Front. Agric. China 2009, 3(4): 374–382
DOI 10.1007/s11703-009-0075-1

RESEARCH ARTICLE

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Evaluation of phenotype and genetic diversity of maize landraces from Hubei Province, Southwest China

Abstract The intelligent exploitation of maize landraces for maize breeding requires a detailed knowledge of genetic and historical relationships among these populations and an understanding of the partitioning of genetic diversity among populations. In this study, the diversity of 102 maize landraces from Hubei Province was evaluated on the basis of phenotype data (collected over two years) and simple sequence repeat (SSR) data. The results showed that significant differences in important traits were present among the landraces, especially in kernel weight and ear height. The comparison of the yield components of two elite populations, BSSSC9 and Suwan2, with those of landraces indicated that the ear length of 28 landraces, the kernel weight of 35 landraces, the row number per ear of 11 landraces, and the kernel number of 3 landraces were better than those of the two elite populations, implicating that abundant genetic diversity and favorable genes were accumulated within these landraces. Thirty-six SSR markers revealed a total of 179 alleles in 102 landraces, with an average of 4.97 alleles per loci, and 0.4362 polymorphism information content (ranging from 0.3141 to 0.5601). Cluster analysis based on the phenotypic data and SSR data divided the 102 landraces into two or three major groups. Integrating the phenotypic data and SSR diversity, we suggested that abundant genetic variability and specific alleles were contained within the set of landraces. A few landraces (including Batangbai, Bairihui, Dongjingbai, and Huangyumi) with large genetic diversity and specific favorable characteristics could be selected for further research and utilization.

Keywords maize (*Zea mays* L.), landrace, phenotype, simple sequence repeat (SSR), genetic diversity

Received February 10, 2009; accepted May 20, 2009

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1 Introduction

There are abundant germplasm resources of maize (*Zea mays* L.) in China; more than 16000 collections are conserved in the Crop Germplasm Resources Pool of China, and about 90% of these collections are landraces and populations. However, research and utilization of these germplasm resources have not fully attracted the breeder's attention during recent years because only 2%–3% of inbred lines broadly used in modern breeding programs are selected from landraces or native populations (Wu, 1989; Li, 1998). However, it is well known that landraces have undergone a long-term natural and artificial selection process during their planting history. Diverse varieties or populations adapted to diverse niches and needs of farmers have been developed, resulting in the genetic diversity that is observed today. This collection diversity is observed by morphological description, isozyme, and/or DNA marker screening. Historically, isozyme markers were the first biochemicals to be used and allowed for the assay of genetic diversity within and among populations (Doebley et al., 1985; Lefor-Buson et al., 1991; Revilla et al., 1998). Subsequently, DNA markers, including restriction fragment length polymorphisms (Livini et al., 1992; Dubreuil and Charcosset, 1998; Gauthier et al., 2002), random amplification of polymorphic DNA (Liu et al., 1999b; Carvalho et al., 2004), and SSR (Liu et al., 2003; Pressoir and Berthaud, 2004; Vigouroux et al., 2005; Yao et al., 2007; Warburton et al., 2008), were used. These techniques allowed not only whole-genome identification of genetic diversity but also the classification of maize inbred with heterotic groups (Melchinger et al., 1991; Labate et al., 2003; Liu et al., 2003).

Recently, the germplasm of more than 1300 landraces from Hubei Province, in the southwest of China, has been collected and conserved in the Crop Germplasm Pool of Hubei. Such collections are considered valuable resources both for the objectives of conservation of natural materials and for broadening of the maize-breeding genetic database. The use of these materials in breeding programs and characterization of favorable traits/alleles and genetic diversity within the collections is urgently required. Morphological descriptions and classifications have been carried out in the past decades (Zhang et al., 1994; Liu et al., 1998; Xu and Wu, 1998). Genetic diversity at isozyme loci was also assayed within and among a few landraces (Zhang et al., 1995; Liu et al., 1998; Lu et al., 2002), but the number of landraces evaluated on phenotype and genotype represents only a minority of the 1300 collections. Further morphological and genetic evaluation of the majority of landraces remains to be performed.

The current study was undertaken to further evaluate phenotypes and simple sequence repeat (SSR) genotypes in order to obtain a better understanding of Hubei maize diversity. We examined a total of 102 landraces for various morphological and less obvious agriculturally important traits. Genetic variability was determined at 36 SSR loci. We found that abundant genetic variability and many favorable traits were contained within the set of landraces, and a few landraces (including Batangbai, Bairihui, Dongjingbai, and Huangyumi) showed large genetic diversity and specific favorable characteristics. We hope to select this genetic diversity for further research and utilization.

2 Materials and methods

2.1 Genetic materials

The collections listed in Table 1 are the 102 maize landraces conserved in the Crop Germplasm Pool of Hubei, China, which we studied. These landraces were collected during the 1980s and 1990s from diverse ecological districts of Hubei Province, including a high mountainous area, the Three Gorges river area, a hill area, and a flat plains area. The present collections represented a small part of the maize germplasm landraces cultivated by some regional farmers of Hubei Province, and their reproductive isolation had been maintained by traditional agriculture through direct selection by farmers for many generations. The collections include the dent and flint kernel types and different kernel colors (Table 1). In this collection, some landraces had the same name despite being collected from different regions. For differentiating those homonymous landraces, we used the landrace name followed by an Arabic numeral to define a specific landrace, for example, Bairizao1, Bairizao2, and so on.

Table 1 The name, kernel color and type, and average polymorphism information content of studied landraces

No.	name	kernel color	kernel type	a*PIC*[a)]
1	Batangbai	yellow	flint	0.4434
2	Baibanshan	yellow	flint	0.3743
3	Baibaogu	white	semi-dent	0.4367
4	Baierhua	white	flint	0.4460
5	Baiheyumi	white	flint	0.3589
6	Baijiuyue	yellow	flint	0.4678
7	Bailijiuyue	red	dent	0.3948
8	Bailiushi	yellow	flint	0.4903
9	Baipiyumi	white	flint	0.5131
10	Baiseyumi	yellow	flint	0.4944
11	Baizibaogu	white	flint	0.4397
12	Bairigui	yellow	semi-dent	0.3325
13	Bairihui	yellow	flint	0.4257
14	Bairizao1	yellow	flint	0.4694
15	Bairizao2	red	flint	0.4005
16	Bendibianyi	yellow	flint	0.4395
17	Bendiyulv	white	flint	0.5292
18	Chaoxianbai	white	flint	0.4381
19	Chiyumim	yellow	flint	0.4756
20	Chutoubang	white	flint	0.4500
21	Chuanbao	white	flint	0.3640
22	Chunyumi1	white	dent	0.4361
23	Chunyumi2	yellow	flint	0.5066
24	Dabaisui	yellow	flint	0.4519
25	Dabanyac	yellow	flint	0.4506
26	Dazhihuang1	yellow	flint	0.4738
27	Dazhihuang2	white	semi-dent	0.5145
28	Dazhihuang3	yellow	flint	0.4227
29	Dazhihuang4	yellow	flint	0.5370
30	Dazhiyumi	white	flint	0.4025
31	Dingzishi	yellow	flint	0.4432
32	Dongjingbai	white	dent	0.4130
33	Dongyaci	white	flint	0.3220
34	Dongtingbai	white	flint	0.4944
35	Erhuazao	yellow	flint	0.4383
36	Erhuangzhi	white	flint	0.3838
37	Erzhibai	red	flint	0.4382
38	Erzhihuang	yellow	flint	0.3626
39	Gaoganqin	yellow	flint	0.4000
40	Hongbaogu1	white	flint	0.5074
41	Hongbaogu2	white	flint	0.4709
42	Honghuabg	yellow	flint	0.4399
43	Hongshanym	yellow	flint	0.4709
44	Hongyumi	yellow	flint	0.4004
45	Houshanhuang	white	semi-dent	0.3439
46	Hunanhuang	yellow	flint	0.4970

(*Continued*)

No.	name	kernel color	kernel type	a*PIC*[a)]
47	Huabaogu	yellow	flint	0.4736
48	Huangbenym	yellow	flint	0.4820
49	Huangluym	Red	flint	0.3598
50	Huangym1	yellow	flint	0.4671
51	Huangym2	yellow	flint	0.3680
52	Huihongp	yellow	flint	0.4164
53	Jiaobenlu	white	flint	0.4582
54	Jinbangcui	yellow	flint	0.4281
55	Jinbangc1	yellow	flint	0.4470
56	Jinbangc2	white	flint	0.3839
57	Jinbaotou	yellow	semi-dent	0.4946
58	Jinyinghua	yellow	flint	0.4045
59	Jiuyueh1	yellow	flint	0.3916
60	Jiuyueh2	yellow/white	flint	0.4064
61	Jiuyuezao	yellow	flint	0.4955
62	Kuhuangbg	yellow/white	flint	0.3531
63	Laohuangbg	yellow	flint	0.4706
64	Laoshuya	yellow	flint	0.5601
65	Liushirih	Red	flint	0.4600
66	Liushizao	yellow	dent	0.4411
67	Liuyueb1	white	flint	0.3894
68	Liuyueb2	red	flint	0.4694
69	Liuyuebao	white	flint	0.3623
70	Liuyueling	white	flint	0.5446
71	Lushuih	yellow	flint	0.4188
72	Luosuobg	yellow	flint	0.4300
73	Mibaoguym	yellow/white	flint	0.4522
74	Niujiaoym	yellow	flint	0.5418
75	nuohongym	white	flint	0.4976
76	Qipianye	white	semi-dent	0.3813
77	Qiyeluym	yellow	flint	0.4673
78	Qiyueling	yellow	flint	0.4001
79	Qimeizhi	yellow	flint	0.4216
80	Sanhuacao	yellow	flint	0.3803
81	Sanjiaocun	yellow	flint	0.4187
82	Shengliym	yellow	flint	0.3949
83	Shifacao	white	flint	0.5014
84	Tiezhih1	yellow	semi-dent	0.3999
85	Tiezhih2	yellow	flint	0.3141
86	Tiezhih3	red	flint	0.4590
87	Wujituiym	yellow	flint	0.3426
88	Wunizhitui	white	flint	0.5473
89	Xiaobaogu	white	flint	0.4147
90	Xiaohuangl	yellow	flint	0.4174
91	Xiaoyangbao	yellow	flint	0.4125
92	Xiaozhib	yellow	flint	0.4616
93	Xiaozhihuang1	white	flint	0.4297
94	Xiaozhihuang2	white	dent	0.4829
95	Xiaozhihuang3	yellow	semi-dent	0.4116
96	Yangxicao	yellow/white	flint	0.4834
97	Yejizhuo1	yellow	flint	0.3784
98	Yejizhuo2	white	semi-dent	0.4488
99	Yumiyumi	yellow	flint	0.4713
100	Zhoubaogu	yellow	flint	0.4020
101	Zhuanwoz	white	dent	0.4063
102	Zhuiziba	white	flint	0.3680

Note: a) a*PIC* represents average polymorphism information content.

2.2 Phenotypic evaluation

The phenotype evaluation of all 102 landraces and two elite populations (Suwan 2 and BSSSC9) was performed at Jingzhou (centre of Hubei Province) in 2006 and 2007. A randomized block design was employed in the field with three replicates. Each block consisted of two rows (3.0 m long and 0.6 m space apart) and a total of 22 individuals. Each replicate contained 104 blocks. All materials were planted under normal condition in all two environments, and about 100 kg N·hm^{-2} and 120 kg N·hm^{-2} were applied during growth season of maize in 2006 and 2007, respectively. About 15–18 individuals in a block were measured for agriculturally important traits as follows: days to silking (DTK), plant height (PH), ear height (EH), nodus number down ear (NNDE), nodus number upper ear (NNUE), ear length (EL), ear diameter (ED), row per ear (RPE), kernel per row (KPR), 100-kernel dry weight (100-KW), length of barren ear tip (LBT), and grain weight per ear (GW). Variance analysis of phenotype was done by SAS software, and clustering analysis was performed using NTSYS2.11a (Rohlf, 2002) based on the data from the Principal Component Analysis.

2.3 DNA extraction and SSR assay

Genetic diversity within or among landraces was examined using SSR screening. Sampling was done as described by Dubreuil et al. (1999) and Liu et al. (2005). The leaf disks of ten individuals were pooled to extract genomic DNA using cTAB procedure (Saghai-Maroof et al., 1984) and forty individuals per landrace were sampled for evaluation of genetic diversity. DNA concentration was estimated using a NanoDrop® (Eppendorf, Germany) spectrophotometer and then adjusted to 10 ng·μL^{-1}. A total of 36 SSR markers, which were a subset of 96 markers used by Liu et al. (2003) for the evaluation of the genetic diversity of maize inbred lines, were chosen on 10 linkage groups of maize (Table 2). PCR, PAGE electrophoresis, and SSR band score were performed as described by Liu et al.

Table 2 The SSR marker, chromosomal location, and revealed allelic number

No.	marker	Bin[a)]	A[b)]	No.	marker	Bin	A
1	bnlg1429	1.02	6	19	nc009	6.04	3
2	bnlg615	1.07	4	20	bnlg1732	6.05	6
3	bnlg1720	1.09	6	21	bnlg2132	7.00	6
4	bnlg1017	2.02	5	22	bnlg1094	7.02	2
5	bnlg1018	2.04	3	33	bnlg1808	7.02	6
6	bnlg1138	2.06	5	24	bnlg1305	7.03	6
7	bnlg1940	2.08	6	25	phi116	7.06	5
8	bnlg1456	3.05	2	26	bnlg1834	8.03	5
9	bnlg1449	3.06	5	27	bnlg1782	8.06	6
10	bnlg1931	3.07	7	28	bnlg1065	8.07	9
11	bnlg1265	4.05	5	29	phi033	9.01	4
12	bnlg1784	4.07	3	30	phi065	9.03	5
13	phi093	4.08	3	31	bnlg1209	9.05	6
14	bnlg1917	4.10	3	32	bnlg1129	9.08	5
15	bnlg589	4.11	7	33	phi050	10.03	4
16	bnlg1287	5.04	3	34	bnlg1526	10.04	5
17	bnlg118	5.07	10	35	bnlg1028	10.06	4
18	bnlg1538	6.01	5	36	bnlg1360	10.07	4

Note: a) location of marker on maize chromosome; b) the number of revealed alleles.

(2005). The mean number of alleles within each landrace was calculated using $A = \Sigma A_i/k$, where A_i is the number of alleles at i loci, and k is the number of SSR loci identified. The polymorphism information content (PIC) of each SSR locus was calculated using $PIC = 1 - \Sigma p^2_i$, where p_i is the frequency of the i allele. The average PIC for each landrace was estimated by a$PIC = \Sigma PIC_j/k (j = 1$ to $k)$. Genetic distances (GD) among 102 landraces were estimated by Nei's distance (Nei, 1978). Clustering analysis was performed using the neighbor joining method by the Numerical Taxonomy Multivariate Analysis System (NTSYS-pc) version 2.11, a software package (Rohlf, 2002). The goodness of fit of the landraces to a specific cluster was determined by Mantel test (Mantel, 1967).

3 Results

3.1 Phenotypic variation of important traits among landraces

3.1.1 Morphological variation

The variance analysis for phenotypic traits on two-year data showed that the variance among replicates was not significant, but the variance from two years was significant ($P < 0.05$). The variances of important traits among landraces were highly significant ($P < 0.01$), indicating that the studied landraces contained dramatic variations of earliness, plant architecture, and ear and kernel characteristics. A detailed comparison of each trait among landraces showed that the phenotypic variation was extensive, and the differences between the extreme landraces were highly significant (Table 3).

For instance, Yejizhuo showed a shorter growth period of days to silk (DTK), i.e., about 47 d in 2007 and 49 d in 2006, while Liuyuepao showed a longer DTK, i.e., about 71 d in 2007 and 78 d in 2006. In addition, Yejizhuo had shorter ears of about 7.4 cm in 2007 and 7.5 cm in 2006, with about 15 kernels per row, compared to both Bairihui and Batangbai that had ears of about 17.0 cm in 2006 and 18.0 cm in 2007, with about 32.0 kernels per row and 34.0 kernels per row in 2007, respectively. Baipiyumi and Chunyumi 1 had only 8–10 rows per ear, while Xiaobaogu had about 16.0–18.0 rows per ear. The 100-kernel weight of Huangbaogu, Batangbai, Dongjingbai, and Bairicao was all more than 30.0 grams. Furthermore, abundant variability among landraces was also shown for other biological traits. Chunyumi 1 and Liuyuepao 1 grew higher, with heavier ears and larger biomass (the data not shown here).

The proportion of double ear of Laoshuyachi was more than 40.0%. The coefficient of variation (COV) is another parameter for measuring the dispersion of a phenotype value. A larger COV of LBT (0.30 in 2007) and EH (0.2 in 2007 and 0.25 in 2006) revealed that the variations of the two traits were abundant among the studied landraces, whereas the COV of ED and DTK was lower, i.e., only 0.07–0.09 for ED and 0.08–0.12 for DTK in two years, respectively (Table 3). This result indicated that the

Table 3 The mean and variance range of eleven traits in 102 landraces of maize

trait	mean		variation range		COV[a)]	
	2006	2007	2006	2007	2006	2007
DTK	64.04	60.49	49.0–87.0**	43.33–74.00**	0.12	0.08
PH/cm	194.03	209.80	144.0–251.0**	150.67–267.96**	0.12	0.12
EH/cm	80.81	90.00	35.0–128.1**	50.98–147.00**	0.25	0.20
NNDE	—	7.14	—	5.04–10.04**	—	0.13
NNUE	—	6.00	—	5.11–6.93**	—	0.06
EL/cm	12.34	13.84	7.49–17.33**	7.43–18.34**	0.14	0.15
ED/cm	3.46	3.82	2.65–4.10**	2.75–4.53**	0.09	0.07
RPE	11.6	11.50	9.20–19.30**	9.07–17.20**	0.12	0.12
KPR	23.58	24.65	14.50–33.80**	15.21–34.93**	0.14	0.13
LBT	—	1.21	—	0.34–2.88*	—	0.30
100-KW/g	21.50	26.12	13.07–34.26**	12.49–32.27**	0.17	0.30

Note: * = significant at $P < 0.05$ level; ** = significant at $P < 0.01$ level; — = data were not measured in 2006; a) COV = coefficient of variation.

phenotypic differences of these traits were not significant. Taking together, the data presented above showed that there was abundant diversity among the 102 landraces from Hubei. Diverse genotypes and alleles could be contained within the germplasm of these landraces.

3.1.2 Difference with the elite populations

Phenotypic comparisons between the landraces and Suwan 2 and/or BSSSC9 showed that the average DTK of landraces was 61.0 d, shorter than that of Suwan 2 (74.0 d) and similar to that of BSSSC9 (62.0 d). The average plant or ear height of the landraces was about 22.0–24.0 cm lower than that of Suwan 2 and BSSSC9 or about 19.0 cm shorter than that of Suwan 2 instead of BSSSC9. Generally, the performance of yield components of Suwan 2 and BSSSC9 was better than that of the landraces, especially in the grain yield per ear and yield components of BSSSC9. However, 19 landraces (18.6%) showed a higher grain weight per ear than that of Suwan 2. Three landraces (Bairihui, Batangbai, and Huangyumi-1) showed higher yields than BSSSC9, indicating that a few of favorable alleles might be contained in those high yield landraces and might be utilized in an advanced breeding program.

3.2 Evaluation of genetic diversity of landraces

3.2.1 Number of alleles

SSR markers were employed to reveal the genetic diversity within and among the landraces. Each marker revealed between two (bnlg1094, bnlg1456, and bnlg1094) and 10 (bnlg118) alleles. A total of 179 alleles were revealed in 102 landraces (Table 2). The average of 4.97 alleles per SSR locus was smaller than that of 6.1 alleles revealed by Yao et al. (2007) in 54 landraces from Sichuan, Yunnan, and Guizhou, and 9.0 alleles reported by Vigouroux et al. (2005) in 45 landraces. Our average value of alleles was similar to that of the 5.4 alleles reported by Wu et al. (2004) in popcorn landraces, but slightly higher than that of 4.1 alleles revealed by Liu et al. (2005) in waxy maize landraces and markedly higher than the average allele number of isozyme loci (Doebley et al., 1985; Lefor-buson et al., 1991; Zhang et al., 1995; Lu et al., 2002).

3.2.2 Genetic diversity

The PIC reflects the genetic diversity level in a population. The set of 102 landraces revealed 0.4362 of average PIC value, ranging from 0.3141 to 0.5601 (Table 1). The PIC of five landraces (4.9%, including Tiezhihuang2 and Dongyaci) was lower than 0.35, whereas the PIC of 11 landraces (10.8%, including Laoshuyachi and Wunizitui) was higher than 0.5. In addition, different SSR loci also possessed diverse PIC in the set of landraces. The PIC of the phi050 and bnlg1018 was lower than 0.01, whereas the PIC of bnlg1429 and bnlg1065 was higher than 0.75. The allele number and PIC revealed by SSR indicated that there was abundant genetic diversity within or among the studied landraces.

3.3 Difference among homonymous landraces

In the studied landraces, some varieties from different regions shared the same name; for example, Dazhihuang, Tiezhihuang, Chunyumi, and Yejizhuo had four, three, two, and two landraces, respectively (Table 1). The comparison of phenotypes with genotypes might identify if the homonymous collections came from the same population. The phenotypic comparison listed in Table 4 showed that there were some nonsignificant differences for

Table 4 The phenotypic comparison of important traits among homonymous landraces

	Bairicao 2	Chunyumi 2	Dazhihuang 2	Dazhihuang 3	Dazhihuang 4	Yejizhou 2	Xiaozhihuang 1	Xiaozhihuang 2
Bairicao 1	0.3143§	—	—	—	—	—	—	—
Chunyumi1	—	0.085	—	—	—	—	—	—
Dazhihuang 1	—	—	0.4262	0.3497	0.0491*	—	—	—
Dazhihuang 2	—	—	—	0.3973	0.0342*	—	—	—
Dazhihuang 3	—	—	—	—	0.0210*	—	—	—
Yejizhou 1	—	—	—	—	—	0.0118*	—	—
Xiaozhihuang	—	—	—	—	—	—	0.0463*	0.0569
Xiaozhihuang 1	—	—	—	—	—	—	—	0.0470*

Note: §= single-tail probability of *T*-test; * = significant at $P < 0.05$ level.

one or two traits between the two Bairicao landraces, and the two collections were clustered into the same group (Fig. 1). However, significant differences were found in two Chunyumi landraces and two Yejizhuo landraces. Consequently, these two homonymous collections were clustered into different subgroups (Figs. 1 and 2). Among four Dazhihuang landraces, the performance traits of Dazhihuang 1–3 were similar, while that of Dazhihuang 4 was significantly different ($P < 0.05$) resulting in cluster differences (Figs. 1 and 2). A pairwise comparison of the three Xiaozhihuang collections also showed distinct differences. The collections with significant phenotypic diversity also showed genotype differences by SSR screening (Table 5). Two Bairicao collections only revealed some differences at bnlg1429 and bnlg1065 loci, whereas 66 alleles revealed differences between Dazhihuang 1 and Dazhihuang 4 mainly at bnlg589, bnlg1931, bnlg118, bnlg1065, and bnlg1720 loci. According to the integrated phenotype and genotype data, we suggest that the two Bairicao collections might originate from the same population. Additionally, we believe that Dazhihuang 1–3 might derive from the same population, but Dazhihuang 4 might derive from a different origin. There were actual genetic differences among the

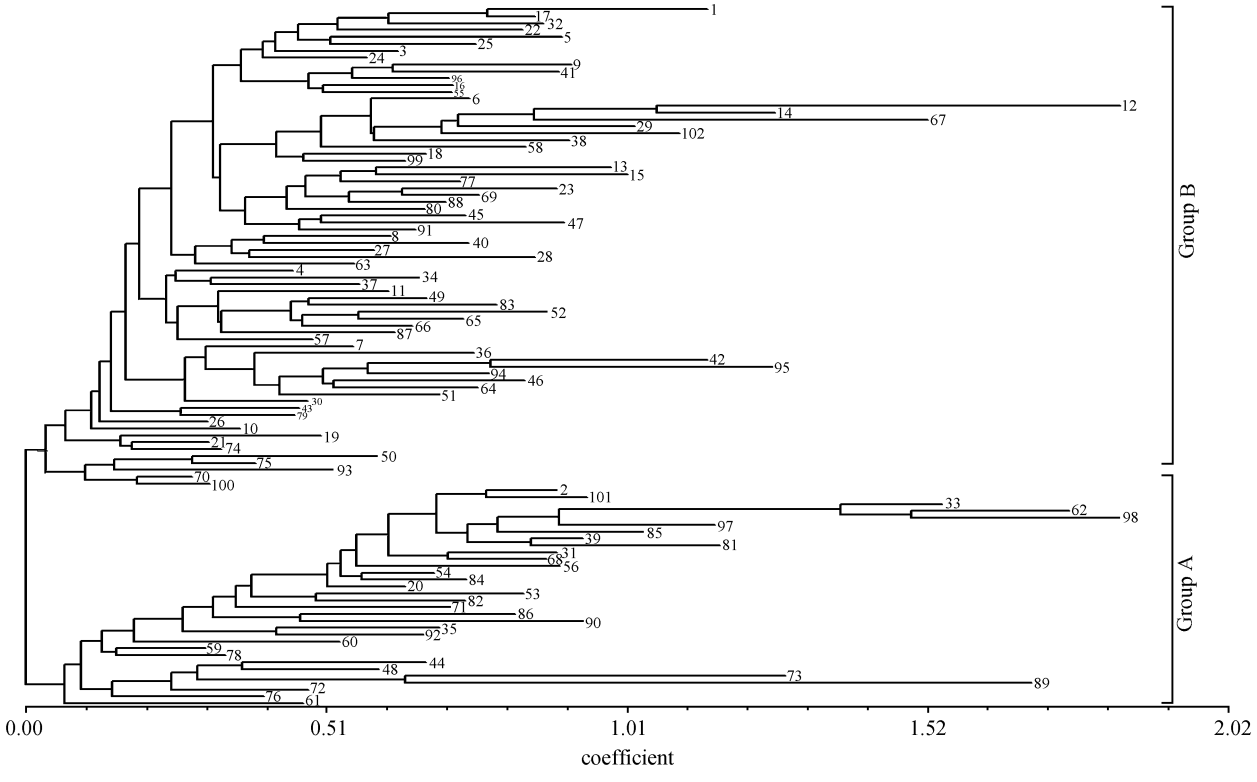

Fig. 1 A dendrogram of 102 corn landraces from Hubei

Note: Clustering analysis was performed based on phenotype data in 2007 using neighbor joining method by the Numerical Taxonomy Multivariate Analysis System (NTSYS-pc) version 2.11a software package (Rohlf, 2002). The number representing each landrace corresponds to the data in Table 1.

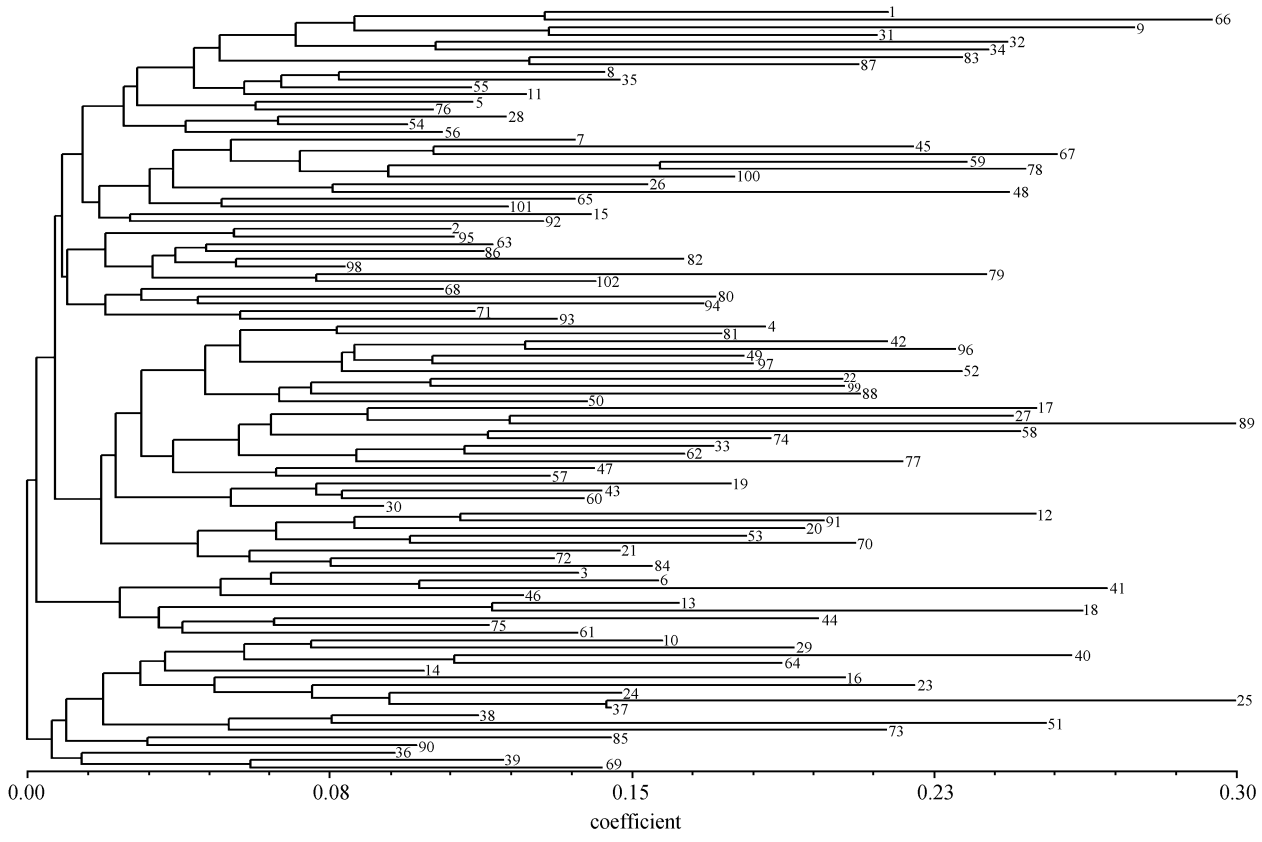

Fig. 2 A dendrogram of 102 corn landraces based on SSR data

Note: Genetic distances among landraces were estimated using Nei's distance (Nei, 1978). The number representing each landrace corresponds to the data in Table 1.

Table 5 The genotypic comparison among homonymous landraces

landrace	A[a)]	Aa[b)]	aPIC[c)]
Bairicao1	90	2.50	0.52
Bairicao2	86	2.39	0.44
Chunyumi1	82	2.78	0.53
Chunyumi2	94	2.61	0.61
Dazhihuang1	80	2.22	0.47
Dazhihuang2	92	2.56	0.50
Dazhihuang3	90	2.50	0.42
Dazhihuang4	104	2.89	0.57
Yejizhou1	79	2.19	0.46
Yejizhou2	84	2.33	0.51
Xiaozhihuang	80	2.22	0.60
Xiaozhihuang1	80	2.22	0.61
Xiaozhihuang2	91	2.53	0.68

Note: a) A = total number of alleles; b) Aa = the average number of alleles in each locus; c) aPIC = average polymorphism information content.

collections of two homonymous Chunyumi, two homonymous Yejizhuo, and three homonymous Xiaozhihuang, indicating that they might belong to different landraces.

4 Discussion

Maize planting areas in Hubei Province are located in the western mountainous areas under a complex ecological environment. The landraces have undergone long-term natural selection during their planting history with occurrence of great differentiation in maize landraces to meet the needs of local environments and farmers. The adaptation of landraces to many niches for many years has resulted in a large variability that can be observed today (Rebourg et al., 2001). The data from isozyme loci show that an abundant diversity exists within or among the landraces, and on the average, about 1.7–2.0 alleles per locus with more than 60% heterozygosity are revealed at a dozen of isozyme loci, which is slightly lower than that found in BSSSC9 and Lancaster from the U.S.A. (Zhang et al., 1995; Lu et al., 2002). However, the genetic diversity of a minority of landraces is yet more abundant than the two populations from the U.S.A., showing favorable traits for yield and abiotic tolerance (Liu et al., 1998). In our study, SSR markers revealed an average of 4.97 alleles per

marker (ranging from 2 to 10) and 0.4362 PIC (ranging from 0.3141 to 0.5601) in the 102 landraces. Specifically, 10.8% landraces showed more than 50% in PIC, indicating that those landraces contained the abundant SSR diversity. Phenotypic evaluation showed that the difference of grain yield was very significant among landraces from the three western mountainous areas of Hubei Province (Zhang et al., 1994; Liu et al., 1998; Lu et al., 2002). In a set of 102 landraces, we found that the kernel weight had the most extensive variability ranging from 12.49 g to 32.27 g, with 30% COV. Another trait with an extensive variability of 20% COV was the plant ear height, ranging from 50.98 cm to 147.00 cm. The phenotype clusters such as earliness, small kernel, larger kernel, and high yield may be further partitioned resulting in specific types of landraces containing specific favorable alleles that might be utilized for advanced breeding programs. Therefore, we suggest that the abundant genetic variability and specific alleles which are contained within the landraces from Hubei Province will be a valuable resource.

Zhang et al. (1994) selected 10 elite populations from more than 100 Hubei landraces by the grain yield evaluation, of which 20% showed a higher yield than BSSSC9, Suwan2, and Lancaster, and 40% manifested a high general combining ability. Similarly, Lu et al. (2002) also found other elite landraces. Based on the combining abilities of these selected populations with BSSSC9, Lancaster, and Suwan2, Liu et al. (1998) artificially recombined four new synthetic populations using elite landraces. Furthermore, favorable alleles for improving yield and yield components of the released maize hybrids were identified in these synthetic populations (Zhang and Wu, 1997). The phenotype variation and genetic diversity of these synthetic populations were more abundant than the corresponding four landraces (Liu et al., 1999a, 1999b). In our study, we found that the grain yield per ear and yield-associated traits of 28 landraces were equal to or excelled those of BSSSC9 and Suwan 2, and a few landraces, including Batangbai, Bairihui, Dongjingbai, and Huangyumi, showed a higher genetic diversity and specifically favorable characteristics. These landraces could be selected for further research and utilization. To utilize these elite landraces, further genetic evaluation, estimation of their combining ability, and heterotic pattern assays are required.

Acknowledgements We are grateful to Feng Teng and Ruixiang Liu from Agricultural University of Hebei for their expert technical assistance in the molecular analyses and to Fanmei Zeng and Weibin Jin from Yangtze University for the field trials. We are also grateful to Dr. Zhikun Li from Agricultural University of Hebei for the data analysis. This work was supported by The Foundation of Germplasm Conservation and Seeking from Hubei Finance Department.

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