# DIVERSITY ANALYSIS OF MAIN AGRONOMIC CHARACTERS OF DIFFERENT SWIDA WILSONIANA CLONES

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#### Abstract

In order to produce high-yield and oil content *Swida wilsoniana* species, 28 agronomic traits in 7 *Swida wilsoniana* clones were measured and analyzed from variance, principle components, cluster, and correlation. Variance analysis results showed that the variation coefficients of the 28 agronomic traits ranged from 8.04% to 94.30%, and the largest variation was from leaf pattern, such as leaf shape, color, and leaf margin character. And the phenotypic differentiation coefficients ranged from 45.27% to 96.40%, which indicated that the characters were relatively genetically stable. Main inheritance was represented by 4 principal components, which were inflorescence, fruit, oil content, and fruit quantity per cluster. Principal components analysis clustered the 7 clones into 4 groups. High-yield and high-oil target species can be produced by hybridizing groups 2 and 3.

Key words: Hybrid parent; Agronomic traits; Phenotypic diversity; Principal components analysis; Cluster analysis.

#### Introduction

Swida wilsoniana (Wangerin) Soják is a deciduous broad-leaved tree species from family Cornaceae with a high fruitoil content ranging from 33% to 36% (Song et al., 2008), S. wilsoniana is an ideal multipurpose woody oil plant (Liao et al., 2005). Which can grow well in marginal land (Jessup, 2009), such as barren hills, wasteland, and soil erosion areas (Ling et al., 2009), based on the Chinese Renewable Energy Law: "Developing oil plant should neither compete with farmers for grain nor compete with grain for land". Increasing number of studies on the resource collection and evaluation of S. wilsoniana were reported (Li et al., 2010), including clones breeding and high-yield species cultivation from wild resources (Li et al., 2008). However, there are few studies on hybrid breeding, parent selection, or cell and molecular biologic analyses of S. wilsoniana (Li et al., 2009; Zhao et al., 2010). Isozyme markers and DNA molecular markers has been widely used in plant germplasm resources identification and classification (Alexander et al., 2009), but morphological characters description is still used as the basic method for germplasm resources identification (Ben et al., 2010). In this study, main growth traits of S. wilsoniana clones were measured in field. Principal components analysis and cluster analysis were applied.

The genetic variation is the prerequisite of plants for adapting to various external environments, which is widely used for plants cross breeding. The effective early character selection of plants usually depend on the appropriate selection method, selection index and selection period of plants (Bao *et al.*, 2009), Based on the correlation between juvenile and adult trees' growth characteristics, some phenotypic traits of adult trees could speculate from their juvenile stage. Therefore, the effective of selection method is largely determined by the genetic correlation between the trees' childhood and adult stages. The appropriate early selection method can greatly shorten breeding period, accelerate breeding process and improve breeding efficiency. The early growth traits of hybrid seedlings including plant height, ground diameter, branches and leaves characters, which were used to evaluate the growth performance of different hybrid offspring seedlings. Comparing to the main characters' differences of genetic parameters, combining ability effect and genetic variance component between parents and progeny could make a great contribution to improving the quality of hybrid seedlings, optimizing the technical parameters of seedling establishment, accelerating the standardization and industrialization of hybrid seedlings production, providing the theoretical basis and experimental materials for forest tree genetic improvement (Stacy et al., 2016).

In order to acquire a new hybrid species with excellent characteristics in the early stages of breeding, the correlation between biological characteristics and economic characters of hybrid offsprings during the early selection were analyzed, such as resistibility and yield of the hybrid species, For example, in order to obtain new poplar varieties with excellent biological characters (Li et al., 2004), a experiment was conducted on hybrid breeding of Populus euphratica. The poplar varieties were obtained with excellent performance of seedling characters including plant height, ground diameter, and disease resistance. The interspecific hybridization test of Picea offspring seedling stage growth traits heredity determination (Zhao et al., 2015) showed that lateral branch length was more susceptible to genetic control than plant height and ground diameter, which can be used as the growth selection index of the hybrid progeny. For oil trees, the genetic variation of height, ground diameter and crown width on oil-tea hybrid progeny were analyzed, and the genetic parameters of oil tea parents were estimated (Lin et al., 2016), the results showed that significant genetic differences were found the in height, ground diameter

crown area between hybrid combinations. and Significant (general combining ability) GCA and (specific combining ability) SCA effects on tree height, ground diameter and crown were found. The fruit and seedlings traits of hickory nuts reciprocal cross between China and the United States were analyzed (Shen et al., 2009), the results showed that the seed germination rate from reciprocal cross was higher than parent seeds form natural pollination. Different pollination ways greatly affected the plant height and number of leaves, but did not affect the ground diameter. The the seedling analysis of mating combinations showed that the progeny growth difference between cross combinations of Liriodendron chinense were remarkable (Pan et al., 2014), which can be used for hybrid combinations or individual selection.

## **Materials and Methods**

**Plant material:** Clones of *Swida wilsoniana*, including 713, 806, A03, B03, B05, B08, and D05 (morphological characteristics are shown in Table 1) were bred by the Hunan Academy of Forestry and grafted in 2005. The experimental site is located in the forest farm of Hunan Academy of Forestry (28°N, 113°E), it has a subtropical humid climate, with an average annual temperature of 16.8°C-17.2°C, the average sunshine is 1496–1850 h, average annual rainfall is 1400~1900 mm, and an annual frost-free period of 274 days. Rainfall mainly occurs in spring and summer. (Song *et al.*, 2009).

## Experiment

**Morphologic measurements:** From March to November of 2013, growth traits of selected clones were measured. Results are shown in Table 2, and each trait was measured with average of 10 biological replicates.

**Determination of oil content in fruits:** Fruits of selected clones were air-dried. Then, oil and moisture content were detected using a DA 7200 near-infrared analyzer [Perten Ruihua (Beijing) Co., Ltd. scientific instruments (Sweden perten), model included]. Each clone was represented by 3 replicates and each replicate was measured 3 times.

### Data processing

Encoding the quality of characters: Morphological characters were standardized using the following model: leaf margin (binary character): non-curling 0, curling 1; Blade shape: 0: strip $\rightarrow$ elliptical wrap around needle $\rightarrow$ elliptic,1: strip $\rightarrow$ strip wrap around needle $\rightarrow$ needle (branch from two characters); Leaf color (orderly polymorphism character): light-green 0, yellowish-green 1, green 2.

**Data analysis:** Data were analyzed using nested analysis of variance, factor analysis (Tan & Mei, 2007a), cluster analysis (Xie *et al.*, 2013), and correlation analysis (Tan & Mei, 2007b) using IBM SPSS statistics 19.0 and Microsoft Excel 2007.

	Hoight	Breast diameter	Cround diamotor	Under brench height	Tree crown		
Clones	Height (cm)	(cm)	(cm)	Under-branch height (cm)	North-south (cm)	East-west (cm)	
713	320.2	4.3	9.8	34.3	450.5	335.5	
806	412.3	5.5	11.6	9.5	513.3	480.6	
A03	420.6	3.7	8.0	9.1	235.5	181.5	
B03	445.8	3.6	13.5	20.5	440.1	401.5	
B05	284.9	3.2	12.5	25.3	306.6	260.3	
B08	165.9	1.8	9.5	50.5	220.7	230.8	
D05	215.4	1.8	6.5	9.5	235.8	185.7	

Table 1. Morphological characteristics of Swida wilsoniana clones.

Table 2. Growth traits of selected clones.

Vegetative growth traits	Reproductive growth traits	Fruit growth traits	
Leaf bud horizontal diameter (LBHD)	Inflorescence length (Primary, Secondary, Tertiary)	Seed horizontal diameter (SHD)	
Leaf bud vertical diameter (LBVD)	(PIL, SIL, TIL)	Seed vertical diameter	
Lear bud vertical dialicter (LD VD)		(SVD)	
Leaf length (LL)		Thousand seed weight	
Lear lengui (LL)	Inflorescence horizontal diameter (Primary, Secondary,	(TSW)	
Leaf width (LW)	Tertiary) (PIHD, SIHD, TIHD)	Fruit horizontal diameter	
Lear width (Lw)		(FHD)	
Loof shape (LS)		Fruit vertical diameter	
Leaf shape (LS)	Inflorescence vertical diameter (Primary, Secondary,	(FVD)	
Leaf color (LC)	Tertiary) (PIVD, SIVD, TIVD)	Thousand fruit weight	
Lear color (LC)		(TFW)	
Leaf margin character (LMC)	Chuster horizontal diameter(CUD)	Oil content	
Lear margin character (LMC)	Cluster horizontal diameter(CHD)	(OC)	
Annual branch longth (ADI)	Chuster vertical diameter (CVD)	Moisture content	
Annual branch length (ABL)	Cluster vertical diameter (CVD)	(MC)	
	Fruit quantity per cluster (FQPC)		

	Tuble 51 vegetative growth traits of afferent clones.											
Measured			C	lone numbe	er			CV	Vst			
traits	713	806	A03	B03	B05	B08	D05	CV	V SL			
LBHD	$2.027^{a}$	$1.610^{ab}$	1.310 <sup>b</sup>	$1.507^{ab}$	1.603 <sup>ab</sup>	1.707 <sup>ab</sup>	1.473 <sup>ab</sup>	15.67%	83.53%			
LBVD	2.173 <sup>c</sup>	2.393 <sup>bc</sup>	$3.487^{ab}$	$2.747^{abc}$	$3.687^{a}$	3.137 <sup>abc</sup>	$2.963^{abc}$	20.84%	45.43%			
LL	101.946 <sup>a</sup>	96.273 <sup>a</sup>	$87.917^{ab}$	97.320 <sup>a</sup>	$100.787^{a}$	75.363 <sup>b</sup>	75.567 <sup>b</sup>	14.06%	68.80%			
LW	$48.997^{a}$	52.193 <sup>a</sup>	46.267 <sup>a</sup>	47.313 <sup>a</sup>	$49.200^{a}$	36.263 <sup>a</sup>	$49.000^{a}$	12.19%	57.16%			
LS	$0^{b}$	$1^{a}$	$0^{b}$	$1^{a}$	$0^{\mathrm{b}}$	$1^{a}$	$1^{a}$	94.30%	73.43%			
LC	3 <sup>a</sup>	$1^{c}$	2 <sup>b</sup>	3 <sup>a</sup>	3 <sup>a</sup>	$1^{c}$	2 <sup>b</sup>	45.27%	45.27%			
LMC	$0^{\mathrm{b}}$	$1^{a}$	$1^{a}$	$0^{\mathrm{b}}$	$1^{\mathrm{a}}$	$0^{b}$	$1^{a}$	94.30%	61.32%			
ABL	$154.280^{a}$	102.593 <sup>a</sup>	195.190 <sup>a</sup>	179.103 <sup>a</sup>	195.483 <sup>a</sup>	$135.350^{a}$	$178.853^{a}$	23.40%	50.47%			

Table 3. Vegetative growth traits of different clones.

Note: Different letters across clones indicate significant differences (p<0.05)

Table 4. Reproductive growth traits of different clones.

Measured			0	lone numb	er			CV	Vst	
traits	713	806	A03	B03	B05	B08	D05	CV.	v St	
PIL	56.140 <sup>a</sup>	43.043 <sup>bc</sup>	47.343 <sup>bc</sup>	24.630 <sup>d</sup>	48.753 <sup>ab</sup>	44.677 <sup>bc</sup>	38.897 <sup>c</sup>	22.69%	93.23%	
PIHD	$76.740^{\rm a}$	61.973 <sup>b</sup>	58.057 <sup>b</sup>	32.200 <sup>c</sup>	64.277 <sup>b</sup>	58.343 <sup>b</sup>	39.433°	27.20%	96.40%	
PIVD	96.603 <sup>a</sup>	74.507 <sup>bc</sup>	81.193 <sup>ab</sup>	43.500 <sup>d</sup>	$85.097^{ab}$	68.833 <sup>bc</sup>	58.433 <sup>cd</sup>	24.33%	91.04%	
SIL	43.923 <sup>a</sup>	28.157 <sup>b</sup>	31.327 <sup>b</sup>	28.030 <sup>b</sup>	30.410 <sup>b</sup>	28.830 <sup>b</sup>	27.797 <sup>b</sup>	18.45%	89.99%	
SIHD	34.703 <sup>a</sup>	23.177 <sup>b</sup>	18.353 <sup>b</sup>	16.837 <sup>b</sup>	19.460 <sup>b</sup>	18.857 <sup>b</sup>	$18.800^{b}$	28.68%	74.37%	
SIVD	47.617 <sup>a</sup>	$38.457^{ab}$	35.177 <sup>ab</sup>	27.467 <sup>b</sup>	$40.430^{ab}$	34.180 <sup>b</sup>	32.597 <sup>b</sup>	17.54%	71.66%	
TIL	$21.987^{a}$	19.307 <sup>ab</sup>	$18.167^{ab}$	15.763 <sup>b</sup>	$19.657^{ab}$	17.917 <sup>ab</sup>	9.207 <sup>c</sup>	23.47%	89.64%	
TIHD	$16.170^{a}$	12.923 <sup>b</sup>	12.523 <sup>bc</sup>	9.767 <sup>bc</sup>	11.653 <sup>bc</sup>	11.643 <sup>bc</sup>	9.207 <sup>c</sup>	19.14%	84.68%	
TIVD	30.573 <sup>a</sup>	24.733 <sup>a</sup>	30.120 <sup>a</sup>	22.557 <sup>a</sup>	$25.870^{a}$	22.297 <sup>a</sup>	15.453 <sup>a</sup>	21.12%	50.02%	
CHD	94.150 <sup>a</sup>	70.963 <sup>bc</sup>	$84.147^{ab}$	97.030 <sup>a</sup>	84.073 <sup>ab</sup>	66.560 <sup>°</sup>	65.113 <sup>c</sup>	16.14%	86.82%	
CVD	59.237 <sup>a</sup>	58.320 <sup>a</sup>	67.883 <sup>a</sup>	68.597 <sup>a</sup>	$58.070^{a}$	60.903 <sup>a</sup>	56.233 <sup>a</sup>	8.04%	49.98%	
FQPC	$45.667^{a}$	25.667 <sup>cd</sup>	17.333 <sup>d</sup>	$42.000^{ab}$	$22.000^{cd}$	$30.000^{\circ}$	32.667 <sup>bc</sup>	33.46%	88.32%	

Note: Different letters across clones indicate significant differences (p<0.05)

#### Results

#### Diversity of traits in Swida wilsoniana clones

Variance analysis and phenotypic differentiation of vegetative growth traits among different clones: Table 3 shows that the significant coefficient of variation was found in leaf bud horizontal/vertical diameter, leaf shape, leaf color, leaf margin character, and annual branch length among different clones. Coefficients of variation for leaf shape, leaf margin, and leaf color were obviously higher than other traits, as leaf shape, leaf color, and leaf margin are qualitative traits that are controlled by a single gene. Meanwhile, leaf bud, leaf area, and annual branch length are quantitative traits that are controlled by multiple genes, and therefore were relatively genetically stable.

Phenotypic differentiation coefficients of vegetative growth traits ranged from 45.27% to 83.53%, with an average of 60.68%. Of these, leaf bud transverse diameter had the largest proportion (83.53%), which showed that variation in this trait was mainly across different clones. Leaf color had the smallest proportion (45.27%), which showed that variation in this trait was mainly from within different clones. The results illustrated that trait performance was associated with both gene regulation and cultivation environment (Wang *et al.*, 2013).

Phenotypic differences in inflorescence and cluster traits among different clones: Table 4 shows that the average longitudinal diameter of cluster traits had less variation between different clones, but the coefficient of variation of other indexes, such as inflorescence and cluster, were larger (over 15%). fruit quantity per cluster

is the largest (33.46%), and also showed that different clones had genetically different yields.

The phenotypic differentiation of inflorescence length was the largest in inflorescence group (ranging from 91.04% to 96.40%), which indicated that variation between different clones represented the greatest differences in the size of inflorescences. This suggested that the size of inflorescences was mainly influenced by the genotype, and that environmental impact was small; therefore, it was relatively genetically stable. Therefore, this trait could be used as the main indicator in selecting clones for breeding. The phenotypic differentiation of fruit quantity per cluster (88.32%) and cluster horizontal diameter (86.82%) also changed greatly between different clones, which showed that the single fruit cluster number and cluster diameter were stable genetic characters.

Analysis of variance and phenotypic differentiation of fruit traits among different clones: The coefficients variation of of longitudinal/transverse diameter in fruit and seeds among different clones were small. However, coefficients of variation in seed weight, fruit weight, and moisture content were larger, which illustrated that phenotypic differences in fruits and seeds were smaller across different clones, while the inheritances of fruit and seed quality traits were relatively genetically stable (Table 5).

Phenotypic differentiation coefficients of fruit traits were higher (ranging from 62.37% to 93.71%), which differentiation coefficients of longitudinal diameter (93.71%), fruit weight (89.21%), and the fruit diameter (87.65%) were the highest. This suggested that fruit traits were genetically stable and the influence of environment on fruit quality was smaller among different clones. This could provide well genetic conditions for benign traits of superposition.

Table 5. Fruit traits of different clones.

Measured			CV	Vst					
traits	713	806	A03	B03	B05	B08	D05	CV	V SL
SHD	4.636 <sup>ab</sup>	4.674 <sup>a</sup>	4.194 <sup>c</sup>	$4.400^{cb}$	4.368 <sup>c</sup>	4.658 <sup>a</sup>	3.784 <sup>d</sup>	7.32%	77.76%
SVD	$4.154^{ab}$	$4.256^{ab}$	$3.988^{b}$	$4.140^{ab}$	$4.030^{ab}$	$4.282^{a}$	$3.618^{\circ}$	5.54%	62.37%
TSW (g)	55.551 <sup>b</sup>	63.214 <sup>a</sup>	41.113 <sup>cd</sup>	50.166 <sup>bc</sup>	45.772 <sup>°</sup>	60.171 <sup>ab</sup>	32.117 <sup>d</sup>	22.11%	80.94%
FHD	6.313 <sup>a</sup>	5.713 <sup>bc</sup>	5.723 <sup>bc</sup>	5.467 <sup>c</sup>	$6.020^{ab}$	6.033 <sup>ab</sup>	5.713 <sup>bc</sup>	4.82%	87.65%
FVD	6.233 <sup>a</sup>	5.883 <sup>ab</sup>	5.627 <sup>b</sup>	$5.927^{ab}$	$5.850^{\mathrm{ab}}$	6.130 <sup>ab</sup>	$5.670^{ab}$	3.76%	93.71%
TFW (g)	$110.810^{b}$	132.423 <sup>ab</sup>	91.667 <sup>°</sup>	$110.442^{b}$	93.848 <sup>bc</sup>	164.045 <sup>a</sup>	91.221 <sup>c</sup>	23.56%	89.21%
OC (%)	$30.46^{ab}$	29.83 <sup>b</sup>	32.68 <sup>a</sup>	35.26 <sup>a</sup>	$30.02^{ab}$	24.26 <sup>c</sup>	29.67 <sup>b</sup>	11.06%	84.26%
<u>MC (%)</u>	12.93 <sup>a</sup>	11.78 <sup>ab</sup>	9.46 <sup>b</sup>	8.96 <sup>b</sup>	9.60 <sup>b</sup>	12.37 <sup>a</sup>	11.32 <sup>ab</sup>	14.37%	71.33%

Note: Different letters across clones indicate significant differences (p<0.05)

Table 6. Eigenvector and contribution rates of principal components of traits of *Swida wilsoniana* clones.

components of trans of <i>Swida witsoniana</i> ciones.										
	1	2	3	4						
SHD	0.182	<u>0.957</u>	0.142	0.119						
SVD	0.346	0.882	0.081	0.245						
TSW	0.207	0.895	-0.084	0.282						
FHD	<u>0.845</u>	0.107	-0.207	0.279						
FVD	0.332	0.577	-0.031	0.679						
TFW	-0.096	0.838	-0.490	0.202						
OC	-0.259	-0.301	0.857	0.012						
MC	0.442	0.202	-0.650	0.556						
LBHD	-0.075	-0.184	0.020	-0.837						
LBVD	0.570	0.273	-0.096	0.737						
LL	0.412	0.122	0.730	0.189						
LW	0.188	-0.495	0.336	0.117						
LS	-0.781	0.205	-0.479	0.261						
LC	0.147	-0.420	0.762	0.268						
LMC	0.119	-0.509	-0.188	-0.661						
ABL	-0.074	-0.606	0.510	-0.339						
PIL	0.965	-0.010	-0.207	-0.073						
PIHD	0.960	0.266	-0.080	0.009						
PIVD	<u>0.994</u>	0.034	0.002	-0.091						
SIL	0.762	-0.030	0.283	0.505						
SIHD	0.746	0.039	0.056	0.631						
SIVD	0.965	0.003	-0.020	0.231						
TIL	0.703	0.610	0.349	0.005						
TIHD	0.863	0.309	0.148	0.263						
TIVD	0.705	0.350	0.552	-0.141						
CHD	0.147	0.053	0.949	0.250						
CVD	-0.396	0.311	0.688	-0.246						
FQPC	-0.125	0.007	0.195	0.960						
Total	11.549	6.158	4.337	3.034						
Variance (%)	41.245	21.992	15.489	10.837						
Cumulative (%)	41.245	63.237	78.725	89.563						

**Principal components analysis:** Bartlett's ball test and the (KMO) test showed that there was a significant genetic difference in the 28 traits across different clones, and using principal component analysis (PCA) as a factor extraction, and orthogonal varimax rotation was used to rotate the load matrix.

From Table 6, significant differences were found in genetic traits of the main component, trait value, and the rate of variance. The 28 agronomic traits were divided into 4 main components. The first 3 principal components cumulatively contributed 78.73%, so the basic information of the original variable was reflected in the first 3 factors. The first principal component had a large eigenvalue (11.55) and the largest contribution rate was

41.26%, which showed a dominant influence; the variance of the second principal component was 21.99%; the third principal component accounted for 15.49% of the variance; and the variance of the fourth principal component was 10.84%.

The eigenvectors showed that the index accounted for the corresponding principal components. Table 6 shows that the first principal component of inflorescence size (including primary, secondary, and tertiary inflorescence length/ horizontal/ vertical diameter) as well as fruit diameter trait. Inflorescence longitudinal diameter (IHD) had the highest load index of the principal component (0.99). The left form had the largest negative absolute value (0.78), which suggested that the first principal component reflected the inflorescence factor. The highest load index of secondary principal component was seed vertical diameter (SHD, 0.96) and load indexes of seed longitudinal diameter (SVD), seed weight (TSW), and fruit weight (TFW) were 0.88, 0.89 and 0.84, respectively, while the annual branch length (ABL,-0.61) and left width (LL,-0.49) were larger and negative. This showed that the second principal component reflected some information of seed index, namely the inflorescence factor and the highest load index of third principal component was cluster horizontal diameter (0.95) followed by fruit oil content (OL, 0.86), leaf color (LC, 0.76), leaf length (LL, 0.73), and average longitudinal diameter (CVD, 0.79), but the whole fruit moisture content (MC) was large and negative (-0.65). These results suggested that the third principal component reflected factors related to oil content. Fruit quantity per cluster was the highest (FQPC, 0.96) in fourth principal component, followed by Leaf bud horizontal diameter (LBHD,-0.84) and leaf bud longitudinal diameter (LBVD, 0.74). Fruit longitudinal diameter (CVD, 0.68) and leaf margin character (LMC,-0.66) were the largest, negative, absolute values. This showed that the fourth principal component mainly reflected the number of fruit and cluster factors.

**Genetic distance and clustering analysis:** Fig. 1 shows the results of cluster analysis and principal component factor scores for the seven *S. wilsoniana* clones. Based on hierarchical clustering, the threshold of 17.5 was set; the seven *S. wilsoniana* clones were divided into 4 groups. Group I represented the small fruit group with the same characters of less fruit quantity per cluster, small fruit longitudinal diameter, big leaf bud horizontal diameter, and small leaf bud longitudinal diameter, curled edges, Group I included two subgenera, and the first subgroup included clones A03 and B05, with the shortest euclidean distance (0.878). The second subgroup included clones B05 and B08, with a euclidean distance of 0.995. Group

II represented high yield group included clones 713, with more fruit per cluster, larger fruit, bigger inflorescence, and non-curling, oval leaves. Group III represented high yield and high oil content group included B03 clones, with the highest oil content, the lowest moisture content, smaller inflorescence, and bigger cluster. Group IV represented low oil content group included D05 cloneswith the highest moisture content, minimum oil content, smaller seeds, smaller clusters, lesser fruit/seed weight, broad leaf with light green, and longer new branch length, Therefore, to achieve the breeding goal, hybridization of group II with group III might produce a high-yield, high-oil content species (Table 7).

Table 7. Factor scores of different clones.

Clanar	Factor score									
Clones	1	2	3	4						
713	713 1.489		0.467	1.553						
806	0.086	0.757	-0.567	-0.059						
A03	0.290	-0.169	0.680	-1.523						
B03	-1.604	0.340	1.412	0.634						
B05	0.726	-0.419	0.390	-0.867						
B08	-0.266	1.362	-1.275	-0.067						
D05	-0.721	-1.802	-1.107	0.329						
CASE Label Num A03 3 B05 5 806 2 B08 6 713 1	]	10	15	20 25 I						
B03 4				II IV						
D05 7			i							

Fig. 1. Dendrogram of cluster analysis based on growth characteristics of seven *Swida wilsoniana* clones.

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# Correlation analysis of growth traits among different clones

**Correlation analysis of nutritional traits, cluster traits, and fruit traits:** Table.8 shows that: (1) nutritional branches, bud longitudinal diameter, and fruit horizontal diameter were significantly positively correlated with the fruit longitudinal diameter, which suggested that larger fruit had larger longitudinal diameter leaf buds; (2) there was a significant, negative correlation between leaf edges traits, longitudinal diameter fruit, and fruit quantity per cluster, which manifested as clones with bigger fruit had more fruits in non-curling leaf edges; (3) the annual branches length, fruit weight, and thousand seed weight were significantly negatively correlated, which indicated that stronger new branches partly affected the quality of the fruit.

**Correlation analysis of fruit, cluster traits and reproductive traits:** The length, horizontal diameter, and longitudinal diameter of primary and secondary inflorescence were significantly positively correlated with fruit longitudinal diameter. Which indicated that the size of fruit was obviously affected by the primary/secondary inflorescences. Length of the tertiary inflorescence was significantly positively correlated with seed horizontal and longitudinal diameter, which showed that the size of seeds was greatly influenced by the length of tertiary inflorescence was positively correlated with fruit quantity per cluster, but was not significant (p>0.05). Larger inflorescence varieties had lower oil content and higher moisture content (Table 9).

able 8.	Correlation	coefficients	between	fruit,	cluster	traits	and	vegetative trait	ts.
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						,		8			
	CHD	CVD	FQPC	SHD	SVD	TSW	FHD	FVD	TFW	OC	MC
LBHD	-0.161	0.171	-0.729	-0.300	-0.406	-0.494	-0.124	-0.544	-0.282	-0.084	-0.602
LBVD	0.207	-0.438	0.635	0.445	0.622	0.568	$0.806^{*}$	$0.912^{**}$	0.384	-0.367	0.744
LL	$0.772^{*}$	0.120	0.207	0.381	0.447	0.312	0.168	0.267	-0.286	0.546	-0.216
LW	0.270	-0.233	0.030	-0.298	-0.206	-0.202	-0.195	-0.332	-0.640	0.592	-0.182
LS	-0.517	-0.078	0.221	0.040	-0.034	0.191	-0.544	-0.002	0.515	-0.207	0.151
LC	$0.821^{*}$	0.201	0.418	-0.231	-0.182	-0.364	0.130	0.078	-0.657	0.626	-0.423
LMC	-0.406	-0.302	$-0.769^{*}$	-0.520	-0.515	-0.474	-0.275	$-0.818^{*}$	-0.523	0.089	-0.300
ABL	0.411	0.347	-0.145	-0.599	-0.652	$-0.808^{*}$	-0.133	-0.479	$-0.773^{*}$	0.479	-0.694

Note: \*p<0.05 level (2-tailed); \*\*p<0.01 level (2-tailed)

	CHD	CVD	FQPC	SHD	SVD	TSW	FHD	FVD	TFW	OC	MC
			e e								
PIL	-0.063	-0.451	-0.212	0.110	0.265	0.152	$0.865^{\circ}$	0.285	-0.006	-0.444	0.533
PIHD	0.078	-0.366	-0.130	0.422	0.568	0.456	$0.846^{*}$	0.473	0.168	-0.388	0.534
PIVD	0.127	-0.341	-0.209	0.198	0.346	0.206	$0.813^{*}$	0.281	-0.087	-0.261	0.402
SIL	0.521	-0.110	0.478	0.172	0.329	0.181	$0.760^{*}$	0.581	-0.123	0.041	0.466
SIHD	0.307	-0.361	0.507	0.252	0.444	0.376	0.731	0.638	0.046	-0.089	0.682
SIVD	0.171	-0.503	0.080	0.218	0.414	0.302	$0.856^{*}$	0.464	-0.043	-0.246	0.556
TIL	0.463	0.099	-0.023	$0.776^{*}$	$0.832^{*}$	0.689	0.577	0.576	0.269	-0.061	0.193
TIHD	0.335	-0.130	0.165	0.492	0.626	0.516	0.735	0.574	0.143	-0.121	0.538
TIVD	0.606	0.339	-0.111	0.504	0.531	0.352	0.443	0.281	-0.079	0.223	-0.013

Note: \*p<0.05 level (2-tailed); \*\*p<0.01 level (2-tailed)

#### Discussion

**Diversity of traits:** Phenotypic variation is not only a fundamental research targetfor genetic diversity, but also a vital foundation for improving breeding (Chen *et al.*, 2012). Selective breeding should identify and add beneficial genes from wild germplasm resources. Coefficients of variation present discrete level of each phenotype (Zhang *et al.*, 2011). Phenotypic differentiation coefficients represented for genetic and habitat diversity (Zhou *et al.*, 2009).

In this study, variance analysis showed different degrees of variation in the 28 growth traits of 7 Swida wilsoniana clones, and the coefficients of variation ranged from 8.04% to 94.30%. Coefficients of variation for qualitative traits, such as leaf shape, leaf color, and leaf margin, were larger than other traits, such as inflorescence length/ transverse diameter/longitudinal diameter, as quantitative traits are regulated by the cumulative effects of multiple genes, while qualitative traits are controlled by a single gene. Wan et al., (2012) and Duan et al., (2013) reported that the coefficients of variation for oliver qualitative traits, such as fuzz on the calyx, were larger (e.g., 80.56%) than number of sepals (e.g., 13.97%) in Camellia sinensis L. Our study also found that the morphology of fruits and seeds were relatively stable genetic traits, and morphological changes in fruits and seeds were less affected by the environment.

This study found that phenotypic differentiation coefficients of the 28 growth traits were ranging from 45.27% to 96.40%, which suggested agronomic traits were genetically stable and less affected by environmental factors and can be used as selective indicators for breeding and was a well genetic conditions for benign traits of superior quality.

The main source of variation and correlations: The 28 measured traits were divided into 4 principal components, which were inflorescence factor, seed factor, oil content factor, and fruit quantity per cluster. The first 3 principal components represented 78.73% of the genetic variation, This showed that major indexes of morphological differentiation in germplasm resources come from inflorescence, seeds, fruit oil content, fruit quantity per cluster, and that these 4 traits also reflected actual morphological identification and classification of *Swida wilsoniana* species.

Cluster analysis was based on the principal components analysis. Seven *Swida wilsoniana* species were clustered into 4 groups. Group II represented high yield group was characterized by more fruit quantity per cluster, bigger fruit, bigger inflorescence, non-curling and oval leaves. Group III represented high yield and high oil content group was characterized by whole fruit with the highest oil content, lowest moisture content, bigger cluster, smaller inflorescence, and green-lanceolate leaves. Therefore, high-yield and high-oil target species may be produced by hybridizing groups II and III. However, considering the influence of environmental factors on phenotypic traits (Liu, 2013), molecular markers or microscopic perspectives should be used for better morphological identification of *Swida wilsoniana*.

**Selection for the early period:** This study showed that the clone which had bigger primary and secondary inflorescence, non-curling leaf margin, or bigger leaf bud longitudinal diameter would have large fruit. The clone with longer tertiary inflorescence would have big seeds. The clone with non-curling leaf margins and larger secondary inflorescence and more fruit per cluster would have a highfruit yield. These results provide some basis for the ideal species and hybrid breeding in the early period.

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