Full Length Article

Assessment of Phenotypic Diversity in Foxtail Millet Core Collections in Shanxi Province

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Abstract

The assessment of genetic diversity in foxtail millet core collection can aid in the selection of best parents with complementary characteristics. It facilitates the introgression of favorable genes from plant germplasm into commercial cultivars and accelerates breeding progress. In this study, 595 foxtail millet landraces collected from Shanxi Province were subjected to a comprehensive assessment of 18 phenotypic traits. The results showed that the phenotypic diversity of foxtail millet genetic resources was abundant. Panicle weight (PW), grain weight (GW), primary branch number per panicle (PBNP), and spikelet number per primary branch (SNPB) showed abundant variation. Moreover, there were differences in foxtail millet genetic resources from different cities in Shanxi Province. The results of cluster analysis showed that the core collections were classified into three categories according to the geographical and ecological distribution of foxtail millet. The results of stepwise regression and principal component analysis (PCA) demonstrated that tillering capacity (TC), peduncle length (PeL), leaf length (LL), leaf width (LW), panicle length (PL), diameter of the main stem (DMS), panicle weight per main stem (PW), and protein content (PC) could be used as main identification indicators of the foxtail millet phenotypic variations. This research will benefit the identification and utilization of foxtail millet landraces and may help breeding values. © 2020 Friends Science Publishers

Introduction

Foxtail millet (*Setaria italica* L.) belongs to Poaceae family (Li 1997) and is one of the most important coarse cereals in Shanxi Province (Chai and Feng 2003; Liang and Cheng 2005). Foxtail millet has developed characteristics such as high temperature, drought resistance, barren tolerance, and strong adaptability (Diao 2011; Jia *et al.* 2013); thus, it can be planted in various areas of Shanxi Province. Qin Zhou Huang, Fen Zhou Xiang, and Dong Fang Liang are the brand name products from foxtail millet which are famous in China. Shanxi is one of the most important foxtail millet producing provinces in China, where its cultivation area accounts for about 25% of the total cultivation area of foxtail millet in China (Gu and Gu 2007; Li *et al.* 2015). Therefore, developing new high yielding foxtail millet varieties suitable to different growing regions along with improving the production level as a way to promote economic development is of great importance.

Foxtail millet is the carrier of inheriting Chinese agricultural civilization. A comprehensive and systematic study on the genetic resources of foxtail millet in the province - selection of a representative core collection was made from a large genetic resource collection to carry out a unified and precise phenotypic identification and a thorough evaluation of the characteristics of local varieties (Li and Wu 1996) were carried out to cultivate new varieties that meet the current social needs and improve the use efficiency of local varieties (Wang *et al.* 2016).

Germplasm resources, which are used to develop new varieties provide basic material for germplasm innovation. The identification of breeding objectives is based on germplasm resources; therefore, the collection and preservation of germplasm resources are important (Zhang 2003). However, the urgent problem is how to study and utilize large germplasm resources. The concept of core collection provides an efficient way of making use of large resources (Frankel 1984; Li *et al.* 1999; Chen *et al.* 2009). The genetic diversity of foxtail millet germplasm is determined to a great extent by the minimum size of the foxtail millet germplasm sample, which provides an effective and practical method for the evaluation of foxtail

millet varieties as well as the promotion of its utilization. Now, more than 27000 foxtail millet germplasm accessions are preserved in the national medium-term genebanks (Liu *et al.* 2009), which account for approximately 80% of the global foxtail millet accessions (Jia and Diao 2017). Jia *et al.* (2013) constructed a core collection from more than 27000 foxtail millet accessions preserved in the national medium-term genebanks. Wang *et al.* (2016) identified the comprehensive set of agronomic traits in core germplasm collections of foxtail millet, which makes it possible to make efficient use of its gene pool in different ecological areas of China.

At present, 5627 foxtail millet landraces are preserved in the seed bank of the Shanxi Province (Wen *et al.* 2002), among which a large number have well-developed traits such as drought resistance, increasing yield potential, resistance to smut, excellent aroma and the good eating quality. Wang *et al.* (2019) made use of 5627 landraces from Shanxi Province as source material and constructed a primary core collection of foxtail millet landraces. In the present study, the material included a foxtail millet core collection comprising of 595 accessions. Comprehensive phenotypic identification of the accessions was carried out, which laid the foundation for further understanding of the phenotypic diversity of a core collection of foxtail millet landraces. The objective of this study is to characterize core collection of foxtail millet using morphological marker and use comprehensive information to evaluate each germplasm, and also for the efficient use of these accessions in future foxtail millet improvement program.

Materials and Methods

Plant materials

For two consecutive years (2017–2018), 18 traits in 595 foxtail millet accessions were investigated at the Dongyang experimental base in Shanxi Academy of Agricultural Sciences (37.6 °N, 112.7 °E). The experimental site has a temperate continental climate, with the annual average temperature of 9.8°C and annual average of 450.5 mm. All accessions were planted on 18th May 2017 and 27th May 2018. Two rows of 3 m long of each genotype were planted with the row- to- row spacing of 35 cm and the plant- to-plant spacing of 10 cm. The experimental soil was red clay loam having pH of 8.1 and medium in organic material (18.2 g kg^{-1}). Fertilizers were applied at the rate of 66:36:54kg/ha $N:P_2O_5:K_2O$ as basal dose during land preparation and 30 kg/ha N was top-dressed 50 days after seeding. The test was irrigated once before heading date. All germplasms were provided by the Institute of Crop Germplasm Resources, Shanxi Academy of Agricultural Sciences.

Investigation of traits

The data were recorded as per the descriptors of foxtail millet [*Setaria italica* (L.) beauv.] (Lu 2006). Phenotypic

traits including sheath color, tillering, panicle type, heading date, stem node number, plant height, peduncle length, leaf length, leaf width, panicle length, panicle diameter, diameter of main stem, panicle weight per main stem, grain weight per main stem, primary branch number per panicle, spikelet number per primary branch, grain weight (1000-seed) and protein content were investigated.

Data analysis

The phenotypic data were entered and analyzed using Microsoft Excel 2007. The fuzzy membership function values for each trait were computed using a membership function whose range is between 0 and 1. The formula is as follows:

$$\mu\,(x_i) = (x_i\text{-}x_{imin})/(x_{imax}\text{-}x_{imin})\ (i{=}1,\,2,\,3,\ldots\ldots,\,595)$$

$\mu\,(x_i)$ is the membership function value of the personality trait of one material, x_i is the personality value, and x_{imax} and x_{imin} are the maximum and minimum values of x_i, respectively.

Shannon-Wiener diversity index (H') was used to evaluate genetic diversity. The formula is as follows:

$$H'{=}-\textstyle\sum\,(p_i\,Ln\,p_i)\ (i{=}1,\,2,\,3,\ldots\ldots,\,595)$$

Data analysis was carried out using correlation analysis, principal component analysis (PCA) and cluster analysis on SPSS 19.5. The scores of each principal component were calculated using Microsoft Excel 2007. The evaluation indices of all traits in foxtail millet germplasm accessions were screened using the stepwise regression analysis.

Results

Genetic diversity of qualitative traits

There were significant differences in the qualitative traits of the core collection of the foxtail millet germplasm in Shanxi Province (Fig. 1). Out of 595 genotypes, the majority were found to have green leaf sheath color (56.66%), while 26.64% of genotypes had a purple color. With regard to tillering capacity, 53.38% of foxtail millet genotypes had tillers and others had no-tillers. In terms of panicle type (Fig. 2), most of the genotypes belonged to type 2, accounting for 72.25%, followed by type 3 (13.87%), type 6 (6.6%) and type 4 (6.4%).

Genetic diversity of quantitative traits

According to the classification of genetic diversity, the quantitative traits were distributed into 10 groups (Fig. 3). The panicle diameter and grain weight (1000-seed) had values between 0.4 and 0.8 on a 10 point (0.1–1) scale, which represented 91.4% and 91.9% of the total genetic diversity, respectively. Furthermore, the diameter of the main stem, primary branch number per panicle and spikelet number per primary branch were in the range of 0.3–0.6,
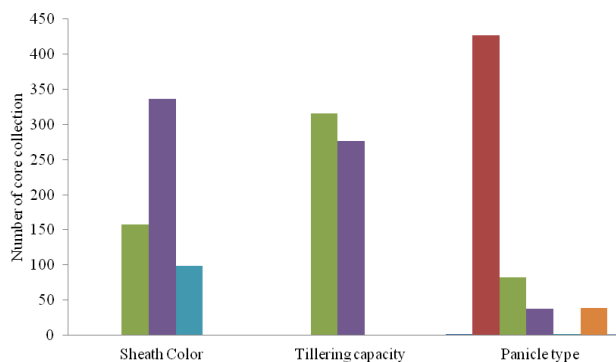
Fig. 1: The number of different types of germplasm in leaf sheath color, tillering capacity and panicle type in 595 core collection
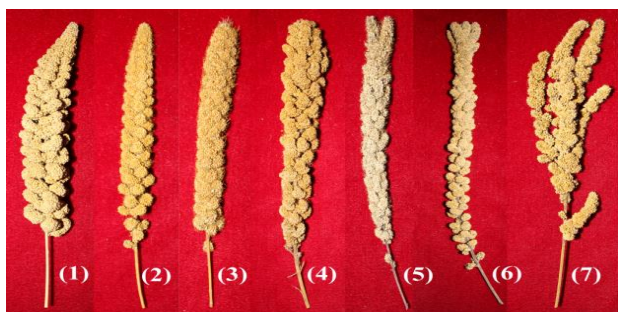
Fig. 2: Diversity panicle types of Shanxi foxtail millet core collection

Fig. 3: Distribution diagram of subordinate function value of fifteen phenotypic traits

accounting for 96.3%, 86.6%, and 94.3%, respectively. Other quantitative traits showed the values between 0.3–0.7, representing 87.4% to 95.6% of the diversity.

The variation and distribution of phenotypic traits in the core collection of foxtail millet are presented in Table 1. The minimum coefficient of variation among 15 quantitative traits was for protein content (6.71), while the maximum was for the grain weight per main stem (26.28). The minimum (1.29) and maximum (1.95) genetic diversity index values were observed for the diameter of the main stem and the protein content, respectively.

The average heading date (HD) was 62.48 ± 5.88 and ranged from 46.0 to 86.5 d. Among them, H526 (Majiangsheng 00018180) had the longest heading date (86.5), while the shortest heading date (46.0) was observed in H087 (Sangenqimaogu 00005564).

Table 1: Phenotypic traits of 595 foxtail millet accessions

Agronomic trait	Mean ±SD	Range	CV (%)	H'
HD (d)	62.48 ±5.88	46.00–86.5	9.42	1.81
SN	12.02 ±1.28	5.10–16.1	10.68	1.58
PH (cm)	114.55 ±17.04	38.90–160	14.88	1.74
PeL (cm)	38.42 ±6.61	20.20–59.7	17.20	1.93
LL (cm)	44.46 ±4.94	29.00–62.8	11.10	1.81
LW (cm)	2.81 ±0.25	1.88–4.47	8.84	1.35
PL (cm)	28.04 ±4.80	14.20–44.5	17.11	1.88
PD (cm)	2.51 ±0.35	1.22–3.68	14.11	1.79
DMS (cm)	0.80 ±0.08	0.46–1.36	10.39	1.29
PW (g)	24.33 ±6.08	5.24–46.84	25.00	1.81
GW (g)	19.48 ±5.12	3.67–37.11	26.28	1.84
PBNP	112.88 ±21.06	54.10–194.6	18.66	1.78
SNPB	90.52 ±19.30	19.50–168.1	21.33	1.69
SW (g)	3.15 ±0.36	1.63–4.19	11.28	1.75
PC (%)	12.37 ±0.83	10.00–14.8	6.71	1.95

HD, heading date; SN, stem node number; PH, plant height; PeL, peduncle length; LL, leaf length; LW, leaf width; PL, panicle length; PD, panicle diameter; DMS, diameter of main stem; PW, panicle weight per main stem; GW, grain weight per main stem; PBNP, primary branch number per panicle; SNPB, spikelet number per primary branch; SW, 1000-seed weight; PC, protein content

Panicle and grain weight per main stem are the two important yield component traits of foxtail millet. The average panicle weight was 24.33 ±6.08 g, ranging from 5.24 to 46.84 g. The average grain weight obtained was 19.48 ±5.12 g, with range values of 3.67 –37.11 g. Among them, H585 (Dagu 00016114) and H252 (Baimaolianggu 00015626) had the lowest panicle and grain weight, while the highest panicle and grain weights were recorded in H180 (Zhuhanchangruangu 00006232) and H266 (Jinjunqu 00015736).

The grain weight (1000-seed) ranged from 1.63–4.19 g, with a mean value of 3.15 ±0.36 g. Of the genotypes, H252 (Baigangu 00015626) had the lowest (1.63 g) and H268 (Huangruangu 00015749) had the highest (4.19 g) 1000-grain weight. The protein content had an average value of 12.37 ±0.83%, with a range of 10.01– 14.81%. The lowest (10.01%) and highest (14.81%) protein contents were found in H031 (Dahonghuanhgu 0004898) and H291 (Huangruangu 00015945), respectively.

Correlation analysis of phenotypic traits

Correlation analysis of the studied traits showed that there were different degrees of correlations among the 18 phenotypic traits (Fig. 4). The correlation between qualitative and quantitative traits was weak. Heading date was positively correlated with SN, PH, DMS, and PBNP, indicating the positive effect of HD on the growth of foxtail millet. The yield component traits PW and GW had highly significant positive correlations with the growth indices such as SN, PH, LL, LW, PL, PD, and DMS. It was found that SNPB and SW were also positively correlated with these traits, indicating the close interaction between vegetative and reproductive growth during the foxtail millet development. The yield of foxtail millet could only be improved by coordinating the vegetative and reproductive growth. The PC was significantly positively correlated with PeL and had a

Table 2: The variation distribution of quantitative traits in different years

Trait	2017		2018	
	Mean	CV	Mean	CV
HD	62.42 ±8.72	13.97	62.54 ±4.97	7.95
SN	12.03 ±1.46	12.14	12.02 ±1.33	11.06
PH	109.82 ±17.33	15.78	119.38 ±18.69	15.66
PeL	40.48 ±7.88	19.46	36.31 ±6.54	18.02
LL	44.75 ±5.83	13.04	44.2 ±5.41	12.24
LW	2.97 ±0.32	10.85	2.66 ±0.28	10.48
PL	27.00 ±4.94	18.31	29.10 ±5.67	19.49
PD	2.54 ±0.4	15.74	2.48 ±0.44	17.59
DMS	0.77 ±0.1	13.69	0.83 ±0.1	12.47
PW	25.78 ±8.04	31.18	22.86 ±6.69	29.25
GW	20.04 ±6.62	33.06	18.92 ±5.78	30.56
PBNP	108.95 ±24.67	22.65	117.10 ±21.76	18.59
SNPB	97.10 ±25.52	26.29	83.76 ±21.18	25.29
SW	3.08 ±0.45	14.67	3.24 ±0.4	12.26
PC	12.64 ±1.19	9.41	12.10 ±0.79	6.57
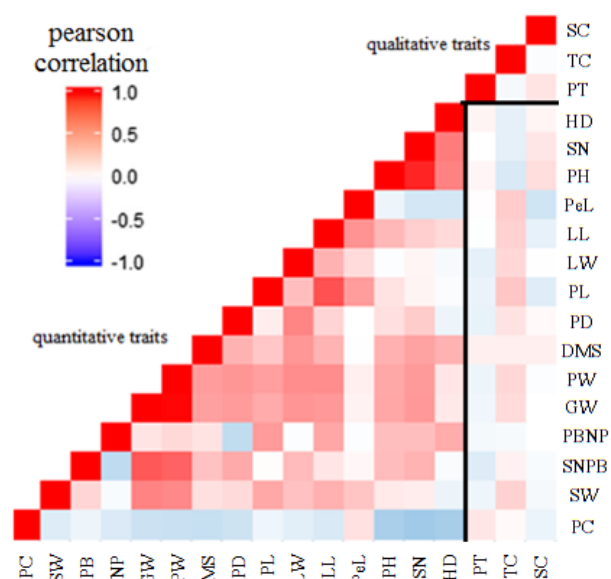
Fig. 4: Correlation matrix between the agronomic traits. Trait codes are given in Supplementary Table 1

negative correlation with other traits except for SW and SNPB. Therefore, the use of breeding processes to improve foxtail millet protein quality is of significant importance.

Annual variation in phenotypic traits

Stability is an important component of germplasm resources. Due to the differences in ecological environments, there might be differences in phenotypic traits in foxtail millet during two consecutive years. Table 2 lists the mean (average) and coefficient of variation (CV) for phenotypic traits in foxtail millet for two years. The mean values of HD, SN, LL, LW, and PD showed small variations between the two years. The highest mean values of PH, PL, DMS, PBNP, and SW were obtained in 2018,

while other quantitative traits had higher values in 2017. There were obvious variations in PL, PW, GW, and SNPB, which were significantly related to yield composition. Except for PL and PD, the coefficients of variation for other quantitative traits were higher in 2017 than those in 2018 and obvious variations were observed for HD, PBNP, SW, and PC.

Comparisons of shannon-wiener diversity indices of 18 phenotypic traits in core collection

According to administrative divisions in Shanxi Province, core collections of foxtail millet genetic resources, representing 11 cities, could be divided into 11 categories, namely, Datong (DT), Shuozhou (SZ), Xinzhou (XZ), Taiyuan (TY), Jinzhong (JZ), Lvliang (LL), Yangquan (YQ), Changzhi (CZ), Linfen (LF), Jincheng (JC) and Yuncheng (YC). Statistical analysis of genetic diversity indices of 18 phenotypic traits in a core collection consisting of 595 accessions was done based on 11 cities.

There were small differences among cities for the mean values of diversity indices (Table 3), indicating that phenotypic diversity in each city was equally abundant. However, the genetic diversity index (H') had the lowest mean value (1.6528) for Jincheng city and the highest value (1.8725) for Taiyuan city. Genetic diversity indices of the qualitative traits were significantly lower than that of the quantitative traits. The H' values of three quality traits (SC, TC and PT) were lower.

Cluster analysis on samplings of different regions in shanxi province

The core collection was divided into three groups with the Euclidean distance of 5.39 (Fig. 5) and the results were analyzed by DPS software. Datong and Shuozhou could be classified under Cluster I, while Cluster II included Jincheng, Jinzhong, Taiyuan, Luliang, Xinzhou, Yangquan, Changzhi and Linfen, and Yuncheng belonged to cluster III.

Principal component analysis of phenotypic traits

Correlation analysis showed correlations among phenotypic traits, which had a certain effect on the evaluation of the core collection. In order to mitigate the adverse effect of the related factors, the core collection was comprehensively evaluated by principal component analysis using DPS software. The cumulative contribution rate of the first nine principal components is over 80%, indicating that these components represented more than 80% of the genetic information for the evaluation of core collections.

The contribution rate of the first principal component was 25.71% and the power vectors of PW and GW were larger than for other traits, thus the first principal component was composed of these two traits (Table 4). The contribution rate of the second principal component was 14.26%, which was dominated by HD, SN, and PH,

Table 3: Comparison of the Shannon-Wiener diversity indexes of the 18 phenotypic traits of foxtail millet core collection

	SC	TC	PT	HD	SN	PH	PeL	LL	LW	PL	PD	DMS	PW	GW	PBNP	SNPB	SW	PC	Mean
DT	1.034	0.621	1.143	1.971	1.881	1.797	1.981	1.907	2.067	1.813	1.728	1.912	1.955	1.918	1.812	1.879	1.750	1.927	1.727
SZ	0.974	0.562	1.180	1.927	1.927	1.808	1.652	1.771	1.841	2.047	2.068	1.602	2.220	2.047	1.841	1.836	1.820	1.927	1.725
XZ	0.954	0.609	0.815	2.076	1.972	2.148	2.107	2.030	2.159	1.784	2.098	1.708	2.019	2.092	2.048	1.904	1.866	1.961	1.797
TY	0.957	0.666	0.536	2.109	2.021	2.172	2.122	2.025	2.139	2.162	2.139	1.998	2.144	2.264	2.055	1.945	2.142	2.107	1.873
JZ	0.959	0.693	0.713	1.908	1.984	1.872	2.069	1.801	1.752	2.012	1.971	1.769	2.094	2.061	1.959	1.931	1.901	1.942	1.744
LL	0.869	0.607	0.842	2.198	1.587	1.747	2.027	2.082	1.923	2.000	2.150	1.333	1.962	2.006	2.037	1.869	1.820	2.095	1.731
YQ	1.028	0.649	0.703	1.956	1.844	1.921	1.905	1.891	2.201	1.787	1.624	1.844	2.038	1.956	1.824	2.069	2.089	2.150	1.749
CZ	0.906	0.640	0.864	2.069	2.051	2.034	1.934	2.044	1.877	2.049	2.123	1.667	2.060	2.082	1.662	1.758	1.991	2.154	1.776
LF	1.020	0.693	0.933	1.909	2.143	1.927	2.079	2.075	1.498	1.724	2.078	1.730	2.227	2.192	2.083	2.091	2.105	2.049	1.808
JC	0.451	0.637	0.824	1.676	1.979	1.864	1.705	1.792	1.864	1.907	1.979	1.864	1.864	1.820	1.979	1.864	1.864	1.820	1.653
YC	0.831	0.257	0.628	1.710	1.767	1.615	2.061	1.864	1.841	1.991	1.859	1.807	1.991	2.119	1.841	2.084	2.084	1.859	1.678
Mean	0.973	0.691	0.914	1.806	1.579	1.738	1.926	1.811	1.348	1.877	1.791	1.289	1.808	1.841	1.777	1.670	1.753	1.948	

Trait codes are given in Table 1

Table 4: Power vector (PV), eigenvalues (E), contribution rate (CR), and cumulative contribution rate (CCR) of the first nine principal components based on 18 phenotypic traits

Trait	PV1	PV2	PV3	PV4	PV5	PV6	PV7	PV8	PV9
SC	0.0034	-0.1620	-0.1186	0.4297	0.2511	-0.6200	0.0422	-0.1491	0.4979
TC	0.0803	0.2654	0.0616	0.2047	-0.0235	-0.2523	-0.4248	0.7754	-0.0345
PT	-0.0418	-0.0753	0.0495	0.3612	0.7277	0.1974	-0.0378	-0.0547	-0.4042
HD	0.1406	-0.4161	0.1691	0.0802	-0.1019	0.1378	-0.1108	0.1861	-0.1736
SN	0.2802	-0.4046	-0.0160	-0.1129	0.0704	0.0866	-0.1436	0.0793	0.1624
PH	0.2659	-0.3902	0.0577	-0.1372	0.1564	0.1006	-0.1853	-0.0292	0.2727
PeL	0.0731	0.3340	0.2763	-0.0315	0.1557	0.3196	-0.3450	-0.1533	0.3670
LL	0.2921	0.1470	0.3749	0.0640	0.0392	0.1086	-0.0183	-0.0974	0.1611
LW	0.2471	0.2181	-0.1317	0.3854	-0.2431	0.1158	0.2518	-0.0944	-0.0280
PL	0.2355	0.2317	0.4194	0.0185	-0.0288	-0.0584	0.1153	-0.0638	0.0896
DP	0.2249	0.1090	-0.3332	0.2833	-0.2139	0.1815	-0.0914	-0.1321	0.1180
DMS	0.2728	-0.0861	-0.0296	0.4180	-0.0472	0.2606	0.1578	0.1157	-0.0835
PW	0.4086	0.0904	-0.1237	-0.1590	0.1137	-0.1444	0.1841	0.0554	-0.1419
GW	0.4012	0.0837	-0.1584	-0.1930	0.1505	-0.1518	0.1612	0.0508	-0.1452
PBNP	0.1138	-0.1757	0.4861	-0.0344	-0.1139	-0.2137	0.4167	0.1164	-0.0562
SNPB	0.2590	0.0605	-0.3844	-0.3072	0.1401	0.1110	0.0535	0.1751	0.1798
SW	0.2255	0.2240	0.0318	-0.1547	0.1255	-0.3397	-0.2893	-0.3479	-0.3495
PC	-0.1786	0.2342	-0.0069	-0.1183	0.3865	0.1656	0.4469	0.2897	0.2597
E	4.6285	2.5671	2.0125	1.1554	1.1041	0.9794	0.8834	0.8254	0.7912
CR%	25.7140	14.2619	11.1806	6.4189	6.1338	5.4410	4.9079	4.5856	4.3956
CCR%	25.7140	39.9759	51.1565	57.5754	63.7092	69.1502	74.0581	78.6437	83.0393

The trait codes are listed in Table 1
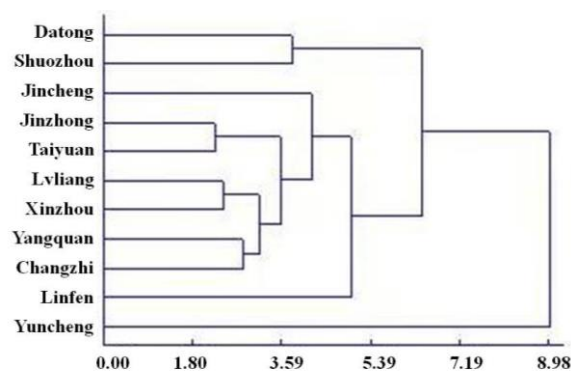
Fig. 5: Clustering dendrogram of foxtail millet germplasm resources from different regions in Shanxi Province

power vectors of LL, PL, DP, PBNP, and SNPB were larger than for other characters, which showed that the third principal component consisted of these characters. The contribution rate of the fourth component was 6.42%, and LW and DMS had larger power vectors than that of other characters. The fifth principal component had a contribution rate of 6.13% and it was composed of PT. The contribution rate of the sixth principal component was 5.44%, and the power vector of SC was the highest. The contribution rate of the seventh principal component was 4.91%, and the PC value was the largest. Moreover, the contribution rate of the eighth principal component was 4.58%, and the power vector of TC was the largest. The contribution rate of the ninth principal component was 4.40%, and PeL and SW had the highest values, indicating that these two traits had the largest contribution to this component.

Comprehensive evaluation of phenotypic traits

The values of 18 phenotypic traits of core collection in

indicating that the second principal component was a comprehensive reflection of these traits. The contribution rate of the third principal component was 11.18%, and the

Table 5: The higher and lower F value of accession

Name	location	Lower F	Name	Location	Higher F
Daheigu	Yanggao	0.3127	Langweiba	Zuoquan	0.6468
Gegu	Pingyao	0.3225	Baidihuang	Xingxian	0.6487
Bayihuang	Tunliu	0.3319	Machangjiang	Qinyuan	0.6542
Qinggu	Tunliu	0.3331	Dabaigu	Puxian	0.6564
Zhuazhuagu	Xiaxian	0.3343	Zhushugu	Yushe	0.6573
Huangruangu	Yingxian	0.3350	Hongxiaoweigu	Shouyang	0.6636
Yanggu	Pinglu	0.3413	Zigangu	Pingyao	0.6640
Honggangu	Yanhu	0.3440	Sanbianlian	Zuoquan	0.6663
Xiaobaigu	Zhangzi	0.3449	Gouchangruangu	Pingyao	0.6881
Qishiliugu	Pingding	0.3456	Zhuhanchangruangu	Lishan	0.7235

Table 6: Correlation coefficients between the 18 phenotypic traits and comprehensive value (F-value)

Trait	Correlation coefficient	Trait	Correlation coefficient
SC	-0.131**	PL	0.752**
TC	0.407**	DP	0.312**
PT	0.016	DMS	0.470**
HD	-0.013	PW	0.637**
SN	0.138**	GW	0.599**
PH	0.165**	PBNP	0.272**
PeL	0.554**	SNPB	0.320**
LL	0.784**	SW	0.358**
LW	0.555**	PC	0.084*

foxtail millet were standardized and then replaced with the 9 principal components. The scores of 9 principal components were obtained from accessions and standardized using the fuzzy membership function. The weight coefficients of each principal component were calculated (0.310, 0.172, 0.135, 0.077, 0.074, 0.066, 0.059, 0.055, 0.053). Furthermore, the composite score (F) for each germplasm was calculated. The higher the F value for each millet germplasm, the better the phenotypic character is. The average F value for the millet core collection was 0.5227 and the F value of H180 (Zhuhanchangruangu 00006232) from Lishi, Lvliang City was the highest (0.7235), while H256 (Dahegu 00015665) from Tunliu, Changzhi City had the lowest F value (0.3127), indicating more comprehensive phenotypes of H180 and less of H256 (Table 5). Correlation analysis showed that F value was positively correlated with all phenotypic traits except PT and HD (Table 6).

The optimal regression equation was constructed based on the composite score values (F) and phenotypic traits and the evaluation index values for traits of millet resources were screened. The equation constructed using the stepwise regression is as follows: $y = (-368.446 + 20.610x_2 + 2.191x_7 + 3.694x_8 + 42.224x_9 + 3.340x_{10} + 147.468x_{12} + 2.796x_{13} + 17.301x_{18}) \times 10^{-3}$, where x_2, x_7, x_8, x_9, x_{10}, x_{12}, x_{13} and x_{18} are representative of TC, PeL, LL, LW, PL, DMS, PW and PC, respectively and their direct path coefficient were 0.163, 0.229, 0.288, 0.166, 0.254, 0.194, 0.269 and 0.227, respectively. The determination coefficient (R^2) for the above equation was 0.984, indicating 98.4% of the variation in these 8 independent variables. The total variation of F was 4396.07 and various coefficients in the equation were highly significant. The F values for each of the variables in the regression equation showed high efficiency

of 8 variables and the value of the phenotypic variation in foxtail millet landraces from Shanxi Province was significant. It was indicated that 8 variables could be used as the core collection comprehensive evaluation indices.

Discussion

The genetic diversity for landraces of foxtail millet is required to evolve in response to complex geographical and ecological variations, climate change and long-term artificial domestication. These varieties are mainly planted in small regions and may be outdated or sporadic, but they have different origins and characteristics, possessed high genetic diversity and are suited to traditional agricultural practices (Li and Wu 1996; Nakayama 2011). A majority of these resources has not been genetically improved and may have obvious shortcomings, but some unusual characteristics are of great importance in breeding (Wang *et al.* 2018). The phenotypic traits of 595 core collection were evaluated for two consecutive years in order to better understand morphological characteristics of germplasm resources in crop breeding.

Genetic variation in the core collection is abundant, but it still is lower than the diversity of foxtail millet core collection at the national level (Wang *et al.* 2016). The range and coefficients of variation for all traits were high. The traits such as plant height, panicle length, panicle weight and grain weight in foxtail millet core collections showed generally higher values compared to those obtained in the studies by Tian (2010) and Qu *et al.* (2018). However, it was lower than that reported by Wang *et al.* (2009) on the germplasm identification of foxtail millet in Gansu Province. In this study, the average coefficient of variation

for 15 quantitative traits was 14.87% and the average genetic diversity index was 1.73. Coefficients of variation for panicle weight and grain weight were 25.00 and 26.28, respectively, and their genetic diversity indices were 1.81 and 1.84, respectively, indicating that core collections had abundant phenotypic diversity and could well represent the diversity in the entire collection of foxtail millet in Shanxi Province. Genetic diversity of different types of germplasm provides opportunities in plant breeding. In the present study, the range of variation for panicle weight, grain weight, 1000-seed weight and protein content could contain analysis results of the study by Zhang *et al.* (2017); Moreover, the range of variation for panicle length, panicle weight, grain weight and 1000-seed weight could contain the analysis results of the study by Xiang *et al.* (2018), indicating that gaining the advantages of landraces and improving the existing main varieties are positive approaches in foxtail millet breeding in Shanxi Province.

The resources of 11 cities from the same geographical origin in Shanxi Province were divided into three categories based on the systematic and cluster sampling. The first category included Datong and Shuozhou, in the north of Shanxi, which was mainly the early maturing spring-sowing areas; the second category included the majority of the cities in the south-central part of Shanxi Province, which were mainly the middle and late-maturing spring-sowing regions. Moreover, the third category included Yuncheng City, in the south of Shanxi, which was the summer-sowing area. This classification basically reflects the geographical and ecological areas of Shanxi for foxtail millet production.

In this study, the principal component analysis (PCA) for 18 traits of Shanxi core collection in foxtail millet was carried out. After the normalization of principal component scores, the composite scores (F) were calculated and the comprehensive performance of each landrace was evaluated and compared based on a quantitative value. Among the landraces, Langweiba, Baidihuang, Machangjiang, Dabaigu, Zhushugu, Hongxiaoweigu, Zigangu, Sanbianlian, Gouchangruangu, and Zhuhanchangruangu showed better comprehensive performance. The comprehensive phenotypic score of Jingu 21 (00024668) (Chen *et al.* 1992) was only 0.4697 and it ranked 494th. The annual cultivated area in Shanxi was about 1.33×10^5 hm^2, which was accepted by farmers and the markets, indicating that the local varieties still maintain allelic variation that needs to be further excavated and utilized.

All 16 traits were significantly correlated with F value. The correlation coefficient between tillering capacity and F value was 0.407 and that of peduncle length, leaf length, leaf width, panicle length, diameter of main stem, panicle weight, and grain weight was relatively high. The higher the comprehensive value, the higher the trait value was. For identification purposes and breeding practices, close attention should be paid to the selection of these traits. The research study of genetic variation in a population, combined with F value, can be conducted.

The correlation analysis showed that there was a correlation between different traits; although some were low, they were still significant. Meanwhile, the correlations between qualitative and quantitative traits were weak or did not exist, which were similar to those found between phenotypic traits and comprehensive score values. With regard to yield components panicle weight, grain weight, and 1000-seed weight, the correlation coefficient was highly significant. In order to improve the yield, the foxtail millet breeding programs and the selection of main traits should be strengthened; however, other secondary factors should also be considered. Varieties whose traits are coordinated and have excellent comprehensive scores could be extensively cultivated (Lu *et al.* 2015; Zhang *et al.* 2017).

Conclusion

Among the 595 accessions of foxtail millet core collection in Shanxi province, high level of diversity was observed for 18 agronomic traits like sheath color, tillering capacity, panicle type, heading date, stem node number, plant height, peduncle length, leaf length and width, panicle length and diameter, panicle and grain weight per main stem, protein content, etc. The protein content was significantly positive correlated with peduncle length. Landraces such as Zhuhanchangruangu, Sanbianlian, Zigangu, Dabaigu, Machangjiang, Langweiba, etc. had the much better comprehensive traits important and can usesd for crop improvement programmes. According to the established regression equation, eight traits were tested as the key phenotypic indicators. The abundant genetic variation of core collection provides utility resources for genetic improvement of foxtail millet.

Acknowledgments

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