



Variability of *Pyrus communis* accessions in China assessed using multivariate analysis

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Summary

Twenty-three morphometric fruit traits for 47 common pear (*Pyrus communis* L.) cultivars and hybrids were recorded from trees growing in the fruit tree resources nursery of the Yantai Academy of Agricultural Sciences, Shandong, China, to provide information for classification and utilization of common pear cultivars. The frequency distribution, coefficient of variation, and Shannon-Weaver diversity index were calculated. A Q-mode cluster analysis and principal component analysis were used to evaluate groups among the accessions and pomological characters. Significant diversity in fruit characters was observed among the accessions. The Shannon-Weaver index ranged from 0.42 to 2.02. The average coefficient of variation was lowest for total soluble solids concentration (8.38%) and highest for fruit peel color (40.6%). The Shannon-Weaver index for 11 qualitative characters ranged from 0.42 to 1.33 and indicated that the qualitative characters showed rich diversity. The first nine principal components accounted for 85.40% of the total variance. Principal component biplots and hierarchical cluster analysis categorized the accessions into five main groups on the basis of the pomological traits. The results provide information on morphological relationships among common pear cultivars grown in China and indicate there is high phenotypic diversity that can be utilized in pear breeding programs.

Keywords

Pyrus communis, fruit quality, biodiversity, numerical classification, principal component analysis

Significance of this study

What is already known on this subject?

- Evaluation of phenotypic diversity among genotypes is an important consideration for classification and utilization of germplasm resources in breeding. However, few studies have examined relationships among pomological traits for common pear in China.

What are the new findings?

- Some characteristics had the highest discrimination power and hence are suggested for morphological evaluation of pear accessions. Fruit weight, fruit length and total soluble solids were highly diverse for creating abundant pear germplasm.

What is the expected impact on horticulture?

- The present investigation detected substantial genetic diversity among *Pyrus communis* accessions, which indicates there is considerable potential to breed pear cultivars. The variability detected among *P. communis* accessions grown in China may be utilized in future traditional breeding programs or advanced biotechnology studies.

Introduction

Pears are considered to have originated in Central Asia. From the ancestral form, the lineage evolved into two broad groups of species: oriental species, native to eastern and northern Asia, and occidental species, native to Europe and northern Asia. Pear is among the most important fruit crops grown in temperate parts of the world. China is the center of origin of the genus *Pyrus* and is a global center of diversity for cultivated pear. Four groups of commercial pear cultivars are recognized in China (Teng et al., 2004): Chinese sand pear (*Pyrus pyrifolia* (Burm. f.) Nakai), Chinese white pear (*Pyrus pyrifolia* White Pear Group), Ussurian pear (*Pyrus ussuriensis*

Maxim.), and Xinjiang pear (*Pyrus x sinkangensis* T.T. Yu). The European species *Pyrus communis* L. (common pear) is the progenitor of more than 5,000 cultivars (Monte-Corvo et al., 2001); only a small number of these cultivars are grown commercially worldwide (Bell et al., 1996). Global pear production is predominantly limited to certain cultivars, such as 'Williams', 'Anjo', and 'Conference', which were selected during the eighteenth and nineteenth centuries. Therefore, it is crucial to evaluate the diversity among extant *Pyrus* accessions to breed new cultivars. Screening of existing genotypes is important to exploit the genetic variability and to identify superior genotypes in breeding programs.

Shandong Peninsula is an important region in China for cultivation of common pear. Yantai was an early area where common pear accessions were introduced to China, including 'Bartlett' and 'Conference', as the environment and climate were highly suitable for common pear. Germplasm resources of *Pyrus communis* have been analyzed in numerous previous studies. For example, the genetic diversity of different *Pyrus* species, including European, Asian, and other commercially less important species, has been evaluated using morphological, biochemical, and molecular markers (Zarei et al., 2019).

Fruit quality parameters may not be independent and, therefore, the relationships among such parameters should be studied to improve the selection objectives for fruit quality and to improve characterization of fruit quality by using a limited number of independent parameters (Ruiz and Egea, 2008). Studies of peach have revealed correla-

tions among certain pomological traits (Byrne et al., 1991; Genard and Bruchou, 1992; Genard et al., 1994; Esti et al., 1997). Variance analysis, correlation analysis, principal component analysis (PCA), and hierarchical cluster analysis have been used to study the diversity of fruit quality traits among pear germplasm in Guizhou province (Zhang and An, 2014).

TABLE 1. Pedigree and origin of the 47 common pear accessions studied.

Cultivars	Pedigree	Origin
Boliarska	Unknown	Bulgaria
Beurre Giffard	A chance seedling	France
Madeleine	Unknown	France
Yubileen Dar	Unknown	Bulgaria
Bunte Julibirne	Unknown	Germany
Red Clapp Favorite	A red sport of Clapp Favorite	United States
Docteur Jules Guyot	A seedling selection	France
Clapp Favorite	Flemish Beauty × Bartlett	United States
Bartlett-Max Red	A red sport of Bartlett	United States
Bosc	Unknown	Belgium
Red Anjou	A red sport of Anjou	United States
Bartlett	Unknown	England
Alexandrine Douillard	Unknown	Unknown
Radana	Unknown	Czech Republic
Zaojinxiang	Ai xiang × Docteur Jules Guyot	China
Maria	Unknown	Unknown
Spalding	Unknown	Unknown
Lecounte	Unknown	China
Chispe	Unknown	Unknown
Xiaozaoashuyangli	Unknown	France
Star	Unknown	Unknown
Fulaoendi'e	Unknown	China
Laikelake	Unknown	China
Chaoxianyangli	Unknown	China
Hayilande	Unknown	China
Lafulansi	Unknown	China
Louis	Unknown	Unknown
Red Beileisha	Unknown	Unknown
Cascade	Unknown	United States
Likert	Unknown	Unknown
Comice	Unknown	United States
Hailante	Unknown	China
Jinxiang	Bartlett × Nanguoli	China
Aixiang	A seedling selection	China
Longyuanyangli	Longxiangli × 63-1-76	China
Bayuehong	Early Barlette × Zaosu	China
Ningmenghuang	Jingbaili × Pyrus	China
Wujiuxiang	Yali × Bartlett	China
Guifei	Unknown	China
Eldorado	Unknown	Bulgaria
Angeliemu	Unknown	China
Gufoenboer	Unknown	Unknown
Pink avocado	Coscia × Beurre Claireau	Italy
Packham's Triumph	Uvedale St. Fermain × Bartlett	Australia
Hardy	Unknown	France
Abate Fetel	Unknown	France
Trapezica	Unknown	Bulgaria

Multivariate techniques, such as PCA and cluster analysis, have been extensively used by researchers to assess correlations among morphometric characters and to analyze germplasm of diverse fruit crops, such as pear (Pereira-Lorenzo et al., 2012; Najafzadeh and Arzani, 2015; Bashiri et al., 2017), grape (Cunha et al., 2007), pomegranate (Khadivi-Khub et al., 2015; Martinez-Nicolas et al., 2016; Zarei, 2017), cherry (Khadivi-Khub, 2014), (Pestanana et al., 2011), longan (Huang et al., 2010), loquat (Chen et al., 2011), mango (Shi et al., 2011), apple (Gong et al., 2014), kiwifruit (Qin et al., 2015), watermelon (Pan et al., 2015) and jujube (Norouzi et al., 2017). However, few studies have examined relationships among pomological traits for common pear in China.

We recorded fruit characters for 47 common pear accessions grown in Shandong province to summarize the phenotypic diversity by calculation of a diversity index and quantitative classification analysis. The results provide a foundation for identification, utilization, and breeding of superior pear germplasm resources. Evaluation of fruit characters for a large number of cultivars and hybrids that show considerable phenotypic variability will provide valuable information on *Pyrus communis* accessions and their potential utilization in breeding programs.

Materials and methods

Plant materials

The study was conducted at the Yantai Academy of Agricultural Sciences, Yantai, Shandong province, China in two consecutive years (2018 and 2019). Forty-seven common pear cultivars and hybrids were grown in the same experimental orchard using standard pear orchard management practices (Table 1). To assess 11 qualitative and 12 quantitative fruit characters for each accession, 25 mature fruit per accession that were free of pests and diseases were randomly selected and hand-harvested at the commercial maturity stage. Immediately after harvest, the fruit were transported to the laboratory where the characters were measured. Three replicates for each cultivar were recorded.

Fruit quality trait evaluation

Fruit shape, fruit peel color, lenticel prominence, degree of russetting, flesh texture, flesh texture type, flesh juiciness, flesh flavor, fruit core size, fruit fragrance, and abundance of stone cells, were described by visual observation and the relevant phenotypic character state was assigned (Table 2). In

addition, the quantitative characters fruit weight, total soluble solids (TSS) concentration, fruit length, fruit diameter, fruit shape index, peduncle length, peduncle diameter, flesh firmness, soluble sugar (SS) concentration, titratable acidity (TA), ratio of TSS to TA, and ratio of SS to TA were measured.

The fruit weight was calculated as the mean weight of 25 fruit sampled per cultivar measured using an analytical balance (model JKH-500, Jadever Co., Taiwan) with accuracy of ± 0.01 g. Flesh firmness was measured using a Bertuzzi Penetrometer (model FT-327, Facchini, Alfonsine, Italy) equipped with an 8-mm cylindrical plunger and was expressed as kg cm^{-2} . Fruit length and fruit diameter were measured with accuracy of 0.1 mm using a vernier caliper. The SS concentration was determined using an Atago N1 handheld refractometer (Atago, Tokyo, Japan) and the data were expressed as °Bx. The TA was determined by acid-base titration. The TSS concentration was measured using a digital refractometer (PAL-1, Japan). The ratio of TSS concentration to TA, and the ratio of SS concentration to TA were calculated. The flesh from the sampled fruit was used for determination of SS and TA. The flesh samples were immediately frozen in liquid nitrogen and stored at -20°C prior to use.

Statistical analysis

The mean of the data for two years was calculated for each character. Microsoft Excel and IBM SPSS Statistics 19.0 software were used for data analysis. Qualitative traits were calculated from the corresponding assignment values of each type, and quantitative traits were classified into 10 classes, ranging from Class 1 ($<x - 2s$) to Class 10 ($>x + 2s$), where s is the standard deviation and the difference between each class was 0.5s, 'x' the mean value for a character. Fruit trait diversity was evaluated by calculating the Shannon-Weaver index (H') using the formula $H' = -\sum(p_i) \ln(p_i)$, where p_i is the proportion of the total sample represented by trait i . Principal component analysis was performed to evaluate the relationships among cultivars in multidimensional space. Minimum and maximum values as well as the mean and coefficient of variation (CV; %) were analyzed for all variables. Pearson's correlation analysis among the fruit traits and hierarchical clustering of the accessions into similarity-based groups using Ward's method were performed. The number of principal components (PCs) considered was determined by the principal component cumulative ($\geq 85.0\%$). The PC score of each accession and the PC load of each character were used to generate biplots of the first and second PCs (PC1 and PC2).

TABLE 2. Eleven qualitative characters for pear fruit and coding of the phenotypic character states.

Character	1	2	3	4	5	6
FS	Oblate	Globose	Ovate	Obovate	Spindle-shaped	Pear-shaped
FPC	Russet	Light russet	Green	Yellow green	Green yellow	Red
LP	Conspicuous	Moderate	Obscure			
DR	Many	Moderate	Few	Absent or rare		
FT	Coarse	Moderate	Fine			
FTT	Dense	Sandy	Soft			
JF	Dry	Moderate	Juicy			
FF	Sour	Sweet-sour	Sour-sweet	Sweet		
FCS	Large	Moderate	Small			
FFC	Absent	Present				
ASC	Abundant	Moderate	Few			

FS: fruit shape; FPC: fruit peel color; LP: lenticel prominence; DR: degree of russetting; FT: flesh texture; FTT: flesh texture type; JF: flesh juiciness; FF: flesh flavour; FCS: fruit core size; FFC: fruit fragrance; ASC: abundance of stone cells.

Results

Morphological traits diversity analysis

Identification and evaluation of pear fruit characters is a primary task of research on pear germplasm resources, which can be used for initiation of breeding programs, management of genetic resources, protection of cultivars, and selection of candidates for local production (Pereira-Lorenzo et al., 2012). In total, 40 character states were distinguished among the 11 qualitative characters recorded. Fruit shape and fruit peel color showed the greatest variation (six states for each character). The CV ranged from 16.45% (fruit core size) to 40.58% (fruit peel color). The Shannon-Weaver diversity index ranged from 0.42 (fruit core size) to 1.33 (fruit peel color), which indicated that the fruit qualitative characters showed abundant variation.

Among the six character states defined for fruit shape, pear-shaped was the most frequent state recorded among the 47 accessions (74.47%). For the other qualitative characters, the most frequent states were green fruit peel, obscure lenticels, degree of russeting, low degree of russeting, fine flesh texture, soft flesh texture type, juicy fruit, sour-sweet flavor, medium fruit core size, fruit fragrance present, and low abundance of stone cells, which were observed in 53.19%, 53.19%, 85.11%, 61.70%, 68.09%, 68.09%, 74.47%, 89.36%, 63.83%, and 51.06% of the accessions, respectively (Figure 1).

Quantitative fruit characters

The CV for quantitative characters ranged from 8.38% (TSS concentration) to 37.25% (RST), which indicated that the fruit traits showed a high degree of variation among the

TABLE 3. Statistics for the diversity of 23 fruit characters recorded for 47 common pear accessions.

Variable	Mean	Max.	Min.	SD	Variation coefficient (%)	Shannon-Weaver diversity index	Class
Fruit shape	5.17	6	1	1.52	29.40	0.93	Low diverse
Fruit peel color	3.09	6	1	1.25	40.58	1.33	Intermediate
Lenticel prominence	2.28	3	1	0.84	37.03	1.01	Intermediate
Degree of russeting	3.72	4	1	0.71	18.95	0.56	Low diverse
Flesh texture	2.57	3	1	0.57	22.30	0.8	Low diverse
Flesh texture type	2.57	5	1	0.68	26.26	0.83	Low diverse
Flesh juiciness	2.4	3	1	0.8	32.44	0.91	Low diverse
Flesh flavor	2.89	4	1	0.66	22.81	0.84	Low diverse
Fruit core size	1.98	3	1	0.33	16.45	0.42	Low diverse
Fruit fragrance	1.6	2	1	0.5	29.33	0.65	Low diverse
Abundance of stone cells	2.28	3	1	0.82	35.91	1.03	Intermediate
Fruit weight (g)	211.8	459.0	54.6	77.37	36.53	2.02	Highly diverse
Total soluble solids (%)	13.0	15.1	10.7	1.08	8.38	2.00	Highly diverse
Fruit length (mm)	84.07	117.1	57.24	19.25	22.65	2.01	Highly diverse
Fruit diameter (mm)	70.37	92.54	49.59	15.24	21.43	1.91	Intermediate
Fruit shape index	1.21	0.89	1.53	0.19	15.84	1.95	Intermediate
Peduncle length (cm)	3.10	1.15	6.78	1.11	35.23	1.98	Intermediate
Peduncle diameter (mm)	0.42	0.27	0.74	1.28	26.81	1.95	Intermediate
Flesh firmness (kg cm ⁻²)	4.3	2.6	7.3	1.52	27.51	1.90	Intermediate
Soluble sugar (%)	7.62	5.93	9.07	1.01	10.79	1.83	Intermediate
Titrateable acidity (%)	0.27	0.13	0.48	0.09	30.51	1.89	Intermediate
Ratio of TSS and TA	53.98	109.23	27.5	21.78	35.26	1.50	Intermediate
Ratio of SS and TA	31.66	13.27	56.33	14.67	37.25	1.27	Intermediate

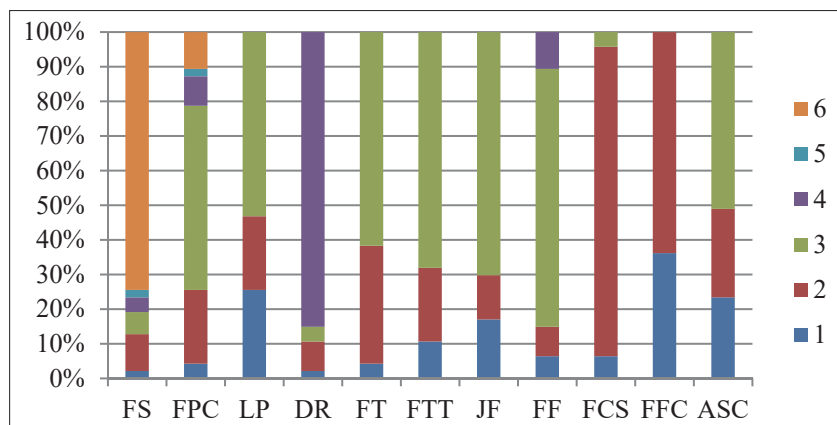


FIGURE 1. Frequency distribution of fruit qualitative characters among 47 common pear accessions.

TABLE 4. Correlation coefficients among the pear fruit characters.

	FS	FPC	DO	AR	FT	FTT	JF	FF	FCS	FFC	ASC	WF	TSS	FL	FD	FSI	SL	ST	FFI	SS	TA	RTT	RST
FS	1	-0.153	0.312*	0.262	0.497**	0.484**	0.532**	0.082	0.210	0.550**	0.510**	-0.082	0.444**	0.198	-0.219	0.566	0.303	0.056	-0.449**	0.396**	-0.315*	0.365*	0.360*
FPC		1	0.179	0.051	-0.009	0.093	0.140	-0.015	0.010	0.051	0.118	0.165	-0.138	0.017	0.090	-0.098	-0.086	0.328*	-0.021	0.027	0.047	-0.112	-0.061
DO			1	0.397**	0.507**	0.468**	0.419**	0.053	-0.056	0.615**	0.476	-0.236	0.160	-0.160	-0.264	0.181	0.299*	0.133	-0.516**	0.298	-0.342*	0.339*	0.353*
AR				1	0.497**	0.155	0.306*	0.028	0.047	0.332*	0.297*	-0.219	-0.041	-0.126	-0.175	0.071	0.305*	0.012	-0.263	-0.066	-0.106	0.130	0.120
FT					1	0.484**	0.093	-0.138	0.771**	0.476**	-0.019	0.510**	0.088	-0.086	-0.189	0.409**	0.264	0.046	-0.703**	0.379**	-0.396**	0.427**	0.460**
FTT						1	0.050	0.089	0.703**	0.771**	0.455**	-0.015	0.426*	0.290*	-0.178	0.401**	0.157	0.167	-0.639**	0.416**	-0.308*	0.369*	0.409*
JF							1	-0.011	0.165	0.212	0.151	0.409**	0.202	0.155	0.121	-0.104	0.032	0.208	-0.213	0.334*	-0.584**	0.439**	0.485**
FF								1	-0.024	0.147	0.189	0.175	0.168	0.409**	0.120	0.237	-0.030	0.128	0.045	0.334*	-0.531**	0.478**	0.441**
FCS									1	0.042	0.238	0.208	0.154	0.312	0.202	0.223	0.007	0.116	-0.135	0.136	-0.242	0.218	0.211
FFC										1	0.722**	-0.128	0.469**	0.222	-0.034	0.343*	0.172	0.382*	-0.658**	0.453**	-0.348**	0.416**	0.443**
ASC											1	-0.0064	0.365*	0.310*	0.074	0.416**	0.138	0.224	-0.472**	0.422**	-0.513**	0.525**	0.529**
WF												1	0.493**	0.414**	-0.144	-0.354*	0.231	0.161	0.075	-0.212	0.246	0.226	0.226
TSS													1	0.374**	0.044*	0.471**	-0.121	0.250*	-0.389*	0.933**	-0.455**	0.636**	0.476**
FL														1	0.740**	0.339*	-0.328*	0.047	-0.153	0.389**	-0.322*	0.446**	0.428**
FD															1	-0.367*	-0.493**	0.003	0.140	0.106	-0.212	0.161	0.180
FSI																1	0.187	-0.011	-0.423**	0.409**	-0.316*	0.415**	0.370**
SL																	1	-0.219	-0.229	-0.103	0.126	-0.153	-0.180
ST																		1	-0.065	0.313*	-0.222	0.217	0.232
FFI																			1	-0.449*8	0.544**	-0.572**	-0.541**
SS																				1	-0.581**	0.725**	0.763**
TA																					1	-0.905**	-0.864**
RTT																						1	0.942**
RST																							1

*: p<0.05; **: p<0.01.

Abbreviations: FS: fruit shape; FPC: fruit peel color; DO: lenticel prominence; AR: degree of russeting; FT: flesh texture; FTT: flesh texture type; JF: flesh juiciness; FF: flesh flavor; FCS: fruit core size; FCC: fruit fragrance; ASC: abundance of stone cells; WF: fruit weight; TSS: total soluble solids concentration; FL: fruit length; FD: fruit diameter; FSI: peduncle length; SL: peduncle length; ST: peduncle diameter; FFI: flesh firmness; SS: soluble sugar concentration; TA: titratable acidity; RTT: ratio of TSS to TA; RST: ratio of SS to TA.

accessions. Characters that show high variability represent strong candidates for selection in the germplasm set. The Shannon-Weaver diversity index ranged from 1.27 (RST) to 2.02 (fruit weight). These results confirmed that the fruit characters showed abundant diversity. Three traits (fruit weight, TSS concentration, and fruit length) showed high diversity (see Table 3).

The mean peduncle length and mean peduncle diameter were 3.10 cm and 0.42 mm, respectively. The CV was 35.23% and 26.81%, and the Shannon-Weaver diversity index was

1.98 and 1.95, respectively. The mean fruit shape index was 1.21, which indicated that the predominant fruit shape of the accessions analyzed was pear-shaped. Weight per fruit ranged from 54.6 g ('Boliarska') to 459.0 g ('Cascade'). Flesh firmness ranged from 2.6 to 7.3 kg cm⁻² for all cultivars and selections. Most of the accessions showed flesh firmness values between 2.6 and 4.0 kg cm⁻², which are suitable for consumers and the processing industry. The TSS concentration ranged from 10.7 °Bx to 15.3 °Bx. The cultivar 'Bayuehong' showed the lowest TSS concentration, whereas

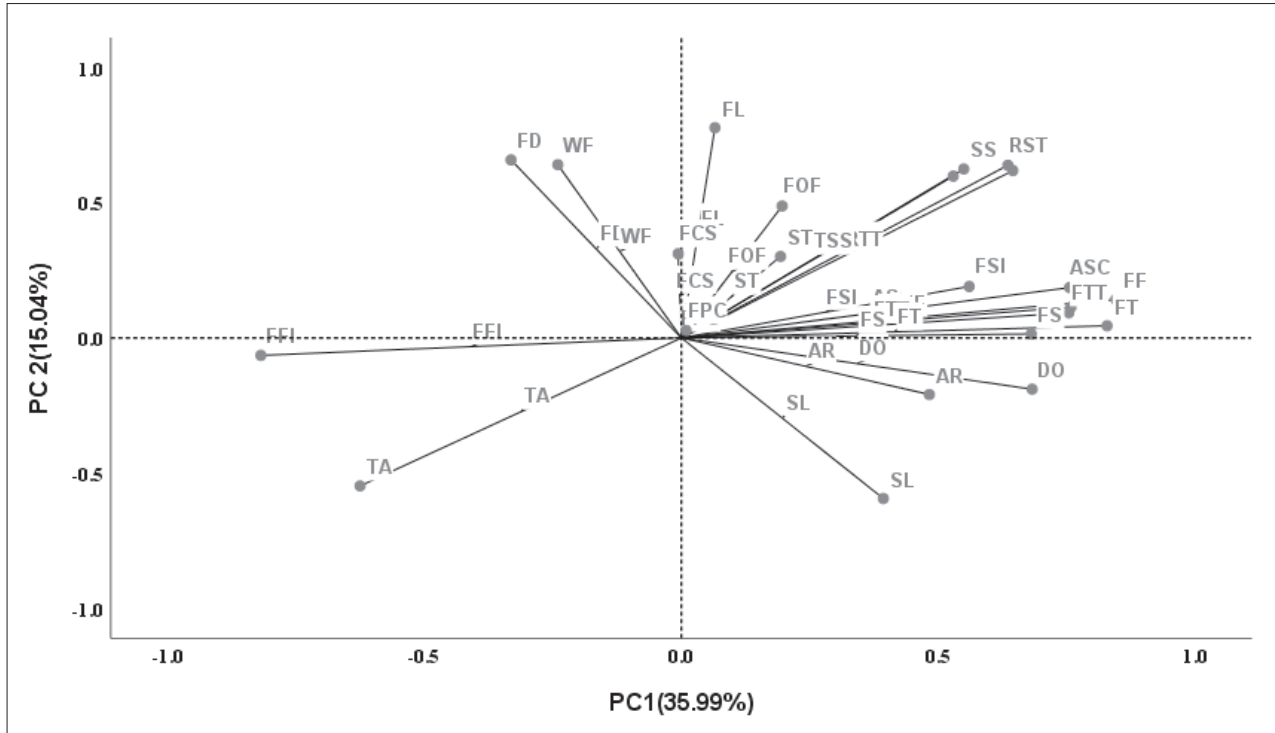


FIGURE 2A. Scatterplot of the 47 pear cultivars according to fruit quality characters on the first and second principal components (PCs) as determined by principal component analysis.

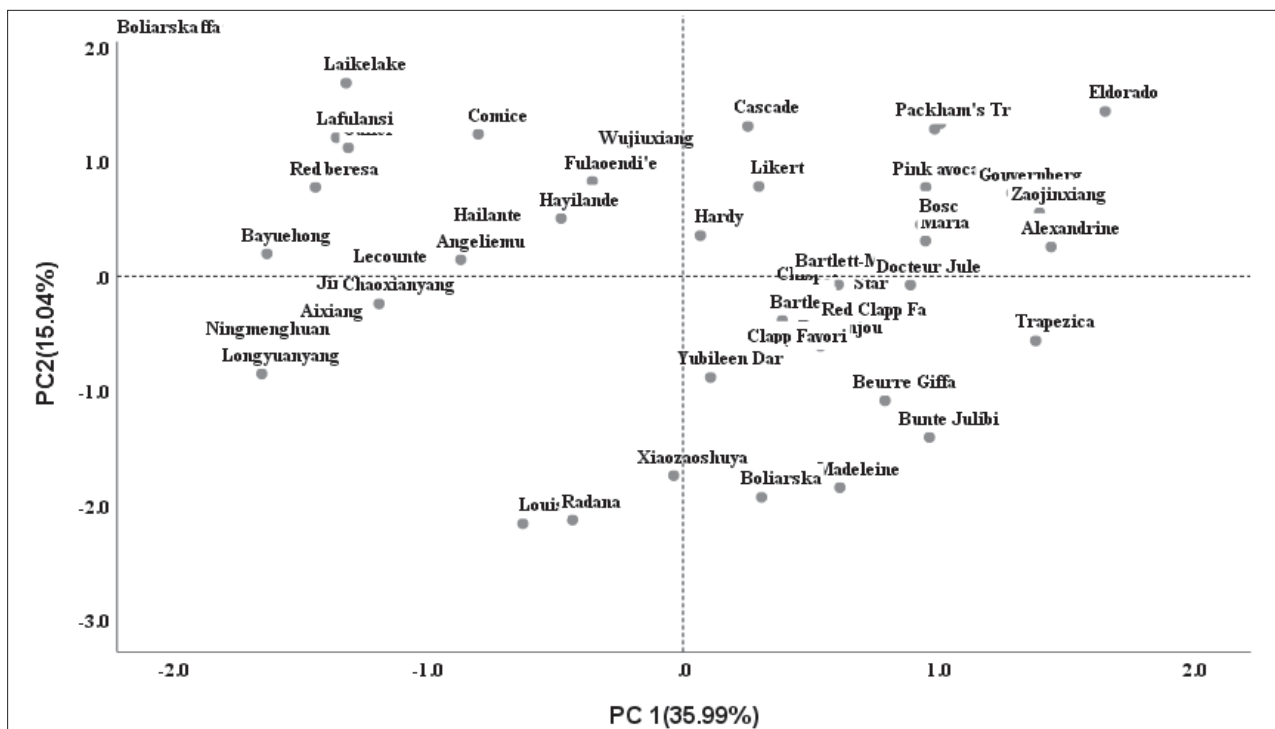


FIGURE 2B. Scatterplot of factors on first and second PCs for the 47 pear cultivars.

the highest was recorded for 'Packham's Triumph'. The SS concentration is an extremely important quality attribute and notably influences the fruit taste. The SS concentration ranged from 5.71 °Bx ('Angeliemu') to 9.37 °Bx ('Packham's Triumph') and the Shannon-Weaver diversity index was 1.83. The TA of cultivars ranged from 0.13% ('Eldorado') to 0.5% ('Longyuanyangli'). The means of the ratio of TSS to TA and the ratio of SS to TA were 54.62 and 30.16, the CV was 35.26% and 37.25%, and the Shannon-Weaver diversity index was 1.50 and 1.27, respectively.

Pearson's correlations among traits

Significant correlations were observed among fruit characters (Table 4). Fruit shape was correlated with lenticel prominence ($r=0.312^*$), fruit texture ($r=0.497^{**}$), fruit texture type ($r=0.484^{**}$), flesh juiciness ($r=0.532^{**}$), fruit fragrance ($r=0.550^{**}$), stone cell abundance ($r=0.510^{**}$), TSS concentration ($r=0.444^{**}$), SS concentration ($r=0.396^{**}$), and TA ($r=-0.315^*$). The SS concentration was strongly correlated with fruit texture ($r=0.443^{**}$), fruit texture type ($r=0.536^{**}$), flesh juiciness ($r=0.378^*$), fruit fragrance ($r=0.584^{**}$), stone cell abundance ($r=0.419^{**}$), flesh firmness ($r=-0.377^{**}$), and RST ($r=0.763^{**}$). Fruit weight was strongly correlated with fruit length ($r=0.493^{**}$), fruit diameter ($r=0.414^{**}$), and peduncle length ($r=-0.354^*$). It is well established that increase in fruit length will result in a higher fruit weight. The TSS concentration was highly correlated with TA ($r=-0.455^{**}$), SS ($r=0.933^{**}$), RTT ($r=0.636$), flesh firmness ($r=-0.389^*$), peduncle diameter ($r=0.250^*$), and fruit shape index ($r=0.471^{**}$). Therefore, the correlated parameters can be used to predict each other.

TABLE 5. Eigenvalues and proportion of the total variance among cultivars explained by individual principal components.

PC	Eigenvalues	Percent var.	Cumulative %
1	8.276	35.985	35.99
2	3.460	15.044	51.028
3	1.700	7.391	58.42
4	1.424	6.189	64.61
5	1.307	5.683	70.29
6	1.151	5.002	75.29
7	0.914	3.974	79.27
8	0.715	3.109	82.38
9	0.695	3.021	85.40
10	0.570	2.477	87.88
11	0.539	2.345	90.22
12	0.460	2.001	92.22
13	0.428	1.860	94.08
14	0.353	1.535	95.62
15	0.310	1.349	96.97
16	0.225	0.979	97.94
17	0.198	0.862	98.81
18	0.102	0.442	99.25
19	0.064	0.278	99.53
20	0.063	0.272	99.80
21	0.039	0.170	99.97
22	0.039	0.162	99.98
23	0.004	0.018	99.99
24	0.003	0.013	100.000

TABLE 6. Principal component analysis of the pear fruit characters measured. Eigenvalues for each character on the first nine principal components are listed. Eigenvalues ≥ 0.412 (highlighted in bold) are significant.

	Components								
	1	2	3	4	5	6	7	8	9
Fruit shape	0.574	0.066	0.013	0.551	0.151	-0.283	0.120	-0.117	0.062
Fruit peel color	0.122	-0.078	0.028	-0.079	0.207	0.845	-0.049	0.095	-0.010
Lenticel prominence	0.567	0.235	-0.310	-0.142	0.143	0.238	0.197	-0.300	0.051
Degree of russeting	0.288	0.096	-0.146	-0.053	0.017	-0.036	0.857	-0.024	0.071
Flesh texture	0.751	0.298	-0.149	0.126	-0.081	-0.038	0.356	0.186	0.052
Flesh texture type	0.793	0.246	-0.172	0.085	0.174	-0.052	-0.152	0.107	-0.186
Juiciness of flesh	0.822	0.138	0.181	0.188	-0.008	0.100	0.180	-0.009	0.015
Flavor of flesh	-0.237	0.683	0.214	0.332	0.220	0.109	0.169	-0.129	-0.282
Fruit core size	-0.078	0.086	0.140	0.112	0.078	-0.015	0.075	0.064	0.927
Fruit fragrance	0.833	0.268	0.067	0.038	0.311	-0.048	0.088	-0.189	-0.057
Amount of stone cells	0.654	0.293	0.186	0.253	0.101	0.200	0.229	-0.213	0.199
Weight per fruit	-0.127	0.116	0.328	0.039	0.212	0.126	0.004	0.824	0.102
Total soluble solids	0.310	0.635	0.048	0.165	0.412	-0.358	-0.159	0.098	0.111
Fruit length	0.159	0.277	0.826	0.261	-0.020	-0.020	-0.136	0.178	0.150
Fruit diameter	-0.067	0.069	0.911	-0.313	-0.002	0.031	-0.042	0.135	0.066
Fruit shape index	0.315	0.326	-0.155	0.776	-0.031	-0.054	-0.139	0.113	0.161
Peduncle length	0.203	-0.182	-0.414	0.352	-0.118	-0.049	0.338	-0.379	0.041
Peduncle thickness	0.133	0.119	-0.025	0.003	0.813	0.296	0.031	0.173	0.067
Flesh firmness	-0.704	-0.463	0.078	-0.129	0.241	-0.117	-0.032	0.175	0.052
Soluble sugar	0.395	0.631	0.082	0.025	0.419	-0.322	-0.163	0.120	0.147
Titrateable acidity	-0.320	-0.881	-0.100	-0.036	0.066	-0.084	-0.099	0.014	-0.041
Ratio of TSS and TA	0.347	0.881	0.089	0.085	0.032	-0.060	0.051	0.083	0.078
Ratio of SS and TA	0.374	0.860	0.099	0.024	0.077	-0.055	0.040	0.123	0.086



PCA grouping of accessions and traits

The Kaiser-Meyer-Olkin index value was 0.702 (sig = 0.000), which indicated that conducting a PCA was acceptable. The first nine PCs (PC1 to PC9) collectively explained 85.40% of the total variance, the contribution of each trait to the PCs was relatively dispersed, and the cumulative contribution rate did not increase significantly, indicating that the trait variation was multidirectional and its classification was influenced by multiple traits. The character's fruit shape, lenticel prominence, flesh texture, flesh texture type, flesh juiciness, fruit fragrance, abundance of stone cells, and flesh firmness were prevalent in PC1 and contributed 35.99% of the total variation. Flesh flavor, TSS concentration, TA, ratio

of TSS to TA, and ratio of SS to TA were significant contributors to PC2 and accounted for 15.04% of the total variance. With regard to PC3, fruit length, fruit diameter, and peduncle length contributed 7.39% of the total variation. These three PCs explained 58.42% of the total variance among the 47 accessions. The six remaining PCs explained 26.98% of the variance and the important traits included fruit shape index, TSS concentration, peduncle diameter, fruit peel color, degree of russeting, fruit weight, and fruit core size. Plots of PC1 and PC2 were generated to visualize the relationship in multidimensional space among the pear accessions (Figure 2a, b). The PC scores for the accessions evaluated are shown in Figure 2b.

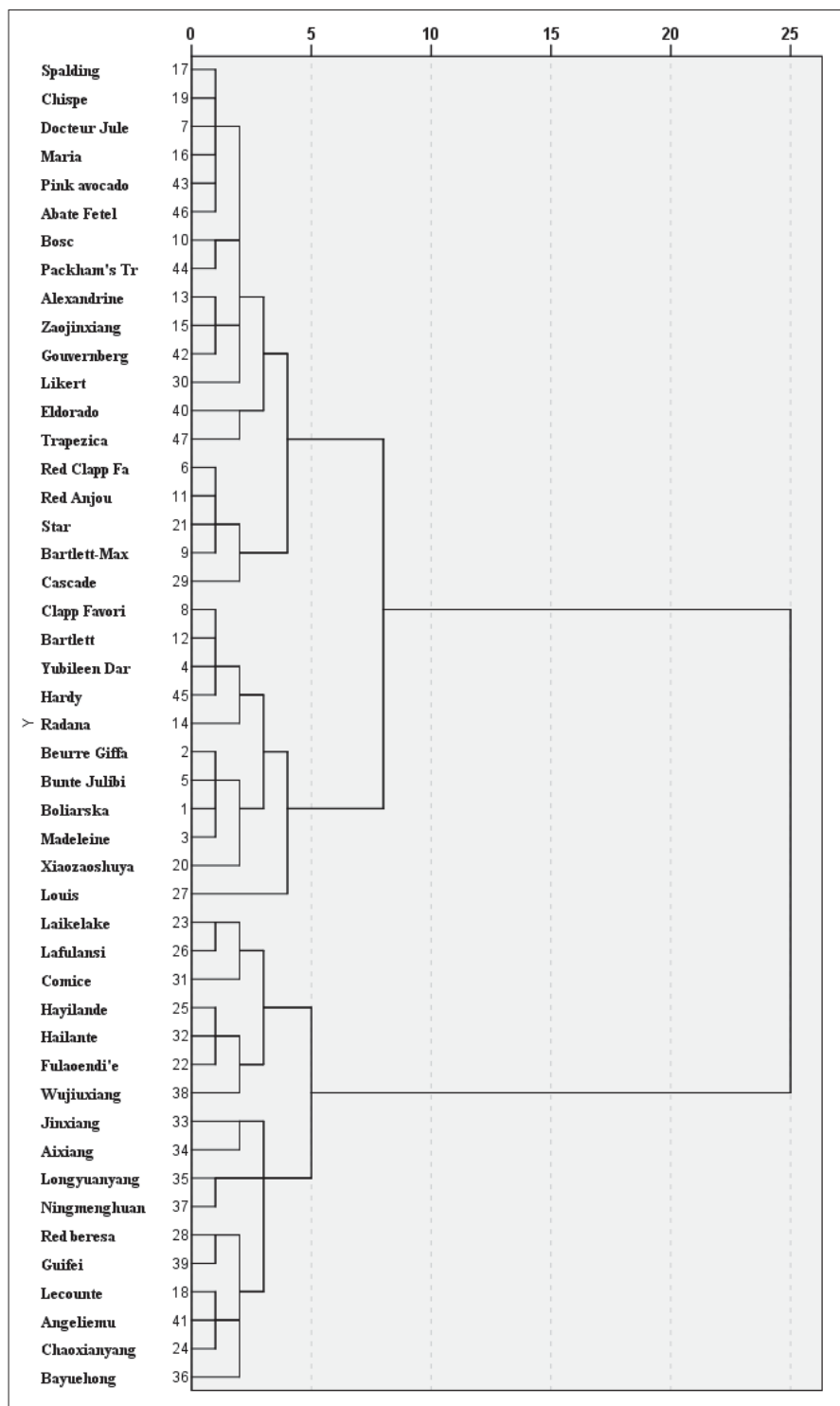


FIGURE 3. Dendrogram generated by Q-mode hierarchical cluster analysis using Ward's method based on 23 fruit phenotypic traits for 47 pear cultivars.

The PC loadings for the fruit quality variables are shown in Table 6. The negative values for PC1 reflected the high flesh firmness, absence of fragrance, and moderate abundance of stone cells in cultivars such as 'Ningmenghuang', 'Longyuanyangli', 'Bayuehong', 'Lafulansi', 'Boliarskaffa', 'Aixiang', 'Chaoxianyangli', 'Red Beresa', 'Hanlante', 'Comice', 'Lecount', 'Hayilande', 'Wujiuxiang' and 'Fulaeodie'. The highest loadings for PC2 reflected the high SS concentration, low TA, high ratio of TSS to TA, and high ratio of SS to TA of cultivars such as 'Eldorado', 'Packham's Triumph', 'Boliarskaffa', 'Laikelale', 'Cascade', 'Pink Avocado' and 'Comice'.

Cluster analysis of dendrogram

The relationships among the 47 pear genotypes was further explored by construction of a dendrogram by a hierarchical cluster analysis based on Euclidean distance using Ward's method (Figure 3). At the dissimilarity value of 10, the accessions were grouped into two main clusters; one cluster included accessions of *Pyrus communis* and the other cluster comprised hybrids of *Pyrus communis*. At a reduced dissimilarity of almost 5, four clusters were resolved. The A and B clusters showed a close similarity, as did the C and D clusters. The A and B clusters showed a higher similarity with the C cluster than with the D cluster. Generally, the accessions in this group were more similar than among those of another group.

The A cluster included 19 accessions of *Pyrus communis*. The members of this cluster were characterized by pear-shaped, juicy fruit, low flesh firmness, high TSS concentration, and low TA. This cluster was divided into two subgroups. The fruit peel color contributed to the distinction of these subgroups. Members of the B cluster were the most homogenous and were characterized by pear-shaped, juicy, fragrant fruit. The members of the C cluster produced pear-shaped or globose fruit with a lower fruit weight and obscure russeting. This cluster was divided into three subgroups. The D cluster was characterized by globose or obovate fruit with the highest TA, dense flesh texture, and low fruit weight.

Discussion

The diversity index is an important indicator with which to evaluate germplasm resources (Pettuccelli et al., 2013). In the present study, we observed abundant diversity among the 47 pear cultivars. The CV reflects the degree of dispersion of the character data. The CV was positively correlated with the range of variation in traits; the larger the CV, the greater the degree of variation in the trait and the greater the differences in the trait among cultivars. The CV for fruit peel color was the highest observed (40.60%), followed by the ratio of SS to TA (37.25%) and fruit weight (36.53%). Li et al. (1995) analyzed the SS concentration and TA in the fruit of 251 cultivars representing Ussurian pear, Chinese white pear, Chinese sand pear, common pear, and Xinkiang pear, the TSS concentration, SS concentration, and TA are important fruit quality parameters that reflect fruit flavor. The average SS concentration and TA of the 47 cultivars were 8.10% and 0.25%, which were moderate and low, respectively. However, the mean TSS concentration was 13.0%, which is an indication of excellent germplasm quality. The Shannon-Weaver index is a measure of the diversity of germplasm resources that is affected by the number of trait groups and the distribution uniformity of individuals in the groups. The higher the index value, the richer the diversity of the traits. The Shannon-Weaver index values for qualitative characters ranged from 0.42 to 1.33 with the highest diversity observed for fruit peel

color and the lowest diversity observed for fruit core size. The Shannon-Weaver index values for quantitative characters ranged from 1.27 to 2.02, and thus showed greater diversity than qualitative characters. Thus, the present panel of cultivars may be a useful source of breeding materials for germplasm innovation and selection of quantitative characters. Rich genetic diversity translates to strong potential for utilization of the germplasm for genetic improvement. The wide range in diversity index values may reflect extensive interspecific and intergeneric hybridization, and thus the genetic complexity and diversity of the parents of the pear cultivars. The low diversity in fruit core size, degree of russeting, and fruit shape index may be due to the stable, consistent culture conditions or selective breeding for certain fruit traits and the diversity decreased after multiple generations of selection. The high diversity observed in fruit weight, fruit length, and TSS concentration may be due to the inheritance of quantitative traits controlled by multiple genes.

Significant or highly significant positive or negative correlations were observed among pomological traits recorded in this study, which may enable reduction in the number of pomological traits analyzed. Flesh firmness showed a significant correlation with SS concentration ($r = -0.449^{**}$) and TA ($r = 0.544^{**}$), which agreed with the findings of Byrne et al. (1991). The breeding response for one trait depends on genotypic variation of that trait within the breeding population and on genotypic correlations between traits (Cantín et al., 2010). Strong correlations were observed among certain fruit quality characters, which would enable reduction in the number of pomological traits recorded in breeding programs and for orchard management. Therefore, phenotypic correlations are important parameters to consider in breeding programs.

The multivariate statistical procedure PCA has been used previously to explore relationships among cultivars and to study correlations among fruit characters within sets of apricot genotypes (Brown and Walker, 1990; Badenes et al., 1998; Gurrieri et al., 2001; Azodanlou et al., 2003) and peach genotypes (Wu et al., 2003; Esti et al., 1997; Crisosto et al., 2006). Principal component analysis and cluster analysis have been widely used in analyses of genetic diversity (Martynov and Dobrotvorskaya, 2006; Masumbuko and Bryngelsson, 2006). A PCA of 32 vegetative and fruit characters, recorded from 48 pear accessions from four pear systems grown in different regions of Iran, revealed that fruit size, pulp texture, and leaf size were the greatest contributors to PC1 (Zarei et al., 2019). It is well documented that characters that are predominant contributors to the main PCs show the highest variation among accessions and have the greatest impact on multidimensional separation of the accessions (Iezzoni and Pritts, 1991). We observed a strong correlation among certain characters and PCs, which may allow the number of traits recorded to be reduced among a set of pear accessions.

Morphological attributes are influenced by environmental factors, such as altitude, rainfall, and other climatic variables, in a variety of fruit crops (Talhouk et al., 2000; Boulli et al., 2001; Said et al., 2013). However, some reports indicate that geographical origin does not influence genotype clustering in certain fruit species. According to Martinez-Nicolas et al. (2016), geographic origin can be reflected in the grouping of accessions collected from their natural distribution areas, where the plant materials have been little modified by human activities. In the present study, the pear accessions were clustered mainly based on their phylogenetic relationships. The differences between the present results and previous

studies may be due to the different ecogeographical groups of pear cultivars analyzed. In future studies, additional phenotypic characters, such as branch, leaf, and flower traits, should be considered and cluster analysis performed in combination with molecular analyses. The genetic diversity among genotypes depends on the extent of variability present in the population for different characters under investigation. In addition, the magnitude of heterosis is largely governed by the degree of genetic diversity among the parental lines (Saran et al., 2006).

Evaluation of phenotypic diversity among genotypes is an important consideration for classification and utilization of germplasm resources in breeding (Khadivi-Khub et al., 2014). The success of any breeding program depends on the extent of genetic variability in the source population. Furthermore, efficient assessment of variability is a basic requirement of breeding programs. Both PCA and cluster analysis are effective tools for differentiation of materials according to pomological traits (Voltas et al., 2007). Information derived from PCA may assist plant breeders to identify a limited number of highly differentiated populations to be selected for further studies (Iezzoni and Pritts, 1991).

Conclusions

The present results emphasize the utility of PCA for evaluation of fruit quality in *P. communis* and to study relationships among pomological traits. Based on the results of the present investigation, it can be concluded that among the attributes that were studied here, lenticel prominence, abundance of stone cells, and ratio of TSS and TA characteristics had the highest discrimination power and hence are suggested for morphological evaluation of pear accessions. Fruit weight, total soluble solids, and fruit length were highly diverse for creating abundant pear germplasm. The present investigation detected substantial genetic diversity among Chinese *Pyrus communis* accessions, which indicates there is considerable potential to breed pear cultivars with improved fruit quality. The variability detected among *P. communis* accessions grown in China may be utilized in future traditional breeding programs or advanced biotechnology studies.

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