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# **RESEARCH ARTICLE**

# **PHENOTYPIC DIVERSITY OF** *ACER GINNALA* **(ACERACEAE) IN CHINA UNDER ENVIRONMENTAL CONDITIONS**

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### **ARTICLE INFO ABSTRACT**

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# **INTRODUCTION**

Plants are vulnerable to rapid environmental changes due to changing climate influnences on floral biodiversity including changed geographical distribution of species, in length of growing season for plants and so on (Iverson and Prasad., 2001; Lucas-Borja *et al*., 2016). So it is essential to gain a comprehensive idea of population genetic variability in order to provide a basis for conservation of the trees (Aitken *et al*., 2008). Phenotypic diversity and variation may reflect both genetic variability and adaption to local environmental characteristics (Ming *et al*., 2006). The relationships between plant phenotypic variation and environment have been reported in many articles (Li *et al*., 2014). *Acer ginnala* (Aceraceae) is a tree or shrub with bisexual flowers and key fruit (Hall, 1951; Bock *et al*., 1980). It is widely distributed in both Japan, North Korea, Russia and over most provinces in China from the northeast to the southwest (Huang *et al*., 2009). This speices is always used for landscaping with highly ornamental value, economic value for industry application, and medical value with its gallic acid (Wang, 2010; Yan *et al*., 2010; Huang *et al*., 2009)*.* Meanwhile*,* with the increase of soil moisture content and soil total potassium, the leaves gradually became oval and the key fruit became shorter, *A. ginnala* have formed different types of phenotypic characteristics in wild community (Wang

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*Acer ginnala* (Aceraceae) is a multipurpose shrub with significant economic and ecological value in China. Considering the fact that various natural and anthropogenic pressures might bring about serious influences to morphological diversity of *Acer ginnala.* In this context, thirty-four phenotypic traits were analyzed to explore the phenotypic variation and pattern of 19 *Acer ginnala* populations by principal component analysis (PCA), nested analysis and cluster analysis. A correlations between phenotypic traits and environment factors were used pearson's correlation coefficient. The results showed that phenotypic traits were significantly different among 19 populations. Phenotypic variation coefficient (*CV*) and Shannon-Wiener index (*HSW*) were 23.53% and 5.22 respectively. The phenotypic differentiation coefficient (*V*st) among populations was 56.996%, which was more than that of within populations (43.004%). The total of four principal components was 87.30% in principal component analysis. Nineteen *A. ginnala* populations were divided into two groups based on cluster analysis. Absolute high temperature and Annual average temperature were negative correlated to leaf length of *A. ginnala*, while Annual precipitation had a positive correlation with length/width ratio of leaf. Environmental factors would affect the phenotypic variation and pattern of *A. ginnala*  populations.

> *et al*., 2010). Very few analyses have been conducted on the genetic diversity and variation of *A.ginnala.* The study on phenotypic diversity of *A.ginnala* in different environments will provide useful information for understand the genetic variation pattern and protection of *A.ginnala.* The objective of this study is to answer the following questions: Are there phenotypic diversity of *A.ginnala* populations? Which environmental factor play a role in these phenotypic diversity?

# **MATERIALS AND METHODS**

### **Sample collection**

From September 2015 to October 2015, A total of 380 samples were collected from 19 populations of *A. ginnala*, covering most of its distribution range in China. About 20 individuals per population were collected. The distances between sampled trees varied from 50 to100 meters depending on the population size, to ensure that the sampled trees truly represented their populations. Each population was positioned by GPS and meteorological factors were provided by the local weather bureau. The detailed locations and environmental factors were listed in Table 1.

### **Measurement of parameters**

According to the method of Falkenhagen (1978), each trait was measured in three replicates and the mean value was used (liu

*et al*., 2016). Eight phenotype traits, Leaf length (LL), blade length (BL), blade width (BW), Petiole length (PL), the high of leaf opex to left side (Hos), the length of leaf opex to left side (Los), the high of leaf opex to  $\alpha$  (Hl $\alpha$ ) and the length of leaf opex to  $\alpha$  (Ll $\alpha$ ), were measured by ruler. Petiole width (PW), Petiole end width (PEW), leaf opex length (LOL), leaf opex width (LOW), caropodium length (CL), length of key fruit handle (KFHL), key fruit length (KFL), key fruit width (KFW), Bears the mark (BM), fruit length (FL), fruit width (FW), Fruit thickness (FT), seed length (SL), seed width (SW)

and seed thickness (ST) were measured by vernier caliper. The angle of key fruit (KFIA) and angle on the left (ɑ) were measured by the protractor. Length/width ratio of key fruit (KFLW), Length/width ratio of fruit (FLW), Length/width ratio of seed (SLW), leaf area (LA), leaf vein (LV), Length/width ratio of petiole (PLW), Length/width ratio of blade (BLW), Leaf length/Petiole length (KLP) and Length/width ratio of leaf opex (LLW) were calculated by EXCEL software.

## **Table 1. The locations and ecological factors of** *A.ginnala* **populations**



#### **Data analyze**

Statistical analysis was performed with SPSS software for Microsoft Windows (SPSS17.0). Analysis of variance (ANOVA) was performed for morphological variables to find significant differences between studied populations. Principal component analysis (PCA) was used to assess contribution rate of variation. And Pearson's correlation coefficient was undertaken to further examine the correlations between phenotypic traits and environment factors. Coefficients of variation (*CV*) and phenotypic differentiation coefficient ( $V_{ST}$ ) were determined as index of morphological variability. Coefficient of variation (*CV*) according to the formula *CV*=stdv/avg were calculated (the average quantity (avg) of target from the standard curve, the standard deviation of the average (stdv) (Zhou *et al*., 2010). Vst was calculated as  $Vst=(\delta t/s2)/(\delta t/s2+\delta s2)$ , where  $\delta t/s2$  is the variance component among regions, and δs2 is the variance component within regions (Ge *et al*., 1988). The phenotype diversity (Shannon-Wiener information index, *Hsw*) of each morphological trait and population was evaluated by BIO-Dap software (Liu *et al*., 2016). Cluster analysis was performed based on Euclidean distance using unweighted pair-group method of arithmetic averages (UPGMA) by cluster function in NTSYSps-2102a software.

length (LLW) exhibited the highest variation (31.612%). The mean *CV* of 34 traits was 23.53%. The average variation among populations was lowest in population HJG (18.076%) and highest in FZL population (36.054%) (Table 3). Shannon-Wiener index  $(H<sub>SW</sub>)$  of 34 traits was used for the estimation of phenotypic diversity.  $H_{SW}$  for 34 morphological traits was ranged from 4.18 to 6.26, and the mean was 5.22. The  $H<sub>SW</sub>$  of 19 populations ranged from 2.18 to 2.43, with a mean value of 2.31. The highest phenotypic diversity was found in WCLC, BDG and LJS population  $(H_{SW} = 2.43)$ , while the lowest phenotypic diversity was in LTG population  $(H_{SW} = 2.18)$ (Table 3). PCA analysis showed that the four principal components of the cumulative contribution rate were 87.300% (Table 4). The first principal component contribution rate was 39.825% with the main contributions from  $H<sub>La</sub>$ , HOS, BL, BW, LA, LL and PW. The second principal component contribution rate was 22.522% with the main contributions from KLP, LLW, PL, KFL, FT and ST. The third principal component contribution rate was 16.499% with the main contributions from BM, KFW, KFHL, KFL and CL. The fourth principal component contribution rate was 8.454% with the main contributions from FLW, KFLW, SLW, FL, ST and SL.

**Table 2. The ANOVE analysis of phenotypic traits among/within populations of** *A. ginnala*

traits	Among populations F value	Within populations F value	traits	Among populations F value	Within populations F value
LL	65.034**	13.993**	$L_{La}$	99.207**	11.828**
BL	95.147**	$16.057**$	LA	97.826**	15.772**
<b>BW</b>	$106.213**$	15.089**	<b>CL</b>	58.922**	1.502
<b>BLW</b>	43.498**	1.784	<b>KFHL</b>	92.446**	1.907
PI.	37.930**	$6.159**$	<b>KFL</b>	154.831**	1.708
<b>PW</b>	56.367**	$10.920**$	<b>KFW</b>	107.604**	1.157
<b>PLW</b>	$36.226**$	0.281	<b>KFLW</b>	69.372**	1.604
<b>FLW</b>	25.714**	13.837**	<b>KFIA</b>	29.134**	$2.255*$
<b>KLP</b>	$61.162**$	0.87	BM	$80.550**$	0.247
LOL	90.207**	$6.940**$	FL	207.473**	0.874
LOW	0.718	0.537	FW	4.822**	0.736
<b>BLW</b>	54.502**	$2.116*$	<b>FT</b>	95.057**	1.434
a	33.619**	$5.129**$	<b>PEW</b>	$16.801**$	$2.664**$
$\mathbf{v}$	$26.612**$	$16.402**$	<b>SL</b>	143.480**	0.837
$H_{OS}$	196.823**	11.886**	<b>SW</b>	5.766**	0.791
Los	22.757**	9.544**	<b>ST</b>	104.487**	1.373
$H_{La}$	331.523**	$11.334**$	<b>SLW</b>	$10.487**$	$3.001**$

Not: LL: Leaf length; BL: blade length; BW: blade width; BLW: Length/width ratio of blade; PL: Petiole length; PW: Petiole width; PLW: Length/width ratio of petiole; PEW: Petiole end width; KLP: Leaf length/Petiole length; LOL: leaf opex length; LOW: leaf opex width; LLW: Length/width ratio of leaf opex; ɑ: angle on the left; LV: leaf vein; Los: the length of leaf opex to left side; L<sub>la</sub>: the length of leaf opex to a; LA: leaf area; CL: caropodium length; KFHL: length of key fruit handle; KFL: key fruit length; KFW: key fruit width; KFIA: angle of key fruit; BM: Bears the mark; FL: fruit length; FW: fruit width; FT: Fruit thickness; SL: seed length; SW: seed width; ST: seed thickness; SLW: Length/width ratio of seed;  $H_{\alpha s}$ : the high of leaf opex to left side;  $H_{\alpha s}$ : the high of leaf opex to ɑ; KFLW: Length/width ratio of key fruit; FLW: Length/width ratio of fruit.

F: means the value of Significant difference.

\*mean significant difference at 0.05 level; \*\* mean significant difference at 0.01 level.

## **RESULTS**

# **Phenotypic differentiation**

## **Phenotypic diversity**

The *F* values of *A. ginnala* phenotypic traits among populations were significantly different (Table 2). Only 16 phenotypic traits (LL, BL, BW, PL, PW, LOL, LOW, ɑ, LV, HOS,  $H_{Ia}$ ,  $L_{Ia}$ , KFIA, PEW and SLW) within the populations were significantly different. The distinct correlation in each phenotypic trait of *A. ginnala* from different populations was confirmed by analyzing coefficient of variation *(CV)*. The average *CV* of the seed length (SL) among the 19 populations exhibited the lowest variation (15.677%), while the leaf opex The phenotypic differentiation coefficients (*Vst*) value of 34 phenotypic traits ranged from 23.134% to 85.287% (Table 5). The *Vst* value of Length/width ratio of seed (SLW) exhibited the lowest value (23.134%), while Length/width ratio of leaf opex (LLW) exhibited the highest value (85.287%). The phenotypic differentiation coefficients (*Vst*) among populations was 56.996%, and that within populations was 43.004%. This result revealed that phenotypic variation among populations was higher than within populations. Nineteen *A. ginnala* populations were mainly divided into two groups (Fig. 1). Ten populations from north of China (MLG, BJ, HHG, BDG, QLY, XTS, JMLC, YDS, HJG and PQG) and four populations

Mean Hsw of phenotypic traits 5.22

Traies	<b>CV</b>	Shannon- Wiener(Hsw)	traies	<b>CV</b>	Shannon- Wiener(Hsw)	Populations	<b>CV</b>	Shannon- Wiener(Hsw)
LL	22.09	6.17	$L_{La}$	27.388	5.81	FZL	36.054	2.34
BL	23.084	6.26	LA	28.346	5.87	<b>BDG</b>	21.719	2.43
BW	21.058	6.23	<b>CL</b>	21.76	4.99	<b>BYS</b>	24.341	2.33
<b>BLW</b>	24.953	5.29	<b>KFHL</b>	24.257	4.98	<b>BJ</b>	18.805	2.23
PL	25.483	5.26	<b>KFL</b>	25.915	4.99	<b>HJG</b>	18.076	2.33
PW	23.8	5.26	<b>KFW</b>	20.297	4.99	<b>HHG</b>	18.231	2.26
<b>PLW</b>	27.657	5.23	<b>KFLW</b>	19.853	4.99	<b>JMLC</b>	19.645	2.25
<b>PEW</b>	27.019	6.26	<b>KFIA</b>	20.775	5	LJL	22.803	2.2
<b>KLP</b>	28.156	5.25	BM	21.979	5	LJS	23.844	2.43
LOL	29.938	6.25	FL	22.046	4.87	<b>LTG</b>	20.703	2.18
LOW	27.392	4.91	<b>FW</b>	23.122	4.86	<b>MLG</b>	21.057	2.35
<b>LLW</b>	31.612	5.22	<b>FT</b>	20.84	5.21	PQG	18.984	2.33
α	22.755	5.27	<b>PEW</b>	19.031	4.98	QLY	20.77	2.33
LV	24.661	5.27	SL	15.677	4.68	TBD	26.787	2.33
$H_{OS}$	25.688	5.14	<b>SW</b>	19.705	4.68	<b>TTZ</b>	33.768	2.3
$\rm L_{0S}$	24.251	4.95	<b>ST</b>	16.963	4.18	<b>TBS</b>	28.327	2.3
$H_{La}$	24.163	4.86	<b>SLW</b>	18.454	4.21	WCLC	34.54	2.43
Mean CV of phenotypic traits		23.53				XTS	19.792	2.35
						<b>YDS</b>	18.907	2.28
Mean Hsw of phenotypic traits	5.22					Mean	23.53	2.31

**Table 3. Shannon-Wiener indices and variation coefficient based on phenotypic traits of** *A. ginnala* **populations**

Not: LL: Leaf length; BL: blade length; BW: blade width; BLW: Length/width ratio of blade; PL: Petiole length; PW: Petiole width; PLW: Length/width ratio of petiole; PEW: Petiole end width; KLP: Leaf length/Petiole length; LOL: leaf opex length; LOW: leaf opex width; LLW: Length/width ratio of leaf opex;  $a$ : angle on the left; LV: leaf vein; Los: the length of leaf opex to left side;  $L<sub>la</sub>$ : the length of leaf opex to ɑ; LA: leaf area; CL: caropodium length; KFHL: length of key fruit handle; KFL: key fruit length; KFW: key fruit width; KFIA: angle of key fruit; BM: Bears the mark; FL: fruit length; FW: fruit width; FT: Fruit thickness; SL: seed length; SW: seed width; ST: seed thickness; SLW: Length/width ratio of seed; H<sub>os:</sub> the high of leaf opex to left side; H<sub>la:</sub> the high of leaf opex to a; KFLW: Length/width ratio of key fruit; FLW: Length/width ratio of fruit.

BDG: Ba daogou Mountain; HJG: Hao jiagou Mountain; HHG: Hou huigou Mountain; JMLC: Jie miaolinchang; PQG: Pang quangou Mountain; QLY: Qi liyu Mountain; XTS: Xing tangsi Mountain; YDS: Yunding Mountain; BJ: Beijing; MLG: Mai ligeng Mountain; BYS: Bai yunshan Mountain; LJS: Lao junshan Mountain; LJL: Lao jieling Mountain; LTG: Long tangou Mountain; TTZ: Tian tangzai Mountain; FZL: Fu ziling Mountain.; WCLC: Wochuanglingchang; TBD: Tai baiding Mountain; TBS: Tong baishan Mountain.





Not: LL: Leaf length; BL: blade length; BW:blade width; BLW: Length/width ratio of blade; PL: Petiole length; PW: Petiole width; PLW: Length/width ratio of petiole; PEW: Petiole end width; KLP: Leaf length/Petiole length; LOL: leaf opex length; LOW: leaf opex width; LLW: Length/width ratio of leaf opex;  $a$ : angle on the left; LV: leaf vein; Los: the length of leaf opex to left side;  $L<sub>lo</sub>$ : the length of leaf opex to ɑ; LA: leaf area; CL: caropodium length; KFHL: length of key fruit handle; KFL: key fruit length; KFW: key fruit width; KFIA: angle of key fruit; BM: Bears the mark; FL: fruit length; FW: fruit width; FT: Fruit thickness; SL: seed length; SW: seed width; ST: seed thickness; SLW: Length/width ratio of seed; H<sub>os</sub>: the high of leaf opex to left side; H<sub>la</sub>: the high of leaf opex to a; KFLW: Length/width ratio of key fruit; FLW: Length/width ratio of fruit.



Not: LL: Leaf length; BL: blade length; BW:blade width; BLW: Length/width ratio of blade; PL: Petiole length; PW: Petiole width; PLW: Length/width ratio of petiole; PEW: Petiole end width; KLP: Leaf length/Petiole length; LOL: leaf opex length; LOW: leaf opex width; LLW: Length/width ratio of leaf opex; q: angle on the left; LV: leaf vein; Los: the length of leaf opex to left side; L<sub>la</sub>: the length of leaf opex to q; LA: leaf area; CL: car length; KFHL: length of key fruit handle; KFL: key fruit length; KFW: key fruit width; KFIA: angle of key fruit; BM: Bears the mark; FL: fruit length; FW: fruit width; FT: Fruit thickness; SL: seed length; SW: seed width; seed thickness; SLW: Length/width ratio of seed; H<sub>os</sub>: the high of leaf opex to left side; H<sub>ig</sub>: the high of leaf opex to a; KFLW: Length/width ratio of key fruit; FLW: Length/width ratio of fruit.

### **Table 6a. Correlation coefficient between phenotypic characters and meteorogical factors**







Note: BDG: Ba daogou Mountain; HJG: Hao jiagou Mountain; HHG: Hou huigou Mountain; JMLC: Jie miaolinchang; PQG: Pang quangou Mountain; QLY: Qi liyu Mountain; XTS: Xing tangsi Mountain; YDS: Yunding Mountain; BJ: Beijing; MLG: Mai ligeng Mountain; BYS: Bai yunshan Mountain; LJS: Lao junshan Mountain; LJL: Lao jieling Mountain; LTG: Long tangou Mountain; TTZ: Tian tangzai Mountain; FZL: Fu ziling Mountain.; WCLC: Wochuanglingchang; TBD: Tai baiding Mountain; TBS: Tong baishan Mountain.

Fig.1. UPGMA-derived dendrogram based on Euclidean distances showing of the 34 phenotype traits of *A. ginnala* 

(LJL, LTG, BYS.LJS) from south of China Fourteen populations were gathered into group I, other five populations (WCLC, FZL, TTZ, TBD and TBS) from south of China were gathered into group II.

#### **Correlation analysis**

The correlation analysis showed in Table 6. FSL, KFW and LA had a positive correlation with the average temperature of January and absolute low temperature, respectively. Nine phenotypic traits (LL, PW, LOL, LOW, LALW, HOS, H<sub>Ia</sub>, KFIA and FW) had a negative correlation with absolute high temperature and annual average temperature, respectively. Annual Precipitation had positive correlation with BLW, CL, and LA, had a negative correlation with eleven phenotypic traits (LL, PL, PW, LOL, LOW, LLW, HOS,  $H<sub>10</sub>$ , KFIA, BM and FW). Nine phenotypic traits (LL, BLW, PW, LOL, LOW, LLW, LV, HOS and  $H<sub>La</sub>$ ) had a positive correlation with annual sunlight hours, while CL and BLW had a negative correlation with annual sunlight hours. Eleven phenotypic traits (BL, BW, PW, PL, LOL, LLW, HOS,  $H<sub>La</sub>$ , BM, FT and ST) had a negative correlation with latitude.

## **DISCUSSION**

### **Phenotypic diversity**

*A. ginnala* existed high phenotypic diversity and variation in populations (Table 2). Similar results were obtained in previous studies (Yang *et al*., 2011). The same genus tree *Acer mono* also occuured a high level of phenotypic variation (Zhang *et al*., 2015). The high phenotypic diversity of *A. ginnala* was related to the broad geographical distribution, selection of cultivator and long evolutionary history of species. First, *A. ginnala* mainly inhabit in Northeast, North, Northwest of China, the environmental conditions in these inhabits were different (Huang *et al*., 2009 such an annual precipitation and annual average temperature in different regions). Futhermore, due to the ornamental and economic value, *A. ginnala* is widely planted in many place, farmers give priority to the amelioration of more attractive characteristics through introducing and maintaining phenotypic with different (Li *et al*., 2007; Wang *et al*., 2013). In addition, *A. ginnala* has been reportd to possess millions years of evolutionary history (Yan *et al*., 2010). Thus, it can be inferred that such a long history, broad distribution range and selection of cultivator may have rendered it possible to accumulate a large amount of phenotypic variability. Analysis of population-level diversity revealed that the phenotypic diversity of WCLC population was higher than those of other populations. Population size of WCLC was the largest and individuals were found to be thriving, which may harbor more phenotypic diversity within this population. LTG population had the lowest diversity. Human activities have been an important cause of population size reduction in LTG in the past years through overexploitation and habitat loss. Reduction in population size may lead to increase inbreeding depression and lower fitness (Ellstrand and Elam, 1993; Frankham *et al*., 1997). This in turn would lower the diversity of LTG population, and also lower its ability to compete with introduced species, to cope with disturbed habitats, and to adapt to natural changes in the environment (Frankham *et al*., 1997).

**Phenotypic differentiation:** The phenotypic differentiation of *A. ginnala* main came from among populations, which was

affected by biological characteristics or geographically isolation of populations. *A. ginnala* has hermaphodite flower and low rate of seed maturity, which reduced pollen flow between populations (Liang *et al*., 2007). Furthermore, the geographical location in the distribution range of *A. ginnala* is complex, with neighboring populations frequently separated by geographic barriers such as high mountains and broad rivers. Under these conditions, pollens or seeds can seldom expand successfully from one population to another. Cluster analysis showed that 19 populations gathered into two distinct groups (Fig.1). Plant species may respond to suitable environment conditions through phenotypic plasticity (Fiorani and Schurr, 2013). In our study, the nine south populations had the similar temperature and precipitation, however, the content of elements in soil is different. Five populations (TBS, TBD, WCLC, TTZ and FZL) located in Dabie Mountain (E: 113°16´~116°45´, N: 30°57´~32°43´), the C, N and P content of soil in Dabie Mountain were  $249$ mg/kg ~ 780.10mg/kg, 59.27mg/kg ~ 190.10mg/kg, 30.95mg/kg ~ 107.10 mg/kg, respectively (Wang *et al*., 2014; Zhang *et al*., 2010). The other four populations (LJL, LTG, BYS, LJS) located in Funiu Mountain (E: 110°30´~113°05´, N:32°45´~34°00´), N content in Funiu Mountain were 26 mg/kg ~220mg/kg (Zheng *et al*., 2011), which possibly lead to that four southern populations of *A.ginnala* were not clustered into a class with the other five southern populations.

### **Conclusion**

In summary, high genetic diversity and high genetic differentiation were detected among the *A. ginnala* populations in China. A large proportion of the genetic variation (56.996%) resides among the populations. Significant correlation was found between phenotypic traits and environmental factors. The strategy of conservation for *A. ginnala* should in-situ methods. In-situ method pays more attention to restore the suitable habitats and the effective population size. Based on the results, in-situ conservation strategies should be adopted to protect and restore all existing populations of *A. ginnala*.

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#### **Conflict of interest**

The authors declare they have no conflict of interest.

# **REFERENCES**

- Aitken, S.N., Yeaman, S., Holliday, J.A., Wang, T., Curtis-Mc Lane, S. 2008. Adaptation, migration or extirpation:climate change outcomes for tree populations. *Evol. Appl*., 1: 95– 111.
- Bock, K., Courl, F.N., Jensen, S.R. 1980. The structure of *Acertannin*. *Phytochemistry*, 19: 2033-2348.
- Ellers, J., Rog, S., Braam, C., and Berg, M.P. 2011. Genotypic richness and phenotypic dissimilarity enhance population performance. *Ecology*. 92: 1605–1615.
- Ellstre, N.C., Elam, D.R., 1993. Population genetic consequences of small population size: implication for plant conservation. *Annu. Rev. Ecol. J*., 24: 238-244.
- Falkenhagen, E.R.1978. Multivariate classification in provenance reach. *Siilvae Genetica*, 27: 14-23.
- Fiorani, F., Schurr, U. 2013. Future scenarios for plant phenotyping. *Annu. Rev. Plant Biol*., 64: 267--291.
- Frankham, R. 1997. Do island populations have less genetic variation than mainland populations. *Heredity*, 78: 311-- 327.
- Ge, S., Wang, M.X., Chen, Y.W. 1988. An analysis of population genetic structure of *Masson pine* by isoenzyme technique. Sci. Silvae. Sin. 24, 399-409 (in Chinese with English abstract).
- Hall, B.A. 1951. The floral anatomy of *the genus Acer*. Am.j.Bot. 38: 793-799.
- Huang, D., Wang, J., Li, D.L. 2009. Biological characteristics and planting technology of *Acer ginnala Maxim*. *Modern Agricultural Sciences*, 16: 112-113.
- Iverson, L.R., and Prasad, A.M. 2001. Potential changes in tree species richness and forest community types following climate change. Ecosystems 4:186–199. Li, L.P., Ma X.Q., Song, L., Liu X.H. 2007. Research Status and Expectation of *Acer ginnala* in Northeast China. *Journal of northeast forestry university,* 35: 79-81.
- Li, S.C., Yang, S.H., Liu, H.X., Guo, N., Fu, L., Ge, H. 2014. Phenotypic Diversity of *Rosa beggeriana* Populations in Tianshan Mountains of Xinjiang. Acta Horticulturae Sinica. 2014, 41(8):1723–1730.
- Liang, M., Zhang, Y., Yang, Y.H., Xu, H.J. 2007. Study on seed anatomy biology of *Acer* plants. *Forestry Science & Technology*, 32: 9-12.
- Liu, L., Chen, W., Zheng, X., Li, J., Yan, D.T., Liu, L., Liu, X., Wang, Y. L. 2016. Genetic diversity of *Ulmus lamellosa* by morphological traitsand sequence-related amplified polymorphism (SRAP) marker. *S. Biochem. Syst.Ecol*., 66: 272-280.
- Lucas-Borja, M.E., Ahrazem, O., Candel-Pérez, D., Moya, D., Fonseca, T., Hernández Tecles, E., las Heras, J.D., Gómez-Gómez, L. 2016. Evaluation of fire recurrence effect on genetic diversity in *maritime pine* (Pinus pinaster Ait.) stands using Inter-Simple Sequence Repeat profiles. Science of the Total Environment.
- Ming, J., Gu, W.C. 2006. Phenotypic variation of *Syringa oblate* line. *Forest Research*, 19: 199-204.
- Shen, L., Xu, R., Liu, S., Jun, C., Xu, C.Q.,, Xie, C,X.,Liu, T,N. 2015. Phenotypic variation of seed traits of *Haloxylon ammodendron* and its affecting factors. *Biochem. Syst. Ecol*., 60: 81-87.
- Stöcklin, J., Kuss, P., Pluess, A.R. 2009. Genetic diversity, phenotypic variation andlocal adaptation in the alpinelandscape: Case studies with alpine plant species. *Botanica Helvetica*, 119: 125–133.
- Wang, D., Pang, C.H. 2010. Phenotypic Diversity of *Acer ginnala* (Aceraceae) Populations at Different Altitude. *Acta Botanica Yunnanica*, 32: 117-125.
- Wang, Q.D. 2013. Ginnala cultivation management. Special economic animals and plants 37: 21-26.
- Wang, W.B., Ping, G.E. 2014. Biological characteristics of soil in different vegetation types at the low altitude of Mt. Dabie. *Guangdong Agric.Sci*., 14: 52-56.
- Yan, N., Wang, D. 2010. Genetic Diversity of *Acer ginnala* Populations at Different Elevation in Qiliyu Based on ISSR Markers. *Sci.Silv. Sin*., 46: 51-56.
- Yang, W.Z., Jin. H., Yang, M.Q., Zhao, Z.L., Zhang, Z.H.,Wang,Y.Z., Zhang, J.Y. 2011. Phenotypic Diversity and Environment Relations in Gentiana rigescens of Yunnan. *Acta Bot.Boreal.-Occident.Sin*., 31: 1326- 1334.
- Zhang, R.H., Liu, X. 2010. Assessment and spatial distribution of soil erosion sensitivity in Tongbai -Dabie Mountainous area. *Science of Soil and Water Conservation*, 8: 58-64.
- Zhang, Z.D., Gao, J., Kong, D., Wang, A., Tang, S.Z., Li, Y.Y., Pang X.M. 2015. Assessing genetic diversity in *Ziziphus jujuba* 'Jinsixiaozao'using morphological and microsatellite (SSR) markers. *Biochem.Syst.Ecol*., 61: 196- 202.
- Zheng, J.G. Hou, G. and Zhang, Y.H. 2011. Study on the Distribution Characteristics of Vegetation and Soil Nutrientsin Funiu Mountain. *J. Anhui Agri. Sci*., 39: 1432  $-1433.$
- Zhou, S.Y., Xie, Z.L., Xiao, O., Yang, X.R., Heng, B.C., Sato, Y. 2010. Inhibition of mouse alkali burn induced-corneal neovascularization by recombinant adenovirus encoding human vasohibin-1. *Mol. Vis*., 16: 1389.

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