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Full Length Research Paper

Genetic diversity and relationships among cabbage (*Brassica oleracea* var. *capitata*) landraces in China revealed by AFLP markers

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Genetic diversity and relationships among Chinese traditional cabbage landraces have not yet been well investigated. To explore the diversity, 83 landraces originating in Northern China, Southern China, Eastern Europe, Western Europe as well as other countries were evaluated by using AFLP markers. Results indicated that cabbage landraces exhibited a relatively low level of diversity. Among the 575 markers, 41.9% were polymorphic with an average PIC value of 0.354. Unweighted pair group method with arithmetic averages (UPGMA) cluster and population structure analysis consistently divided all landraces into two major groups reflecting geographic origins. Group 1 was a distinct group comprised of Northern China landraces and Eastern European landraces, whereas Group 2 was comprised of populations of Southern China landraces, Western European populations and other countries. Landraces with varied maturing times or head types could not be distinguished based on molecular data. The Northern China population was closely allied to the Eastern Europe population (*D* = 0.037). The integration of our data with historical documents confirmed that traditional cabbage landraces cultivated in North of China were first introduced from Russia.

Key words: Amplified fragment length polymorphism (AFLP), genetic diversity, cabbage (*Brassica oleracea* var. *capitata*), landraces, population structure.

INTRODUCTION

Cabbage (*Brassica oleracea* var. *capitata*) is one of the most widely grown and important vegetable crops consumed worldwide and are particularly widespread in many agricultural regions of China. More than 937 thousand hectares cabbage is planted in china every year (Fang, 2008). Although, local landraces have been widely cultivated in many Chinese provinces prior to the 1970s, during the last 40 years, these populations were rapidly replaced by many modern hybrid cultivars developed from genotypes with a restricted genetic base. The traditional local cabbage landraces distributed primarily throughout Northern China exhibitt many high quality agronomic traits including disease resistance and ecological adaptation following a long history of natural and artificial selection in China. For instance, in the past four decades, most of the commercial cabbage hybrid cultivars in China were developed by crossing a traditional cabbage landraces with a newly introduced foreign cabbage breeding line (Fang et al., 2002). One of the most important black rot resistant cabbage accession PI436606 was developed from a Chinese traditional landrace Heiyedapingtou cultivated in North of China before 1970s (Dickson and Hunter, 1987).

To preserve the local germplasm, China launched a large scale nationwide germplasm collection for traditional head cabbage landraces. At the beginning of the 1980s, there were totally 221 head cabbage landraces

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collected and deposited into the National vegetables Gene Bank at the Institute for Vegetable and Flowers (IVF) of the Chinese Academy of Agricultural Sciences (CAAS). Some of them have been used as breeding materials of hybrid cultivars such as Heyexiaopingtou, Jingzhaoshen, Heyepingtou, Jixinganlan, Niuxinganlan, Dapingtou, Erwuye, Nanmuye and Erhutou. However, most of them have not been fully utilized up to till now.

Thus, to explore the promising breeding materials in the cabbage landraces conserved in China and improve cabbage varieties adapted to various biotic and abiotic stresses, genetic diversity, gene communication and cultivar exchange between different countries and planting regions must be explored to address these aims.

Several methodologies have shown efficacy in assessing genetic diversity within and among populations, including morphologic traits and isozymes. Among these molecular approaches, RAPDs have been the most commonly used PCR-based fingerprinting technique applied to analyze genetic diversity in *B. oleracea* to date (Hu and Quiros, 1991; Kresovich et al., 1992; Santos et al., 1994; Margalé et al., 1995; Lanner-Herrera et al., 1996; Phippen et al., 1997; Lazaro and Aguinagalde, 1998; Koutita et al., 2005), largely due to its simplicity, efficiency in performance and no requirement for sequence generation. Recently, simple sequence repeat (SSR) and amplified fragment length polymorphism (AFLP) have been advocated as the most common and effective marker systems for genetic analyses in different Brassica species cultivars (Sobotka et al., 2004; Tonguç and Griffiths, 2004; Zhao et al., 2005; Louarn et al., 2007; Van Hintum et al., 2007; Mei et al., 2010). Compared with codominant SSR, although, AFLPs might be associated with the inability to distin-guish heterozygotes from homozygotes, many research suggested that the genetic estimates based on AFLPs and SSRs are highly correlated because the high numbers of polymorphic loci counterbalance the loss of information resulting from dominance (Powell et al., 1996; Gerber et al., 2000; Baraket et al., 2011; Mei et al., 2010). Recently, Van Hintum (2007) conducted research on the genetic diversity distribution in a selection of very similar groups of Dutch white cabbage accessions and confirmed that AFLP markers are extremely sensitive and especially possessed great utility in measuring minor genetic changes between some of the more similar cabbage accessions.

Although, lots of works on genetic diversity analysis in *B. oleracea* have been reported, most of them pay attention to the divergency among different subspecies. To date, little work has been reported to evaluate genetic diversity and relationships between local cabbage landraces in China. In this paper, we used the fluorescence-based AFLP approach to investigate genetic diversity and relationships among head cabbage landraces collected from different planting regions of China. Such information will be of great interest for future genetic improvement of heading cabbage in China.

MATERIALS AND METHODS

Plant materials

A total of 83 heading cabbage landraces were obtained from the Institute for Vegetable and Flowers (IVF) at the Chinese Academy of Agricultural Sciences (CAAS), including 43 landraces collected from the provinces to the north of the Yangtze River (Northern China Population), 10 landraces from areas to the south of the Yangtze River (Southern China Population), 13 landraces from Russia and Ukraine (Eastern Europe Population), six landraces or open pollinated cultivars from Netherlands, Denmark and Germany (Western Europe Population) and 11 from Africa, India, Japan and Korea (here referred to as other countries population). All accessions, origins and main morphotype are summarized in Table 1.
All accessions were raised in the field at the IVF experimental center. Young leaves were collected from a pool of five plants of each accession and used for DNA preparation.

DNA extraction and AFLP analysis

Total genomic DNA was extracted from young leaves using the protocol of Doyle and Doyle (1987) with minor modifications. A total of 300 mg of fresh plant material was ground and initially extracted in tubes containing CTAB extraction buffer (100 mM Tris-pH 7.5, 700 mM NaCl, 50 mM EDTA pH 8.0) and iron bullets in a Retsch shaker. Two more extraction steps were preformed with chloroform/isoamilic alcohol (24:1). The DNA of each sample was retained in a final chloroform extraction and subsequently diluted in 100 µl dd water.

AFLP fingerprints were generated based on the protocol described by Vos et al. (1995) with minor modifications. Total genomic DNA (300 to 500 ng) was digested using two restriction enzymes (*EcoR* I and *Mse* I) and then ligated to adaptors. Pre-amplifications were carried out using E00 (5´-GACTGCGTA CCAATTC-3´) and M00 (5´ -GATGAGTCCTGAGTAA-3´) primers. Selective amplification was performed with primers having three selective nucleotides each. Only E-NNN primers were labeled with IRD-700 or IRD-800 at the 5´ end for selective amplification. In order to identify primer combinations that yielded well scorable polymorphisms approximately, 80 primers were tested on six samples. Finally, 12 suitable combinations were selected for further analysis based on the number of unambiguously scorable polymorphic bands (Table 2). The AFLP amplification products were analyzed with a LI-COR model 4200 dual-dye automated DNA sequencing system. Electrophoresis conditions and data collection were as described by Myburg and Remington (2000)

Data analysis

All AFLP bands were treated as dominant markers and all weak and unresolved bands were discarded. Only clearly distinguishable polymorphic bands in the range of 50 to 500 bp were scored as present (1) or absent (0) to generate an binary data matrix for genetic analysis.

POPGENE version 1.32 (Yeh et al., 1999) was used to calculate Nei's genetic diversity (Nei, 1973) and Shannon-Weaver diversity index (*I*) (Shannon and Weaver, 1949) within populations. The probability of a polymorphism between two random genotypes (the polymorphism information content or PIC) was estimated using the following formula:

Table 1. List of accessions.

Accession name	Label	Accession number	Type of line[a]	Origin[a]	Accession name	Label	Accession number	Type of line[a]	Origin[a]
Jinyuanganlan	Jiny	V04A0014	L	Gansu	Damiandongganlan	Dam	V04A0213	L	Xingjiang
Erzhuanzhi	EZ	V04A0019	L	Gansu	Xiaojixin	Xiao		L	Shanghai
Pingdinbaoxincai	Pin	V04A0020	L	Gansu	Liushitianzhaoyecai	Liu		L	Guangdong
Hongjinbai	Ho	V04A0021	L	Gansu	Shanghaijixin	Sha	V04A0125	L	Shang Hai
Baotoucai	Ba	V04A0167	L	Gansu	Heiyexiaopingtou	HY		L	Shanghai
Heyepingtou	Hey	V04A0016	L	Gansu	Dawuyelianbai	Daw	V04A0005	L	Sichuan
Dapingtou	Dapi	V04A0166	L	Gansu	Dananmuye	Dan	V04A0138	L	Sicuan
Baobaocai	Bao	V04A0169	L	Gansu	Taiwan1	TA1		L	Taiwan
Hailaerwanganlan	Hail	V04A0060	L	Heilongjiang	Taiwan2	TA2		L	Taiwan
Kaifengniuxin	Kai	V04A0047	L	Henan	Taiwan3	TA3		L	Taiwan
Hongqimopan	Hon	V04A0057	L	Heilongjiang	Xiafeng	Xiaf		L	Taiwan
Manzhouliganlan	Man	V04A0058	L	Heilong jiang	Yaluoshilaka	Yal	V04A0191	L	Ukraine
Hailaerganlan	Hai	V04A0059	L	Heilong jiang	Licaganlan	Lic	V04A0192	L	Ukraine
Hongqipingtou	Hong	V04A0062	L	Heilong jiang	Russian1	RU1		L	Russia
Erdazhiyuancai	Erd	V04A0091	L	Neimenggu	Russian2	RU2		L	Russia
Heshangtou	Hes	V04A0092	L	Neimenggu	Russian3	RU3		L	Russia
Dazhiyuancai	Daz	V04A0093	L	Neimenggu	Russian4	RU4		L	Russia
Hanghoudayuancai	Han	V04A0095	L	Neimenggu	Russian5	RU5		L	Russia
Sumuqinerhutou	Sum	V04A0096	L	Neimenggu	Russian6	RU6		L	Russia
Nongmudapingtou	Non	V04A0100	L	Neimenggu	Russian7	RU7		L	Russia
Erheiganlan	Erh	V04A0183	L	Neimenggu	Hope	Hop		OP	Russia
Dapingding	Dap	V04A0184	L	Neimenggu	Russian9	RU9		L	Russia
Qiaokaoshanbandun	Qia	V04A0185	L	Neimenggu	Slava	Sla		OP	Russia
Erdariqi	Erda	V04A0187	L	Neimenggu	Gift	Gif		OP	Russia
Daheiganlan	Dah	V04A0188	L	Neimenggu	Beijingzhaoshu	Be		OP	Denmark
Wuyan711	Wuy	V04A0094	L	Neimenggu	Danjinzhaosu	Danj		OP	Denmark
Rentoucai	Ren	V04A0098	L	Neimenggu	Goldacre	Gol		OP	Denmark
Wangoudapingding	Wan	V04A0072	L	Ji Lin	Copenhagenmarket	Cop		OP	Denmark
Dapingtouerhao	Da	V04A0074	L	Ji Lin	Deguo1	DE1		L	German
Jinzhaoshen	Jin		L	Liaoning	Helan1	HE1		L	Netherland
Gaoganganlan	Gao	V04A0102	L	Ningxia	Feizhou1	FE1		OP	Africa
Yancidaganlan	Yan	V04A0189	L	Ningxia	Feizhou2	FE2		OP	Africa

Table 1. Continue

Duanbaganlan	Dua	V04A0106	L	Qinghai	Feizhou3	FE3	OP	Africa
Changbaganlan	Cha	V04A0107	L	Qinghai	Feizhou4	FE4	OP	Africa
Liuyuehuang	Liuy	V04A0105	L	Qinghai	Feizhou5	FE5	OP	Africa
Dingbiandapingtou	Din	V04A0115	L	Shaanxi	Yindu1	YI1	L	India
Xiandapingtou	Xia		L	Shaanxi	Qiude	Qiu	L	Japan
Luowenhuangyuanbaicai	Luo	V04A0199	L	Shanxi	Fuji early	Fuj	OP	Japan
Yibaiershitianhuizhibai	Yib	V04A0202	L	Shanxi	Huangmiao	Hua	L	Japan
Datongdariyuan	Dat	V04A0206	L	Shanxi	Korea1	KO1	L	Korea
Wushidongganlan	Wus	V04A0130	L	Xingjiang	Korea2	KO2	L	Korea
Dalianhuabai	Dal	V04A0209	L	Xingjiang				

[a]Type of line abbreviated as L = landrace, OP = open pollinated cultivar.
[b]Origin refers to either a country or to a province within China.

Table 2. Data recorded for the 12 AFLP primer combinations employed to detect polymorphisms among 83 heading cabbage landraces.

Primer combination	Number of band	Polymorphic band	Polymorphism rate (%)	PIC
E-AGG/M-CCT	39	10	25.6	0.339
E-AGC/M-CGC	19	6	31.6	0.412
E-AGT/M-CCG	52	19	36.5	0.303
E-AGG/M-CCG	81	49	60.5	0.333
E-ACC/M-CCT	48	30	62.5	0.318
E-AAG/M-CCC	66	28	42.4	0.345
E-ACA/M-CCT	50	37	74.0	0.348
E-AGC/M-GAG	18	7	38.9	0.412
E-AGA/M-CCG	43	18	41.9	0.409
E-AGT/M-CCT	49	18	36.7	0.387
E-AGA/M-CCT	45	11	24.4	0.345
E-ACC/M-CTG	65	18	27.7	0.301
Total	575	251	-	-
Average	47.9	20.9	41.9	0.354

$$PIC = 1 - \sum_{i=1}^{k} P_i^2 \quad (1)$$

Where, k is the total number of alleles detected for a given marker locus and P_i is the frequency of the ith allele in the set of genotypes investigated (Anderson et al., 1993).

Similarity was calculated as the proportion of AFLP markers where the comparison of two accessions exhibited the same score (SM_{xy}= (n_{11}+n_{00})/n) and where n was the number of markers scored. Cluster analysis was performed using the unweighted pair group method with arithmetic averages (UPGMA). Dendrograms were constructed using the UPGMA algorithms in the MEGA 4.0 software (Tamura et al., 2007).

A Bayesian approach with the program structure 2.2 was used to identify population groups (Falush et al., 2007; Pritchard et al., 2000) The number of population clusters (K) was set to vary between 1 and 10 with 600,000 Markov Chain Monte Carlo (MCMC) iterations and a burning period of 60,000. The value of K with the highest likelihood was selected as the optimal number of clusters in the sample at which, Pr(X/K) no longer increased with increasing values of K.

All cabbage landraces were subdivided into five geographical populations (Northern China, Southern China, Eastern Europe, West Europe and other countries) according to the accession country of origin. A classical analysis of molecular variance (AMOVA) within and among population components was analyzed using WINAMOVA 1.55 (Excoffier, 1992).

RESULTS

Levels of polymorphism

In this study, 12 pairs of *EcoR* I/*Mse* I primers, which were

selected from 128 pairs of primer combinations, showed clear banding patterns with notable polymorphisms. These primer pairs were used to fingerprint 83 *B. oleracea* accessions of different geographical origins. A total of 575 scorable amplification products ranging from 50 to 600 bp were obtained, of which 251 were polymorphic with an average of 20.9 polymorphic bands per primer combination. The levels of polymorphism were calculated based on the percentage of polymorphic bands, which varied from 24.4% for the E-AGA/M-CCT primer combination to 74.0% for the E-ACA/M-CCT primer combination (Table 2). The polymorphism content estimation information for the 12 primer combinations ranged from 0.301 to 0.412, with an average of 0.354.

Table 2 shows the selected primers, number of polymorphic bands, rate of polymorphism and PIC among accessions.

Genetic relationship and population structure among all landraces

In this study, all possible pairwise comparisons were used to assess genetic similarities of the 83 head cabbage based on the 251 polymorphic AFLP markers; a high range of similarity among landraces was observed. The genetic similarities ranged from 0.413 in a pairs of genotypes ('Da pingtouerhao' versus 'Kaifengniuxin') to 0.933 in a pair of genotypes ('Sumuqinerhutou' versus 'Erheiganlan'), with an average value of 0.736.

A UPGMA dendrogram was generated to evaluate similarity values among landraces (Figure 1). The resulting dendrogram resolved two major clusters of genotypes with low bootstrap values. However, general interpretations can be made from the results. The Chinese landraces from the Northern provinces of China (36 of 43 or 84%) and Eastern European landraces (5 of 8 or 63%) were allied in Group 1. Group 2 was comprised of the Chinese landraces in the Southern provinces of China (7 of 10 or 70%) and Western European landraces (4 of 6 or 67%). The landraces from other countries (Africa, India, Japan and Korea) were distributed in both groups. No obvious clustering based on morphotypes was evident, because landraces with various maturing times or head types were not clearly distinguished based on molecular data. These results suggested that most polymorphisms do not contribute to the phenotypic variation in head cabbage.

Population structure generated similar results using structure 2.2 software (Figure 1). The results indicated that a K=2 value was the best average assignment rate. The software provided the coefficients of estimated ancestry per individual in each group. In the plot of ancestry estimates shown in Figure 1 (parallel to the UPGMA dendrogram), each individual is represented by a single horizontal bar broken into two segments, with lengths proportional to the individual's estimated ancestry fraction from each of the two groups. Model-based groups were congruent with dendrogram classifications.

The 'red bar' group corresponds to the first cluster in the UPGMA dendrogram (Group 1), while the 'green bar' corresponds to the second cluster (Group 2). Population composition of Groups 1 and 2 generated by structure 2.2 showed a more defined delimitation supporting different geographical origins. Group I included 51 landraces, representing the Northern China population (represented by 37 landraces) and the Eastern European population (represented by 10 landraces). 32 landraces comprised Group 2 and circumscribed the Southern China population (represented by 7 landraces), the Western European population (represented by 5 landraces) and the other countries population (represented by 11 landraces).

Genetic diversity among geographical populations

Genetic diversity among cabbage landraces was congruent with geographical origins based on AFLP data. To further explore the genetic diversity among the five geographical populations, POPGENE 1.32 was used to calculate Nei's genetic diversity (h) and the Shannon-Weaver index (I). Total genetic diversity (h) and the Shannon-Weaver index (I) for all cabbage landraces was 0.317 and 0.483, respectively. Genetic diversity was greatest in the Northern China population, with a mean h-value of 0.319 and I-value of 0.477. These measures were lower in the Southern China population, which exhibited an h-value of 0.261 and I-value of 0.398. AMOVA partitioned population genetic diversity and indicated that the major portion of genetic diversity was within geographical populations, even when all the landraces were analyzed together (Figure 2a) or only Chinese landraces (Figure 2b) were analyzed independently. Genetic differentiation between different geographical origins was extremely low. This result suggested that local differentiation in Chinese head cabbage landraces did not arise following introduction into China. Low genetic differentiation among landrace populations was confirmed by high gene flow (Nm = 3.509).

Genetic relationships among geographical populations

Gene differentiation between the five geographical populations was further explored by generating estimates of genetic distance based on AFLP allele frequencies. Pairwise comparisons of the five populations revealed high genetic identity values ranging from 0.906 to 0.964, which also indicated high similarity and closer genetic distance between different geographical populations.

Relationships between populations were further illustrated by a UPGMA dendrogram, based on Nei's

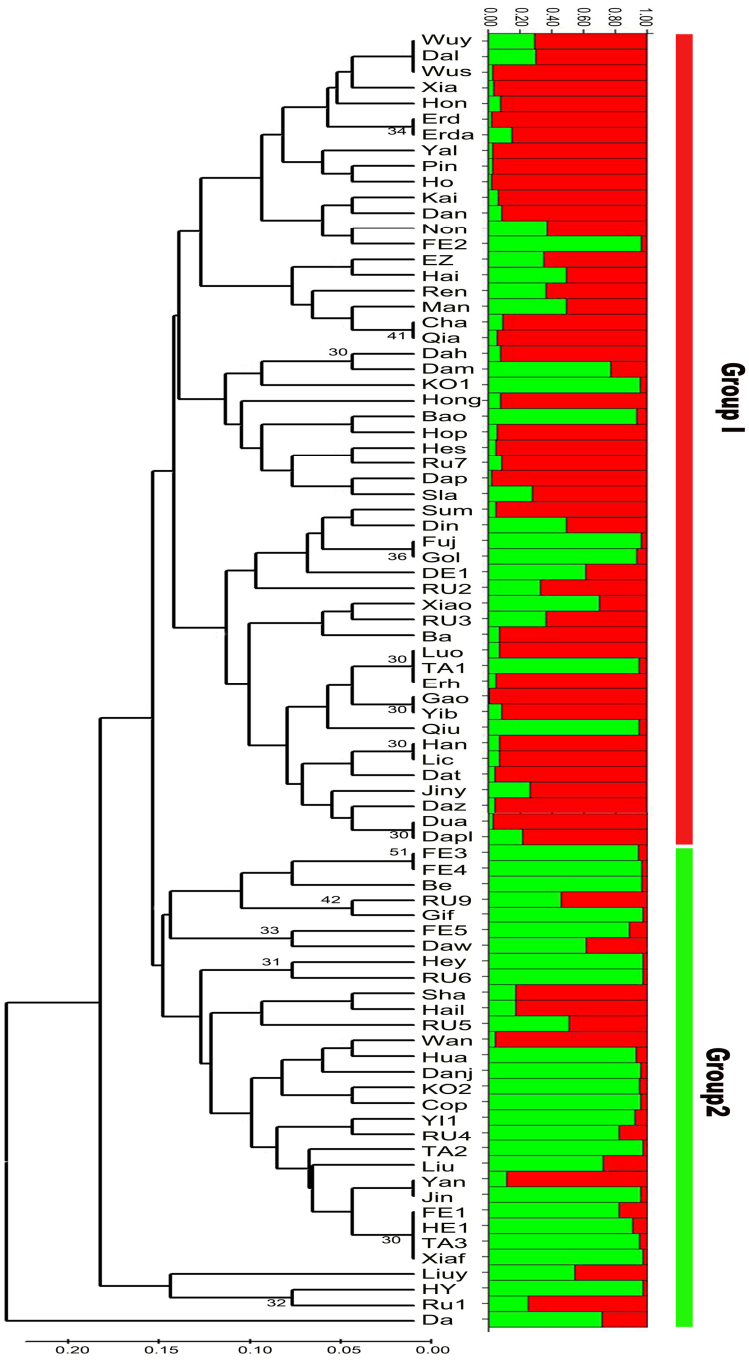

Figure 1. UPGMA dendrogram and population structure analysis of the 83 head cabbage landraces based on AFLP data. Numbers on the branches correspond to bootstrap values (values smaller than 30 were not included). Estimated population structure of each landrace is represented by a horizontal bar, which is partitioned into two colored segments that represent the individual estimated levels of the two groups.

genetic distance (Figure 3). The dendrogram showed that the Northern China population was closely related to the Eastern Europe population genetic distance (0.037), but distant from the Southern China population (0.059). Conversely, the Southern China population showed a close genetic relationship to cabbage landraces of other countries (0.047), but appeared to be more distant from the Eastern Europe population (0.087) and Western

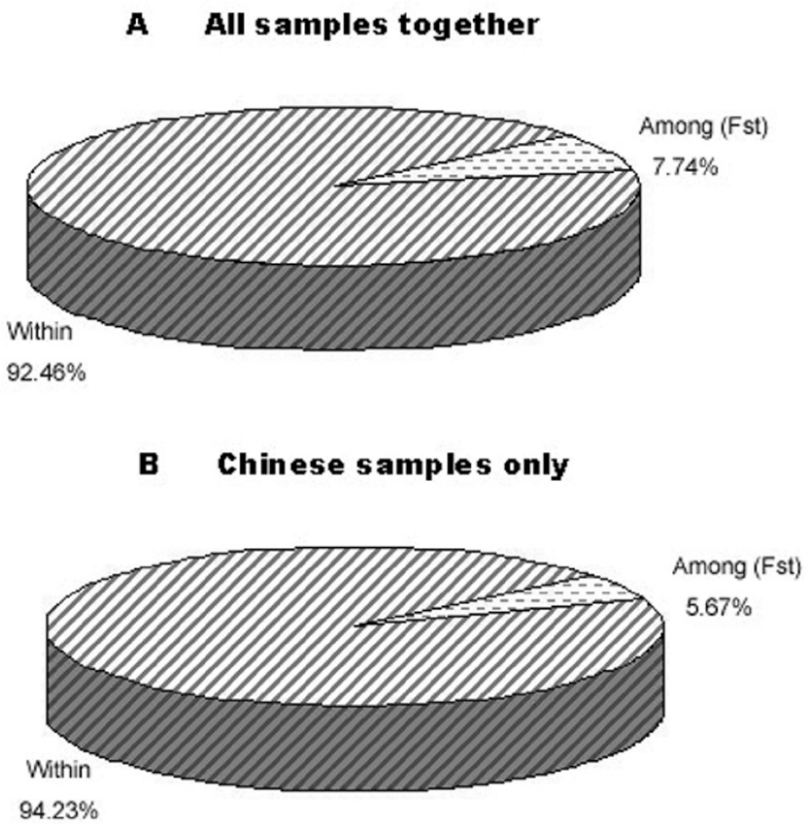

Figure 2. Summary of the genetic differentiation (Φst = F_{st}) among and within groups as determined by AMOVA. (A) All landraces together; (B) China landraces (1,000 permutations); P < 0.001.

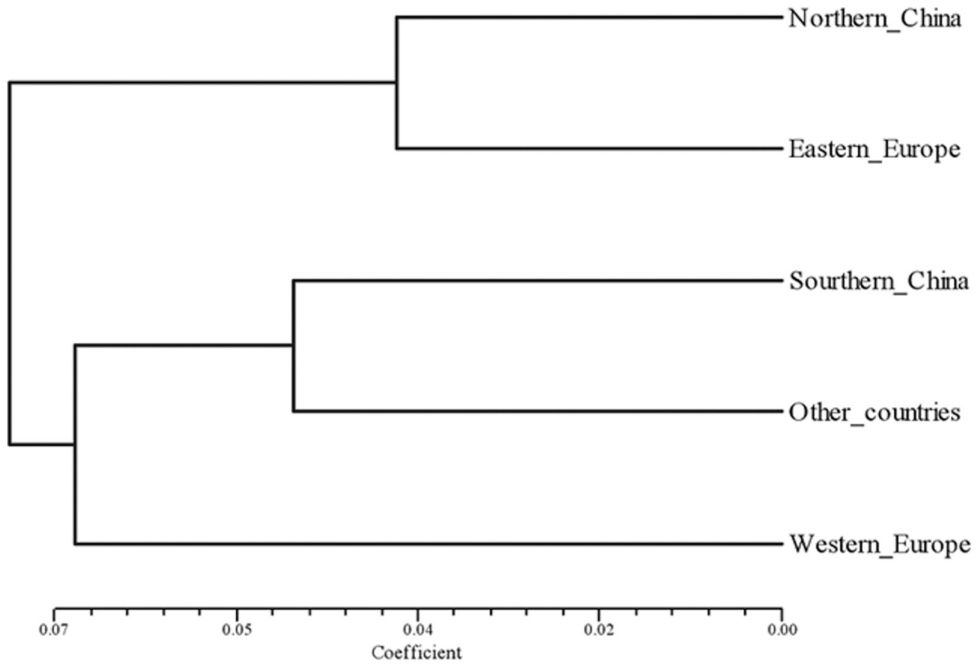

Figure 3. UPGMA cluster analysis dendrogram based on Nei's genetic distances among the five populations of head cabbage landraces.

Europe population (0.086).

DISCUSSION

This study makes the first report of the investigations into genetic diversity in a collection of 53 Chinese head cabbage landraces compared with 30 representatives from Europe, Africa, India, Japan and Korea. The rates of polymorphisms were relatively lower (41.6%) compared with polymorphisms (70%) between *B. oleracea* subspecies (Farnham et al., 1996), which demonstrated that head cabbage landraces are very similar in genotype and had relatively low diversity among all genotypes analyzed. PIC has been used in marker comparison studies analyzing levels of polymorphism in various *B. oleracea* subspecies (Tonguç and Griffiths, 2004; Louarn et al., 2007). The PIC value of dominant markers ranged from zero for monomorphic markers to 0.5 for markers that are present in 50% of the plants and absent in the other 50% (Anderson et al., 1993). In our work, relatively lower PIC values (average 0.317) suggested that *B. oleracea* var. *capitata* cultivars represent populations of low genetic diversity. This result confirmed the narrow genetic diversity observed in main cabbage breeding materials reported in a previous investigation (Fang et al., 2002).

The UPGMA dendrogram and population structure analysis divided all 83 head cabbage landraces into two groups. Group 1 was a distinct group of Northern China and Eastern European landraces (mainly from Russia and Ukraine), whereas Group 2 is primarily comprised of landraces from the Southern China population, Western European population and other countries. Northern China landraces and Eastern Europe landraces are intermingled in Group 1 and do not form a clear sub-cluster between the eco-geographical populations. Similar results were observed in Group 2. These observations suggested that landraces from the North of China possess a relatively close relationship to that from their Eastern European neighboring countries. The differentiation between Northern China and Southern China landraces was suggestive of different ancestry and cultural history of head cabbage in the Northern and Southern areas of China.

Another important observation was that landraces with varied maturing times or head types could not be definitively distinguished based on molecular data. The incongruity between morphological and molecular data can be explained by the absence of significant genetic distance between these main economical traits in cabbage cultivars relative to diversity in geographical origin. Most polymorphisms observed did not contribute to phenotypic variation, which indicated that only a few genes are involved in the favored economical traits.

To further explore the genetic diversity within and among geographical populations, POPGENE 1.32 was used to calculate Nei's gene diversity (*h*) and the Shannon-Weaver diversity index (*I*). The results indicated that the old China landraces had a relatively higher genetic diversity, which revealed a more valuable gene pool in the landraces reserved at IVF. Partitioning of population genetic diversity among geographical populations showed that the major portion of genetic diversity was within geographical populations and the genetic differentiation between different geographical origins was extremely low.

Many factors, including breeding-system, seed exchange and agricultural practices influence genetic diversity, including the proportion of variation distributed within and between populations (Hamrick and Godt, 1996). The high genetic similarity among different geographical populations can be explained by the short cultural history of head cabbage and the active exchange of seeds among different countries.

Late-maturing cabbages are the oldest group of head cabbages (http://www.history.org/history/CWLand/resrch3.cfm) and have been popularly planted at large scales in the north of China in the 19th century, according to historical documents in China (Wu, 1848). To date most of the head cabbage landraces reserved in IVF were originated in Northern China (78.9%). One of the most valuable observations of this study was that the Northern China population had closer relationships with the Russia and Ukraine landraces (representing the Eastern Europe populations) and relatively lower relationships with other European countries and the Africa, India, Japan and Korea populations.

There are different opinions about the cultivation history of cabbage in China. Some Chinese researchers believed that Chinese traditional head cabbage was first introduced from Russian (Jiang, 1981). Alternatively, some others suggested that head cabbage was first introduced from the Netherlands or some other Western European country through the south of China (Ye, 1986). Based on molecular data, the close genetic relationships between head cabbage landraces originating in Northern China and Eastern European countries confirmed the Chinese historical documents relative to the cultivation history of head cabbage by the end of 17-century (Fang, 1690). Due to the significantly lower levels of diversity within the Southern China population, we can presume a fairly shorter history of head cabbage cultivation in the south compared with the north. Combining the historical documents to date, we support the hypothesis that head cabbage was first introduced from Europe through the Mediterranean Sea, the Middle Asian Region, Russia and then to different parts of North China by the end of the seventeenth century.

In conclusion, we presented a profile of the genetic diversity among cabbage landraces of different geographical origins. Our findings also provided a systematic reference for future cabbage breeding programs, contri-

buting to the traditional China head cabbage germplasm bank. In addition, we also contributed information regarding the genetic diversity and allocation of possible heterotic groups. For the last 50 years, the majority of commercial hybrid head cabbage cultivars in China has been and is presently crossed with cultivars introduced from outside China. The literature did not provide much information regarding the diversity among traditional China landraces and landraces from outside China. Our study analyzed 83 China landraces from varied geographical sources and disclosed another important genetic pool in the limited head cabbage germplasm. The divergence exhibited in this group provided us valuable information regarding the relationship among these accessions and will assists breeders in generating new F_1 hybrids.

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