

Phenotypic Diversity In Natural Populations of *Docynia Delavayi* (Franch.) Schneid.

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Abstract

Docynia delavayi (Franch.) Schneid. is a wild fruit tree with high medicinal, edible, ecological, and ornamental values. This paper investigates the phenotypic diversity of nine traits in fruit and leaf from 17 *Docynia delavayi* natural populations. The results of coefficient of variation showed petiole length and leaf area contributed the highest mean coefficient of variation (CV = 36.85% and 43.71%, respectively), while fruit vertical diameter had the lowest contribution index (CV=12.17%). The principal component analysis (PCA) revealed that first six PC axes explained 95.417% of the total variance among the *Docynia delavayi* populations tested, and the first three PCs explained 76.413% of the variation in multiple traits. PC1 was the most important genetic factor and the main indicator of its interpopulation variation, accounting for 51.428% of the total variation. Based on the nine phenotypic data of leaf and fruit from 17 natural populations of *Docynia delavayi*, the UPGMA method was used to broadly classify these populations into four main groups. This study provides a theoretical basis for further utilization and conservation of *Docynia delavayi* germplasm resources.

1. Introduction

Docynia delavayi (Franch.) Schneid. is an evergreen tree belonging to the Rosaceae family, genus *Docynia*, which is a medicinal plant mainly distributed in southwest China. (Flora of China. 1987; Wu et al. 1984; Han et al. 2014). With the increasing emphasis on health, the beneficial bioactive of *Docynia delavayi* is gaining more and more attention. (Dong et al. 2013). *Docynia delavayi* fruit are rich in antioxidants and phenolic compounds (Deng et al. 2014; Zhao et al. 2012). *Docynia delavayi* has a higher antioxidant capacity compared to other plants in the Rosaceae family, which makes it being one of important healthy fruit resource for human health benefits. (Guan et al. 2000). In the last decades, the research objectives of *Docynia delavayi* have focused on reproduction techniques and the extraction and analysis of active ingredients, etc(Xu et al. 2015; Dong et al. 2013).

The prerequisite for the improvement and utilization of wild species is to have a detailed understanding of the genetic traits of germplasm resources. (Day Rubenstein et al., 2006; Upadhyaya et al., 2008). Phenotype is one of the most important means of studying diversity and is the most direct expression of plant adaptation to the environment (Li et al. 2018). Evaluating the diversity of plant phenotypes is conducive to the protection and utilization of plants. (Shao et al. 2013; Su-Kyung et al. 2016; Yin et al. 2016). The characterization of the phenotypic trait diversity includes the evaluation of the pattern variation of the phenotypic structure, identifying the traits that contribute the most to the overall diversity in the collection, and establishing the similarity/dissimilarity level between the parents based on the traits considered (Nikolic' et al., 2010; Oliveira et al., 2012). In the study of plant phenotypic diversity, researchers often describe or measure the genetically stable traits of fruits and leaves, and use statistical methods for relational analysis, so as to reflect the degree of biological phenotypic diversity (Su-Kyung et al. 2016).-

The domestication and improvement of *Docynia delavayi* germplasm has a prerequisite which is information of phenotypic and gentic variation. In the present study, models of fruit and leaf variation were determined between and within 17 *Docynia delavayi* natural populations from different sites. The objectives are to elucidate the natural distribution of wild *Docynia delavayi* resources by measuring the phenotypic diversity of these wild populations in different locations. These findings will provide a theoretical basis for the rational utilization of its germplasm resource.

2. Materials & Methods

2.1 Sample Collection

The leaves and fruits from 17 natural populations of *Docynia delavayi*, were collected from different sites located in Yunnan and Sichuan provinces (Figure 1, Table 1). The distance between sampled trees exceeded 50 m to reduce the probability of sampling closely related trees. More than 30 mature individuals per population, total of 525 individuals have been selected. The young, disease-free leaves of new shoots were collected, numbered according to sampling locations and individual plants, and placed in pre-numbered self-sealing bags.

2.2 Phenotypic Traits Measurement

To measure leaf traits, 30 leaves per individual were selected, the distance between the selected individuals was controlled to be more than 50m in order to minimize the possibility of the influence of the sampled related individuals. (Yin et al. 2016; Liu et al. 2017). Petiole length (PL), leaf width (LW), and leaf length (LLE) were measured with a vernier caliper, and count the leaf venation number (LVN). The leaf area (LA) of fresh leaf samples was determined by delta-T image analysis system (Bartelink. 1997). In summary, each individual fruit has its own unique traits. There were thirty fruits from each tree were used to estimate fruit vertical diameter (FV) and fruit lateral diameter (FLD). Leaf index (LI) and fruit index (FI) were followed by the formula:

$$LI = \frac{LLE}{LW} \times 100\% \quad FI = \frac{FV}{FLD} \times 100\%$$

2.3 Statistical Analyses

The data of 17 natural populations were initially grouped and then averaged for statistical analysis. Quantitative variables were assessed with Microsoft Excel 2010 for the following parameters: mean, maximum, minimum, coefficient of variation (CV), and standard deviation (SD). Other or the rest of statistical analyses were performed using SPSS 22.0. When comparing the difference within or between the different accessions origin, ANOVA F test ($P \leq 0.05$) was be used. The correlations among traits were measured by Pearson correlation coefficient, $P \leq 0.05$, to expose possible connections based on

the 3-year average data of 3 trees for each addition and year. The principal component analysis (PCA) was employed to study correlations among traits. Then, based on normalized data about 9 phenotypic traits, UPGMA was used for clustering of different *Docynia delavayi* resources materials.

3. Results

3.1 Variation in Phenotypic Traits

The ANOVA results showed that in each accession, the probability of difference was high for all measured traits (LVN, PL, LA, LLE, LW, FV and FLD) ($P \leq 0.01$, Table 2). The leaf traits reported that the LVN value ranged between 4.46 ± 0.65 cm (YM) and 7.83 ± 1.11 cm (YJ). The PL value ranged from 7.22 mm to 17.18 mm, the highest PL values were observed in XY (7.22 ± 1.53 mm) and the lowest values, in YJ (17.18 ± 3.29 mm). A range of 4.67 ± 3.16 cm² (RH) to 21.53 ± 6.07 cm² (YJ) was found for LA. LLE varied from 2.97 ± 0.34 cm (DC) to 8.68 ± 0.34 cm (YJ), while LW ranged from 1.78 ± 0.60 cm (RH) to 3.66 ± 0.69 cm (YJ) (Table 3). The LI value means there was no remarkable differences among all populations. (Table 2). The mean value of LI was 2.15, with a variation ranged from 1.10 ± 0.23 for DC to 2.45 ± 0.32 for ML.

The fruit traits showed that the highest value for FV (43.59 ± 4.67 mm) and FLD (46.23 ± 6.42 mm) were determined in the LC population, while the ML presented the lowest value for FV (28.39 ± 3.33 mm) and the DC for FLD (26.44 ± 3.31 mm). The FI value had a average of 1.05, ranging between 0.89 ± 0.09 and 1.39 ± 0.21 for the ML and DC population, respectively. And average FI value did not differ among populations.

The CV for nine traits in the tested *Docynia delavayi* populations showed (Table 3) that PL and LA exhibited relatively high variation (the CV were 36.85% and 43.71%, respectively). In all phenotypic traits of *Docynia delavayi*, the LA had the largest CV (43.71%), while FV had the smallest CV (12.17%). The CV value of traits was in the order of LA (43.71%) > PL (36.85%) > LW (25.33%) > LLE (24.47%) > LVN (17.50%) > FLD (13.30%) > FV (12.17%). On average, populations showed higher variation in leaf traits than fruits traits (the CV were 28.13% and 12.48%, respectively)

3.2 Correlation Analysis

The correlations between features were found at $p \leq 0.05$, and the Pearson correlation coefficients were reported between pairs of traits shown that LVN observed significant and positive correlations with LA, PL, LLE, LW, while PL and LA had the most strongly correlation with LVN ($R = 0.816$, $p \leq 0.01$). Significant positive correlations were also found between PL and LVN ($R = 0.816$, $p \leq 0.01$), LA ($R = 0.752$, $p \leq 0.01$), LLE ($R = 0.682$, $p \leq 0.01$), LW ($R = 0.734$, $p \leq 0.01$), and FV ($R = 0.681$, $p \leq 0.01$); between LA and LLE ($R = 0.974$, $p \leq 0.01$), LW ($R = 0.927$, $p \leq 0.01$), FV ($R = 0.735$, $p \leq 0.01$) and FLD ($R = 0.562$, $p \leq 0.05$); between LLE and LW ($R = 0.845$, $p \leq 0.01$), LI ($R = 0.639$, $p \leq 0.01$), FV ($R = 0.679$, $p \leq 0.01$) and FLD ($R = 0.612$, $p \leq 0.01$); and between FV and FLD ($R = 0.767$, $p \leq 0.01$). FLD was negatively correlated with FI ($R = -0.658$, $p \leq 0.01$) (Table 4).

Nevertheless, a significant negative correlation was found between longitude and LVN ($R = -0.543$, $p \leq 0.05$), LA ($R = -0.789$, $p \leq 0.01$), LLE ($R = -0.788$, $p \leq 0.01$), LW ($R = -0.696$, $p \leq 0.01$), and FV ($R = -0.465$, $p \leq 0.01$); and between latitude and LVN ($R = -0.454$, $p \leq 0.01$), LA ($R = -0.660$, $p \leq 0.01$), LLE ($R = -0.644$, $p \leq 0.01$), LW ($R = -0.710$, $p \leq 0.01$), FV ($R = -0.735$, $p \leq 0.01$), and FLD ($R = -0.488$, $p \leq 0.05$) (Table 4). In a word, the result showed that traits had no correlated with altitude, but the negative and significant correlated with longitude and latitude. The internal links between individual and geographical conditions was to be further research.

3.3 Principal Component Analysis in Traits

The results of the PCA analysis indicated that over 76% of the observed variance could be explained by the first three components (Table 6). The total variance explained by PC1 axis and PC2 axis was 51.428% and 15.190%, respectively. The Rotated Component Matrix of factorial analysis of *Docynia delavayi* showed that there is a clear separation between leaf traits, fruit traits, and geographical conditions (Table 6). PC1 represents mainly LW (0.940), LA (0.914), LLE (0.859), PL (0.843) and LVN (0.711). PC2 explains mainly FI (-0.835), FLD (0.721) and FV (0.257). Longitude (0.339) and Latitude (0.216) occupied a certain position in PC3.

The first principal component largely represents these interrelated leaf traits, so it is the most important genetic factor, and it accounts for 51.428% of the total variance. (Table 7). The susceptibility of FV and FLD was positively correlated with the second principal component, and negatively correlated with FI (-0.835). Therefore, PC2 represents the second in importance genetic element, accounting for 15.19% of the overall variance. The third principal component is negatively correlated with longitude and latitude. ($r = 0.339$ and 0.216 , respectively). Therefore, this principal component explains 9.796% of the total variance.

3.4 Clustering Analysis

The Ward clustering of the six most important principal components of nine standardized phenotypic traits resulted in a tree showing that four groups (clusters) were distinguished (Figure 2). The Group I consist of three populations (LC, MS, and YJ). Only one population, DC, belongs to Group II. Group III consists of three populations, including CN, LL, and MJ. The ten populations in Group IV represent different geographic sites (YB, RH, NL, LJ, MY, YL, XY, CX, ML, and YM).

4. Discussion

Morphological markers have been recognized as an efficient and useful marker system which has several advantages such as simplicity, speed and cost-effective. (Zhang et al. 2018; Munthali et al. 2012; Eticha et al. 2005). In this study, phenotypic diversity of nine leaf and fruit traits was investigated in 17 populations of *Docynia delavayi* with the result that there was a high degree of variability among populations. Similar results have been reported in some species of Rosaceae before (Bella et al. 2021; Forcada et al. 2012). It may be indicated that most of species in Rosaceae had a high degree of phenotypic diversity in the important traits (Zargar et al. 2021).

The CV value is a parameter independent of the tested trait unit, which is effective in comparing the tested traits, and a good indicator that phenotypic traits distinguish the ability of the accessions. (Elhoumaizi et al. 2002; Petruccelli et al. 2013). Phenotypic features with lower CV values were more homogenous and reproducible among different populations, and the descriptors that have higher CV values are better discriminative than in other populations than those studied here and may become reliable markers for characterizing fruit trees. (Petruccelli et al. 2013). In the case of the work, the CV value in three fruit phenotypic characters were all lower than 20% (varied from 11.69–13.30%). It indicated that the fruit traits showed lower average CV value as would be expected because of the higher stability. Compare with the leaf traits, the CV value were all higher than 20%, showed a higher environmental influence, which was similar to other plants (Zeng et al. 2021; Lu et al. 2021), indicated that the fruit traits were more stable than leaf characters in much of arbor species (Petruccelli et al. 2013, Li and Gu, 2005). It could be due to the effective of environment, that the leaf traits had greater environment influence, whereas, fruit traits had stronger genetic control.

Information on the most important traits in evaluating phenotypic diversity is provided by correlation coefficients. (Milatovic' et al., 2010; Norman et al., 2011). In our study, the six leaf traits were positively and significantly correlated. It implied that the main traits with the significant correlation reflecting the important indication role of leaf and fruit morphology in variation identification (Forcada et al. 2012; Petruccelli et al. 2013; Ahmed et al. 2011). The results of the correlation analysis between phenotypic traits and geographical conditions showed that with the increase of longitude and latitude, the size of leaf and fruit showed a trend of decreasing. The different result has been showed in *Quercus mongolica* (Li and Gu, 2005), which showed that the traits had an increasing tendency when the longitude and latitude were magnified. It might be on account of the existence of different genetic mechanisms among different species (Acosta-Quezada et al., 2011). Interestingly, the correlations were observed between *Docynia delavayi* traits and longitude and latitude, but were not altitude. It was similar to previously reported results (Liu et al. 2021), indicated that the complex internal links between phenotypic traits and geographic conditions, and the exact genetic mechanisms need to be further investigated. (Milatovic' et al., 2010).

The principal component analysis (PCA) can help identify resources with better quality performance (López-Upton et al. 2015). It identifies highly discriminative variables, which are important for the characterization of the population. (Petit et al. 1998; Vinceti et al. 2013). In this study, leaf traits such as LA, LLE and LW are consistent with the high contribution to the first component in the *Docynia delavayi* population, which can be used for the identification of *Docynia delavayi* germplasm. The similar conclusions have been reached in previous studies on morphological traits of Rosaceae family. (Lacis et al., 2010; Nikolic et al., 2010). But some studies were not consistent with those of Lansari et al. (1994) who compared phenotypic traits of Moroccan almonds and variables contributing towards leaf traits were found to be less important than other traits for explaining the differences in variation among the selected. It might be attributed to the specific genetic structure of Rosaceae, and the further research is needed to investigate the intent of genetic control.

In the present work, cluster analysis showed some correlation between populations with similar fruit traits, while the correlation between populations of the same geographic origin was weak. During the investigation and measurement, the Group Ⅱ, which the populations were near at the northeast of Yunnan and southwest of Sichuan, showed the smaller fruit size. It was a probable adaptation to the complex geographic position and natural environment of the regions of species, which similar with the reported findings (Elhoumaizi et al. 2002; Saddoud et al. 2008).

Current findings supported these opportunities in native germoplasm of *Docynia delavayi* which has been found the higher phenotypic variability, suggested that the *Docynia delavayi* cultivar program could yield richer genetic diversity. Generally, some traits such as LL, LW, LA that reflected the phenotypic information of *Docynia delavayi*, were susceptible to the interference of natural environment, so that it was difficult to grasp the evolutionary relationship and genetic relationship between *Docynia delavayi* only by traits (Shao et al. 2013). Therefore, further studies of their mechanism must be carried out on molecular level.

Conclusions

In the present study, high levels of genetic variation were found among and within populations of *Docynia delavayi*. The variation in fruit traits of *Docynia delavayi* was more stable than that in leaf traits, while the correlations were observed between *Docynia delavayi* traits and longitude and latitude. The further study should explore the relationship between the climate and soil factors and the phenotypic traits of *Docynia delavayi*, which will help to gain insight into the mechanisms between genetic and abiotic factors that contribute to the phenotypic variation of this species. Meanwhile, for the purpose of understanding the genetic mechanisms at the molecular level of *Docynia delavayi* populations, it is still necessary to use molecular markers or other molecular biology techniques to investigate the genetic relationships among *Docynia delavayi* populations.

Declarations

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Tables

Table 1. Collection locations of *D. delavayi* and associated geographical factors.

Location	Number of leaf investigations	Number of fruit investigations	Latitude	Longitude	Elevation
Xiangyun (XY)	30	30	100°54'	25°56'	2360
Yunlong (YL)	35	35	99°37'	25°88'	1674
Ninglang (NL)	30	30	100°846'	27°203'	2550
Lijiang (LJ)	31	31	100°00'	26°80'	2450
Yanbian (YanB)	38	38	101°370'	26°895'	2148
Muli (ML)	31	31	101°276'	27°957'	2712
Miyi (MY)	30	30	101°973'	27°058'	1770
Renhe (RH)	30	30	101°665'	26°621'	2035
Chuxiong (CX)	30	30	101°412'	24°999'	2353
Yuanmou (YM)	30	30	101°986'	25°498'	2368
Dongchuan(DC)	30	30	103°201'	26°19'	2360
Mojiang (MJ)	30	30	101°629'	23°408'	1385
Lancang (LC)	30	30	100°179'	22°598'	1664
Changning (CN)	30	30	100°12'	25°12'	1741
Longling (LL)	30	30	99°11'	24°50'	1768
Mangshi (MS)	30	30	98°44'	24°39'	2041
Yingjiang (YJ)	30	30	98°16'	25°20'	2291

Table 2. ANOVA of studied phenotypic traits of *D. delavayi*

Note: **indicates significant difference at the 0.01 level.

*indicates significant difference at the 0.05 level.

LVN- Leaf veantion number; PL- Petiole length; LA- Leaf area; LLE- Leaf length; LW- Leaf width; LI- Leaf index; FV- Fruit vertical; FLD- Fruit lateral diameters; FI- Fruit index.

Phenotypic Traits		Sum of Squares	Mean Square	F	Sig.
LVN	Between Groups	367.768	1.620	2.322	0.000**
	Within Groups	18.840	0.698		
PL	Between Groups	4934.127	21.736	2.473	0.000**
	Within Groups	237.302	8.789		
LA	Between Groups	9335.148	41.124	3.272	0.000**
	Within Groups	339.316	12.567		
LLE	Between Groups	820.542	3.615	1.723	0.001**
	Within Groups	56.647	2.098		
LW	Between Groups	145.642	0.642	1.658	0.000**
	Within Groups	10.450	0.387		
LI	Between Groups	64.477	0.284	1.079	0.426
	Within Groups	7.106	0.263		
FV	Between Groups	9987.995	44.000	1.939	0.021*
	Within Groups	612.834	22.698		
FLD	Between Groups	14065.196	61.961	3.258	0.000**
	Within Groups	513.515	19.019		
FI	Between Groups	7.921	0.035	0.948	0.604
	Within Groups	0.994	0.037		

Table 3. Mean and Standard Deviation of leaf and fruit traits of *D. delavayi*

Mean Number	Leaf veantion number (LVN)	Petiole length/mm (PL)	Leaf area/cm ² (LA)	Leaf length/cm (LLE)	Leaf width/cm (LW)	Leaf index (LI)	Fruit vertical/mm (FV)	Fruit lateral diameters/mm (FLD)	Fruit index (FI)
XY	5.10±0.89	7.22±1.53	8.59±3.04	5.34±1.02	2.36±0.61	2.41±0.41	33.08±3.24	27.86±3.26	1.19±0.12
YL	5.04±0.73	8.25±1.87	9.23±4.13	4.95±0.74	2.65±1.05	1.91±0.37	31.18±4.04	27.38±2.87	1.14±0.11
NL	4.52±1.13	9.70±4.48	7.81±4.00	4.64±1.24	2.36±0.81	2.08±0.63	34.89±3.08	31.69±3.50	1.11±0.14
LJ	5.13±0.91	7.67±1.92	6.59±3.09	4.48±1.21	2.11±0.52	2.15±0.47	28.90±4.74	27.89±4.29	1.04±0.07
YanB	4.84±1.01	7.78±2.45	4.94±2.66	3.72±1.12	1.87±0.56	1.95±0.42	34.73±5.33	31.44±4.67	1.10±0.13
ML	5.17±0.98	9.56±2.84	6.48±2.65	4.74±1.10	1.95±0.50	2.45±0.32	28.39±3.33	32.24±5.12	0.89±0.09
MY	5.25±0.87	11.32±5.56	6.25±2.92	4.54±1.23	1.97±0.42	2.30±0.33	33.17±5.46	29.79±3.31	1.12±0.14
RH	5.06±0.92	7.42±3.26	4.67±3.16	3.49±1.51	1.78±0.60	1.94±0.40	32.05±3.73	28.94±2.15	1.11±0.12
CX	6.10±0.87	10.90±4.15	9.78±4.66	5.73±1.53	2.46±0.62	2.37±0.47	38.27±2.84	34.50±4.35	1.12±0.11
YM	4.46±0.65	7.87±1.64	8.04±3.02	5.13±0.99	2.28±0.46	2.28±0.28	38.78±3.81	44.13±6.32	0.90±0.16
DC	5.60±0.81	13.12±2.81	4.81±0.85	2.79±0.34	2.60±0.41	1.10±0.23	36.20±3.40	26.44±3.31	1.39±0.21
MJ	5.38±0.86	9.32±2.51	10.59±3.59	5.46±1.02	2.84±0.58	1.95±0.32	36.89±3.72	29.61±4.59	1.26±0.17
LC	6.01±0.84	12.18±8.93	16.43±4.85	7.58±1.69	3.22±0.64	2.45±0.78	43.59±4.67	46.23±6.42	0.95±0.10
CN	5.70±0.92	11.12±3.40	15.81±3.73	6.83±0.80	3.44±0.50	2.01±0.27	38.88±3.12	29.96±4.19	1.31±0.17
LL	7.08±0.95	11.80±2.84	14.34±5.78	6.92±1.50	3.00±0.69	2.35±0.40	33.78±2.89	28.34±3.04	1.20±0.18
MS	6.49±1.08	13.10±4.49	18.05±7.04	7.90±1.73	3.32±0.61	2.38±0.30	42.16±4.88	39.35±4.85	1.08±0.14
YJ	7.83±1.11	17.18±3.29	21.53±6.07	8.68±1.15	3.66±0.69	2.42±0.29	43.18±6.05	43.02±4.95	1.00±0.09

Table 4. Coefficient of variation of phenotypic traits of *D. delavayi*.

CV Number	LVN	PL	LA	LLE	LW	LI	FV	FLD	FI	Mean
XY	17.60%	22.58%	67.89%	33.05%	25.60%	15.00%	12.83%	11.68%	10.84%	24.12%
YL	14.40%	22.69%	35.69%	14.99%	32.42%	42.00%	12.96%	10.49%	9.48%	21.68%
NL	24.91%	46.22%	51.21%	26.79%	34.21%	32.00%	8.82%	11.04%	12.44%	27.51%
LJ	17.59%	65.66%	50.00%	27.00%	31.00%	25.00%	13.11%	11.85%	7.22%	27.60%
YanB	20.93%	31.48%	56.65%	32.58%	31.76%	21.00%	19.33%	14.65%	11.99%	26.71%
ML	19.10%	29.75%	40.91%	23.25%	25.39%	13.00%	11.71%	15.88%	9.65%	20.96%
MY	15.91%	53.74%	49.00%	25.21%	25.60%	12.00%	16.18%	9.27%	12.94%	24.43%
RH	18.09%	43.95%	67.66%	43.35%	33.95%	21.00%	11.63%	7.45%	10.83%	28.66%
CX	12.50%	48.21%	46.23%	29.14%	24.64%	27.00%	9.21%	17.76%	14.25%	25.44%
YM	14.56%	20.85%	37.54%	19.29%	20.16%	12.00%	9.84%	14.33%	17.61%	18.46%
DC	12.87%	20.72%	24.43%	18.01%	18.75%	26.00%	12.55%	13.66%	16.34%	18.15%
MJ	15.93%	26.85%	33.84%	18.95%	20.04%	17.00%	12.80%	20.93%	14.06%	20.04%
LC	13.96%	73.26%	29.54%	22.35%	19.82%	33.00%	10.72%	13.89%	10.57%	25.23%
CN	14.91%	50.26%	27.73%	15.94%	15.63%	15.96%	11.30%	18.82%	16.73%	20.81%
LL	33.30%	16.84%	57.62%	30.97%	34.42%	18.77%	8.39%	10.58%	6.82%	24.19%
MS	16.66%	34.24%	39.00%	21.89%	18.41%	12.67%	11.56%	12.33%	12.81%	19.95%
YJ	14.19%	19.13%	28.19%	13.22%	18.75%	11.99%	14.01%	11.51%	8.74%	15.53%
Mean	17.50%	36.85%	43.71%	24.47%	25.33%	20.91%	12.17%	13.30%	11.96%	/

Table 5. Correlation analysis results between phenotypic traits and geographical factors of *D. delavayi*

Phenotypic Traits	LVN	PL	LA	LLE	LW	LI	FV	FLD	FI	Longitude	Latitude	Altitude
LVN	1.000											
PL	0.816**	1.000										
LA	0.816**	0.752**	1.000									
LLE	0.756**	0.682**	0.974**	1.000								
LW	0.750**	0.734**	0.927**	0.845**	1.000							
LI	0.315	0.193	0.469	0.639**	0.135	1.000						
FV	0.540*	0.681**	0.735**	0.679**	0.746**	0.133	1.000					
FLD	0.328	0.422	0.562*	0.612**	0.420	0.477	0.767**	1.000				
FI	0.056	0.098	-0.068	-0.215	0.200	-0.657**	-0.034	-0.658**	1.000			
Longitude	-0.543*	-0.387	-0.789**	-0.788**	-0.696**	-0.461	-0.465**	-0.270	0.117	1.000		
Latitude	-0.454**	-0.388	-0.660**	-0.644**	-0.710**	-0.155	-0.735**	-0.488*	-0.115	0.292	1.000	
Altitude	-0.199	-0.093	-0.327	-0.282	-0.409	0.053	-0.252	0.057	-0.378	0.213	0.601*	1.000

Note: **Correlation is significant at the 0.01 level (2-tailed).

*Correlation is significant at the 0.05 level (2-tailed).

Table 6. Rotated Component Matrix of factors analysis of *D. delavayi*

Factors	Component		
	1	2	3
LVN	0.711	-0.011	0.086
PL	0.843	0.050	0.033
LA	0.914	-0.092	0.334
LLE	0.859	-0.100	0.482
LW	0.940	-0.168	0.143
LI	0.156	0.116	0.884
FV	0.774	0.257	-0.282
FLD	0.611	0.721	-0.024
FI	0.050	-0.835	-0.308
longitude	-0.673	0.040	-0.339
latitude	-0.713	0.422	-0.216
altitude	-0.395	0.556	-0.230
Extraction Method: Principal Component Analysis.			
Rotation Method: Varimax with Kaiser Normalization.			

Table 7. Total Variance Explained of *D. delavayi*

Component	Initial Eigenvalues			Extraction Sums of Squared Loadings			Rotation Sums of Squared Loadings		
	Total	% of Variance	Cumulative %	Total	% of Variance	Cumulative %	Total	% of Variance	Cumulative %
1	6.171	51.428	51.428	6.171	51.428	51.428	5.789	48.242	48.242
2	1.823	15.190	66.618	1.823	15.190	66.618	1.835	15.295	63.537
3	1.175	9.796	76.413	1.175	9.796	76.413	1.545	12.876	76.413
4	0.961	8.012	84.425						
5	0.752	6.265	90.690						
6	0.567	4.726	95.417						
7	0.273	2.274	97.690						
8	0.210	1.753	99.443						
9	0.055	0.458	99.901						
10	0.006	0.052	99.953						
11	0.004	0.035	99.989						
12	0.001	0.011	100.000						

Extraction Method: Principal Component Analysis.

Figures

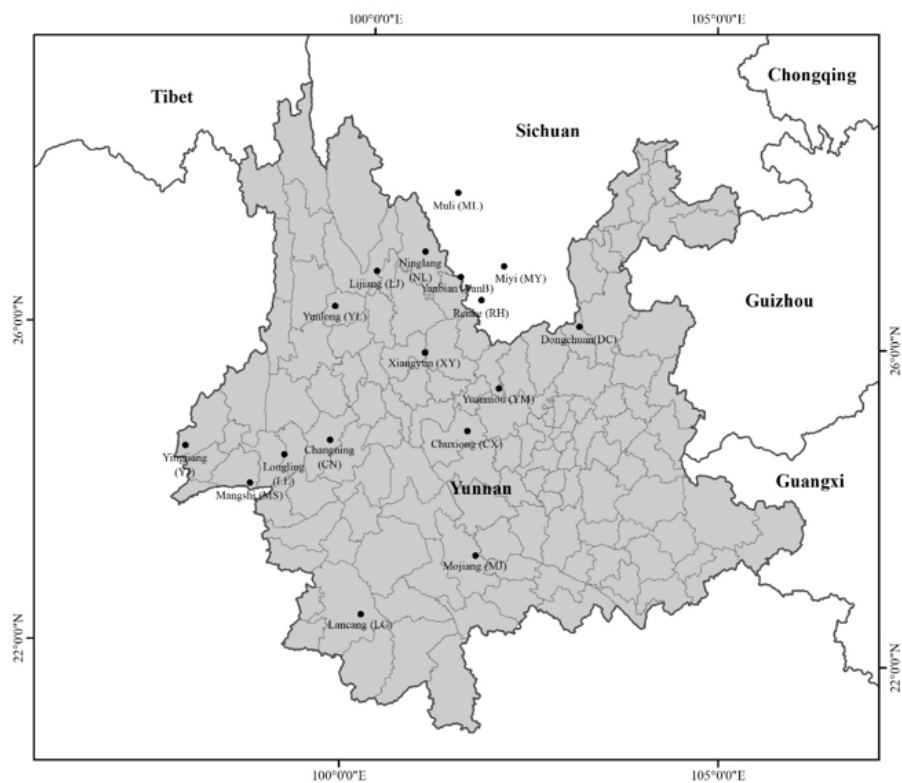


Figure 1

Map of Southwest China showing locations of 17 sampled *D. delavayi* populations

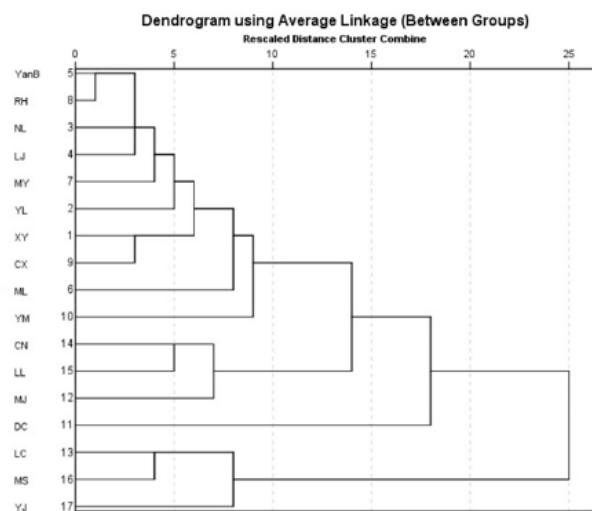


Figure 2

Clustering analysis (UPGMA) using variables of phenotypic traits and geographical factors of *D. delavayi*.