Phenotypic and genetic diversity of sugarcane（*Saccharum* L.）protospecies and landraces

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Abstract：In order to explore genetic diversity and relationship among different sugarcane species，select excellent sugarcane germplasm and parental combination for hybridization，the present study was conducted for genetic diversity analysis using 18 genotypes of protospecies and landraces of sugarcane（*Saccharum* spp.）with 14 quantitative traits. The results showed that the phenotypic and genetic diversity of sugarcane was highly significant in sucrose % cane，stalk weight，leaf width，stalk diameter and fiber % cane by coefficient of variation and correlation analysis of 14 quantitative traits. Four principal components of quantitative traits named quality factor，growth factor，maturity factor and photosynthetic factor，respectively，were extracted from principal component analysis，and the cumulative contribution rate of four principal components was 83.48%. Ten desirable genotypes of sugarcane had higher values of quantitative traits than the averages in factor analysis in turn as follows：Sampana→Tiangeda→Heqingcao Ganzhe→Guilin Zhuzhe→Tanzania→Mango→Guzhizhe→Dadaozailai→Tuojianghong→Chunnee. The 18 accessions could be divided into five clusters based on the genetic distance，and potential hybrid may be developed by crossing Sampana with Tiangeda and/or Sampana with Heqingcao Ganzhe. It suggested that we should not only consider the complementary of main traits，but also genetic distance when we select parents for crossing in sugarcane breeding. The present study proved that factor analysis was good to help the parental selection and determine crossing combinations in sugarcane breeding program.

Key words：sugarcane；quantitative traits；genetic diversity；factor analysis

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不同基因型甘蔗种质资源的表型遗传多样性

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摘　要：为探明甘蔗原种和地方种的遗传多样性和亲缘关系，以期筛选出优良甘蔗种质和优良杂交亲本。该研究对 18 份甘蔗原种和地方种的 14 个数量性状进行了表型遗传多样性分析。结果表明：通过 14 个数量性状的

变异系数（coefficient of variance，CV）和性状之间的相关分析，18 份甘蔗原种和地方种的数量性状遗传变异主要来自甘蔗蔗糖分、单茎重、叶宽、茎径和纤维分；对 14 个数量性状进行主成分分析提取获得了 4 个主成分因子，分别命名为"品质因子"、"生长因子"、"成熟度因子"和"光合因子"，主成分因子累积贡献率达 83.482%；进一步通过对主成分因子开展综合评价分析，获得数量性状综合表型高于平均水平的 10 份材料，依次为 Sampana→甜圪塔→合庆草甘蔗→桂林竹蔗→坦桑尼亚→芒戈→古芝蔗→大岛再来→托江红→春尼；聚类分析基于不同的遗传距离可将 18 份种质聚为 5 个类别，潜在的优良杂交组合是 Sampana 和甜圪塔或 Sampana 和合庆草甘蔗，表明在甘蔗遗传育种亲本选择上既要考虑各性状主要因子的互补，又要保持一定的遗传距离。该研究认为，在甘蔗育种工作中，利用因子分析法进行表型遗传多样性分析，将更加有助于亲本和杂交组合的选择。

关键词：甘蔗；数量性状；遗传多样性；因子分析

Sugarcane is an important cash crop of the tropics and subtropics, and is grown in more than 90 countries between 40°N and 32°5′S, encompassing half of the globe (Waclawovsky et al., 2010; Silva et al., 2012). It provides 60%−70% of the world's sugar (Prabu et al., 2011; Silva et al., 2012) and produces numerous valuable by-products like ethanol used as a fuel, alcohol used in pharmaceutical industry, bagasse used in paper industry and aquaculture, and press mud used as a rich source of organic nutrients for crop production (Li 2010; Yang et al., 2012; Alonso-Pippo et al., 2013). It has been demonstrated that modern sugarcane varieties are highly complex polyploids derived from a few crosses carried out more than a century ago between the high sugar content species *Saccharum officinarum* ($x = 10, 2n = 8x = 80$) and the wild species *S. spontaneum* ($x = 8, 2n = 5x − 16x = 40 − 128$) and backcrossed with *S. officinarum* (Bhat et al., 1985; D'Hont et al., 1996, 2002; D'Hont 2005). However, previous studies have also showed that sugarcane belongs to the genus *Saccharum* L. composed of hybrids derived from *S. officinarum* (Noble clones), *S. sinense* (Chinese clones), *S. barberi* (North Indian clones) and *S. spontaneum* (Ha et al., 1999; Irvine 1999; Brown et al., 2002; Selvi et al., 2003; Cuadrado et al., 2004). At present not more than 15 varieties of *S. officinarum* species have been used as parents, and only 2 genotypes of *S. spontaneum* and *S. barberi* have been utilized (Li, 2010). Consequently, most of the sugarcane varieties around the world have the same ancestors. The fact that only a few innovative parents have been used in sugarcane breeding leads to high genetic similarity in commercial sugarcane cultivars and the genetic basis tended to narrow (Selvi et al., 2003; Cordeiro et al.,

2003; Hemaprabha et al., 2006; Lavanya et al., 2010). Parent selection is the first step in plant breeding program through hybridization, so it is urgent to introduce protospecies or landraces to broaden the genetic base and then improve the potential traits of modern sugarcane varieties (Salem et al., 2008).

Morphological traits are valuable tools to identify genotypes as they reflect external resemblance more than genetic relatedness (Demey et al., 2003; Perera et al., 2012; Ahmed et al., 2012). Morphological traits are phenotypic characteristics of genetic variations, and there are a series of complex aspects like gene expression and regulation, and ontogeny in the process from genotype to phenotype (Li et al., 2010; Liu et al., 2010). The regulation of genetic variation can be revealed by reasonable sampling and adopting effective mathematical statistical methods (Liu et al., 2010; Hussain et al., 2010; Perera et al., 2012). Many researchers have studied the morphological genetic diversity in crops such as sorghum, wheat, rice (Durrishahwar et al., 2012; Khodadadi et al., 2011; Rampant et al., 2011). Principal component analysis (PCA) and cluster analysis as the main means have been widely used in diversity analysis and satisfactory traits selection (Ahmed et al., 2010; Iiyas et al., 2010; Smiullah et al., 2013).

Most of the reports on morphological and genetic diversity of sugarcane have aimed at the commercial varieties in one particular region or country (Wagih et al., 2004; Sajjad et al., 2009; Perera et al., 2012), while references on studying protospecies or landraces are very limited. In the present study, 18 sugarcane protospecies or landraces were employed to investigate the genetic diversity based on 14 quantitative traits by u-

sing PCA,factor analysis and cluster analysis methods to provide a reference for appropriate parent selection in sugarcane breeding.

1 Materials and Methods

1.1 Plant materials

Eighteen sugarcane accessions of protospecies and landraces conserved in Sugarcane Research Center,Chinese Academy of Agricultural Sciences/Sugarcane Research Institute,Guangxi Academy of Agricultural Sciences,including 7 sugarcane protospecies namely Mango (S. barberi),Chunnee (S. barberi),Loethers(S. officinarum),Robustum (S. robustum),Heqingcao Ganzhe (S. sinense),Luzhe (S. sinense),Guilin Zhuzhe (S. sinense) and 11 landraces namely Sampana,Jiagudao,Tanzania ,Tuojianghong ,Hekou Qingpi, Luoguzhe,Guzhizhe,Senbaina,Dadaozailai,Tiangeda, Hongpi S17,were selected for experiment.

The experiment was carried out at the Sugarcane Research Institute,Guangxi University,Nanning,China (22°13′−23°32′N and 107°45′−108°51′E) during January 2011 and December 2012. The experiment was laid out in a randomized block design with 3 replications. Each variety was accommodated in a plot having 3 rows of 5 m in length with spacing 1.2 m between rows. The field management was done as for commercial sugarcane production. Observations were recorded for 14 agronomic traits viz. leaf length,leaf width,leaf length/width, plant height, stalk diameter, stalk weight,field brix,juice brix (after milling),gravity purity,juice yield,reducing sugar ％ juice,sucrose ％ cane,sucrose ％ juice and fiber ％ cane. The standardization of data was according to Cai et al.(2006).

1.2 Statistical analysis

Coefficient of variation was calculated according to following formula：$CV=\dfrac{SD}{X}\times100$

Where $CV=$Coefficient of variation；$SD=$Standard deviation；$X=$Mean.

The original data were organized by using Excel program,and then analyzed by using SPSS (18.0) for ANOVA (Analysis of Variance),correlation analysis, principal component analysis （PCA）,factor analysis and cluster analysis (Steel et al.,1980;Xue,2006).

2 Results and Analysis

2.1 Analysis on coefficient of variation

Coefficient of variation for quantitative trait is adopted to reflect the discrete degree and phenotypic diversity. The coefficients of variation for the 14 quantitative traits in the present study were showed in Table 1. The highest value was recorded for fiber ％ cane (34.07％),followed by stalk weight,stalk diameter, sucrose ％ juice,sucrose ％ cane. Plant height showed relatively low coefficient of variation, and juice yield the lowest. This indicated that the heritable variation of quantitative traits mainly came from fiber ％ cane, stalk weight,stalk diameter and sucrose content. This view was consistent with Chaudhary (2002),Sajjad et al.(2009), and Ahmed et al.(2012). Sajjad et al. (2009) found that fiber ％ cane is the highest contributor to genetic diversity,however,which was opposite to the results reported by Ahmed et al.(2012) that cane fiber (％) showed low genetic advance and heritability values,indicating difficulty of improvement of this trait by the means of direct selection. The differences may be due to different genotypes used and experimental conditions. In the present study，plant height showed a low coefficient of variation. Sajjad et al.(2009) and Ahmed et al.(2012) also reported similar results in their studies.

2.2 Correlation analysis

Correlation analysis among phenotypic traits may reflect biological processes that are of considerable evolutionary interest,correlation can be the result of genetic,functional and physiological or even developmental characters （Wagner et al.,2000；Soomro et al., 2006）.

The data in Table 2 revealed that the correlations of leaf width with field brix,juice brix,sucrose ％ juice and sucrose ％ cane were positively significant at 0.05 level,and that with stalk weight was positively and highly significant at 0.01 level. Stalk weight was positively and highly significantly correlated with leaf

Table 1　Genetic diversity evaluation on quantitative traits

Trait	Minimum	Maximum	Variation amplitude	Mean	Standard deviation	Coefficient of variation（％）
Leaf length（cm）	106.9	183.93	77.03	153.63	19.62	12.77
Leaf width（cm）	3.81	6.69	2.88	5.13	0.77	15.01
Leaf length/width	21.73	40.69	18.96	30.40	5.04	16.57
Plant height（cm）	234.1	344	109.9	299.88	28.15	9.39
Stalk diameter（mm）	9.66	29.37	19.71	18.02	5.17	28.71
Stalk weight（kg）	0.49	2.3	1.81	1.44	0.45	31.09
Field brix（％）	12.07	20.03	7.96	16.06	2.88	17.91
Cane brix（％）	9.72	17.14	7.42	14.49	1.90	13.13
Juice yield（％）	53.38	77.14	23.76	70.60	4.73	6.7
Juice gravity purity（％）	53.04	89.12	36.08	79.03	9.79	12.39
Fiber ％ cane	1.24	3.58	2.34	2.10	0.71	34.07
Reducing sugar ％ juice	0.14	2.67	2.53	0.87	0.15	17.24
Sucrose ％ juice	7.4	17.42	10.02	13.05	2.74	21.02
Sucrose ％ cane	5.83	14.69	8.86	11.15	2.30	20.65

Table 2　Correlation analysis among quantitative traits

	A	B	C	D	E	F	G	H	I	J	K	L	M	N
A	1													
B	0.332	1												
C	0.493＊	−0.637＊＊	1											
D	−0.044	0.016	−0.04	1										
E	0.048	0.23	−0.087	0.4	1									
F	0.306	0.679＊＊	−0.362	0.555＊	0.589＊	1								
G	0.586＊	0.557＊	−0.025	−0.187	0.132	0.301	1							
H	0.079	0.477＊	−0.423	0.193	0.101	0.563＊	0.446	1						
I	−0.289	0.254	−0.479＊	0.374	0.351	.642＊＊	−0.268	0.535＊	1					
J	−0.113	−0.075	−0.036	−0.364	−0.395	−0.411	−0.292	−0.467	−0.3	1				
K	0.233	0.468	−0.249	0.095	0.379	0.607＊＊	0.311	0.562＊	0.650＊＊	−0.513＊	1			
L	0.366	0.580＊	−0.274	0.164	0.28	0.679＊＊	0.577＊	0.844＊＊	0.531＊	−0.557＊	0.863＊＊	1		
M	0.292	0.550＊	−0.309	0.2	0.28	0.691＊＊	0.534＊	0.892＊＊	0.584＊	−0.576＊	0.837＊＊	0.992＊＊	1	
N	−0.321	−0.313	0.115	0.008	0.517＊	−0.292	−0.188	−0.598＊＊	−0.353	0.058	−0.363	−0.540＊	−0.553＊	1

Note：Letters A-N represent leaf length,leaf width,leaf length/width,plant height,stalk diameter,stalk weight,field brix,cane brix,juice yield,reducing sugar ％ juice,juice gravity purity,sucrose ％ juice,sucrose ％ cane,fiber ％ cane,respectively. ＊ significant at 0.05 level； ＊＊ highly significant at 0.01 level.

width,juice yield,gravity purity,sucrose ％ juice and sucrose ％ cane,while positively and significantly correlated with stalk diameter,plant height and juice brix. Juice brix was significantly and positively correlated with leaf width,stalk weight,juice yield,gravity purity,sucrose ％ juice and sucrose ％ cane but was significantly and negatively correlated with fiber ％ cane. Juice yield was significantly and positively correlated with stalk weight,gravity purity,juice brix,sucrose ％ juice and sucrose ％ cane while significantly and negatively with leaf length and leaf width. Gravity purity was positively and significantly correlated with stalk weight,juice yield,juce brix,sucrose ％ juice and su-

crose ％ cane while negatively and significantly with reducing sugar ％ juice. Sucrose ％ cane was positively and significantly correlated with leaf width,stalk weight,field brix,juice brix,juice yield and gravity purity but was negatively and significantly correlated with reducing sugar ％ juice and fiber ％ cane. The variation of sucrose ％ juice was in accordance with that of sucrose ％ cane. Fiber ％ cane was significantly and negatively correlated with cane brix,sucrose ％ juice and sucrose ％ cane. Reducing sugar ％ juice was significantly and negatively correlated with gravity purity,sucrose ％ juice and sucrose ％ cane.

Based on the present study,sucrose content,stalk

weight, leaf width and brix are desired selection parameters to evaluate the agronomic performance of the sugarcane varieties, followed by juice yield, gravity purity, fiber and reducing sugar. Khan *et al.*, (2007, 2012), Mahmood *et al.*, (1990), Ramdoyal (1991) and Soomro *et al.*, (2006) also reported similar results in sugarcane.

2.3 Principal component analysis

The eigenvalue of correlation matrix, variance contribution rate and principal factors were obtained via principal component analysis (Table 3). Based on the principle of eigenvalues greater than 1, four independent factors were extracted from the 14 quantitative traits, which explained 83.48% of the total variation in the dependence structure. Factor loadings that greater than 0.5 were considered important. A summary of the composition of variables of the four extracted factors with loading are given in Table 4.

Factor I included six variables which accounted for 44.16% of the total variation. The six variables were sucrose % cane, sucrose % juice, juice brix, fiber % cane, gravity purity and juice yield. The sign of the loading values indicates the direction of the relationship between the factor and its related characters. The negative sign of fiber % cane indicated the negative correlation coefficients with each of the other variables in factor I (Table 4). Each variable had a high loading in the factor and all of them were associated with cane quality, therefore, this principal component could be called quality factor.

Factor II was responsible for 16.41% of the total variation in the dependence structure. It included four characters, namely stalk diameter, plant height, stalk weight and reducing sugar % juice. The highest loading value in the factor is stalk diameter, followed by plant height, stalk weight and reducing sugar % juice in turn. The variables of this principal component were regarded as growth factor. These results were in agreement with the finding of El-Geddawi *et al.*, (1992) and Hussein *et al.* (2012).

Factor III was made up of field brix and leaf length. The maximum loading value was field brix, which was slightly higher than the second, leaf length.

As the variables of field brix concerned with cane maturity, it was referred to as maturity factor. It accounted for 13.14% of the total variation in the dependence structure.

Factor IV contained two variables, namely leaf length and leaf width. Both variables had a high loading in the factor. For the leaf is the key organ for photosynthesis and it plays an important role on plant growth and metabolism. This principal component was feasibly called photosynthetic factor.

Principal component analysis based on different agronomic traits would get different results. Many component analyses have been performed for complex traits based on morphological and physiological characterizations (Petrasovits *et al.*, 2007; Khan *et al.*, 2012). For sugarcane, previous studies tended to focus on cane yield components (Hussein *et al.*, 2012; Smiullah, 2013), while this study lied emphasis on cane its own traits in order to explore the good traits of cane itself and revealed that higher sucrose content and stalk weight, endowed with higher fiber % cane, gravity purity, leaf length and leaf width were the important characters which should be considered for sugarcane genotype selection.

Taking advantage of principal component analysis by plant breeders has the potential of increasing the comprehension of the casual relationship of variables and can help to determine the desirable traits to be selected in a breeding program (Hussein *et al.*, 2012; Smiullah, 2013).

2.4 Factor analysis

The factor analysis of 18 accessions was done by utilizing the Comprehensive Evaluation Model $F = a_1 F_1 + a_2 F_2 + a_3 F_3 + \ldots\ldots + a_m F_m$ (Xue 2006), where $a_1 = 44.156\%$, $a_2 = 16.413\%$, $a_3 = 13.141\%$, $a_4 = 9.772\%$, obtained from Table 3, and F_m means factor score ("0" is the mean of factor score and standard deviation is "1". Positive values indicate above-average, and negative values indicate below-average). The factor score of each accession was used in above equation for calculating the composite score F value (Table 5). The performances of the 18 accessions in phenotypic traits were evaluated, and ranked in descending from superior

Table 3　Eigenvalues in principal component correlation matrix

Principal component	Characteristic root	Variance contribution (%)	Cumulative contribution (%)
1	6.182	44.156	44.156
2	2.298	16.413	60.569
3	1.840	13.141	73.710
4	1.368	9.772	83.482
5	0.959	6.852	90.334
6	0.716	5.112	95.446
7	0.315	2.253	97.699
8	0.190	1.357	99.056
9	0.087	0.620	99.675
10	0.021	0.149	99.824
11	0.014	0.100	99.924
12	0.006	0.045	99.969
13	0.004	0.029	99.998
14	0.000	0.002	100

Table 4　Principal component load matrix

Trait	The first principal component	The second principal component	The third principal component	The fourth principal component
Sucrose % cane	0.893	0.241	0.250	0.207
Sucrose % juice	0.867	0.234	0.329	0.206
Canebrix	0.853	0.061	0.077	0.257
Fiber % cane	-0.808	0.486	-0.053	0.046
Juice gravity purity	0.737	0.334	0.152	0.187
Juice yield	0.662	0.350	-0.517	0.251
Stalk diameter	-0.046	0.927	0.112	0.216
Plant height	0.226	0.645	-0.278	-0.157
Stalk weight	0.566	0.587	0.146	0.360
Reducing sugar % juce	-0.499	-0.559	-0.130	0.235
Field brix	0.263	0.017	0.857	0.236
Leaf length	0.205	0.018	0.846	-0.244
Leaf length/width	-0.232	0.010	0.330	-0.886
Leaf width	0.360	0.087	0.408	0.774

Table 5　Factor analysis

Species	Factor score					
	F_1	F_2	F_3	F_4	F	Ranking
Sampana	1.281	0.606	0.816	-0.328	0.74	1
Tiangeda	0.894	-0.037	1.098	0.842	0.615	2
Heqingcao Ganzhe	1.19	-0.71	0.58	-0.133	0.472	3
Guilin Zhuzhe	0.475	0.663	0.771	0.159	0.436	4
Tanzania	0.424	1.203	0.274	0.042	0.425	5
Mungo	0.886	-0.631	0.956	-0.494	0.365	6
Guzhizhe	0.997	-0.105	-0.564	-0.5	0.3	7
Dadaozailai	-0.871	2.134	0.158	2.202	0.202	8
Tuojianghong	0.131	-1.569	0.406	1.809	0.03	9
Chunnee	0.232	0.624	-0.394	-1.407	0.015	10
Loethers	-0.112	0.22	-0.276	0.193	-0.031	11
Hongpi S17	0.314	-0.857	-1.179	-0.275	-0.184	12
Luoguzhe	-0.338	-0.197	-0.673	-0.153	-0.285	13
Robustum	-0.597	1.27	-0.399	-1.999	-0.303	14
Hekou Qingpi	-1.118	0.631	-1.677	0.676	-0.545	15
Senbaina	-0.606	-1.219	-0.891	0.385	-0.547	16
Luzhe	-0.394	-1.183	-1.288	-0.133	-0.55	17
Jiagudao	-2.788	-0.842	2.281	-0.888	-1.156	18

tion, irrigation etc. will not lead to appreciable improvement in cane or sugar yield. Hence, the top accessions should be paid more attention to in practical.

2.5 Cluster analysis

In Q cluster analysis the 18 genotypes were grouped into five clusters A, B, C, D and E based on the Euclidean squared distance of 5-10 (Fig. 1), while clusters A, B, C and D got together into one group at Euclidean squared distance of 15, and cluster E as an independent group. Cluster A included Heqingcao Ganzhe, Guzhizhe, Senbaina, Loethers, Hongpi S17 and Chunnee. Cluster B consists of Tiangeda and Mango. Six clones viz. Tanzania , Robustum, Luoguzhe, Guilin Zhuzhe, Sampana and Dadaozailai fell into Cluster C. Two genotypes Luzhe and Hekou Qingpi came into Cluster D. Cluster E consisted of two genotypes Tuojianghong and Jiagudao.

Clustering analysis can clearly reveal the genetic relationship between different accessions and provide the basis for evaluation of screening (Kashif et al., 2007;Sajjad et al.,2009). Sajjad et al.(2009) suggested that one parent may select from each cluster to produce a hybrid having desirable results. It is not wise to cross in intra-cluster for the accessions are not ge-

to inferior based on the F values in Table 5.

Ten genotypes showed positive F values, which could be regarded as excellent germplasm in this research, and the lists were Sampana → Tiangeda → Heqingcao Ganzhe→Guilin Zhuzhe→Tanzania →Mango→Guzhizhe→Dadaozailai→Tuojianghong→Chunnee. EL-Geddway et al.,(2002) and Arain et al.,(2011) stated that sugarcane varieties are greatly affected by genetic make-up. According to Keerio et al.,(2003), unless the genetic potentialities of a variety are high, mere provisions of growing conditions such as fertiliza

netically diverse enough to produce a good hybrid. According to the result of factor analysis, the known desirable genotypes viz. Sampana, Tiangeda and Heqingcao Ganzhe belong to different clusters so these accessions can be coupled to develop a potential hybrid. While other well-behaved genotypes like Tanzania, Guilin Zhuzhe and Sampana gathered into one group, which denoted that these genotypes are genetically more similar so they are not suggested to be used together to produce a hybrid combination. The most distant cluster is E. As the genotypes in this cluster are not very good, therefore, they are also not suggested to be crossed with other clusters to breed a sugarcane hybrid combination. Kashif et al.(2007) stated the genotypes with high index scores and falling into different clusters can be crossed to have maximum variability of good combinations of characters. Similarly, if one is interested in improving a specific character which is undesirable or otherwise weak on genotype. The genetic divergence information will be helpful to select parent combinations in sugarcane breeding (Doule et al., 1997; Kadian et al., 1997; Verma et al., 2000). In this study, a potential hybrid combination may be developed by crossing Sampana with Tiangeda and/or Sampana with Heqingcao Ganzhe.
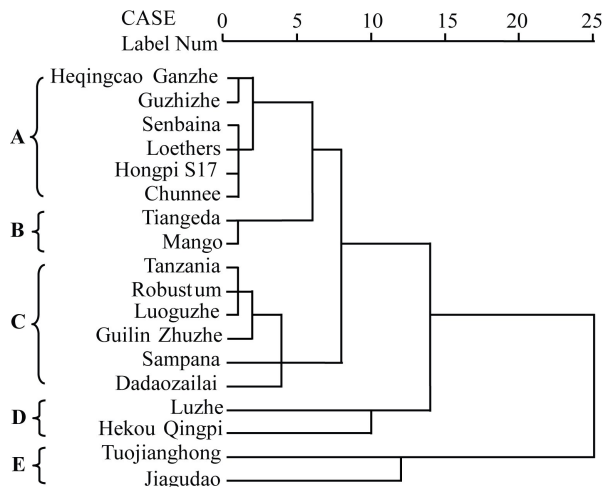

Fig. 1 Dendrogram based on Euclidean squared distance (Q cluster analysis)   18 genotypes were grouped into five clusters A, B, C, D and E at Euclidean squared distance of 5-10, while clusters A, B, C and D got together into one group at Euclidean squared distance of 15, and Cluster E became an independent group.

3　Conclusions

Based on the present study, coefficient of variation, correlation analysis, principal component analysis (PCA), factor analysis and cluster analysis were effective for investigating the phenotypic traits in different genotypes of sugarcane. Especially factor analysis was proved to be helpful for parental selection in sugarcane breeding.

By comprehensive consideration of the results of coefficient of variation, correlation analysis and principal component analysis, the phenotypic and genetic diversity of sugarcane mainly came from sucrose % cane, stalk weight, leaf width, stalk diameter and fiber % cane. It inferred that these traits could be used as desired selection parameters to evaluate the agronomic performance of sugarcane germplasms. Four principal components of 14 quantitative traits were obtained, viz. quality factor, growth factor, maturity factor and photosynthetic factor.

Combining consideration of factor analysis and cluster analysis might be effective to select the admirable parents for hybridization. Several desirable genotypes were obtained such as Sampana, Tiangeda, Heqingcao Ganzhe, Guilin Zhuzhe, and potential hybrid combinations might be developed by crossing Sampana with Tiangeda and/or Sampana with Heqingcao Ganzhe. It is concluded that screening parents not only needs to consider the complementary of main traits, but also needs to keep certain genetic distance.

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