

CHAPTER 2

REVIEW OF THE LITERATURES

2.1 Civilization of northern Thailand

According to the archeological evidences, the area of northern Thailand had been inhabited by human ancestors since prehistorical period. Many archeological sites were excavated, including Tham Lod rockshelter, Pang Mapha district, Mae Hong Son province, where stone tools, human remains, and other evidences have been found. Those stone tools were dated back to between Pleistocene (22,350 BP) and early Holocene periods (7,290 BP) but only two skeletal remains of *Homo sapiens sapiens* were dated back to late Pleistocene (13,720 BP and 12,160 BP) (Shoocongdej, 2004). A number of tools were founded in various younger archeological sites, dated to Neolithic period (6000-600 BC) and Metal age (800-500 BC). During this long prehistoric time, northern Thailand must have been underwent a number of prehistorical civilization, some following one after the other and some contemporaneous. Also there must be different prehistoric populations, different peoples and different races. But it is not yet possible to describe what became of these prehistorical peoples. Did they die out, go away, stay on, evolve, or occasionally mix with later arrival groups. Mlabri, who lived like prehistoric hunter-gatherers, was believed to be the descendent of these local prehistoric peoples, as well as Kha, H'tin, and Lawa who practice simple gathering and gardening culture. The languages of all these groups belong to the Mon-Khmer subfamily in Austro-Asiatic

language family. However, it is not confirmed whether they are descended from local prehistoric populations or just more recent immigrants (Penth, 2000).

The first known history of northern Thailand began on the west bank of the Mae Ping river in Lamphun region. The culture of writing and administration were developed in Haripunchai. Haripunchai was the Mon's capital city which was founded in 750 A.D. and lasted until 1300 A.D. The first ruler of Haripunchai was Phra Nang Chamadevi, daughter of the king of Lop Buri, the center of Mon Dvaravati kingdom in central Thailand. Mon of Haripunchai improved many advanced culture which partly influenced from Myanmar and India. The historic period became fully description with the earliest datable stone inscriptions from 1218 to 1219 A.D. The inscriptions also mentioned Lawa as another local population (Condominas, 1990).

In the thirteenth century, the main group of Tai, who was called by its neighbors as Yuan or Yonok, moved southward from the area where now three countries meet: Myanmar, Laos, Thailand or somewhere further north. The first fully known historical ruler was Phaya Mang Rai, a relative of Lue dynasty of Chiang Rung in Yunnan, China. He founded Chiang Rai in 1263 A.D. and occupied Haripunchai (Lamphun) in 1281 A.D. During the Tai attacking, Lamphun's last Mon ruler fled south to central Thailand but some Mon people stayed on. In 1296 A.D., Phaya Mang Rai founded Chiang Mai as the new capital of Lan Na Kingdom (literally mean "one million rice field"), with help from allies Phaya Ngam Mueang of Phayao and King Ramkhamheang of Sukhothai. Within relatively short time, the Yuan had replaced the Mon as the region's administrators on a state level and controlled a wider area. By then, the Yuan had become more numerous and the kingdom quickly grew by unifying many local rulers of the area under his leadership (Penth, 2000).

The Yuan of Lan Na reached their golden age in 1400 A.D. to 1525 A.D. They became a leading power and many of their cultural features and achievements were exported to neighboring regions such as Lan Chang, Chiang Tung, Chiang Rung. The people of Lan Na had also become deeply attracting to Buddhism and the eighth Buddhist council was opened in 1447 A.D. during Phaya Tilokaraja reign to improve the Buddhist scriptures. There were also well-organized government bureaucracy and many infrastructure projects. The previously independent state Nan, capital of Lue people, was added to the Lan Na kingdom in 1449 A.D. (Penth, 2000).

The decline of Lan Na slowly began after 1500 A.D. and worsens after the death of Phaya Kaeo in 1526 A.D. There was fighting over who should succeed him. In 1558 A.D., Lan Na had to surrender and fully lost its independence under the Burmese army hands. Chiang Mai city became the frontier between the Burmese and Ayuthaya wars for many times. Until 1775 A.D., a joint Yuan and Siamese army seized Chiang Mai from the Burmese when Prince Kawila of Lan Na and King Tak Sin of Ayuthaya combined their resources to overcome the Burmese. It was likewise the beginning of Lan Na renaissance and also of its integration to Siam. However, Chiang Mai was nearly deserted from 1775 A.D. to 1797 A.D. because the city had suffered much physical damage and a serious loss of population along with a loss of food supply. Until after 1800 A.D., in order to solve the pressing problem of a lack of population, the scattered peoples had to be brought back and their numbers were occasionally augmented by resettlement campaigns (*"Kep Phak Sai Sa, Kep Kha Sai Mueang"*, literally mean "putting vegetables in the basket and people in the city"). King Kawila first had to coax and persuade the people from the Shan state and Xishuangbanna to move. Those who agreed went voluntarily to Chiang Mai. If they

did not agree, force was used. Once a town had been captured, the people were first taken as prisoners of war, but later they given status as ordinary citizens. (Malasam, 1997). During this period, many Tai ethnic groups such as Lue, Yong, Khuen had settled and placed themselves under Lan Na territory.

The process of incorporating the semi-independent city-state of Lan Na into the Kingdom of Siam had been in the greater context in the reign of King Rama V (1868-1910 A.D.). The arrangement of having northern vassal king was slowly discontinued and officially ended in 1939 A.D. By then, Lan Na became the northern part of Thailand but the royal Thai court still acknowledge the northern princes and thus honour and remember those northern kings and princes (Penth, 2000).

2.2 Khon Mueang: where are they from?

Nowadays, Yuan peoples usually called themselves as “Khon Mueang”. But the word Khon Mueang is not the name of any specific ethnic groups. As mentioned above, peoples who occupied this area can be divided into two major groups: Mon-Khmer and Tai. It is quite interesting why and how these peoples had developed themselves to become Khon Mueang.

Literally, “Khon” is human being and “Mueang” is the city. Thus, Khon Mueang means the peoples who live in the city. This meaning was suggested to be different from “Khon Phuen Mueang” or indigenous peoples. Because Tai peoples were the newcomers in thirteenth century, and the indigenous population in northern Thailand was the Mon-Khmer speaking peoples, not Tai (Vaddhanaphuti, 2000). Bhumisak (1990) purposed that this word was used since 1558 A.D. when the Lan Na

was ruled by Burmese. During that period, the Burmese, as the ruler, used many derogatory terms to call Lan Na peoples. To oppose the Burmese power, Tai peoples used the word Khon Mueang to proclaim that they were civilized peoples, not a savage, and also made a distinction between Tai and Burmese. Mueang (city) is one of the political domains or the principalities. There were many cities during the Lan Na period and the peoples used the name of the city to refer where they were from, such as Khon Mueang Chiang Mai (Chiang Mai's citizens), Khon Mueang Phare (Phare's citizen). Later, the full words were reduced and became Khon Mueang. However, Charoenmuang (2001) suggested that the Yuan started using the word "Khon Mueang" since the early Rattanakosin period. In the reign of King Rama V of Thailand, Tai in central Thailand usually called northern Thai peoples as Lao because they shared similar language and cultures. However, northern Thai peoples consider Lao as their nearby ethnic group and they are not Lao. Thus, they called themselves as Khon Mueang, used Khum Mueang (Mueang language) and write Tua Mueang (Mueang alphabet).

The transforming process of Khon Mueang is still controversial as well as the history of their biological ancestors. There are two main hypotheses about the Khon Mueang's biological ancestors: the "immigrant" and "endogenous" hypotheses (Figure 1). The immigrant hypothesis states that the present day Khon Mueang is the descendent of Tai who migrated from southern or southeastern China in thirteenth century. The Tai then conquered the native populations on their southern route until they reached the present northern Thailand (Penth, 2000). In contrast, the endogenous hypothesis believes that their ancestors were not the Tai from China, but the native Mon-Khmer peoples who were later, through an influence of Tai politics and culture,

assimilated by the small group of Tai rulers (Condominas, 1990). Until now, using different sources of evidence from archaeologists, anthropologists, and linguists, the strong debate between believers of these two hypotheses is still going on. This research, therefore, used the genetic markers to look at general patterns of historical relationship among populations who residing in northern part of Thailand and make tentative suggestions about Khon Mueang's biological ancestors.

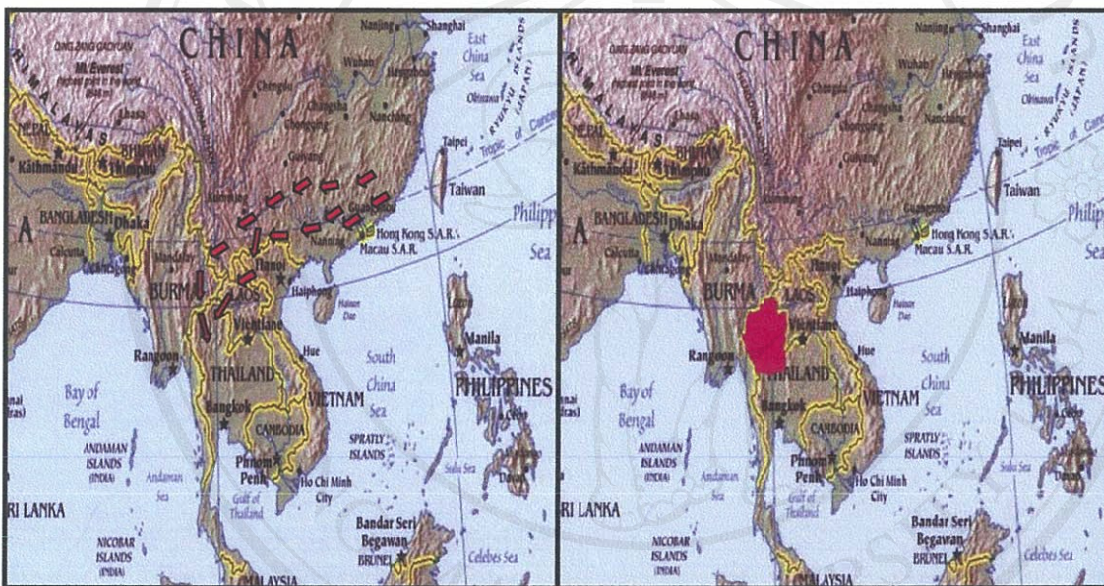


Figure 1 Two main hypotheses about the Khon Mueang's biological ancestors: immigrant (left) and endogenous (right)

2.3 Ethnic and village history of population studied

Yuan or **Yonok** who now call themselves as “Khon Mueang” is the major population of northern Thailand. According to an immigrant hypothesis, Yuan moved southward from the area where now three countries meet: Myanmar, Laos, and Thailand, or somewhere further north in the thirteenth century. They then conquered the native Mon-Khmer peoples along their southern migration route until they reached

the present day northern Thailand (Penth, 2000). Due to the limitation of archaeological and anthropological evidences, the geographic origin, biological ancestors and demographic history of Khon Mueang are not clearly confirmed. Nowadays, 87.5% of Tai people in northern Thailand use northern Thai dialect or Khum Mueang. Their script had been used to write Buddhist sermons and inscriptions for a long time, but only few people can read it now (Gordon, 2005). Architecture and painting can be found in many Lan Na style temples especially in Chiang Mai-Lamphun basin. The stone inscription and the oldest known three dimensional images were found in Wat Chiang Man in Chiang Mai city from 1427 A.D. The largest building was the Stupa Jedi Luang in Chiang Mai. Begun in about 1400 A.D., and was given its final form in 1481 A.D. (Penth, 2000). The earth walls can be seen around Chiang Mai city, which reflect the civilization of the Lan Na Kingdom.

Studied Yuan or Khon Mueang in northern Thailand were from 3 villages around Chiang Mai and Lamphun cities:

Yuan-1 (YU1): Mae Faek Mai sub-district, San Sai district, Chiang Mai province.

Yuan-2 (YU2): Ban Pao sub-district, Mae Taeng district, Chiang Mai province.

Yuan-3 (YU3): Si Tia sub-district, Ban Hong district and Wiang Nong Long district, Lamphun province.

Yuan settled in Chiang Mai-Lamphun basin along the Ping River about 700 years ago. YU1 and YU2 reside in Chiang Mai province on eastern and western banks of the Ping River, respectively, while YU3 lives in Lamphun province. Another well-known Yuan group (YU4) living in Sao Hai district, Saraburi province in Central Thailand, is believed to be the direct descendent of Yuan who used to

occupy Chiang Saen city in northern Thailand. They migrated from the north to central Thailand in 1804 A.D. (about 200 years ago). These people still call themselves Yuan and speak Yuan language.

Lue's historical homeland is Xishuangbanna, Yunnan, southern China, but now they are dispersed in some parts of southern China, upper Myanmar, northern Laos, and northern Thailand. Lue (Lü) or Xishuangbanna Dai (Tai) in Yunnan is an official group under Dai (Tai) ethnicity. The mass migration of Lue people into northern Thailand had occurred in 1804 A.D. according to King Kawila's resettlement campaign. Lue people have their unique dialect and costume, especially Lue women who always cover their head with white or pink cloth (Prangwatthanakun and Naenna, 1996). The most well known Lue temple is Wat Phumin, Mueang district, Nan province. Wat Phumin underwent a major restoration in 1867 A.D. after it was built some 27 years before that. It is believed that the murals were commissioned during this time. The wall paintings in Lue style are considered highly valuable and depict legends concerning the Lord Buddha as well as local legends and the local way of life, which include native attires and weaving, including trading with foreigners. Another temple is Wat Nong Bua in Nong Bua village of Tha Wang Pha district, Nan province. It was built by Lue craftsmen who had earlier migrated from southern China. Apart from the Vihara which is adorned with elaborate carvings, there are also murals painted by Lue artists about one hundred years ago. Their artistic value and degree of perfection equal to those at Wat Phumin.

Lue under this study were from 4 villages in northern Thailand with different village history:

Lue-1 (LU1): Hia village, Silalaeng sub-district, Pua district, Nan province.

People of this village had migrated from Chiang Rung (Jinghong) city, Yunnan, passed through Laos in 1772 A.D.

Lue-2 (LU2): Nong Bua village, Pa Kha sub-district, Tha Wang Pha district, Nan province. This Lue village is well known for the Lue typical architecture and weaving. Their ancestors had used the same migrated route as Lue-1 at the same period of time but they were from Mueang La, Xishuangbanna, Yunnan, China.

Lue-3 (LU3): Ko Klang village, Mae Sai sub-district, Mae Sai district, Chiang Rai province. Most of these people came from Chiang Rung (Jinghong) city, southern Yunnan via Myanmar and settled in Chiang Rai recently (less than 100 years).

Lue-4 (LU4): Luang Nuea village, Luang Nuea sub-district, Doi Saket district, Chiang Mai province. This Lue village was first founded in 1389 A.D. during King Saen Mueang Ma of Chiang Mai period but more Lue migrated into this village later in 1804 A.D.

Yong (YO) (Nyong) are the native people of Yong City founded in the thirteenth century in Shan state, Myanmar and ruled by Lue King. Some scholars suggested that Yong might be the same ethnic group as Lue (Malasam, 1997). The mass migration of Yong into northern Thailand occurred in 1805 A.D., the same period as Lue migration, when King Kawila tried to rebuild Lamphun city. Yong immigrants first settled in Pa Sang district but nowadays they live dispersedly in Lamphun and nearby provinces. Chom Yong Pagoda (Chedi) is one of the symbols of Yong settlement in Pa Sang district, Lamphun province. This pagoda has similar

structure and the same name as pagoda in Yong city of Myanmar. Until now, most of Yong people live in Lamphun and still speak their own dialect, which is similar to that of Lue. Yong in this study was from Ma Kok village and Wai village, Ma Kok sub-district, Pa Sang district, Lamphun province. These two villages were founded since the first settlement of Yong people in Lamphun (1805 A.D.). They are the most well known Yong villages where Yong tradition and language can be maintained.

Khuen (KH) (Khün) is named after a river in Shan state, their homeland in Myanmar. The migration of Khuen into Thailand occurred in the same period as Lue and Yong (1804-5 A.D.). In Thailand, Khuen resides in Mae Wang and San Pa Tong districts, Chiang Mai. Khuen language and script as well as their spoken dialects are closely related to Lue and Yong. Khuen believes in Buddhism and supernatural spirit. Khuen village in this study is located at Thung Ruang Thong sub-district, Mae Wang district and Ban Mae sub-district, San Pa Tong district, Chiang Mai province.

Mlabri (MA) (literally means forest people) is the term called by themselves, but they are called by others as *Phi Tong Lueang* (spirit of yellow leaves) because they usually used banana leaves to build their shelter and when the leaves turn yellow, they disappear shortly after that. Mlabri has ancient Mongoloid features. They used to live dispersedly in Laos and Thailand but nowadays they were found only in Rong Kwang district, Phrae province and Wiang Sa district, Nan province. Mlabri migrated from Sayaburi province in Laos into Thailand during last century (Pookajorn, 1992). The overall number is about 125 individuals. Mlabri was a hunting and gathering society. They usually live in such fertile area and wandering within approximately 30 square kilometers. They strictly follow their lifeways as endogamous marriage. Mlabri language is classified as Khmuic branch, Mon-Khmer subfamily, Austro-

Asiatic family (Gordon, 2005). Mlabri samples in this study were from Huai Yuak village, Wiang Sa district, Nan province.

Palaung (PA) usually call themselves as Ta-Ang (Di-Ang). Their homeland is in southern Shan state, Myanmar. Paluang was the latest hill tribes who migrated into northern Thailand. They have been settling since 1983 A.D. in the area of Doi Ang Khang, west of Fang district, Chiang Mai province. The first Paluang village was No Lae village, Mon Pin sub-district, Fang district, Chiang Mai. A few years later, some of them moved to live at Pang Duang village, Chiang Dao sub-district, Chiang Dao district, Chiang Mai province. Paluang women wear rattan hoop or “Nong Wong” around their waist all the time, as a symbol that they are the descendent of an angel. Some individuals plate their teeth with gold and jewels. They practice an endogamous marriage and patrilocal post-marital residence tradition (Princess Maha Chaki Siridhorn anthropology centre, 2005).

Plang (PL) (Blang) is a small ethnic group living scatter in China, Myanmar, and Thailand. Chinese call them as Blang, Hkawa, or Pulang. Plang people in Thailand called themselves as Tai Doi, Khon Doi, or Tai Loi. Plang samples in this study are from Pa Yang village, Wiang Pang Khum sub-district, Mae Sai district (PL-1) and Lua Pattana village, Pa Tung sub-district, Mae Chan district (PL-2), Chiang Rai province. They migrated from Xishuangbanna, Yunnan, China, through Myanmar and into Thailand in 1974 A.D. They are agriculturist and believe in Buddhism.

2.4 Genetic markers in population studies

Genetic markers are the basic tool which the geneticist used for studying populations. Three properties of a genetic marker are locus-specific, polymorphism, and easy genotyping. Genetic marker can be phenotypes which their variation is observed in the population of interest such as blood group. As the Human Genome Project is progressing rapidly, the DNA molecular markers are become widely appreciated. Molecular markers are a segment of DNA with an identifiable physical location on a chromosome and whose inheritance can be followed. A marker can be a gene or it can be some section of DNA with unknown function. There are three types of chromosome change which create pattern of molecular markers.

- indels are insertions or deletions of the DNA at particular locations on the chromosome. The well known one is *Alu* insertion. *Alu* is a sequence of approximately 300 base pairs fragment which has inserted itself into a particular region of the DNA. There have been some half a million *Alu* insertions in human DNA. YAP or Y chromosome *Alu* polymorphism is one of the recent and widely used in population studies.
- SNPs are polymorphisms on chromosome due to single nucleotide substitution (transition or transversion) or single nucleotide insertion/deletion. SNPs are mostly biallelic markers. The heterozygosity is therefore limited at 50%.
- Tandem repeats are the short sequence of nucleotides repeating over and over again. There are two classes of tandem repeats i.e. minisatellites and microsatellites. Minisatellites are normally 10-60 base pairs repeat long and the number of repeats often extends to several dozen. Microsatellites are smaller with 2-6 base pair in repeat. The mechanism in changing number of

repeats also differs in two classes. The minisatellites have the multistep mutations while the microsatellites have single step mutations.

Choosing and using of genetic markers to study the demography and relationship among populations rely heavily on the different rates of mutation among these markers. Changing in tandem repeat length occurs much more frequently than indels or SNPs. On the evolutionary clock, indels and SNPs can be perhaps compared to be the hour hand, while microsatellites and minisatellites are minute and second hand, respectively (Bradman and Thomas, 1998).

Recently, the potential of using microsatellites as polymorphic markers was increased, as only one *Alu* insertion and one minisatellite on Y chromosome were described, but dozens of microsatellites both autosomal and Y-linked are known (Hammer, 1994; Jobling 1994). Even the number of SNPs had been discovered during the last few years, the usage of microsatellites is still going on because of the relative high mutation frequency. Variability at microsatellite loci is being used for individual identification, forensic science, and population genetic analysis (Kayser *et al.*, 2001).

2.5 Short tandem repeats or microsatellite marker

Short tandem repeats (STRs) or Microsatellite is a short sequence of nucleotides repeated that consists of repeating units of 2 to 6 base pair motif. The repeated sequence is often simple, consisting of two, three, or four nucleotides (di-, tri-, and tetranucleotide repeats, respectively) and can be repeated ranging from 10 or greater. This kind of marker spreads throughout the genome and shows high level of polymorphism. As there are often many alleles present at STRs locus, genotyping

them is often fully informative. In this way, STRs are ideal for determining paternity and population genetic studies.

Mutation of the STRs is explained most frequently by slipped strand mispairing (slippage) during DNA replication on a single DNA double helix. This slippage is usually assumed that increases or decreases in the number of repeats take place in a single repeat unit under a stepwise mutation model (Levinson and Gutman, 1987). Some errors in slippage are rectified by proofreading mechanisms but some mutations can escape repair. The descent DNA strand may reanneal out-of-phase with the template strand and becomes longer or shorter than the template after the process ends.

The rate of STRs mutation occurs much more frequently than the rate of point mutation in other neutral regions of DNA, resulting in a high degree of variability. The dinucleotides repeats appear to have mutation rates 1.5–2 times relatively higher than the tetranucleotides and the non-disease-causing trinucleotides have mutation rates intermediately between the di- and tetranucleotides (Chakraborty *et al.*, 1997). The specific number of repeats in a particular or allele usually remains unchanged from generation to generation, apart from novel changing in STRs length.

The high degree of variability and the fact that they are relatively dense in the genomes has made autosomal STRs popular for use as markers in population genetic studies. Rolf *et al.* (1998) genotyped autosomal STRs of seven Asian populations i.e. 4 groups from China (Han, Bai, Dai, Qiang), Thai, Korean, Japanese and compared with the Ovambos from Namibia and Europeans - the Germans from northwestern Germany. A phylogenetic tree based on allelic frequencies indicated close relationship of the Asian populations, while the Germans and the Ovambos were

outside the cluster. Among studied Asian populations, Bai and Dai (Tai) populations were clear outliers of the cluster of all other Asians, indicating an unexpected pattern of genetic heterogeneity of the Chinese nation. Two clusters of Asian populations could be established: the Korean and Japanese together with the Han and Qiang, then, Bai, Dai (Tai), and Thai populations forming a separate cluster. The autosomal STRs evidence also suggested that the ancestor of the populations currently residing in East Asia entered from Southeast Asia (Chu *et al.*, 1998). However, due to the meiotic recombination between pair of autosomal homologous chromosome, these genetic evidences failed to make a tentative suggestion about ethnic ancestor and the estimation of population genetic structure based on autosomal STRs might be unreliable.

2.6 Human X chromosome

The X chromosome is one of the two sex chromosomes in humans, another is Y chromosome. It is notably larger in size and has more active euchromatin region than its Y counterpart. It contains more than 153 million base pairs encoding 1,134 genes. Even though, it carries thousand of genes but few of these have anything to do directly with sex determination. Each person normally has one pair of sex chromosome in each cell. Females have two X chromosomes, while males have one X and one Y chromosome. Therefore, in female, the genetic recombination may occur between a pair of X chromosome. Early in embryonic development in females, one of the two X chromosomes is randomly inactivated in nearly all somatic cells, called as X-inactivation and creates a Barr body. The X chromosome is remarkably

as gene poor region. It is composed primarily of repeated segment of DNA, mostly associated with CT family, which do not code for proteins or any known function.

Due to its unequal number between two sexes and genetic recombination in female as well as its relative abundance of dinucleotide repeated segments, X chromosome is not widely used to study population relationship but can be used to investigate population genetic structure as basic information for human identification, paternity analysis, and genetic mapping. Matsushita *et al.* (2003) had analyzed allele frequency data of 18 STRs loci on the X chromosome in a Japanese population by means of multiplex PCR and the ABI PRISM Linkage Mapping Set MD 10 Panel 28. Allele frequency profiles showed that there were no significant differences between male and female alleles. The distribution of genotypes of these 18 markers fitted the Hardy-Weinberg equilibrium ($0.05 < P < 0.95$). The heterozygosity levels of these STR loci, except for DXS1106 and DXS8055, ranged from 62.9% to 87.5%.

Deep to the human evolution, Harris and Hey (1999) revealed a fixed DNA sequence difference of X-linked PDHA1 (pyruvate dehydrogenase *E1* a subunit) locus between African and non-African samples. They dated the onset of population subdivision to be about 200,000 years ago. The pattern of nucleotide haplotypes showed no share between African and non-African populations. PDHA1 revealed very low variation among non-Africans, which was consistent with reports from other X-linked and autosomal data set. These DNA sequence results did not suggest evidence of human population expansion and thus were in conflict with mitochondrial DNA data.

2.7 Human Y chromosome

Y chromosome is male specific sex determination involving the development of the testis and constitutively haploid. It consists of approximately 60 million base pairs containing 247 genes, mostly for male reproduction related protein and associated male development. Unlike other chromosomes, it passes from father to son and largely escapes from meiotic recombination. Human Y chromosome comprises two small pseudoautosomal regions at two ends of the chromosome allowing pairing and exchanging with the X chromosome but these two regions amount less than 3,000 bases. Therefore, Y chromosome refers to the non-recombining majority which is also variously known as Non Recombining Portion of Y chromosome (NRPY).

The importance of escaping from recombination of the human Y chromosome provides a unique system of haplotype, the combinations of allelic states of markers along the chromosome transmitted from generation to generation. The polymorphisms along Y chromosome may arise only by mutation and do not reshuffling as other chromosome experience. Thus, the entire Y chromosome preserves a simpler record of male history and uniparentally inherits to their lineages. The advantage of tracing the male genetic line makes the Y chromosome an important tool in the study of modern human origins, migration, and population differentiation. By examining the differences between modern Y chromosomes we can attempt to reconstruct history of human paternal lineages.

Rather than complete sequencing, data of Y chromosome is generally gathered from STRs loci and single nucleotides polymorphisms (SNPs) sites. Efforts to discover genome-wide sequence variation have identified vast numbers of Y-specific markers. There are now more than 200 binary SNPs that are well characterized, and

100–200 potentially useful new STRs, as well about 30 published polymorphic tri-, tetra-, and pentanucleotide repeat markers. It represents an almost unlimited source of phylogenetic information.

As mutation is the only force that causes diversify of Y haplotypes, understanding mutational dynamics is important to understanding the origins of haplotype diversity. Knowledge of the rates and processes of mutation at different classes of marker is fundamental to evolutionary interpretations of Y chromosome data. The biallelic SNPs markers have low mutation rates, while STRs are more rapidly mutated. As results, the robust haplogroups are well defined by biallelic SNPs markers, while phylogeny of Y chromosomal haplotypes can be unified using set of STRs data (Hammer and Zegura, 1996; Underhill *et al.*, 1997).

A number of Y chromosomal STRs markers were being described and more are expected in the near future. Thomas *et al.* (1999) reviewed eight STRs loci on Y chromosome i.e. DYS19, DYS388, DYS389I, DYS389II, DYS390, DYS391, DYS392, and DYS393. These loci were globally used to distinguish populations. The methods of multiplex PCR were developed to amplify all of these loci within only two reactions, which beneficially reduce cost and increase the rate that data are generated. Six more STRs were derived from available sequence database by Ayub *et al.* (2000) i.e. DYS434, DYS435, DYS436, DYS437, DYS438, and DYS439. This set of STRs was assembled into a single multiplex reaction and was used to investigate degree of polymorphism in nine ethnic groups in Pakistan as well as to build up the database. The same set of six STRs loci were analyzed in Han Chinese population (Hou *et al.*, 2001). There were distinct differences in the allele distributions and several alleles were not common to Pakistan and Han Chinese.

Some novel STRs were not yet designated in DYS system as recommend by DNA commission of the International Society of Forensic Genetics (Gill *et al.*, 2001). Y-GATA-A7.1, Y-GATA-A7.2 and Y-GATA-A10 were obtained from a cosmid library of human Y chromosomes (White *et al.*, 1999).

The use of Y chromosomal STRs polymorphism has become commonplace in population genetic studies. Kayser *et al.* (1997) arranged a multicenter study on evaluation of 13 Y-chromosomal STRs in 48 populations around the world. They suggested that this system had an advantage in detecting and discriminating male DNA in addition to well-established autosomal systems. Y chromosomal STRs were frequently used to investigate genetic structure and affinities among global populations. The genetic variance at seven Y-chromosomal STRs loci was studied among male individuals from 20 globally dispersed human populations (Kayser *et al.*, 2001). Analyses of haplotype diversity and population-specific haplotypes revealed marked population structure differences between more-isolated indigenous populations (e.g. Central African Pygmies or Greenland Inuit) and more-admixed populations (e.g., Europeans or Surinamese). Furthermore, male individuals from isolated indigenous populations shared haplotypes mainly with male individuals from their own population. Phylogenetic analysis identified close genetic affinities among European populations and among New Guinean populations.

Many population histories were reconstructed using genetic material data. Based on 16 Y-STRs loci, Zerjal *et al.* (2003) identified Y chromosomal lineage of 16 populations throughout a large region of Asia, stretching from the Pacific to the Caspian Sea. A single male line, probably originating in Mongolia about 1,000 years ago (95% confidence interval limits about 700-1,300 years) and spread to represent

about 8% of males in a region stretching from northeastern China to Uzbekistan. The estimated time met the historical records in the period of Genghis (Chingis) Khan (1162–1227 A.D.) and his male relatives. He established the largest land empire in history and often slaughtered the conquered populations, and he and his close male relatives had many children. Although the Mongol empire later disintegrated as a political unit, his male-line descendants ruled large areas of Asia for many generations. On the mainland Japanese, Hammer and Horai (1995) investigated the relationship among Japanese, Okinawan, and Taiwanese populations in order to trace back their origin by using Y chromosome polymorphisms. Their study supported the historical theory that the modern Japanese were the result of the admixture between their two ancestors, the ancient Jomon, used to live there in the past, and Okinawa-Yayoi people who migrated from Korea or Mainland China.

During the last few years, in addition to the description of new Y chromosomal STRs polymorphisms, there has been a large amount of population and sequencing data published. These data were applied to various scientific points of view especially in forensic science. The haplotypic distributions of 9 STRs loci were investigated among African-Americans, European-Americans, and Hispanics, in order to find out the existence of significant genetic differences among geographic subgroups of U.S. populations (Kayser *et al.*, 2003). There were no significant differences in the distribution of Y-STRs haplotypes among African-American groups, whereas European-American and Hispanic groups exhibited significant geographic heterogeneity. The lack of significant geographic heterogeneity among Y-STRs haplotypes in U.S ethnic groups means that DNA databases do not need to be constructed for separate geographic regions in the U.S.

Each Y chromosomal STRs locus has different power of discrimination. Kangwanpong *et al.* (2004) had developed a computational science approach to calculate the minimum number and selected the most suitable STRs markers for evaluating the diversity and genetic distance among the hilltribes in northern Thailand. Using the decision tree induction algorithm, seven STRs loci out of fifteen were selected. Thereby, this approach could reduce the number of Y-chromosomal STRs used in population studies and still achieves the same information.

2.8 Mitochondrial DNA

Human mitochondrial DNA (mtDNA) is a naked circular double-stranded genome with 16,569 base pairs (bp) in length. It contains 37 genes i.e. 13 subunits of the oxidative phosphorylation system, 2 ribosomal RNAs (rRNAs), and 22 transfer RNAs (tRNAs). It presents in high number of copies in each cell, not within the nucleus, but within the cell's energy-generating organelles, the mitochondria. As those genes are essential for the survival of human species, they are well conserved and have little variations. Although, mtDNA consists predominantly of coding sequences, the 1,100 bp fragment functions mainly in regulation and is therefore termed the control region or displacement loop region (D-loop region).

MtDNA presents in high copy number in human cells. Each cell in the body contains 10 to 100 mitochondrial compartments with each of these housing between 0 to 11 copies of the mitochondrial genome (Ingman, 2003). This property, along with the cytoplasmic location of mtDNA and completely separate from the nuclear DNA, makes it easier to obtain mtDNA from various kind of specimen even fossil remains. The multiple copies of the mtDNA genome within an individual may not all be

identical. The presence of mitochondrial copies differing by one or more nucleotide substitutions in the same individual is known as heteroplasmy. However, this heterogeneity of mtDNA is not common because during fertilization, paternal mitochondria are labeled for degradation through the ubiquitin pathway. Therefore, heteroplasmy remains as an exceedingly rare phenomenon in human individual.

Like Y chromosome, mtDNA is uniparentally inherited but through maternal lineage. This is one of the great advantages as it enables to trace maternal ancestry of a population back through time, without the confounding effects of biparental inheritance and recombination inherent in nuclear DNA. MtDNA molecules had been known as lack of recombination and completely transmitted as a block of haplotype. But, recently, on the basis of linkage disequilibrium (LD) studies, evidence of recombination has been claimed among paternal and maternal human mtDNA (Awadalla *et al.*, 1999). However, leakage of paternal mtDNA to their children is very rare, recombination in mtDNA is not the major issue and can be eliminated.

The mutation rate of mtDNA genome is typically 5 to 10 times higher than that of nuclear DNA (Ingman, 2003). The reason for this high rate is thought to be due to either a high rate of nucleotide misincorporation or low DNA polymerase repair efficiency. The rate of nucleotide substitution is even higher in the non-coding control region, 5 to nearly 20 times faster than that of the coding region (Stoneking, 2000). However, there is now a debate among the exact estimate of mtDNA mutation rates and which to use for studies of population history. In this study, the author used the mutation rate that was estimated by Ward *et al.* (1991), assuming a mutation rate of 1.65×10^{-7} per bp per year or 33% divergence per million years and a generation of 20 years.

Compounding of these high copy number, maternal inheritance, lack of recombination, and a generally higher mutation rate features, human mtDNA has become widely used for studying human evolution, migration, and population history. The analysis of mtDNA has been heavily utilized to investigate a direct genetic line of women in a population. To date, the mitochondrial D-loop fragment is focused as particular sites that are thought to be variable or rapidly evolving, due to high degree of polymorphism that can be found in this relatively short sequence. The D-loop contains two hypervariable regions, called hypervariable segment I (HVS-I) and hypervariable segment II (HVS-II). The HVS-I and HVS-II are ranged from nucleotide (nt) positions 16024 to 16383 and from nt positions 57-372, respectively, according to the revised Cambridge Reference Sequence human mitochondrial genome database (Andrew *et al.*, 1999). Nucleotide substitution in HVS-I is approximately twice as high as in HVS-II (Meyer *et al.*, 1999). The HVS-I segment also contains a homopolymeric tract that exhibits length polymorphisms. The length polymorphism is due to the polycytosine (C) tract between 8 to 14 bases (nucleotide position 16184 to 16193). The mutation, such as C16189T, can be located within and interrupts the tract (Bendall and Sykes, 1995; Malik *et al.*, 2002a, 2002b).

Initial studies of human mtDNA variation were based on restriction fragment length polymorphisms (RFLPs) of either purified genomicDNA or purified mtDNA (Brown, 1980). In recent years, with the advent of the polymerase chain reaction (PCR), the methods of rapid sequencing of PCR products took over and huge amount of mtDNA data for population studies were generated. Molecular anthropologists have been using mtDNA for almost a decade to examine both the extent of genetic variation in humans and the relatedness of populations all over the world (Horai *et al.*,

1996; Bamshad *et al.*, 2001; Oota *et al.*, 2002; Thomas *et al.*, 2002; Yao *et al.*, 2002a, 2002b; Yao and Zhang, 2002; Cordaux *et al.*, 2003; Maruyama *et al.*, 2003; Tajima *et al.*, 2003).

As mtDNA presents in high copy number in an individual, it is ideal to extract mtDNA from fossil remains. Depending on the age of the fossil samples, often only mtDNA will still be present, and therefore this is the only insight one can get into the genetic affinities of ancient populations such as Mongolian (Keyser-Tracqui *et al.*, 2003), Columbian (Cruzado, 2002), Etruscan (Vernesi *et al.*, 2004). However, a major problem with ancient DNA studies is contamination. This is particularly a problem when ancient samples of modern humans are analyzed because the contaminating mtDNA will not differ greatly from the authentic mtDNA. Therefore, caution should be exercised when evaluating studies of ancient DNA in modern humans.

2.9 Genetic evidence and human evolution

“How did our specie originate and spread around the world to become the most dominant specie on the planet?” is the major theme that human population geneticist focused intensely during the past few decades. The greatest journey of human being left behind a trail of such unanswered questions. Although some past evidences were discovered, it seemed unable to fulfill human curiosity and many pieces of the puzzle could not be assembled. Most geneticists have considered two opposing hypotheses: the Multiregional and Out of Africa hypothesis.

The multiregional hypothesis of modern human origin posited that modern humans evolved simultaneously from the descendants of archaic *Homo sapiens* and

even *Homo erectus* throughout the Old World, perhaps, by some amount of gene flow among archaic populations. The anatomically modern human derived directly from locally found fossil types in at least four centers like the Near East, South and East Africa, North China and Southeast Asia. Fossil records were the real evidences that some paleontologists used to support this polycentric hypothesis (Jobling *et al.*, 2004). The major difficulty of this hypothesis is that it requires parallel evolution over all of the Old World for a long period. It is questionable from a genetic point of view whether parallel evolution can continue for a long period and eventually produce organisms very different from the original ones but highly similar to each other (Cavalli-Sforza *et al.*, 1994).

The Out of Africa or single origin hypothesis suggests that anatomically modern humans evolved in Africa before supplanting archaic populations in Europe and Asia. Genetic evidences supported this hypothesis via the recent replacement model. In 1987, study of polymorphism on mtDNA had stunned the world with the finding that all humans alive today can claim as having a common female ancestor who lived in Africa some 150,000 years ago and so called “Matrilineal Most Recent Common Ancestor, Mt-MRCA) or “Mitochondrial Eve” (Cann *et al.*, 1987). However, Mitochondrial Eve was not the only living human female of that time. Many women alived at the same time but only Mitochondrial Eve produced an unbroken line of female descendents carrying her mitochondrial DNA that persist today. Africa was favored to be the originating place of modern human since the greater genetic diversity in African populations than elsewhere had been observed. Phylogenetic analyses also presented mtDNA tree whose first branch separates African from non-African populations, just as expected if all non-African populations

were descendants of an African one. However, the estimated time Mitochondrial Eve living was calculated based on the controversial molecular clock technique. Many subsequent studies had put the human mitochondrial coalescence broadly within the last 200,000-100,000 years (Cann *et al.*, 1987; Vigilant *et al.*, 1991; Harpending, 1994). Human life then sprouted east across the Red Sea into where is now Yemen, and separated into two branches, one up northward to Europe and another traveled through India and all the way to the far reaches of Australia and some upward crossing over the Bering Strait land bridge into America. Studies of mtDNA gained a better understanding of the migrations that shaped human populations, such as the peopling of the New World (Kolman *et al.*, 1996), the colonization of the Pacific (Lum and Cann, 2000), the initial migration to New Guinea and Australia (Ingman *et al.*, 2003), and the settlement of Europe (Cavalli-Sforza and Minch, 1997).

However, mtDNA is only one locus, and only reflects the maternal history of a population. It has therefore become abundantly clear that studies of mtDNA variation need to be complemented with data on the male-specific Y-chromosome, and ideally with autosomal data as well (Jorde *et al.*, 2000). The counterpart of Mitochondrial Eve is known as Y-chromosomal Adam, the patrilineal most recent common ancestor. Judging from molecular clock Y-chromosomal Adam probably lived between 60,000 and 90,000 years ago. The more recent age of the Y-MRCA compared to the mt-MRCA corresponds to a larger statistical dispersion of the probability distribution for a paleolithic man to have living descendants compared to that of a paleolithic woman. While fertile women had equally distributed chances of giving birth to a certain number of fertile descendants, chances for fertile men varied more widely, with some fathering no children and others fathering many, with multiple women (Wikipedia,

2001). However, the Y chromosome, like mtDNA and autosomes, appears to support a recent African origin. Although no locus taken alone would be sufficient to demonstrate support for the out of Africa hypothesis, the consistency of so many loci in supporting a recent African origin builds a compelling case (Seielstad *et al.*, 1999).

2.10 Paternal vs maternal genetic histories

Y-chromosome and mtDNA have been used widely in the population genetic works. As they are transmitted uniparentally, through either paternal or maternal lineages, the story of population were reconstructed on different sides, male and female. Thus, some contexts of unequal contribution factors between males and females such as migration rate, polygamy, rules of postmarital residence were observed to have strongly effect on these sex-specific transmitted markers and known as sex-specific migration patterns. Seielstad *et al.* (1998) found that Y chromosome variants tend to be more localized geographically than those of mtDNA and autosomes. A higher female migration rate than male (via patrilocality, the tendency for wife to move into her husband's house) was used to explain most of this discrepancy, because diversified Y chromosome would enter a population at a lower rate than mtDNA or autosome.

Since this sex-specific migration phenomenon was proposed, the geneticist has paid more concern on asymmetry in the paternal and maternal genetic histories. An unequal contribution of male and female lineages is not uncommon in the American continents, as a consequence of directional gene flow from European men into African and Hispanic Americans in the 16th-17th centuries are historically well known

(Cavajal-Carmona *et al.*, 2000; Seielstad, 2000). Although the postmarital residence was believed to be a major factor in sex-specific migration rate, there has been found to have no important throughout the history of native South American populations. The genetic diversity on autosomal, mtDNA, and Y-Chromosome were used to evaluate sex-specific differences in gene flow of five Native American populations from Columbia. The concordance of these estimates does not support an important difference in migration rates between the males and females. It could be indicating that neither matrilocality nor patrilocality has predominated. In fact, half were considered predominantly patrilocal and half predominantly matrilocal. However, these analyses suggested a pattern of directional mating that preferentially involved immigrant men to native women and established neo-American populations (Mesa *et al.*, 2000).

Analysis of Y-chromosomal and mtDNA polymorphism in two Central Asian lowland populations (Uighurs and Kirghiz) and two highland populations (Kazakhs and Kirghiz) suggested a very different migration pattern in males versus females, in an extended historical frame, with a higher migration rate for females. The reduction of the haplotype genetic diversity was observed in the villages at high altitude, especially in the highland Kirghiz, when compared with the villages at low altitude, which suggests a male founder effect in the settlement of high-altitude lands. Nonetheless, mtDNA genetic diversity in these highland populations is equivalent to that in the lowland populations (Perez-Lezuan *et al.*, 1999).

The Han Chinese, Japanese, and Vietnamese in East and Southeast Asia were also found to have higher migration rate in females than in males. This might reflect patrilocality, as suggested previously by Seielstad *et al.* (1998). But mtDNA

homogeneity observed in Asian populations might indicate a recent demographic expansion arising from successful subsistence due to rice agriculture. The less homogeneity for the Y-chromosome than for mtDNA in these cultivators could reflect the influence of patrilocality operating within this demographic expansion (Oota *et al.*, 2002).

2.11 Linguistic, geographic, and genetic diversity

The most fundamental mechanism by which humans share information is language. There are now 6,912 known living languages all over the world (Gordon, 2005). Classically, language was used and become an important criterion to distinguish human relationships in terms of linguistic affinity. There are a number of ways of classifying the thousands of languages of our world but the most important properties for linguistic classification is paying attention to the internal structure of language (grammar) and common words across languages. The world's languages have been grouped into families that are believed to have common ancestors.

Theoretically, languages in the same group must be originated in one area and can be distributed to be the local languages in several places. Closely related populations were believed to have a short linguistic distance as well as genetic distance. The shared features of languages in one family can be due to shared ancestry and historical evolution of languages might be due to genetic classification. By analyzing Y-chromosomal biallelic and STRs markers, the genetic affinities of populations in Europe, Africa, and Asia were correspondence to linguistic relatedness (Quintana-Murci *et al.*, 1999). The relationship among genetic variability, geographical distance, and linguistic affiliation in South Amerinds also fell in this

category. Migration of females in these peoples generally occurs within the same linguistic group, thereby maintaining the group's genetic homogeneity (Fagundes *et al.*, 2002). The significant correlation between genetic and linguistic relatedness were suggested as a resulting of co-evolution under the condition of genetic isolation (Lum *et al.*, 1998).

However, languages, like any other cultures, can be horizontally acculturated among populations when populations come into contact, even they are not descending from the same ancestor. This evidence was supported by the correspondence between the genetic affinity and the geographic relatedness, but not the linguistic affinity. The interpretation of Y chromosomal data among European populations showed that these peoples were related primarily on the basis of geography rather than on the basis of linguistic affinity. Genetic-barrier analysis also indicated the primacy of geography in the shaping of patterns of variation (Rosser *et al.*, 2000). This scenario had also found between two major linguistic families within Europe: the Indo-European speakers (Norwegians, Swedes, Gotlanders, Lithuanians, Latvians) and Uralic speakers (Saami, Finns, Estonians). The genetic difference based on of Y chromosomes diversity was not ascribable to linguistic affinity. Nevertheless, the differentiation among geographic grouping can be observed (Zerjal *et al.*, 2001).

2.12 Social stratification and genetic variation

Not only language and rules of postmarital residence that have influenced on human genetic variation, the social stratification is another socio-cultural that can transmit from one generation to the next and was widely believed to leave its imprint on population genetic structure. Social stratification which induced by the caste

system are extremely conservative and transmitted quite faithfully. The caste society in India is one of the good examples to find out the effects of the cultural practice and social system on genetic variation. The peoples in India are remarkable as the segmentation of the large population into thousands of endogamous groups. Many of these groups are however clusters of endogamous groups with similar traditional occupations and social status which known as caste. Caste became an important element of Indian politics and was broadly ranked as upper, middle, and lower caste clusters. Members within a caste generally marry among themselves and inter-caste marriages are the incest taboo.

The mitochondrial DNA studies provide some notable insights into the structure of this social mosaic. The Haviks and Mukris communities were chosen from the same district in Uttara Kannada. The difference in their genetic structure suggested that even these two populations were living together in such a restricted geographical locality as a single district of Uttara Kannada but there is no assimilation between them (Gadgil *et al.*, 1997). Such scenario has probably characterized the Indian social mosaic for a long time and probably maintenance of large number of communities in isolation from each other. The evidence on Y chromosome also indicated the same results. There was very little Y chromosomal haplotype sharing among caste clusters, indicating that there was minimal gene flow across the caste (Bamshad *et al.*, 2001; Majumder, 2001).

2.13 Population genetic studies in Thailand

There are conflicting opinions of the origins of the Thai peoples. Since language and culture of Thai peoples are similar to some ethnic groups in southern and southeastern China, scholars presumed that the Thai originated somewhere in China, maybe thousands of years ago (Sunsite, 1998). However, the Thai history had been challenged by some archaeological and skeletal evidences. Nakhbunlung (1994) used craniofacial metric and discrete traits of skeleton to investigate the biological relationships among archaeological and modern Thais and Chinese. The results also refused the immigrant hypothesis from China but failed to clarify that modern Thais were descended from endogenous groups in Thailand. The controversy over the origin of the Thais shows no sign of definite conclusion as many more hypotheses have been put forward. Since then, the origin of the Thai and their relationship to other ethnics become the challenging theme for the population genetic studies in Thailand.

Allele frequencies of 13 gene loci were used to investigate the biological affinities among Thai populations who used languages in different families: Tai-Kadai, Mon-Khmer, Austronesian, and Sino-Tibetan. Measuring of genetic distance showed that the Tai-Kadai was closer to Mon-Khmer, farther to Austronesian, and farthest to Sino-Tibetan. Moreover, the Yuan from Chiang Mai, who related to Lue in Xishuangbanna, China, and Khuen in Myanmar, was not genetically closed to Sino-Tibetan groups. This study concluded that the Thai ancestors might be endogenous people of Southeast Asia who have close biological affinity to Mon-Khmer peoples. However, the mentioned study did not compare Thai population to the Tai groups in

China. The unequivocal results, therefore, need further study and information (Poolsuwan, 2001).

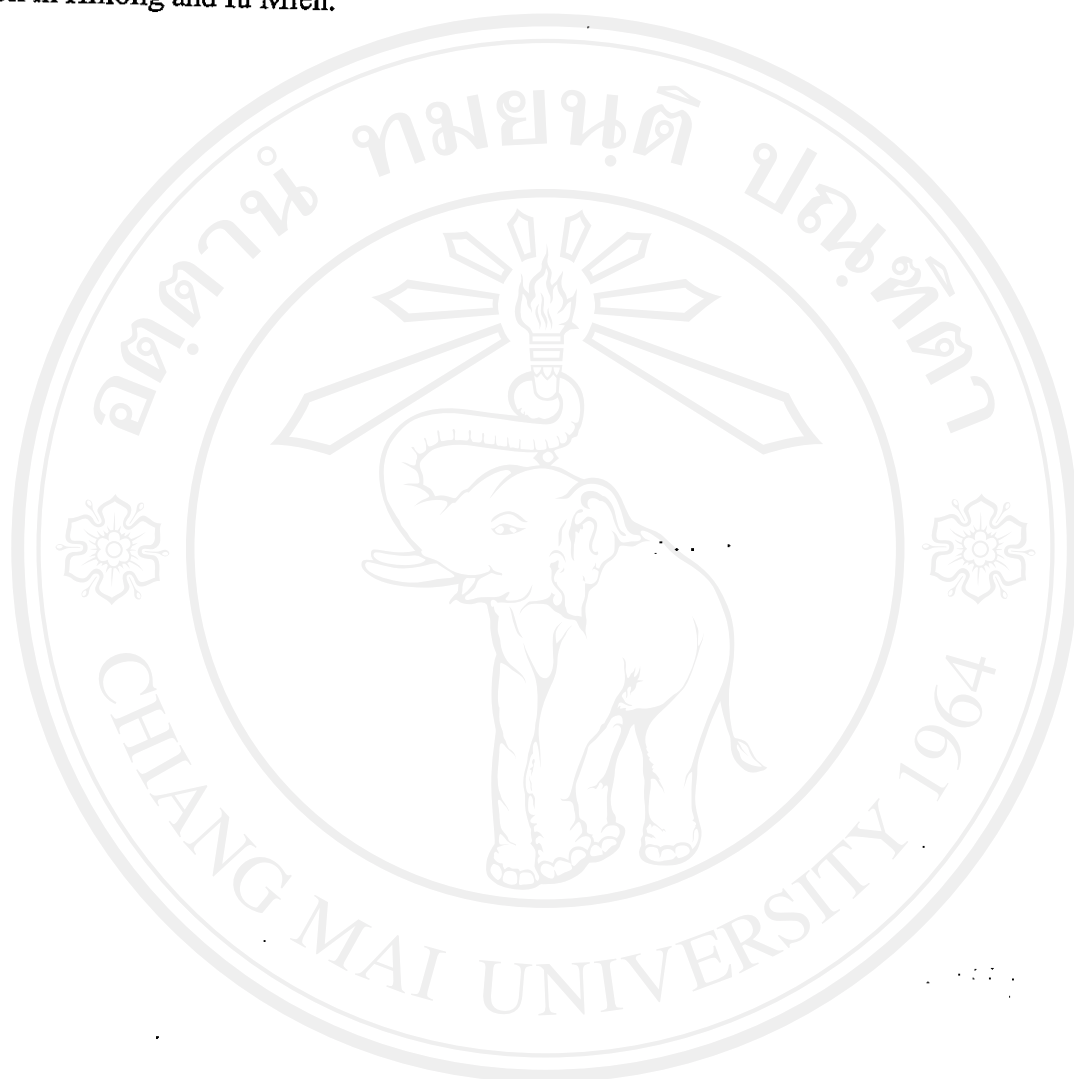
In recent years, with the advent of high-throughput technology in the polymerase chain reaction (PCR) and methods of rapid sequencing of PCR products, it has become more and more common to sequence the mtDNA sequences, even in Thailand. The mtDNA D-loop nucleotide sequences of native Thai populations from two provinces, Chiang Mai and Khon Kaen were analyzed and compared with six ethnic groups of Thailand: hill-tribes (Lisu and Muzur), Phuthai, Lao Song, Chong and aboriginal Sakai. The mtDNA variation and phylogenetic analysis suggested that the 9-bp deletion had occurred in a very ancient ancestry of Southeast Asians, although multiple origins of the deletion could not be identified. Genetic distances among the populations revealed that the Sakai was not related to other Thai populations while Lao Song and Chong were grouped together. The hill tribes, Phuthai, and native northeast Thai (Khon Kaen) were close in genetic affinities. This finding showed some degree of sharing common maternal ancestral lineages (Fucharoen *et al.*, 2001).

The origin of Tai peoples was also under the interest of scientist in other countries. Jin *et al.* (2002) beneficially used the geographic distribution and linguistic relatedness to understand the relationship among Dai (Tai) speaking populations. The Y chromosomal polymorphisms were studied and the origin of these populations was proposed. The Tai speaking populations might be originated in the southern part of East Asia, then migrated northwards and eastwards, with Kam-Sui probably being the oldest.

MtDNA hypervariable sequence I (HVS I) polymorphisms were used to find out the genetic relationship and affinity as well as ethnic origins among four populations of Yunnan province, China (Tibetan, Wa, Tai, and Lahu) by Qian *et al.*, (2001) and Yao and Zhang (2002). The phylogenetic tree showed the correlation between geographic distribution and genetic affinities. Tibetan populations were set with the north-prevalent haplogroups (clades of mtDNA phylogeny) while Tai and Lahu were set with the south one. The Wa populations showed the admixture of north and south haplogroups. The Tai, Wa, and Lahu were also closely related to Han Chinese, while Tibetan and mainland Japanese formed another group. The studies suggested that there were at least two different origins among the minority populations in Yunnan province.

DNA polymorphism has also been used to investigate the hilltribe population relatedness. Kangwanpong *et al.* (2001) investigated three loci of Y chromosomal tetranucleotide repeats among 6 hill-tribes in the northern part of Thailand - Karen, Hmong, Yao (Iu Mien), Lahu, Akha, and Lisu. This study indicated the difference in genetic structure and diversity among these populations. The results also showed an interesting pattern of correlation between the genetic diversity and matrilineal/patrilineal culture. Moreover, the phylogenetic tree constructed from *Fst* genetic distances could revise these populations into two groups which were consistent to the known linguistic clusters. The relationship among the Karen, Hmong, and Iu Mien were more clarified by Srikummool (2005). The difference in the genetic structure of these hilltribes, based on X-, Y-chromosomal and mtDNA markers, was influenced by the rules of the post-marital residence. The adoption tradition had increased the variation of Y chromosome in Iu Mien. Moreover, the

higher male migration rate was observed in Karen, whereas females had higher migration in Hmong and Iu Mien.



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