomee

Duration of using Bue Chomee ranged from >2 to >20 years. Most farmers have grown Bue Chomee more than 20 years (Table 4.3.17). No relationship was found between number of year grown and genetic diversity of farmers' seed ($r=-0.042$, Figure 4.3.11).

Muey Nawng

Similar to Bue Chomee, most farmers have grown Muey Nawng more than 20 years (Table 4.3.18). In contrast to that of Bue Chomee, significant negative correlation ($r=-0.498^*$) between number of year grown and genetic diversity of farmers' seed was observed (Figure 4.3.12).

Table 4.3.17 Distribution of genetic diversity and no. of year farmers grown Bue Chomee variety

Gene diversity	Number of farmers					Total
	1	2-5	5-10	10-20	>20	
>0 – 0.1					1	1
>0.1 – 0.2		1	1	1	6	9
>0.2 – 0.3		1		3	7	11
>0.3 – 0.4						
>0.4 – 0.5						
>0.5 – 1.0						
Total	-	2	1	4	14	21

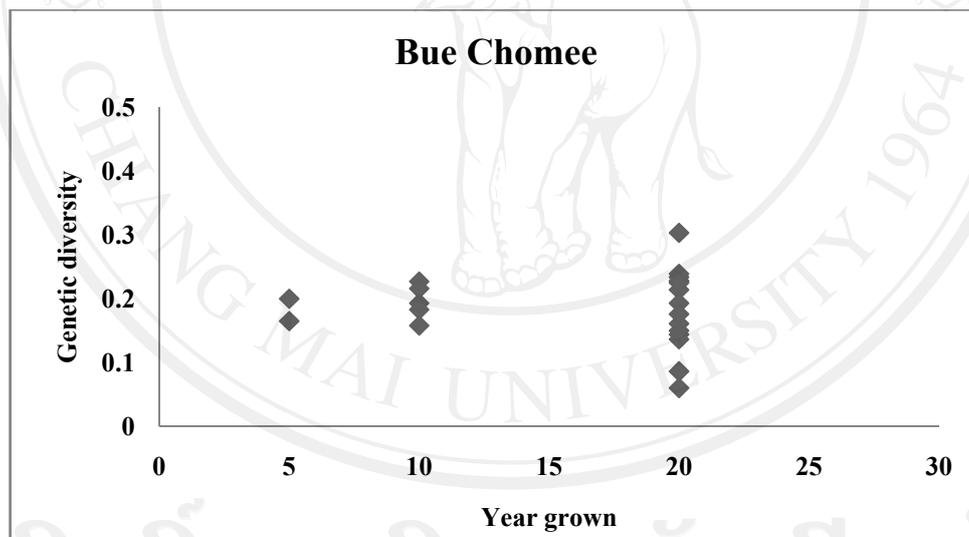


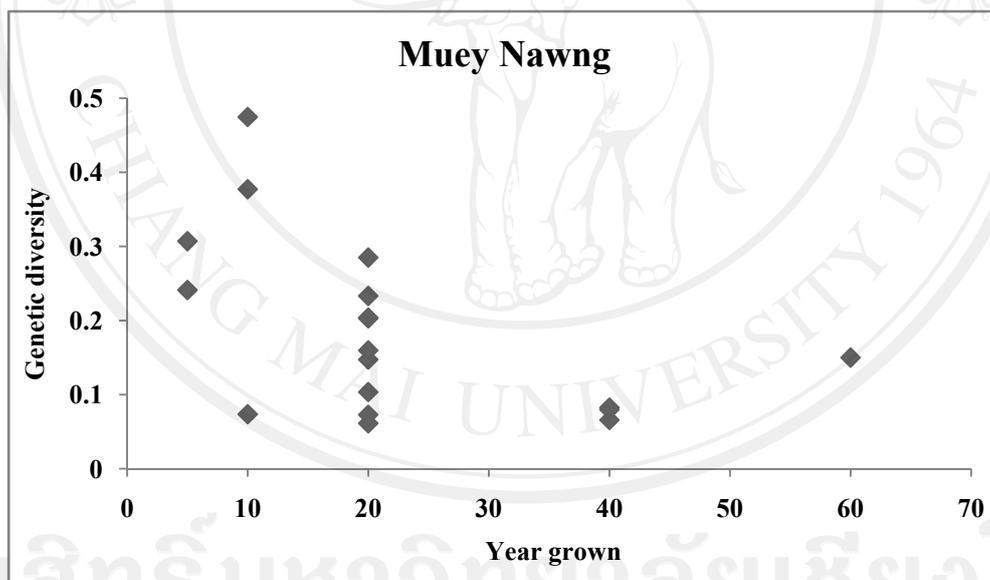
Figure 4.3.11 Relationship between genetic diversity and number of year grown

Bue Chomee rice variety ($r = -0.042$).

Table 4.3.18 Distribution of genetic diversity and no. of year farmers grown Muey

Nawng variety

Gene diversity	Number of farmers					Total
	1	2-5	5-10	10-20	>20	
>0 - 0.1				1	6	7
>0.1 - 0.2					5	5
>0.2 - 0.3			1		4	5
>0.3 - 0.4			1	1		2
>0.4 - 0.5				1		1
>0.5 - 1.0						
Total	-	-	2	3	15	20

**Figure 4.3.12** Relationship between genetic diversity and number of year grown Muey Nawng rice variety ($r=-0.498^*$).

4.3.3.3 *Ethnic group*

As farmers who grown Bue Chomee are all Karen ethnic group (Table 4.3.19), therefore relation between ethnic groups was considered only within Muey Nawng variety (Table 4.3.20). Muey Nawng seed lots kept by Karen farmers were more diverse than Muey Nawng kept by lowland Thai farmers. Genetic diversity of most seed lots of Muey Nawng grown by the Karen was distributed among 0.2 to 0.4 while genetic diversity of the Thai was distributed among >0.0 to 0.2 (Table 4.3.20).

4.3.3.4 *Selection methods*

Farmers selected seeds and panicles either before or after harvesting the crop. Most farmers of both Bue Chomee (18) and Muey Nawng (14) selected their rice seeds for the next season before harvesting (Table 4.3.19 and Table 4.3.20). Different patterns of distribution within each selection method were observed between varieties. Most Bue Chomee seed lots those were selected before harvest had genetic diversity between 0.2-0.3 while all seed lots from those selected after harvest were between 0.1-0.3 (Table 2.3.19). For Muey Nawng variety, genetic diversity of seed lots those selected before harvest were evenly distribute in $>0.0-0.1$, $>0.1-0.2$ and $>0.2-0.3$ ranges (Table 4.3.20).

Furthermore, relationship between genetic diversity and selection method of each ethnic group were plotted in Figure 4.3.11. Genetic diversity of Bue Chomee were between 0.060-0.260 and of Muey Nawng were between 0.017-0.475 and not differed between those selected before or after harvested. In Muey Nawng, genetic diversity of seed lots grown by the Thai farmers were much lower from those of the Karen seed lots. No different between selection method was also found (Figure 4.3.13).

Table 4.3.19 Distribution of genetic diversity (h) of farmers' seed lots relate to ethnic groups and selection methods of Bue Chomee

Gene diversity (h)	Number of farmers			
	Ethnic group		Selection methods	
	Lowland Thai	Karen	Selection of panicles and seeds before harvest	Selection of panicles and seeds after harvest
>0 - 0.1		1	1	
>0.1 - 0.2		9	6	3
>0.2 - 0.3		11	11	
>0.3 - 0.4				
>0.4 - 0.5				
>0.5 - 1.0				
Total	-	21	18	3

Table 4.3.20 Distribution genetic diversity (h) of farmers' seed lots related to ethnic groups and selection methods of Muey Nawng

Gene diversity (h)	Number of farmers				
	Ethnic group		Selection methods		
	Lowland Thai	Karen	Selection of panicles and seeds before harvest	Selection of panicles and seeds after harvest	No selection
>0 - 0.1	6	1	4	2	1
>0.1 - 0.2	4	1	3	1	1
>0.2 - 0.3	1	4	4	1	
>0.3 - 0.4		2	2		
>0.4 - 0.5		1	1		
>0.5 - 1.0					
Total	11	9	14	4	2

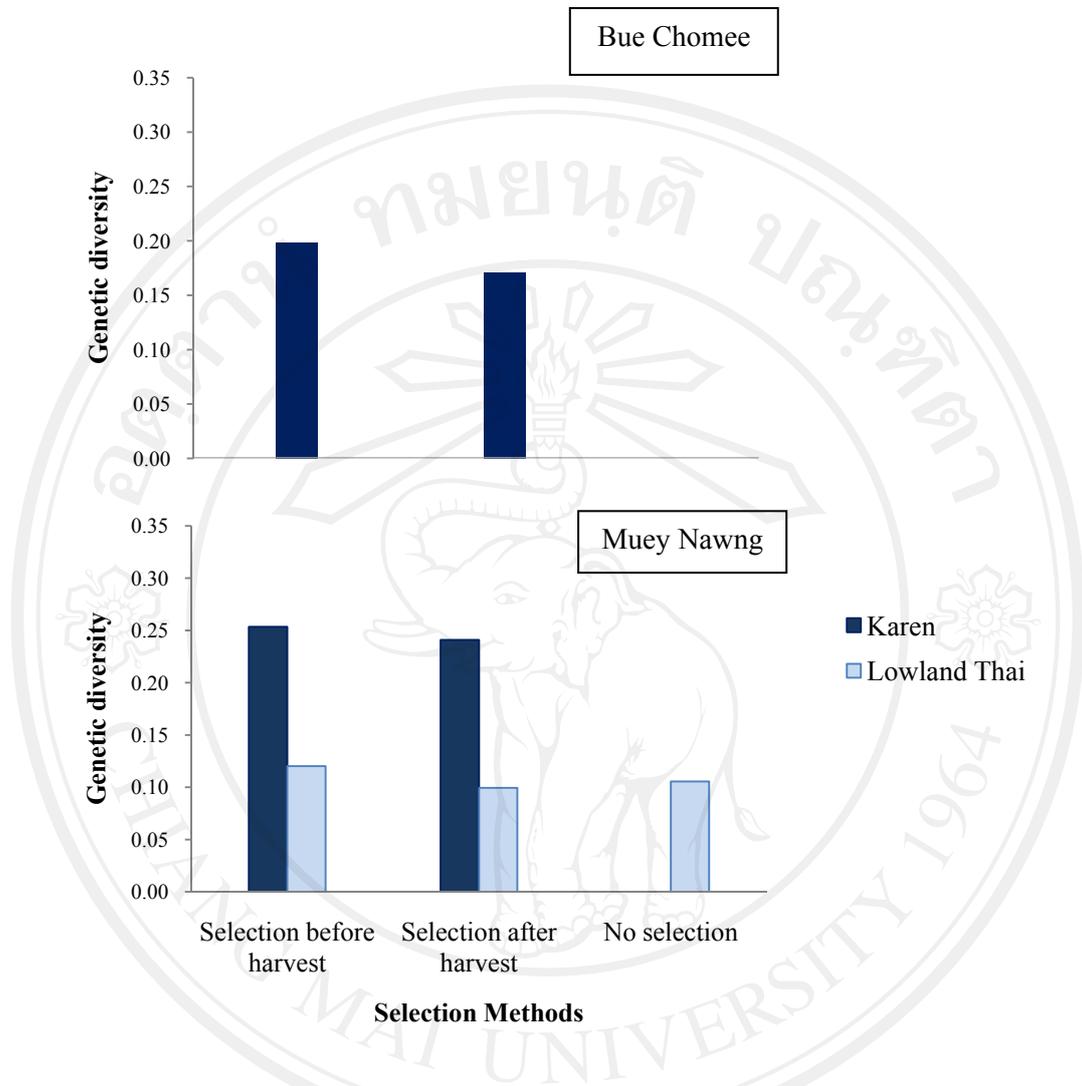


Figure 4.3.13 Genetic diversity and selection methods of Bue Chomee and Muey

Nawng varieties of Karen ethnic and Lowland Thai

4.4 Discussion

The results of Chapter 3 illustrated that Thai landrace rice maintained genetic diversity and was structured by geography which was assumed to be the consequence of farmer's managements. Several studies illustrated the influence of farmers' managements on genetic diversity of local crop germplasm (Dennis, 1987; Bellon and Brush, 1994; Brown, 2000; Parzies *et al.*, 2004). Addition to farmers' managements, natural selection through adaptation to local environments has also been reported to influence genetic diversity of landrace populations (Almekinders *et al.*, 1994; Alvarez *et al.*, 2005; Tiranti and Negri, 2007; Lazrek *et al.*, 2009). As landraces crop germplasm were grown, selected, and kept mostly by indigenous farmers worldwide because they are better adapted to specific local conditions (Parzies *et al.*, 2004). In addition, ethnic group as social factor was expected to be one of an important factor that influenced genetic diversity of landraces germplasm (Orlove and Brush, 1996; Sirabanchongkran *et al.*, 2004). Thus, studies in the present Chapter was performed to examine how farmers' management influenced genetic variation of Thai landraces rice by using seed exchange network approach in fine scale at only single year information which could not addressed to greater temporal or spatial scales. The Chapter found main results as followed: (1) farmers' seed lots of landrace rice Bue Chomee and Muey Nawng varieties were genetically diverse at both within and among seed lots, and networks levels, (2) genetic diversity and population structure of Bue Chomee was strongly influenced by patterns of seed exchange among farmers those were predominantly exchanging seeds within village particularly among relatives and mostly provided from older farmer to the younger, (3) genetic diversity and populations of Muey Nawng was mainly influenced by the managements of

ethnic groups and number of year grown, (4) the dynamics of genetic diversity and differentiation among sources and sinks were shaped through the process called genetic drift ,as only a hand full or small amount of seeds were provided from source therefore only a few genotype was randomly transferred and grown and kept by sink.

Genetic diversity of landraces rice Bue Chomee (BC) and Muey Nawng (MN) varieties were assessed base on six SSR loci. Both Bue Chomee and Muey Nawng were genetically diverse revealed by total genetic diversity while landraces rice Bue Chomee ($H_T=0.468$) was more diverse than Muey Nawng ($H_T=0.281$). Genetic diversity analysis indicated that Bue Chomee was diverse both within ($h=0.060-0.260$) and among seed lots ($F_{ST}=0.308$) which consistent with the results found in Chapter 3. No correlation between genetic diversity and farmers' age ($r=0.07$) and between genetic diversity and number of years grown ($r=-0.042$) were found. Bue Chomee might have its unique characteristics those easy for farmers to select and recognize. Cultural practice played the role to maintain level of genetic diversity of Bue Chomee. Farmers of Bue Chomee may have good practice and transferred their knowledge from generation to generation, from parents to their descendant.

Population structure of Bue Chomee reflected the consequence of seed those were exchanged among farmers mostly within village lead to the reduction of genetic differentiation (F_{ST}). Degree of average pairwised F_{ST} with other seed lots within network and F_{ST} among seed lots within network was lower than F_{ST} between networks indicated that seed lots within networks were more genetically similar than those from different networks. Furthermore, lower F_{ST} between BC1 and BC2 than those between BC3 and BC4 networks was explained by less distance between the villages of the villages of BC1 and BC2 networks (Huai-e-cang and Huai-khao-leep,

respectively) than distance to the village of BC3 and BC4 networks (Huai-yen). In the other word, the possibility of seed exchange among farmers of BC1 network of Huai-e-cang and BC2 network of Huai-khao-leep may be higher than the exchange with farmers of BC3 and BC4 networks of Huai-yen village. Similar result was revealed in maize populations by Perales *et al.*, (2005) illustrated that maize seeds those moved between nearby communities showed less distinct based on isozyme analysis. In contrast, high level of genetic differentiation was found among 4 popcorn landraces populations (*Zea mays* spp. *mays*) in nearby communities of Northeastern Argentina could be explained in term of low local exchange (Bracco *et al.*, 2009).

In case of Muey Nawng, genetic diversity analysis indicated that Muey Nawng were diverse both within (0.061-0.475) and among seed lots ($F_{ST}=0.211$) but lower than those detected in Bue Chomee. Farmers' seed lots within MN1 (0.061-0.233) showed less diverse than those within MN2 (0.160-0.475) networks. Moreover, level of genetic differentiation (F_{ST}) between seed lots within MN1 was also lower than that in MN2 networks. The different levels of genetic diversity and differentiation of MN1 and MN2 networks were clearly explained by the analysis of seed exchange pattern by different ethnic groups. Farmers of MN1 are lowland Thai (Sam-sob village) while farmers of MN2 are Karen (Mae-ming village). Patterns of seed exchange between lowland Thai and Karen farmers of Muey Nawng were clearly different. Lowland Thai of Muey Nawng showed similar frequency of seed exchange between within or outside village and relatives or non-relatives. While Karen farmers of Muey Nawng revealed pattern of seed exchange similar to those illustrated in Karen farmers of Bue Chomee (Figure 4.3.3 a and b) mostly preferred exchange within village especially with relatives.

Lower level of genetic diversity of Muey Nawng than those in Bue Chomee was associated with significant negative correlation between levels of genetic diversity of MN and number of years grown ($r=-0.498$, $p<0.01$). The results suggested that the longer the farmers grown Muey Nawng the lower variation was detected. The results implied that the longer the farmers grown Muey Nawng the more farmers maintain or select their seed and approaching homozygosity with less number genotypes than the former crops. For example, MN23 seed lots revealed the highest genetic diversity ($h=0.475$) and grown Muey Nawng variety for only 5 years (Table 4.2.2). In addition, lower level of genetic diversity of Muey Nawng than Bue Chomee may associated with selection pressure i.e. rice gall midge resistance as Muey Nawng is the variety resistance to rice gall midge. Oupkaew (2009) revealed that genetic diversity of Muey Nawng accessions vary with different level of gall midge resistance from highly resistance to susceptible. The present results consistent with genetic diversity assessment in the Batini barley from Oman (Jaradat *et al.*, 2004) that low level of genetic variation indicating an adaptive response to environmental conditions including abiotic or biotic stress and human selection.

In summary, genetic diversity and population structure of landrace rice variety Bue Chomee was influenced by the pattern of seed exchange among farmers. The exchange pattern of Bue Chomee was predominantly within village and among relatives and preferentially provided from older to younger farmers. While genetic diversity and population structure of Muey Nawng was mainly influenced by managements of different ethnic groups. These results implied that Karen farmers seem to maintain more genetically diverse landrace rice germplasm than lowland Thai farmers.

Furthermore, there were few seed lots of both Bue Chomee and Muey Nawng displayed higher level of average pairwise F_{ST} within network than total F_{ST} among all seed lots within network. The result may due to the data of seed exchange in the present study was collected in one year but the dynamics of farmers' seed exchange occurred all the time. Farmers may have a chance to exchange his/her seed with other farmers lead to the high differentiation of those seed lots within network. These results were confirmed the finding of Chapter 3 that seed lots within the same village showed more genetic similarity than those from different villages resulting the structure as genetic isolation by geographical distance of Bue Chomee landrace rice. Such structure was the consequence of farmers' managements of their rice seeds by the mechanism of seed exchange among farmers predominantly within village as revealed in the results of the present chapter. The expected mechanism that maintained variation within landraces rice varieties demonstrated in the present study is farmers' management especially seed exchange among farmers combination with social factors. The combination of farmers' managements with seed exchange, and social rule including ethnic groups are the dynamics to keep balancing of landraces rice genetic diversity in the present study.