

Genotype-Environment Interaction and Stability of Fiber Properties and Growth Traits in Triploid Hybrid Clones of *Populus tomentosa*

Jian Wu

Beijing Forestry University

Qing Zhou

Beijing Forestry University

Yaru Sang

Beijing Forestry University

Xiangyang Kang

Beijing Forestry University

Pingdong Zhang (✉ zhangpd@bjfu.edu.cn)

Beijing Forestry University <https://orcid.org/0000-0001-6006-360X>

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1 **Genotype-environment interaction and stability of fiber properties and growth traits in triploid hybrid clones**
2 **of *Populus tomentosa***

3 Jian Wu^{1,2,3,4}, Qing Zhou^{1,2,3,4}, Yaru Sang^{1,2,3,4}, Xiangyang Kang^{1,2,3,4} and Pingdong Zhang^{1,2,3,4*}

4 ¹ Beijing Advanced Innovation Center for Tree Breeding by Molecular Design, Beijing Forestry University, Beijing
5 100083, China

6 ² National Engineering Laboratory for Tree Breeding, Beijing Forestry University, Beijing 100083, China

7 ³ Key Laboratory of Genetics and Breeding in Forest Trees and Ornamental Plants, Ministry of Education, Beijing
8 Forestry University, Beijing 100083, China

9 ⁴ College of Biological Sciences and Technology, Beijing Forestry University, Beijing 100083, China

10 * Correspondence: zhangpd@bjfu.edu.cn

11 **Abstract**

12 **Background:** Clones provide a sensitive method for evaluating genotypic stability and detecting genotype-
13 environment (G × E) interactions because of non-additive genetic effects among clones and no genetic effect among
14 ramets of an ortet. The experiments aimed at confirming and expanding the earlier findings, estimating stability
15 parameters, and providing accurate estimates of clonal repeatabilities and genetic gains for an triploid breeding
16 programme of *Populus tomentosa* Carr.

17 **Results:** Six 5-year-old clonal trials established in Northern China were used to determine the clonal variation, clone
18 × site interactions and the stability parameters of fiber properties of wood and growth traits. Three hundred sixty
19 trees from ten hybrid clones were collected in the six sites. The clonal and site effects had a highly significant effect
20 ($P < 0.001$) for all studied traits. The clone × site interactions had a highly significant effect ($P < 0.001$) on fiber
21 length (FL), coarseness (C), and tree growth (tree height [H], diameter at breast height [DBH] and stem volume
22 [SV]), and a moderate effect ($P < 0.05$) on fiber width (FW) and fiber length/width (FL/W). For FL and SV, most of
23 the triploid hybrid clones had higher reaction norms to the improvement in growth conditions and higher phenotypic
24 plasticity. The estimated clonal repeatability of FW (0.93) was slightly higher than for FL (0.89), FL/W (0.83), C
25 (0.91), DBH (0.76), H (0.85), and SV (0.80). Three clonal testing sites were sufficient to estimate quantitative
26 parameters of fiber properties. However, more than three clonal testing sites will help improve the accuracy of
27 quantitative parameters of growth traits.

28 **Conclusions:** Our results unraveled that accurate estimation of quantitative parameters for growth traits in triploid
29 hybrid clones of *Populus tomentosa* required more clonal testing sites than fiber properties.

30 **Keywords:** genotype-environment interactions; stability parameter; clonal repeatability; fiber property; growth trait;
31 *Populus tomentosa*

32 **Background**

33 Chinese white poplar, *Populus tomentosa* Carr. (section *Populus*, family Salicaceae, genus *Populus*), is a widely
34 distributed tree species in northern China and generally grows in mixed-species forest with *Robinia pseudoacacia* L.

35 Since the first triploid hybrid of *P. tomentosa* was artificially synthesized in 1998, the triploid hybrid clones has
36 exhibited superior growth in China [1]. The latest research progress in wood fiber have led to the use of short fibers
37 mixed with coniferous long fibers to produce high-quality paper, or even without the long fibers [2]. The Chinese
38 forestry industry has shown a new focus on the using hybrid poplar for manufacturing evenly short fibers. Thus, An
39 obvious increase in Chinese white poplar use is expected, which in turn arouse interest in breeding selected triploid
40 hybrid clones [3-5].

41 The triploid hybrid clones of *P. tomentosa* have been shown to display a high degree of variability in growth, fiber
42 traits, wood basic density, wood chemical properties [1,3-6]. This variability indicates that intriguing gains may be
43 obtained through selection. The potential advantages of utilizing clonal methods in poplar hybrid clones were
44 reviewed by several authors [7-8]. Genotype \times environment ($G \times E$) interaction normally refers to the performance
45 differences of genotypes between environments [9]. Testing and selection in tree improvement programmes are
46 complicated by this interaction, and leading to reduced total genetic gains. In general, the literature on $G \times E$ is
47 plentiful for forest trees [10-11]. However, the number of studied clones is relatively limited [12]. It is expected that
48 clones are more interactive in different environments than either seed or families origins, because there is no genetic
49 effects among ramets of an ortet and non-additive genetic effects among clones are substantial. Therefore, Clones
50 can provide a sensitive method for evaluating genotypic stability and detecting $G \times E$ interactions [13].

51 To obtain a better understand the genetic control of growth traits, fiber properties, wood basic density and wood
52 chemical properties, basic genetics such as $G \times E$ interactions, inter-trait and inter-site correlations, clonal genetic
53 variation and repeatabilities for triploid hybrid clones of *P. tomentosa* were recently estimated [4-5,14-15]. Both site
54 effects and clonal effects were found to be significant for all tested traits and $G \times E$ interactions were also significant
55 for all studied traits except for fiber length and holocellulose [5,14]. This basic information is crucial to estimate
56 expected genetic gains and develop suitable strategies for clonal forestry. However, most of the studies were
57 conducted on three or four sites, whereas the present study was performed on six sites. For the purpose of tree
58 improvement, accurate estimate of quantitative parameters requires that different genotypes are tested at more
59 locations.

60 The objectives of the present study were: (1) to confirm and expand the earlier findings; (2) to estimate stability
61 parameters of these triploid clones; and (3) to provide accurate estimated values of genetic gains and clonal
62 repeatabilities for improvement program of Chinese white poplar.

63 **Results**

64 **Basic statistics and variation within and between sites**

65 The mean values, standard error (SE) of the mean, ranges of maximum and minimum values, and coefficients of
66 phenotypic variation of all traits in the six clonal trials are presented in Table 3. A fairly obvious difference in growth
67 was found between the six locations, with trees exhibiting the largest growth was observed at the Taiyuan. For fiber
68 properties, the longest fiber length (FL) and the greatest fiber length/width ratio (FL/W) were found at the Gaotang.
69 Trees from the Pinggu site had the shortest FL and the lowest FL/W. The difference between the longest and shortest
70 means of FL was 7.9% (Table 3). However, the thinnest fibers were observed at Xiangfen, and the thickest, at
71 Pinggu. The combined analysis of all six trials displayed that all studied traits had significant site effects (Table 4).

72 FL, fiber width (FW), and FL/W showed a small phenotypic variation (CV = 3.2 - 5.5%) and the values were much
73 lower than those of coarseness (C), diameter at breast height (DBH; at 1.3 m above ground level), tree height (H),
74 and stem volume (SV).

75 **Clonal variation and repeatability**

76 The results of the analysis of variance for the combined six sites are presented in Table 4. Significant clonal effects
77 for all tested traits were been seen (Table 4). For all studied traits, the variance caused by error (That is, the
78 differences between ramets within a clone within a site) accounted for most of the variation, accounting for 48.4 to
79 75.4 % of the overall variation. However, most of the variance in FW (35.7 %) was caused by the clone. Hence, the
80 highest estimated repeatability of clone mean (0.93) and the estimated individual-tree clonal repeatability (0.36)
81 were observed for the FW.

82 The estimated clonal repeatability and estimated individual-tree clonal repeatability of all the studied traits at the
83 each site are shown in Table 5. No significant differences were found between the clones for H, DBH, and SV at the
84 Yanzhou sites, FL/W at the Gaotong sites, as well as FW and FL/W at the Pinggu sites. Therefore, we did not
85 estimate the clonal repeatability for the six traits. The estimated clonal repeatability varied from 0.73 to 0.90 for FL,
86 from 0.68 to 0.95 for FW, from 0.54 to 0.90 for FL/W, and from 0.78 to 0.93 for C. The estimated clonal
87 repeatability of the growth traits ranged from 0.58 to 0.90 (Table 5). However, these differences in estimated clonal
88 repeatability were often non-significant.

89 **Clone × site interaction, stability, and reaction norms of triploid hybrid clones**

90 In this study, all fiber properties and growth traits were observed to have significant interaction of clone × site (Table
91 4). The level of significance for FW (0.031) and FL/W (0.014) was moderate and a highly significant effect ($P <$
92 0.001) was observed for FL, C and tree growth. Higher estimated ratio (57.9%) in H of clone × site interaction
93 variance component to the total variance component of clone×site interaction plus clone were observed than the
94 other traits.

95 The intersite (B-type) genotypic correlations are shown in Table 6. Some intersite genotypic correlations between
96 the same traits were not estimated because no significant differences were observed between the clones for H, DBH,
97 and SV at the Yanzhou site, FL/W at the Gaotong site, and FW and FL/W at the Pinggu site. Most of the intersite
98 genotypic correlations between the same traits at different sites were either moderate or strong, except for H at
99 Zhengzhou-Taiyuan and FL at Pinggu-Taiyuan (Table 6). For FL, FL/W, and the growth traits, the correlations were
100 lower when the Taiyuan site was included.

101 The stability parameters for FL and SV of the individual triploid hybrid clones across the six clonal trials,
102 including the Finlay-Wilkinson parameters and the Shukla stability variances that characterize the reaction norms of
103 the clones are shown in Table 7. The stability parameters of the all studied clones were estimated only for FL and SV.
104 For FL, the Shukla's stability of clones B330 and B331 was slightly higher than those of the other clones due to their
105 lower stability variance (1.01×10^{-4} and 2.28×10^{-4} , respectively). However, for SV, lower stability variances were
106 observed in clones B302, B303, and B306. Therefore, clones B302, B303, and B306 had higher stability for SV than
107 the other clones. For FL, in the Finlay-Wilkinson's method, the regression coefficient (b_i) of clones B302, B303,

108 B304, and B306 varied from 1.214 to 1.429, indicating that the four clones had higher reaction norms. However, the
109 clone, B304, B330, and B331 had higher reaction norms for SV because their regression coefficients (b_i) were
110 1.315, 1.411, and 1.477, respectively.

111 **Inter-trait genetic correlations, correlated genetic response, and genetic gain**

112 The genotypic and phenotypic correlations between all the studied traits at individual sites are presented in Table 8.
113 At all sites, a positive estimated correlation was found between FL and growth traits. A significant positive estimated
114 genetic correlation between FW and C was also observed at each site. However, a negative estimated genotypic
115 correlation between growth traits (except for H) and the C existed. The results suggested that selection for growth
116 traits (except for H) might lead to a slight decrease in C. SV, H, and DBH had some strong positive autocorrelations
117 since SV was derived from H and DBH.

118 The predicted genetic gains of the hybrid clones at the six sites for different selection are presented in Table 9.
119 The results are based on the assumption of the estimated repeatabilities and correlations from direct clonal selection
120 and the related genetic responses in all the studied traits. The predicted genetic gains were identical in C for Pinggu
121 and Zhengzhou (6.1%), while the Taiyuan site had the highest gain (8.4%). However, the gains in C were about
122 twice the gains observed for FL. The selection for C led to the equal gains in FW as direct selection for FW. The
123 selection for DBH led to the gain in SV equal to that of the direct selection for SV but resulted in a slight decrease in
124 C (Table 9). Among growth traits, selection for C resulted in the lowest gains in DBH and SV. However, it had a
125 greater negative impact on SV.

126 **Discussion**

127 Site effects represent the response of trees to the combined influences of edaphic and regional climatic conditions
128 [16]. Even though the current trials were not designed to separate these different effects, some conclusions can still
129 be drawn [16]. The poor field performance in growth at Yanzhou was may be owing to poor drainage (due to soil
130 compression) and wet weather at early stages of the experiment. Significant site effects were observed in the
131 combined analysis of all traits (Table 4). Moreover, a positive correlation between SV and latitude and negative
132 correlations between SV and longitude, as well as rainfall and mean annual temperature, were observed (Fig. 1.),
133 suggesting that edaphic and regional climatic conditions had significant effects on the growth traits. Our findings
134 agreed with the results of former studies of triploid hybrid clones of *P. tomentosa* [4-5], poplar hybrids [16-17], and
135 *P. tremuloides* Michx. [18]. At all sites, the fiber properties of the triploid hybrid clones had less phenotypic
136 plasticity than the growth traits, as evidenced by the lower CV values, indicating that site effects were relatively
137 lower for fiber properties than growth traits.

138 Former studies recorded that the effect of clone \times site interactions on the growth traits at three clonal trials was
139 greater than the clonal effect [4-5]. Randall and Cooper [19] reported that the complexity of testing increased due to
140 such a high interaction. If the correlations between test and planting environments were alike and the objectives of
141 an improvement program were restricted enough to allow selection for certain types of locations, then these
142 interactions may be utilized. The effect of clonal effects on the growth traits in this study was, on the contrary,
143 greater than the clone \times site interactions when the number of testing sites was six. This suggested that an increase in

144 the number of clonal testing sites help improve the accuracy of clonal effects, thus reducing the complexity of clonal
145 testing.

146 It seems that most selected triploid hybrid clones of *P. tomentosa* will probably be exploited on a relatively wide
147 range of sites. In this situation, the effectiveness of selection will be greatly reduced because of large clone \times site
148 interactions unless performance is measured on a relatively large number of sites. Additionally, this interaction will
149 probably be decreased when the region split into planting zones according to the type of terrain. An increase in gain
150 from clonal selection within each site type will be expected. This interaction may be, also, decreased by using stable
151 clones. The gain from a decrease in clone \times site interaction must be compared with the loss from eliminating clones
152 characterized with high growth potential.

153 Zhang et al. [5] reported that the clone \times site interactions were significant for growth traits and fiber properties in
154 triploid hybrid clones of *P. tomentosa* except for FL. In this study, the clone \times site interactions had a highly
155 significant effect on all the studied traits, indicating that triploid hybrid clones of *P. tomentosa* exhibited various
156 relative performances on the six sites. The ratio of the variance component of clone \times site interaction and clone is
157 1.4 for H, 0.5 for DBH and 0.9 for SV. In an example recorded by Lindgren [20], the ratio ranged from 0 to 3, and in
158 most cases it was lower than 1.

159 In this study, no significant positive type B genotypic correlations between genotypic values at Xiangfen-Taiyuan
160 sites for all studied traits were observed (Table 6), which suggested that a true $G \times E$ interaction existed. The
161 differences between these sites may be contributed to the clone \times site interaction. However, the type B genotypic
162 correlations for FL and C between the sites were mostly positive (Table 6), which indicated that the fiber properties
163 were more stable than the growth traits. This result corresponded to the findings of Yu et al. [21] that the relative
164 performance of genotypes in different environments with regard to fiber traits was quite stable.

165 In forest tree breeding, it is crucial to predict the yield of a genotype in different environments. The relative
166 performances in stability analysis are determined by regression coefficient. This information can contribute to
167 develop suitable genotypes for specific environments in forest tree breeding. However, this information is irrelevant
168 if all the tested environments are in one planting region, and each represents the same scale of zone to be planted.
169 Selection for the total mean is all, nonetheless, that is necessary to ensure the highest total gains.

170 For forest tree breeding, what is more important is to predict yield of a genotype in different environments. This
171 concept of stability may be determined by the stability variances [22] and the regression coefficients [23]. In this
172 study, the results indicated that each of the studied clones had various magnitudes of phenotypic plasticity and
173 specific patterns of FL and SV at the six sites. One hypothesis considers that genetic variation and plasticity
174 represent alternative strategies for dealing with environmental heterogeneity [24]. However, other hypotheses
175 believe that a positively correlated between phenotypic plasticity and genetic variation [25]. Higher sensitivity
176 regarding changes in the FL was found for clone B305 and B306 because they had high Shukla's stability variances.
177 However, the regression coefficients (b_i) of clones B302, B303, B304, and B306 for FL ranged from 1.214 to 1.429,
178 suggesting that the four clones had higher reaction norms than the other clones. The stability values for the FL of the
179 triploid hybrid clones were different for the different methods. This could be partially explained by the different
180 principles that are used to estimate the stability parameters. Similar results were found for temporal stability of vigor

181 in rubber by Gouvêa et al. [26] and for wheat yield by Mohammadi and Amri [27]. High values of the Finlay-
182 Wilkinson stability parameter, i.e., the regression coefficient of the clone values on location value, determine the
183 clones that benefit from a productive location, while high intercept coefficients determine the clones that can grow
184 well under limited resource conditions. As shown by the higher regression coefficient means of clone B304, B330,
185 and B331 for SV, these clones have higher norms of reaction to the improvement in growth environments and higher
186 phenotypic plasticity.

187 Generally, an increase in tree growth was related to a slightly higher FL. A number of previous studies have
188 shown that FL increased as the increasing tree growth [28-30]. For example, Xie et al. [31] reported that a
189 significant positive estimated genetic correlation between FL and growth traits was observed in *Populus*
190 *euramericana* (Dode) Guinier. In the present study, the genetic correlations between growth traits and FL were also
191 positive at the six sites, indicating that triploid breeding of *Populus* not only improved the FL, but also increased the
192 tree growth.

193 Clonal repeatability of the fiber properties and growth traits across all six sites were medium to high (Table 4).
194 For fiber properties, the estimated clonal repeatabilities ranged from 0.83 to 0.93, which was consistent with those
195 that has been recorded in the literature [4-5,32]. This suggested that three clonal testing sites were enough to
196 estimate quantitative parameters for fiber properties. However, clonal repeatabilities were estimated to be 0.76 for H,
197 0.85 for DBH and 0.80 for SV, which were slightly higher than those estimated at three clonal trails [5]. This implied
198 that increasing the number of testing sites help improve the accuracy of clonal repeatabilities of growth traits.

199 The analyses of the present study were based on nine genotypes and a relative small number of testing sites
200 measured over only five years. Therefore, The results from this study should be further verified by subsequent larger
201 and longer trials. The implication of the G × E interaction for estimating the gain of genetically improved triploid
202 hybrid clones of *P. tomentosa* should be further studied.

203 **Conclusions**

204 The experiments and analyses lead to the conclusion that the clone and site had a highly significant effect ($P < 0.001$)
205 for all studied traits. The clone × site interactions had a moderate effect on FW and FL/W, and a highly significant
206 effect ($P < 0.001$) on FL, C, and tree growth. The stability parameter analysis showed that most of the triploid clones
207 had higher reaction norms to the improvement in growth conditions and higher phenotypic plasticity. The estimated
208 clonal repeatability of FW (0.93) was slightly higher than for C (0.91), FL (0.89), FL/W (0.83), H (0.85), DBH
209 (0.76), and SV (0.80). Three clonal testing sites were good enough to estimate quantitative parameters of fiber
210 properties. However, more than three clonal testing sites will help improve the accuracy of quantitative parameters
211 of growth traits. The findings in this study were due to a certain number of triploid hybrid clones derived from
212 several parents ($n = 5$). Therefore, the implication of G × E interaction for calculating the gain of genetically
213 improved triploid hybrid clones of *P. tomentosa* should be further investigated.

214 **Methods**

215 **Designing of experiments**

216 In the present study, the materials used were sampled from six triploid hybrid poplar clonal trials in northern China.
217 These trials were established by Beijing Forestry University using cuttings of *P. tomentosa* on sandy loam with
218 typical soil fertility. The clonal trials at Yanzhou, Gaotang and Xiangfen were built in the spring of 2004 and the
219 clonal trials at Pinggu, Taiyuan and Zhengzhou were established in the spring of 2005. The characteristics of the six
220 clonal experiments are shown in Table 1. The planted cuttings were 1.5-2.0 cm in diameter and 20-25 cm in length.
221 The experiments were repeated three times in the nursery. The experiments included one diploid clone and nine
222 triploid hybrid clones at each site (Table 2). The nine triploid hybrid clones were preselected among the triploids
223 derived from five parent trees because they exhibited good growth rate [33]. The diploid clone (M1319) was an elite
224 tree of *P. tomentosa* which grows faster. A randomized complete block design with three replications was used in
225 each clonal trial (240 trees per plot, resulting in a total of 720 trees per clone per trial). Ten clones were planted on
226 the rectangular plots at each location, and each plot contained 240 trees (4 × 60 trees) with 2 m × 3 m spacing. No
227 thinning was conducted during the testing period.

228 **Measurement of fiber properties and growth traits**

229 A total of 360 trees were randomly selected from the six trials sites. Trees were collected randomly, 6 ramets (the 6
230 trees) each clone were sampled fully at random on per location. In the triploid poplar breeding program of Beijing
231 Forestry University, the overall H and DBH of all tree samples were measured by workers at the age of 5 years. The
232 SV of each sample was estimated according to the volume function of DBH and H used by Chen [34]. All sampled
233 trees were shipped to Beijing Forestry University. For laboratory measurements, a 10-cm-thick stem disk was
234 harvested from the breast height of each sample. Matchstick-sized wood samples (each sample implying two pairs of
235 annual rings) were cut from the stem disks to evaluate the fiber properties, and then immersed in a boiling 1:1 (v/v)
236 mixed solution of hydrogen peroxide and acetic acid. Afterwards, FL, FW, and C was measured according to the
237 methods described by Zhang et al. [4] using the Lorentzen & Wettre (LW) Fiber Tester (AB Lorentzen & Wettre,
238 Kista, Sweden).

239 **Statistical analysis**

240 When the main statistical analysis and the estimation of genetic statistics were conducted, the diploid clone (M1319)
241 was not included. Thus, only the nine triploid clones took part in the main variance analysis and estimates of genetic
242 parameters. Analyses of variance were performed according to the UNIVARIATE program of the SPSS software
243 (SPSS for Windows, version 13, SPSS, Chicago, IL). Analysis of variance was used to analyze the variation between
244 the ramets of the sample clones at a location based on the following linear model (Equation (1)):

$$245 X_{ik} = \mu + C_i + \varepsilon_{ik}, \quad (1)$$

246 where X_{ik} represents the observation of the k th ramet of the i th clone; μ represents the general mean; C_i represents the
247 effect attributed to the i th clone and ε_{ik} represents random error. The clone × replicate effects were not included in the
248 linear model (Equation (1)) as the six sampled trees per clone per location were randomly selected.

249 The clonal repeatabilities were calculated within a location as:

250
$$R_c^2 = \frac{\hat{\sigma}_c^2}{\hat{\sigma}_c^2 + \frac{\hat{\sigma}_e^2}{k}} \quad (2)$$

251 and the clonal repeatability of the individual-tree (R_b^2) was estimated according to the following equation:

252
$$R_b^2 = \hat{\sigma}_c^2 / (\hat{\sigma}_c^2 + \hat{\sigma}_e^2), \quad (3)$$

253 where k is the average value of tree samples per clone within a location; $\hat{\sigma}_c^2$ is the estimated variance of clone; $\hat{\sigma}_e^2$ is
254 the variance among the ramets within the clones.

255 The six locations were jointly analyzed using the following linear model [17] (Equation (4)):

256
$$X_{ijk} = \mu + C_i + L_j + C_i L_j + \varepsilon_{ijk} \quad (4)$$

257 where X_{ijk} represents the performance of the k th ramet of the i th clone within the j th location; μ represents the
258 general mean; C_i represents the effect attributed to the i th clone; L_j represents the effect attributed to the j th location;
259 $C_i L_j$ represents the interaction between the i th clone and j th location, and ε_{ijk} represents random error. Only the
260 location was regarded as a fixed effect and all other terms were regarded as random effect.

261 The clonal repeatabilities were estimated using the equation:

262
$$R_c^2 = \frac{\hat{\sigma}_c^2}{\frac{k_2 \hat{\sigma}_c^2}{k_2} + \frac{k_1 \hat{\sigma}_{L \times c}^2}{k_2} + \frac{\hat{\sigma}_e^2}{k_2}} \quad (5)$$

263 and the clonal repeatability of individual-tree was calculated across locations according to the following equation:

264
$$R_b^2 = \hat{\sigma}_c^2 / (\hat{\sigma}_c^2 + \hat{\sigma}_{L \times c}^2 + \hat{\sigma}_e^2), \quad (6)$$

265 where k_1 is the coefficient related to the variance caused by the clone \times site interaction item ($\hat{\sigma}_{L \times c}^2$); k_2 is the
266 coefficient related to the variance caused by the clonal variation ($\hat{\sigma}_c^2$). The standard errors (SE) for the estimates of
267 clonal repeatability were estimated according to the following equation [35]:

268
$$SE(R_c^2) = \sqrt{\frac{2(1 - R_c^2)^2 [1 + (k_2 - 1)R_c^2]^2}{k_2(k_2 - 1)(N - 1)}}, \quad (7)$$

269 where N is the number of tested clones. The SE for the clonal repeatability estimates of individual-tree were also
270 estimated according to the Equation (7), where R_b^2 was used instead of R_c^2 .

271 The genetic correlation coefficients ($r_{A(X,Y)}$) between traits at a location were computed using the equation [36]:

272
$$r_{A(X,Y)} = \frac{\hat{\sigma}_{c(x,y)}}{\sqrt{\hat{\sigma}_{c(x)}^2 \hat{\sigma}_{c(y)}^2}}, \quad (8)$$

273 where $\hat{\sigma}_{c(x,y)}$ is the clonal component of covariance estimated among traits x and y ; $\hat{\sigma}_{c(x)}^2$ is the clonal variance
274 component estimated for trait x ; $\hat{\sigma}_{c(y)}^2$ is the clonal variance component estimated for trait y . Similar to using the
275 mean squares for estimating variance components, the cross-products were used to estimate the corresponding clone
276 component of variance from the data collected from the same individual tree.

277 The approximate SE of genetic correlation estimates were estimated based on the following formula [9]:

$$SE = \frac{1-r^2}{\sqrt{2}} \sqrt{\frac{\hat{\sigma}_{(R_x^2)} \hat{\sigma}_{(R_y^2)}}{R_x^2 R_y^2}}, \quad (9)$$

278 where r is the estimate of genetic correlation; R_x^2 is the estimate of the clonal repeatability of the trait x ; R_y^2 is the
 279 estimate of the clonal repeatability of the trait y ; $\hat{\sigma}_{(R_x^2)}$ and $\hat{\sigma}_{(R_y^2)}$ are the standard error for R_x^2 and R_y^2 , respectively.
 280 Using Equation (7) as the basis for the t -tests, the significance of the genetic correlations between the trait was
 281 tested.
 282

283 The genetic correlation estimates among the same traits for pairs of locations were estimated to assess the
 284 contribution of each pair of treatments to the overall clone \times environment. These type B genotypic correlations were
 285 computed according to the measurements of sample ramets at different locations from the same clones planted
 286 using the equation [37]:

$$r_{B(X,Y)} = \frac{r_{p(x1,y2)}}{R_{C(x1)} R_{C(y2)}}, \quad (10)$$

287 where $r_{p(x1,y2)}$ is the coefficient of phenotypic correlation between the clonal means estimated between x measured at
 288 location 1 and y measured at location 2; $R_{C(x1)}$ and $R_{C(y2)}$ are the square roots of the mean repeatability of the clones x
 289 and y estimated at location 1 and 2, respectively.
 290

291 The SPSS PROC CORR software was used to calculate the phenotypic correlations of the clonal means for each
 292 pair of sites, and the significance test was performed using the F -test.

293 In the present study, it is assumed that the selection intensity is equal to 1.271, which corresponds to selecting
 294 four clones from 18 or three clones from 14 [16]. According to the relevant response of the clonal selection in trait x ,
 295 the expected genetic gain in trait y ΔG_y can be predicted using the formula [9]:

$$\Delta G_y = i_x \sqrt{R_x^2} \sigma_y r_{xy}, \quad (11)$$

297 where i_x ($i_x = 1.271$) is the selection intensity; R_x^2 is the clonal repeatabilities for trait x ; σ_y is the standard deviation
 298 of clonal for trait y ; r_{xy} is the genetic correlation coefficients between trait x and y ($r_{xy} \leq 1$).

299 Estimation of stability parameters

300 To evaluate the stability of the individual clones across the six experimental locations, the stability variances were
 301 estimated using the Shukla model [22], where lower values indicate higher stability, and the significance test was
 302 conducted using the F -test. Subsequently, the stability of the individual clones across locations was also estimated
 303 using the Finlay and Wilkinson stability parameter [23]. The triploid clones were grouped according to the size of
 304 their regression coefficients (b_i), less than, equal to, or > 1 . Clones with $b_i > 1$ are more adapted to favorable
 305 growing conditions, those with $b_i < 1$ are adapted to unfavorable environmental conditions, and those with b_i equal
 306 to 1 have an average adaptation to all environments [23].

307 Abbreviations

308 CV p %: coefficients of phenotypic variation; FL: fiber length; FW: fiber width; FL/W: fiber length/width; C:
309 coarseness; H: tree height; DBH: diameter at breast height; SV: stem volume; R_b^2 : repeatability of individual-tree
310 clonal; R_c^2 : repeatability of clonal means; SE: standard errors; YZ: Yanzhou; GT: Gaotang; XF: Xiangfen; PG:
311 Pinggu; ZZ: Zhengzhou; TY: Taiyuan; F : Fisher's criteria; P : probability levels; t : Student's criteria; b_i : regression
312 coefficient

313 **Declarations**

314 **Ethics approval and consent to participate**

315 Not applicable.

316 **Consent for publication**

317 Not applicable.

318 **Availability of data and materials**

319 All data generated or analysed during this study are included in this published article.

320 **Competing interests**

321 The authors declare that they have no competing interests.

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325 **Authors' contributions**

326 JW was responsible for generating the phenotypic data set, analyzing the results, and writing the paper. QZ and YS
327 was responsible for tree growth measurements. XK was responsible for planning and guiding this research. PZ was
328 responsible for planing and building the clonal trails, collecting wood discs sample, fiber properties measurements
329 and revised the paper. All authors have read and approved the manuscript.

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Table 1 Location, climatic conditions, and description of six clonal trials

Site	Latitude (°N)	Longitude (°W)	Mean annual T (°C)	Rainfall (mm/year)	Number of clones	Sample trees
Yanzhou	35°10'	116°49'	13.6	660	10	54
Gaotang	36°51'	116°04'	13.1	556	10	54
Xiangfen	35°50'	111°21'	11.5	550	10	54
Pinggu	40°13'	117°12'	11.5	640	10	54
Zhengzhou	34°27'	113°57'	14.2	641	10	54
Taiyuan	37°52'	112°33'	10.5	431	10	54

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Table 2 Identity and origin of the hybrid clones

No.	Clone identity	Parents	Level of ploidy	Sex
1	B301	<i>(P. tomentosa × P. bolleana) × P. tomentosa</i>	Triploid	♀
2	B302	<i>(P. tomentosa × P. bolleana) × P. tomentosa</i>	Triploid	♂
3	B303	<i>(P. tomentosa × P. bolleana) × P. tomentosa</i>	Triploid	♀
4	B304	<i>(P. tomentosa × P. bolleana) × P. tomentosa</i>	Triploid	♀
5	B305	<i>(P. tomentosa × P. bolleana) × P. tomentosa</i>	Triploid	♀
6	B306	<i>(P. tomentosa × P. bolleana) × P. tomentosa</i>	Triploid	♀
7	B312	<i>(P. tomentosa × P. bolleana) × P. tomentosa</i>	Triploid	♂
8	B330	<i>(P. alba × P. glandulosa) × P. tomentosa</i>	Triploid	♀
9	B331	<i>(P. alba × P. glandulosa) × P. tomentosa</i>	Triploid	♀
10	M1319	<i>P. tomentosa × P. tomentosa</i>	Diploid	♂

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Table 3 Clone mean values, standard error (SE) of the mean, ranges of maximum and minimum values, and coefficients of phenotypic variation (CV p %) for fiber properties and growth traits at the six clonal trials.

Site	Traits	Triploid clones			Diploid clone (M1319)	
		Mean ± SE	Range (min-max)	CV p %	Mean ±SE	Range (min-max)
Yanzhou	FL (mm)	0.77±0.04	0.68±0.84	5.3	0.67±0.01	0.65±0.69
	FW (µm)	24.7±0.9	23.2±26.6	3.5	22.7±1.2	21.9±25.0
	FL/W	31.3±1.4	28.4±33.4	4.5	29.4±1.1	27.6±30.7
	C (µg/m)	105.8±8.9	86.5±124.3	8.4	91.8±10.9	83.3±113.4
	H (m)	12.5±1.2	10.6±15.4	9.7	9.9±0.5	9.2±10.6
	DBH (cm)	10.7±1.0	8.5±13.3	9.4	9.0±1.2	7.1±10.4
	SV (dm ³)	48.2±11.0	26.2±70.4	22.9	28.7±8.2	16.4±39.5
	FL (mm)	0.82±0.04	0.73±0.90	4.9	0.69±0.03	0.64±0.74
Gaotang	FW (µm)	24.2±0.9	22.6±26.0	3.6	22.1±0.5	21.5±22.7
	FL/W	33.9±1.5	30.7±37.1	4.3	31.1±1.2	29.7±32.6
	C (µg/m)	102.2±7.4	85.7±118.9	7.3	85.5±3.0	82.5±89.0
	H (m)	13.6±1.2	9.4±16.0	8.9	12.0±0.6	11.1±12.9
	DBH (cm)	11.6±1.5	7.8±14.9	12.9	9.7±0.8	8.6±10.8
	SV (dm ³)	61.8±18.4	23.6±113.9	29.8	38.6±7.3	28.1±48.9
	FL (mm)	0.80±0.04	0.73±0.90	5.0	0.67±0.02	0.64±0.71
	FW (µm)	24.2±0.9	22.6±26.0	3.7	22.0±0.7	21.3±22.9
Xiangfen	FL/W	33.1±1.1	30.3±35.4	3.4	30.4±1.6	28.1±32.7
	C (µg/m)	99.6±9.3	68.6±120.3	9.3	82.0±5.7	76.5±92.4
	H (m)	13.2±1.1	11.4±15.8	8.4	11.5±0.4	10.8±12.1
	DBH (cm)	11.7±1.2	9.0±14.6	10.3	10.0±0.7	8.8±10.7
	SV (dm ³)	60.8±15.6	31.5±107.1	25.7	39.4±5.7	28.8±46.4
	FL (mm)	0.76±0.04	0.67±0.85	5.3	0.61±0.02	0.58±0.63
	FW (µm)	26.1±1.0	23.7±28.8	3.8	22.9±0.2	22.5±23.1
	FL/W	29.1±1.6	25.8±31.7	5.5	26.5±0.9	25.2±28.1
Pinggu	C (µg/m)	112.5±7.8	97.8±129.4	6.9	85.2±2.2	80.9±87.2
	H (m)	11.4±1.5	7.8±15.8	13.2	10.6±0.9	9.1±11.8
	DBH (cm)	13.8±2.2	8.7±19.3	15.9	10.4±1.3	8.2±11.9
	SV (dm ³)	75.3±28.0	21.1±133.4	37.2	39.8±10.6	21.3±52.9
	FL (mm)	0.81±0.04	0.74±0.89	4.9	0.68±0.03	0.64±0.72
	FW (µm)	25.3±0.8	23.5±27.1	3.2	22.2±0.6	21.6±23.1
	FL/W	32.2±1.5	28.8±34.8	4.7	30.6±1.1	29.1±32.2
	C (µg/m)	111.2±8.6	88.2±127.5	7.7	87.5±3.8	82.3±91.4
Zhengzhou	H (m)	13.0±1.5	9.2±15.1	11.5	11.1±0.8	10.4±12.6
	DBH (cm)	14.4±1.8	9.8±18.5	12.5	12.3±1.0	11.1±13.6
	SV (dm ³)	91.0±26.7	32.9±152.7	29.3	57.2±12.2	44.3±75.5
	FL (mm)	0.78±0.04	0.72±0.87	5.1	0.65±0.03	0.61±0.68
	FW (µm)	24.6±0.9	22.6±27.4	3.7	21.6±0.4	21.0±22.1
	FL/W	31.7±1.1	29.0±34.2	3.5	29.9±1.4	27.9±31.4
	C (µg/m)	103.5±8.4	84.4±120.0	8.1	80.0±1.6	77.7±81.8
	H (m)	13.9±1.7	9.5±16.4	12.2	11.7±0.5	11.0±12.2
Taiyuan	DBH (cm)	14.8±1.9	11.3±18.5	12.8	13.0±0.8	11.7±13.6
	SV (dm ³)	100.9±31.1	46.1±172.4	30.8	65.5±9.2	50.7±74.6

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Table 4 Analysis of variance results, estimates of repeatability (\pm SE) at the clonal mean and individual-tree levels of all traits of the nine triploid hybrid clones at the six sites combined

Traits	P-value			R_b^2	R_c^2	Percentage (%)
	Clones	Sites	Sites \times clones			
FL	0.000	0.000	0.000	0.29 \pm 0.11	0.89 \pm 0.05	73.9
FW	0.000	0.000	0.031	0.36 \pm 0.13	0.93 \pm 0.03	87.6
FL/W	0.000	0.000	0.014	0.17 \pm 0.08	0.83 \pm 0.07	68.4
C	0.000	0.000	0.000	0.35 \pm 0.13	0.91 \pm 0.04	72.7
H	0.000	0.000	0.001	0.18 \pm 0.09	0.76 \pm 0.09	42.1
DBH	0.000	0.000	0.001	0.21 \pm 0.10	0.85 \pm 0.06	66.2
SV	0.000	0.000	0.000	0.19 \pm 0.09	0.80 \pm 0.08	52.9

447 Note: Estimated percentage ratio (%) of clonal variance component to the total variance component of clonesite
448 interaction and clone. The degrees of freedom are 5 for the site, 8 for the clone, 40 for the clone \times interaction, and
449 270 for the error

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Table 5 The results of analysis of variance and estimates of repeatability of all studied traits of the nine triploid hybrid clones at individual site

Site		Trait						
		FL	FW	FL/W	C	H	DBH	SV
Yanzhou	P value	0.000	0.000	0.000	0.000	0.389	0.516	0.786
	R_b^2	0.58	0.57	0.60	0.53	-	-	-
	R_c^2	0.90 \pm 0.05	0.95 \pm 0.03	0.90 \pm 0.07	0.87 \pm 0.08	-	-	-
Gaotang	P value	0.000	0.000	0.054	0.000	0.000	0.000	0.000
	R_b^2	0.49	0.46	-	0.70	0.45	0.44	0.43
	R_c^2	0.85 \pm 0.07	0.84 \pm 0.10	-	0.93 \pm 0.05	0.83 \pm 0.08	0.82 \pm 0.08	0.82 \pm 0.08
Xiangfen	P value	0.000	0.000	0.041	0.000	0.000	0.020	0.005
	R_b^2	0.38	0.54	0.17	0.44	0.39	0.21	0.29
	R_c^2	0.79 \pm 0.09	0.88 \pm 0.08	0.56 \pm 0.20	0.83 \pm 0.11	0.79 \pm 0.09	0.61 \pm 0.14	0.70 \pm 0.12
Pinggu	P value	0.000	0.073	0.062	0.000	0.030	0.000	0.001
	R_b^2	0.45	-	-	0.45	0.19	0.38	0.33
	R_c^2	0.83 \pm 0.08	-	-	0.83 \pm 0.08	0.58 \pm 0.15	0.78 \pm 0.10	0.74 \pm 0.11
Zhengzhou	P value	0.002	0.000	0.020	0.000	0.000	0.030	0.014
	R_b^2	0.31	0.38	0.21	0.37	0.47	0.19	0.23
	R_c^2	0.73 \pm 0.11	0.79 \pm 0.10	0.61 \pm 0.14	0.78 \pm 0.10	0.84 \pm 0.07	0.58 \pm 0.15	0.64 \pm 0.14
Taiyuan	P value	0.000	0.007	0.047	0.000	0.000	0.000	0.000
	R_b^2	0.42	0.26	0.17	0.64	0.61	0.39	0.48
	R_c^2	0.81 \pm 0.09	0.68 \pm 0.13	0.54 \pm 0.16	0.91 \pm 0.04	0.90 \pm 0.05	0.79 \pm 0.09	0.85 \pm 0.07

455 Note: The degree of freedom for the clone is 8 and 45 for the error

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Table 6 The estimates of type B genetic correlations among all possible pairs of sites for fiber properties and growth traits (with approximate SE in brackets) of the nine triploid hybrid clones

Pairs of site	Genetic correlation						
	FL	FW	FL/W	C	H	DBH	SV
YZ-GT	0.91(0.01)*	0.97(0.01)*	-	0.63(0.03)	-	-	-
YZ-XF	0.90(0.01)*	0.59(0.02)	0.67(0.03)	0.58(0.05)	-	-	-
YZ-PG	0.92(0.01)*	-	-	0.91(0.01)*	-	-	-
YZ-ZZ	0.68(0.04)	0.86(0.01)*	1.13(0.01)**	0.70(0.02)	-	-	-
YZ-TY	0.12(0.05)	1.01(0.01)**	0.20(0.09)	0.54(0.02)	-	-	-
GT-XF	0.98(0.01)*	0.90(0.01)*	-	0.55(0.04)	0.69(0.03)	0.57(0.07)	0.51(0.07)
GT-PG	0.99(0.01)*	-	-	0.74(0.01)	1.32(0.04)**	0.96(0.01)*	0.98(0.01)*
GT-ZZ	0.91(0.01)*	0.96(0.01)*	-	0.67(0.02)	0.88(0.01)*	1.13(0.02)**	1.01(0.01)**
GT-TY	0.35(0.06)	1.03(0.01)**	-	0.66(0.01)	0.16(0.04)	0.61(0.03)	0.44(0.04)
XF-PG	0.90(0.01)*	-	-	1.05(0.01)**	1.06(0.01)**	0.91(0.01)*	0.84(0.02)
XF-ZZ	1.05(0.01)**	0.79(0.02)	0.84(0.03)	1.16(0.01)**	0.79(0.02)	1.25(0.04)**	1.08(0.01)**
XF-TY	0.26(0.07)	0.56(0.04)	0.01(0.01)	0.70(0.02)	0.45(0.03)	0.22(0.09)	0.19(0.07)
PG-ZZ	0.96(0.01)*	-	-	1.10(0.01)**	1.13(0.01)**	1.27(0.03)**	1.26(0.03)**
PG-TY	0.08(0.07)	-	-	0.68(0.02)	0.55(0.04)	0.66(0.03)	0.60(0.03)
ZZ-TY	0.28(0.08)	0.96(0.01)*	0.64(0.07)	0.64(0.02)	-0.02(0.01)	0.59(0.05)	0.36(0.06)

Note: *Significant correlations $p < 0.05$. **denotes $p < 0.01$

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Table 7 Stability parameters for FL and SV of the nine triploid hybrid clones across six sites

Traits	Clones	Shukla stability variance			Finlay-Wilkinson stability parameters			
		Variance x 10 ⁻⁴	<i>F</i>	<i>P</i>	Intercept	<i>t</i>	<i>bi</i>	<i>t</i>
FL	B301	4.31	3.14	0.009	0.068	0.22	0.929	2.41
	B302	4.56	3.33	0.006	-0.241	-0.91	1.321	3.97
	B303	3.80	2.77	0.018	-0.188	-0.68	1.214	3.49
	B304	4.06	2.96	0.013	-0.204	-0.74	1.250	3.59
	B305	6.34	4.62	0.000	0.043	0.12	0.893	1.91
	B306	6.59	4.81	0.000	-0.315	-0.94	1.429	3.37
	B312	5.83	4.25	0.001	0.193	0.58	0.750	1.79
	B330	1.01	0.74	0.594	0.115	0.80	0.893	4.93
	B331	2.28	1.66	0.143	0.246	1.35	0.679	2.95
	B301	3.16	5.39	0.000	18.673	0.78	0.667	2.10
SV	B302	0.56	0.95	0.448	11.26	0.73	0.870	4.27
	B303	0.95	1.63	0.153	13.233	0.83	0.908	4.28
	B304	2.43	4.14	0.001	-25.668	-1.11	1.315	4.26
	B305	2.02	3.44	0.005	14.072	1.12	0.466	2.79
	B306	0.72	1.22	0.298	0.923	0.07	0.941	5.07
	B312	1.23	2.11	0.065	13.508	0.74	0.919	3.78
	B330	2.12	3.61	0.004	-26.084	-1.39	1.411	5.64
	B331	2.04	3.48	0.005	-19.436	-1.22	1.477	7.00

Note: *F*: Fisher's criteria; *P*: probability levels; *t*: Student's criteria; *b_i*: regression coefficient

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Table 8 Phenotypic correlations (below the diagonal) and genotypic correlations (above the diagonal) among all traits at individual sites of the nine triploid hybrid clones

Site	Traits	FL	FW	FL/W	C	H	DBH	SV
Yanzhou	FL		0.59	0.77*	0.87*	-	-	-
	FW	0.55		-0.25	0.97*	-	-	-
	FL/W	0.69*	-0.23		0.16	-	-	-
	C	0.77*	0.88*	0.14		-	-	-
	H	0.10	-0.14	0.24	-0.29		-	-
	DBH	0.26	-0.34	0.59	-0.05	0.24		-
	SV	0.29	-0.49	0.75*	-0.12	0.74*	0.90**	
Gaotang	FL		0.92*	-	0.71	0.65	0.32	0.35
	FW	0.78*		-	0.99**	0.25	-0.19	-0.16
	FL/W	0.68*	0.08		-	-	-	-
	C	0.63	0.88**	0.04		-0.01	-0.34	-0.30
	H	0.55	0.21	0.64	-0.01		0.82*	0.93*
	DBH	0.27	-0.16	0.60	-0.30	0.68*		1.20**
	SV	0.29	-0.13	0.61	-0.26	0.77*	0.98**	
Xiangfen	FL		0.96**	0.63	0.84*	0.52	0.66	0.56
	FW	0.80**		-0.27	0.96**	-0.01	0.07	0.03
	FL/W	0.42	-0.19		-0.19	1.04*	1.16*	1.03*
	C	0.68*	0.82**	-0.13		-0.32	-0.11	-0.21
	H	0.41	-0.01	0.69*	-0.26		1.37**	1.31**
	DBH	0.46	0.05	0.68*	-0.08	0.95**		1.51**
	SV	0.42	0.02	0.65	-0.16	0.98**	0.99**	
Pinggu	FL		-	-	0.75*	1.10**	0.56	0.62
	FW	0.49		-	-	-	-	-
	FL/W	0.81**	-0.11		-	-	-	-
	C	0.68*	0.86**	0.20		0.40	-0.19	-0.16
	H	0.88**	0.17	0.90**	0.31		1.05**	1.11**
	DBH	0.51	-0.25	0.80*	-0.18	0.80**		1.16**
	SV	0.54	-0.24	0.83**	-0.15	0.83**	0.99**	
Zhengzhou	FL		0.63	0.89*	0.68	0.49	0.46	0.43
	FW	0.54		-0.33	0.93**	-0.23	-0.52	-0.53
	FL/W	0.68*	-0.26		-0.06	0.85*	1.10*	1.07*
	C	0.58	0.82**	-0.05		0.29	-0.20	-0.10
	H	0.44	-0.21	0.69*	0.26		0.97*	1.08**
DBH	0.34	-0.40	0.74*	-0.15	0.76*		1.42**	

	SV	0.34	-0.42	0.75*	-0.08	0.88**	0.97**	
	FL		0.97**	1.01*	0.83**	0.33	0.24	0.34
	FW	0.82**		0.36	1.01**	0.17	-0.28	-0.11
	FL/W	0.76*	0.25		0.43	0.47	0.84	0.83
Taiyuan	C	0.82**	0.91**	0.34		-0.05	-0.23	-0.15
	H	0.32	0.15	0.37	-0.05		0.67	0.82*
	DBH	0.21	-0.23	0.61	-0.22	0.62		1.09**
	SV	0.31	-0.09	0.63	-0.15	0.79*	0.97**	

Note: *Significant correlations = 0.01 < p < 0.05; **denotes p < 0.01

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Table 9 Expected response ($\Delta G/\bar{X} \times 100$) in fiber properties and growth traits at the six sites for different selection criteria of the nine triploid hybrid clones

Selection criterion	Response (%)							
	FL	FW	FL/W	C	H	DBH	SV	
Yanzhou	FL	4.9	2.2	3.3	6.6	-	-	-
	FW	3.6	3.9	-1.1	7.5	-	-	-
	FL/W	3.9	-0.9	4.3	1.2	-	-	-
	C	4.2	3.6	0.7	7.5	-	-	-
Gaotang	FL	4.1	2.7	-	5.2	3.7	6.6	13.7
	FW	3.8	3.0	-	7.3	1.8	-1.9	-3.9
	FL/W	-	-	-	-	-	-	-
	C	3.1	3.1	-	7.8	-0.1	-3.5	-7.7
	H	2.3	0.7	-	-0.1	7.0	6.7	17.6
	DBH	1.1	-0.6	-	-2.5	4.7	9.8	22.3
Xiangfen	SV	1.2	-0.5	-	-2.2	5.3	9.6	22.7
	FL	3.2	3.0	1.0	6.0	3.0	3.4	13.4
	FW	3.2	3.3	-0.5	7.2	-0.1	0.4	0.8
	FL/W	1.7	-0.7	1.4	-1.1	5.1	4.4	10.8
	C	2.7	3.1	-0.3	7.4	-1.9	-0.6	-5.2
	H	1.3	-0.1	1.6	-2.2	5.8	4.6	13.5
	DBH	1.3	0.2	1.4	-0.7	4.8	4.7	14.9
	SV	1.4	0.1	1.6	-1.7	5.3	4.5	15.4
	FL	3.8	-	-	4.6	7.9	9.0	17.8
Pinggu	FW	-	-	-	-	-	-	-
	FL/W	-	-	-	-	-	-	-
	C	2.9	-	-	6.1	2.9	-3.1	-4.7
	H	3.5	-	-	2.0	6.0	14.0	26.9
	DBH	2.1	-	-	-1.1	7.3	15.5	32.5
	SV	2.2	-	-	-0.9	7.6	17.4	27.4

	FL	3.3	1.6	2.6	4.0	4.4	4.0	8.4
	FW	2.2	2.6	-1.0	5.7	-2.1	-4.6	-10.6
	FL/W	2.7	-0.8	2.7	-0.3	7.0	8.7	19.0
Zhengzhou	C	2.3	2.4	-0.2	6.1	2.7	-1.8	-2.0
	H	1.8	-0.6	2.7	1.8	9.6	9.1	22.4
	DBH	1.4	-1.2	2.9	-1.0	7.8	7.8	24.6
	SV	1.4	-1.2	2.9	-0.6	9.0	11.5	18.1
	FL	4.0	2.6	2.3	6.6	3.7	2.7	9.3
	FW	3.5	2.4	0.7	7.4	1.7	-2.9	-2.7
	FL/W	3.3	0.8	1.9	2.8	4.3	7.9	18.8
Taiyuan	C	3.5	2.8	1.0	8.4	-0.6	-2.8	-4.5
	H	1.4	0.5	1.1	-0.4	11.9	8.1	24.0
	DBH	0.9	-0.7	1.9	-1.8	7.4	11.3	29.6
	SV	1.4	-0.3	1.9	-1.3	9.5	12.7	28.2

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Figures

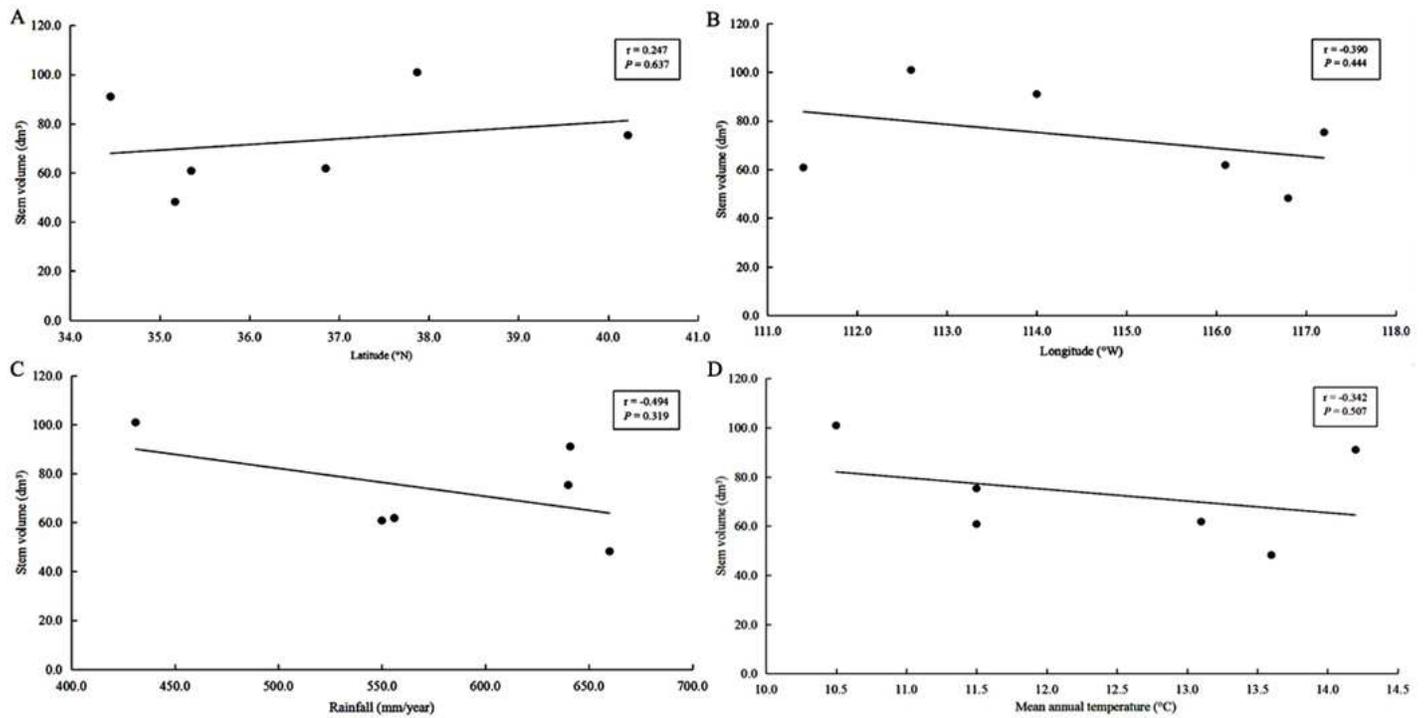


Figure 1

Correlations between stem volume and (A) latitude, (B) longitude, (C) rainfall, and (D) mean annual temperature