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G×E Analysis of Early Growth Traits of *Populus deltoides* in East China by Using BLUP-GGE

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Abstract: In temperate and subtropical climates, *Populus deltoides* is an important poplar species. To analyze the stability, adaptability, and high yield of *P. deltoides* hybrid genotypes in East China, 38 *P. deltoides* genotypes were screened at three experimental sites in Shandong Province, and the coefficients of variation and genetic characteristics of 5-year growth were examined using BLUP-GGE. Results showed that all coefficients of variance were higher for diameter at breast height (DBH) than for tree height at all sites; the repeatability and heritability of tree height were greater than those of DBH at all sites. The fitting degree of tree height and DBH was 93.72% and 92.22%, respectively. The optimum genotype varied by location and grouping, of which Shanxian County divisions are the most powerful and representative of the three sites. The growth of 5-year-old *P. deltoides* was highly varied because of hereditary factors. Shanxian County is the more appropriate site for growth of *P. deltoides* in the tested sites in East China. In East China, genotypes 16, 5, 21, and 7 are regarded as superior. The genotypes 8, 26, and 36 are better for the site Rizhao; 16, 5, and 21 for site Shanxian; and 22, 21, and 5 for site Boxing.

Keywords: excellent genotype; BLUP-GGE; *Populus deltoides*; east China; genotype selection

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Citation: Yuan, Z.; Dong, Y.; Liu, N.; Li, S.; Zhang, W.; Wang, Y.; Han, Y.; Zhuang, R.; Zhang, X.; Su, X.; et al. G×E Analysis of Early Growth Traits of *Populus deltoides* in East China by Using BLUP-GGE. *Forests* **2022**, *13*, 1808. https://doi.org/10.3390/f13111808

Academic Editor: Tadeusz Malewski

Received: 27 September 2022
Accepted: 27 October 2022
Published: 30 October 2022

1. Introduction

Populus trees are the fastest-growing woody species with the largest cultivated area and highest wood yield in the mid-latitude plains of the world [1]. The fast-growing and high-yielding characteristics of poplar plantations benefit to relieve the strain on natural forests and to slow down the greenhouse effect. Additionally, afforesting the poplar plantations can maximize space utilization and enhance biomass per unit area [2]. In temperate and subtropical parts of China, poplar trees are economically and ecologically significant commercial tree species. Therefore, the selection of regionally and commercially superior poplar genotypes has become a major concern for modern breeders. However, *Populus* is a perennial tree genus with a long growth cycle and low breeding efficiency. Evaluation on the early growth traits of poplar trees can shorten the breeding cycle to a certain extent and improve the breeding efficiency [3,4].

Multi-environmental testing (MET) is a crucial step in the process of creating superior plant genotypes. MET can be used to verify candidate genotypes in terms of high yield and field stability [5]. However, when a scientific experimental design is used, many years of forest MET provide unreliable results. In analyzing the phenotypic variations in growth traits, genotype–environment interaction (G×E) is considered to be more useful than plant MET [5–8]. Currently, many statistical models based on random effects are being utilized. Extensive usage of mixed linear models with random effects is prevalent in experimental data analyses [9]. Best linear unbiased prediction (BLUP) is more trustworthy than observations and can provide precise representations.

The genotype main effect plus genotype by environment interaction effects model (GGE) [7,8] was used to fully exploit the inhibitory or promoting effects of G×E on growth traits, and the target planting area of hybrid genotypes was divided into several relatively homogeneous varieties of ecological areas (mega-environment (ME)) [10] to reduce the interaction within the variety of ecological area. Variants with exceptional adaptability can be used to scientifically examine and exploit genotypes and habitats in expansive areas. *Populus deltoides* is an important parental source for the selection and cultivation of excellent clones of *Populus* and occupies an irreplaceable position in the cultivation of high-yield *Populus* plantations. However, up to now, there are only a few studies on the early selection of *Populus* using BLUP-GGE in China. For example, Liu [9] used BLUP-GGE technology to analyze the growth performances of 4-year-old *Populus euramericana* in six experimental sites in four provinces in China. He found a strong correlation of the BLUP value with the observed value and recommended that Shandong Province is the most suitable site for cultivation and breeding of *P. euramericana*. In East China, Shandong Province, Anhui Province, and Jiangsu Province are the main cultivation areas of *P. deltoides*, among which Shandong Province is a representative province of poplar productivity and intensive cultivation in China [11]. Therefore, in this study, three experimental sites in Shandong Province were selected as typical cultivation environmental conditions of *P. deltoides* in East China. The site Shanxian is alluvial sandy loam soil formed by the Yellow River, Rizhao is coastal hills with barren soil, and Boxing is coastal saline-alkali land. In this study, BLUP-GGE was used to examine the outcomes of MET. The results of the study can provide theoretical reference for the breeding and application of *P. deltoides* in East China.

2. Materials and Methods

2.1. Test Sites and Conditions

Eleven *P. deltoides* half-sib family seeds were obtained and sown in the experimental nursery of Shandong Academy of Forestry in mid-May 2014. The seedlings were transplanted to the nursery stock experimental site (Changqing, Jinan) in mid-July, and the measurements were obtained after the growing season. Seedling height and basal diameter of half-sib families of *P. deltoides* were comprehensively evaluated by character expression level method, and excellent individuals were screened out. In 2015, different genotypes were propagated, and seedling height and basal diameter were measured in the end of the growing season. Seedling height and basal diameter of *P. deltoides* genotypes were comprehensively screened for two consecutive years by the Bregkin multi-trait evaluation method, and 35 genotypes (Table 1) with excellent performance were finally selected.

Table 1. Genetic background of 38 *P. deltoides* genotypes (including 3 control). The control genotypes are 15, 37, and 38.

Number	Parents	Number	Parents
1	*P. deltoides* ‘1’ × *P. deltoides*	20	*P. deltoides* ‘1’ × *P. deltoides*
2	*P. deltoides* ‘1’ × *P. deltoides*	21	*P. deltoides* ‘1’ × *P. deltoides*
3	*P. deltoides* ‘1’ × *P. deltoides*	22	*P. deltoides* ‘1’ × *P. deltoides*
4	*P. deltoides* ‘1’ × *P. deltoides*	23	*P. deltoides* ‘1’ × *P. deltoides*
5	*P. deltoides* ‘1’ × *P. deltoides*	24	*P. deltoides* ‘3’ × *P. deltoides*
6	*P. deltoides* ‘3’ × *P. deltoides*	25	*P. deltoides* ‘3’ × *P. deltoides*
7	*P. deltoides* ‘3’ × *P. deltoides*	26	*P. deltoides* ‘3’ × *P. deltoides*
8	*P. deltoides* ‘4’ × *P. deltoides*	27	*P. deltoides* ‘2’ × *P. deltoides*
9	*P. deltoides* ‘4’ × *P. deltoides*	28	*P. deltoides* ‘2’ × *P. deltoides*
10	*P. deltoides* ‘4’ × *P. deltoides*	29	*P. deltoides* ‘2’ × *P. deltoides*
11	*P. deltoides* ‘0’ × *P. deltoides*	30	*P. deltoides* ‘8’ × *P. deltoides*

Table 1. *Cont.*

Number	Parents	Number	Parents
12	*P. deltoides* '0' × *P. deltoides*	31	*P. deltoides* '8' × *P. deltoides*
13	*P. deltoides* '0' × *P. deltoides*	32	*P. deltoides* '0' × *P. deltoides*
14	*P. deltoides* '6' × *P. deltoides*	33	*P. deltoides* '0' × *P. deltoides*
15 (Zhonghe 1)	*P. deltoides* cv. 'Zhonghe 1'	34	*P. deltoides* '0' × *P. deltoides*
16	*P. deltoides* '1' × *P. deltoides*	35	*P. deltoides* '6' × *P. deltoides*
17	*P. deltoides* '1' × *P. deltoides*	36	*P. deltoides* '6' × *P. deltoides*
18	*P. deltoides* '1' × *P. deltoides*	37 (I-69)	*P. deltoides* cv. 'Lux I-69'
19	*P. deltoides* '1' × *P. deltoides*	38 (T-66)	*P. deltoides* cv. 'PE-19-66'

2.2. Test Design

In the field test, 1-year-old saplings with 2-year-old roots and diameter at breast height (DBH) greater than 2 cm were used, and I-69 (*P. deltoides* cv. 'Lux I-69'), T-66 (*P. deltoides* cv. 'PE-19-66'), and Zhonghe 1 (*P. deltoides* cv. 'Zhonghe 1') were used as control genotypes. METs were conducted in sites Rizhao, Shanxian, and Boxing in the spring of 2017, and two protected rows were erected around the test forest (Table 2). Row-and-column spacing was 4 m × 6 m. In the three sites, completely randomized block design with four blocks (replicates) and four plots were used. Tree height and DBH were measured at the end of the growing season every year, and the 5-year growth data were used for subsequent analysis.

Table 2. Natural conditions of the three experimental sites. Some differences in natural conditions were observed among the sites. Site Rizhao is located in a hilly and humid area in eastern Shandong Province, Shanxian is located in a plain and semi-arid area in southwestern Shandong Province, and Boxing is located in a mountainous and arid area in central and southern Shandong Province.

Environment Factor	Rizhao (RZ)	Shanxian (SX)	Boxing (BX)
Longitude/E	119°31′	115°91′	118°29′
Latitude/N	35°46′	34°66′	37°19′
Average annual temperature/°C	11.6	13.9	12.5
Maximum monthly average temperature/°C	23.9	27.8	26.5
Minimum monthly average temperature/°C	−0.3	−0.9	−3.0
Average annual rainfall/mm	813.0	737.1	627.3
Average annual sunshine duration/h	2432.8	2388.1	2632.5
Agrotype	loam	sandy loam	saline-alkali soil

2.3. Statistical Analysis

Excel 2010 and SPSS 20.0 were used to input and organize the measurement data and calculate the coefficient of variation and repeatability. ASReml-R4.1 was used to fit a single-site mixed linear model to calculate heritability, phenotypic variation coefficient, and genetic variation coefficient as well as a multi-site mixed linear model with heterogeneity of site variance for the significance of fixed effects and random effects [12]. The "predict ()" function was used to extract the BLUP value of each genotype growth trait in the multi-site mixed linear model. The GGEBiplotGUI package was used to generate the GGE biplot with the following parameters: scaled set to 0 (non-standardized), centered set to G+GE, and SVP set to symmetrical [9]. The genetic parameter formula [13–15] used was as follows:

$$\text{Coefficient of variation of traits } CV = \sigma/\overline{X} \times 100\% \tag{1}$$

$$\text{Repeatability } R = 1 - 1/F \tag{2}$$

$$\text{Heritability } H^2 = V_g/(V_g + V_e) \tag{3}$$

$$\text{Phenotypic coefficient of variation } CV_P = \sqrt{(V_g + V_e)}/\overline{X} \times 100\% \tag{4}$$

$$\text{Coefficient of genetic variation } CV_G = \sqrt{V_g}/\overline{X} \times 100\% \tag{5}$$

where $\overline{X}$ is an overall mean, σ standard deviation, F ANOVA genotype f value, V_g genotype variance component, and V_e error variance component.

The single-site mixed linear model used was as follows:

$$Y_{ijk} = \mu + \beta_i + c_j + \beta_i \times c_j + e_k \tag{6}$$

where [14] Y_{ijk} is the measured value of the jth genotype trait in the ith block, μ overall mean value, β_i block effect, c_j genotype effect, $\beta_i \times c_j$ is the block × genotype, and e_k error. The genotype effect is a random effect, and the effect of block × genotype is the fixed effect.

The multi-site mixed linear model used was as follows:

$$Y_{ijkl} = \mu + \delta_i + \beta_j + c_k + \delta_i \times c_k + e_l \tag{7}$$

where [14] Y_{ijkl} is the measured value of the kth genotype trait in the jth block at the ith site, μ overall mean value of the trait, δ_i site effect, β_j is block effect, c_k genotype effect, $\delta_i \times c_k$ is G×E, and e_l is the error. The site effect is a fixed effect, and the effect of block, genotype, and G×E is a random effect.

3. Results

3.1. Genetic Variation Analysis of Tree Height and DBH

According to the tree height and DBH descriptive statistics (Table 3), SX had the highest tree height and DBH, followed by RZ and BX. At each site, coefficient of variation, phenotypic variation coefficient, and genetic variation coefficient of DBH were higher (7.6%–22.3%) than those of tree height (7.1%–17.2%). The coefficient of variation, phenotypic variation coefficient, and genetic variation coefficient of tree height were the highest in BX, followed by RZ and SX. The phenotypic variation coefficient of DBH was higher at BX than at RZ, whereas the coefficient of variation and genetic variation coefficients were the highest at RZ, followed by BX and SX. Tree height was consistently more repeatable and heritable at each location (0.87–0.96 and 0.47–0.66, respectively) than DBH (0.79–0.93 and 0.33–0.47, respectively). For tree height, SX showed the highest repeatability and heritability, followed by RZ and BX; for DBH, RZ exhibited the highest repeatability and heritability, followed by SX and BX.

Table 3. Genetic parameters of growth traits of *P. deltoides* genotypes at three test sites.

Trait	Site	Mean (±S.E.)	Coefficient of Variation (%)	Repeatability	Heritability	Phenotypic Coefficient of Variation (%)	Coefficient of Genetic Variation (%)
H/m	RZ	11.9 ± 0.08	15.4	0.95	0.56	11.2	8.4
	SX	19.8 ± 0.12	11.8	0.96	0.66	8.8	7.1
	BX	9.0 ± 0.10	17.2	0.87	0.47	15.0	10.3
DBH/cm	RZ	13.4 ± 0.14	22.3	0.93	0.47	18.5	12.7
	SX	20.1 ± 0.16	15.0	0.86	0.34	13.3	7.6
	BX	11.1 ± 0.15	21.3	0.79	0.33	19.0	10.9

3.2. Mixed Linear Model Test for Tree Height and DBH

Because of the major issue of data imbalance in multi-year forest data, the ASReml-R4.1 program package in R environment was used to create a mixed linear model, and the significance test of fixed effects and random effects were conducted. The results of the fixed effect analysis (Table 4) indicated that the environmental effects on 5-year-old tree height and DBH were extremely significant ($p < 0.01$); RZ (hilly area), SX (sandy area), and BX (saline-alkaline land) have similar climatic conditions but vastly different soil textures. The random effects analysis (Table 5) revealed that the block effects of tree height and

DBH were not significant (z ratio < 1.50); however, the genotype effects were significant (z ratio > 1.50). The G×E effects were extremely significant (z ratio > 4). Different site conditions greatly affected the performance of the *P. deltoides* genotype; the tree height and DBH of 5-year-old *P. deltoides* genotype trees were significantly affected by the genotype and G×E effects.

Table 4. Fixed effects of mixed linear effect models for tree height and DBH of 5-year-old *P. deltoides* genotypes.

Effect Variable	DBH				Height			
	Df	SSD	Wald	Pr(X^2)	Df	SSD	Wald	Pr(X^2)
Site	2	583.77	583.77	$<2.2 \times 10^{-16}$ **	2	1715.7	2341.7	$<2.22 \times 10^{-16}$ **
Residual (MS)	-	1.0	-	-	-	1.0	-	-

** Means extremely significant difference ($p < 0.01$).

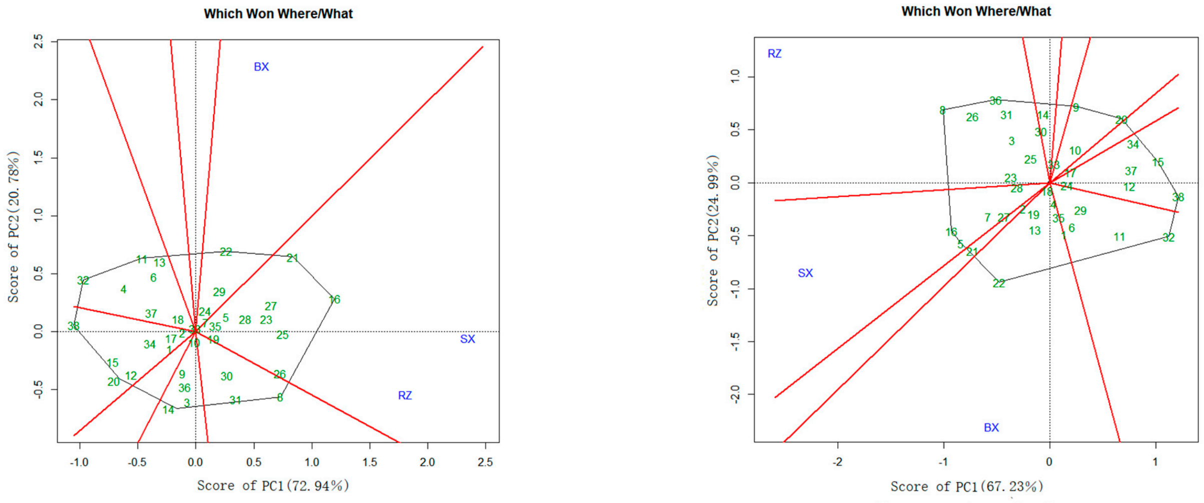
Table 5. Random effects of mixed linear effect models for tree height and DBH of 5-year-old *P. deltoides* genotypes.

Effect Variable	DBH			Height		
	Variance Component	Standard Error	z Ratio	Variance Component	Standard Error	z Ratio
Block	0.1083	0.1055	1.03	0.2036	0.1703	1.20
Genotype	0.8261	0.4411	1.87 *	0.5462	0.2417	2.26 *
G×E	1.9202	0.4527	4.24 **	0.9467	0.2142	4.19 **

* Means significant difference (z ratio > 1.5), ** means extremely significant difference (z ratio > 4).

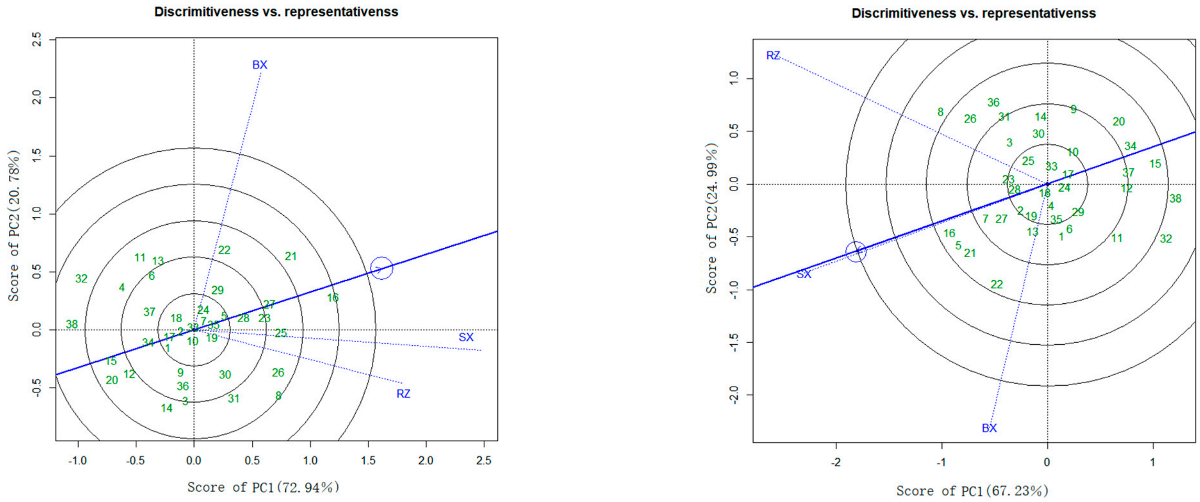
3.3. BLUP-GGE Analysis for Tree Height and DBH

The GGE biplot results (Figures 1–3) indicated that the variance explanation rates of the first principal component (PC1) of tree height and DBH were 72.94% and 67.23%, respectively, and the variance explanation rates of the second principal component (PC2) were 20.78% and 24.99%, respectively. The sums of the variance explanation rates [16] of the first two principal components were 93.72% and 92.22%, which are both greater than 90%. Therefore, the GGE biplot results for tree height and DBH were very reliable.



Tree height
Diameter at breast height

Figure 1. The optimal genotypes on the basis of MET and mega−environment. The blue dots represent the test sites, and the green dots 1–38 represent the genotypes. The test sites between the red lines are the same ME. The green dots furthest from the origin in each ME are the optimal genotypes for the test sites in that ME.



Tree height

Diameter at breast height

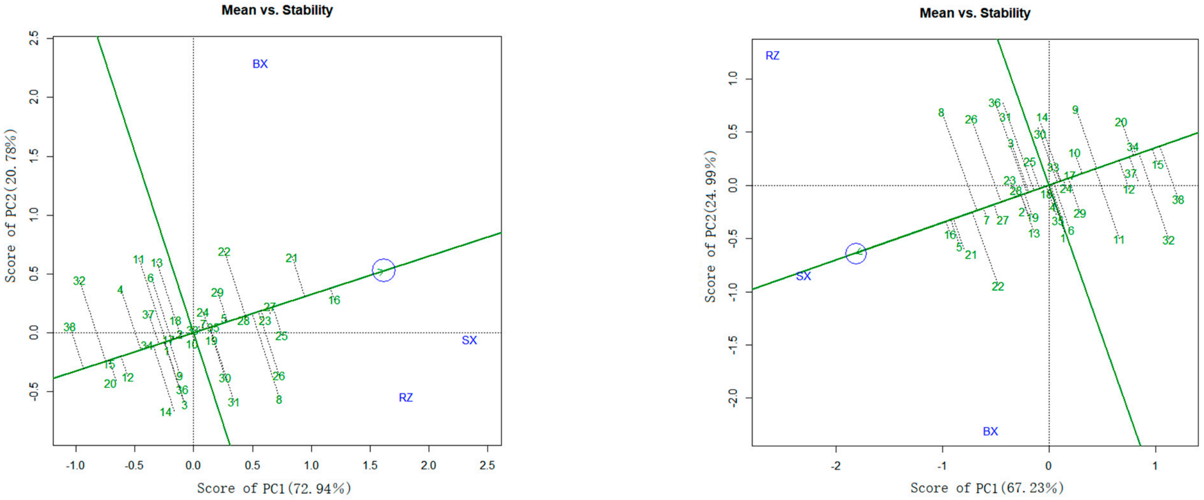
Figure 2. Discrimination and representativeness. The solid blue line with arrows passing through the center of the circle is the average environment axis, and the small circle above it represents the average environment. The length of the dotted blue line vector represents the discriminating power of each test site: the greater the length, the greater the discrimination. The angle between the blue dotted line vector and average environmental axis represents the representativeness of each test point: the smaller the angle, the stronger the representativeness. The angle between the dotted blue line vector represents the correlation of test sites. The greater the correlation between the test sites, the narrower the angle between the vectors of the test sites. When the angle is acute, the correlation is positive; when it is a straight angle, it is irrelevant; and when it is obtuse, the correlation is negative.

3.3.1. Group of the Locations and Optimal Genotypes for Each Location

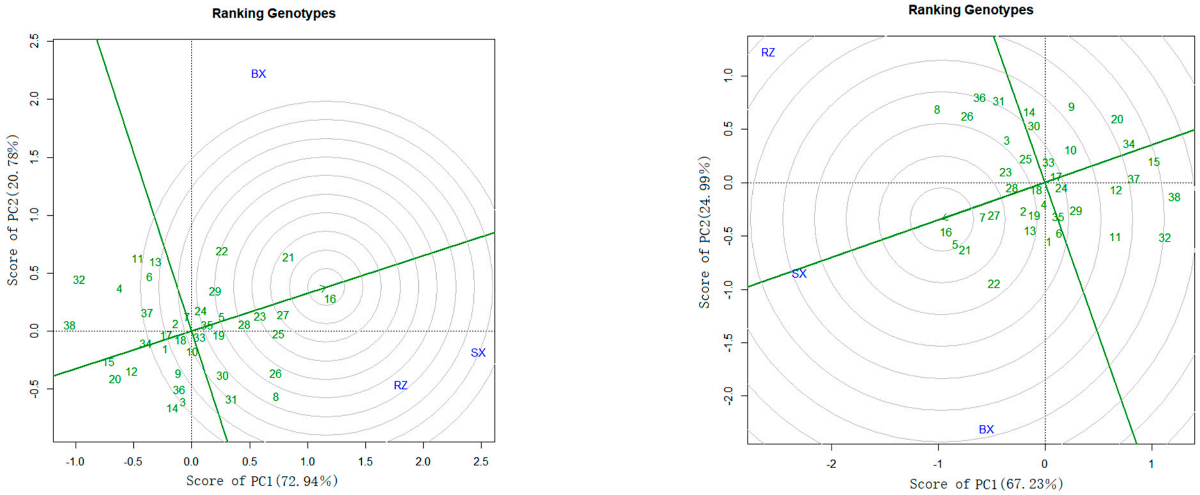
GGE biplots grouped test sites with the same optimal genotype and similar genotype ranking into one group, and test sites in the same group existed in the same ME [9]. The environmental conditions of the test sites of the same ME are similar, and the correlation between test sites is high. The grouping results (Figure 1) revealed that the three experimental sites were classified into two MEs on the basis of tree height, with RZ and SX in one ME and BX in the other; a better genotype for RZ and SX was 16, and a better-performing genotype for BX was 22. An optimal genotype for DBH in sites RZ, SX, and BX was 8, 16, and 22, respectively. The correlation analysis of the three sites (Figure 2) revealed that the vectors between RZ and SX and BX and SX were all acute angles, and the angle between RZ and SX is smaller, showing a positive association between SX and the other two sites and a stronger correlation between RZ and SX. RZ and BX showed a straight angle for tree height but an oblique angle for DBH, revealing that RZ and BX have no correlation for tree height but a negative correlation for DBH.

3.3.2. Discrimination and Representativeness of the Trial Sites

GGE biplots allow for the discrimination and representativeness assessment of trial sites to screen for ideal trial sites [16]. Figure 2 shows the discriminative and representativeness of each experimental site in *P. deltoides*. In terms of tree height, the SX dotted line vector was the longest and the clip degree was the smallest, the RZ dotted line vector was the shortest, and the BX clip degree was the largest, indicating that SX has the best discrimination and representation, RZ has the worst discrimination, and BX has the worst representation. In terms of DBH, the SX clip degree was the smallest and the RZ dotted line vector was the longest, indicating that, among the three sites, SX has the best representation and RZ has the best discrimination. These results showed that SX had better discriminative power and representativeness among the three sites and was the most suitable test site for the *P. deltoides* genotype.



(a) Tree height (b) Diameter at breast height



(c) Tree height (d) Diameter at breast height

Figure 3. High yield and stability. (**a**,**b**) Genotype evaluation results. The green dashed line segment represents the average growth and stability of each genotype: the shorter the dashed line segment, the stronger the stability. The green thick solid line perpendicular to the mean environment axis represents the overall average value of the trait. The average value of the genotype trait on the side of the blue circle is higher than the overall average value. The farther the genotype is from the green thick solid line, the better the trait performance. The average value of the genotype trait on the opposite side of the blue circle is lower than the overall average value. The farther the genotype is from the green thick solid line, the worse the trait performance. (**c**,**d**) Comprehensive evaluation of high yield and stability of each genotype. The smaller the radius of the concentric circles where each genotype is located, the better the overall performance of its high yield and stability.

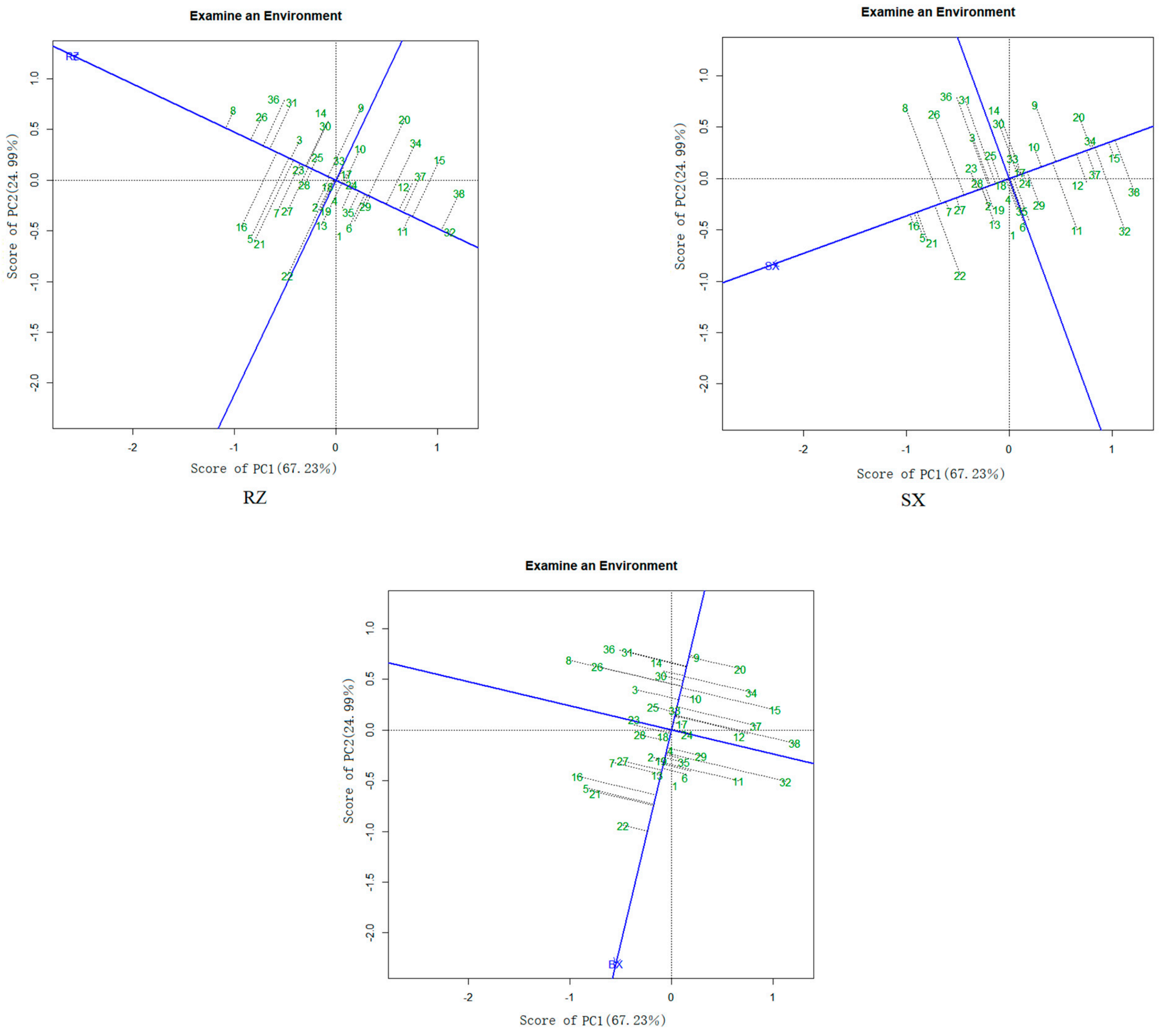
3.3.3. High Yield and Stability

GGE biplots evaluate the high yield and stability of each genotype, and then screen the excellent genotypes with better comprehensive performance. Figure 3 shows that the genotype with the greatest growth in tree height is 16, and 29 genotypes are greater than the 3 control genotypes (15, 37, and 38). Eighteen genotypes showed a growth rate greater than the overall average, among which ten genotypes (such as 16, 27, and 23) had stronger stability; a genotype with general stability was 21, and five genotypes (such as 26, 8, and 22) showed weaker stability. The genotype with the largest growth in DBH was 16. Twenty genotypes exhibited greater growth than the overall average, ten of which were more stable genotypes, including 16, 5, and 7, etc.; five other genotypes, as the stable genotypes, were

19, 25, 21, 13, and 3; and five other genotypes, the less stable genotypes, were 22, 31, 26, 36, and 8. When tree height and DBH are combined, 16, 27, 23, 28, and 5 are better. The genotypes with the best overall performance in terms of tree height, high yield, and stability were 16, 21, 27, and 25; the genotypes with the best overall performance in terms of high yield and stability in DBH were 16, 5, 21, and 7.

3.4. High DBH Yield of Genotypes

On the basis of the breeding objective (wood with a large diameter), the DBH of each genotype in MET was analyzed. In site RZ, the top three DBH genotypes were 8, 26, and 36; in SX, 16, 5, and 21; and in BX, 22, 21, and 5 (Figure 4). They can be chosen as the optimal genotypes for each experimental site.



RZ

SX

BX

Figure 4. High−yield genotypes on the basis of DBH. The origin of the coordinates and point of the test site are connected to form a solid blue line with an arrow (L1), and the direction of the arrow points to the genotype DBH with a high yield. A vertical line (L2) has been drawn through the coordinate origin to L1 to represent the group mean of the trait. The farther the genotypes are from L2 in the direction of the test site, the larger the DBH. The farther the genotypes are from L2 in the opposite direction of the test site, the smaller the DBH.

4. Discussion

Forest tree populations have numerous genetic variations, and their properties are influenced by both genetic and environmental factors [17–19]. In this study, genetic variation analysis showed that the total mean value of tree height and DBH in BX was low, whereas the coefficients of variation, phenotypic variation, and genetic variation were all high. This may be the result of serious soil salinization in BX, which restricts water absorption by roots. The repeatability and heritability of tree height and DBH were greater at each site, with a certain gap between the experimental sites. This indicated that the performance of *P. deltoides* was primarily influenced by genetic factors, and environmental conditions had an impact on the genetic variation of poplar. These findings are consistent with the results of previous studies [20–22].

It was difficult to establish the homogeneity of the test sites because the MET range of the forest trees was broad, and the duration was considerable [23]. Moreover, the measured data frequently lacked or included damaged plants within the blocks and sites, resulting in anomalous and unbalanced data [9,24]. The implementation of mixed linear models plays a significant role in solving this issue in future agroforestry METs. Phenotypic value is the dual response of a genotype to genetic and environmental factors. Unlike phenotypic values, BLUP values exclude the influence of environmental factors, reflect true genetic effects, and improve the accuracy of selection [24]. In this study, the mixed linear model was used to analyze the genetic variation and calculate BLUP values for poplar growth traits. The tree height and DBH were strongly affected by genotype, environment, and G×E impact, indicating that the growth of *P. deltoides* is regulated by genetics and environment and regional breeding strategies need to be established. A large number of studies have confirmed that the genotype, environment, and G×E impacts of poplar [9,25], *Pinus elliottii* [26], *Catalpa bungei*, and *Catalpa fargesii* f. Duclouxii [27] are significant, and regional analyses should be performed to select the genotype suitable for planting at each location.

MET is a crucial component in the breeding and selection of improved tree varieties. G×E alters the genotype ranking and genotype differences at various test sites: a phenomenon known as the rank change and scale effect [7,14,24]. The ecosystems of the three test sites in Shandong Province are highly distinct: the three test sites have a temperate monsoon climate, but the eastern hilly zone (site RZ) is near the coast, and the southwest plain area (SX) and the south-central hilly region (BX) are located on land. In addition, the precipitation, light, and temperature exhibit a distinct shift from southeast to northwest Shandong Province. The region's complex and variable landform types and climatic conditions make it very difficult to breed outstanding genotypes with broad adaptability, and it is essential to select excellent genotypes well-suited to the area. In this study, the tree height and DBH of the three test sites were grouped differently, and an optimal genotype and genotype ranking of each site showed a certain gap. The most suitable genotypes for promotion are those with high growth volume and high adaptability; however, regionally excellent varieties are not always suited for large-scale promotion. These findings are consistent with the research results of *Populus euramericana* [9], *Picea koraiensis* [24], *Pinus massoniana* [28], and *Michelia chapensis* [29]. SX was the most suitable one for planting and breeding of *P. deltoides* among the three experimental sites, which may be related to the similar environmental conditions between SX and place of origin of *P. deltoides*. In addition, SX is located in the alluvial plain of the Yellow River, with fertile soil and excellent drainage, suitable for the growth of *P. deltoides*.

For the selection and breeding of superior genotypes of forest trees, their growth, shape, texture, and resilience must be considered [30]. This experiment will continue to analyze growth traits of *Populus* until the poplar matures to validate the association between the initial growth stage and maturity stage, which will provide empirical evidence for the early selection strategy in future breeding. Poplar breeding goals have changed from a single trait to multiple traits, and wood quality is as important as growth [31,32]. In addition, the cost of forest management should be considered [33]. In this study, only 5-

year-old *P. deltoides* genotypes and DBH were selected and assessed for high yield, stability, and adaptability. In the future, a comprehensive study of many yield attributes is necessary to determine a high-yield and high-quality genotype.

5. Conclusions

The tree height and DBH of 5-year-old *P. deltoides* genotypes varied greatly, with the DBH being greater than tree height. The repeatability and heritability of growth traits (tree height greater than DBH) were greater at each site. The effects of genotype, environment, and G×E were all highly significant. Comprehensive analysis of ME and large-diameter timber revealed that site RZ was optimal for genotypes 8, 26, and 36; BX, 22, 21, and 5; and SX, 16, 5, and 21. Among the three sites, SX showed better discrimination and representativeness and was the most suitable MET site for *P. deltoides*. For commercially preferred large-diameter poplar, genotypes 16, 5, 21, and 7 have great potential and are widely applicable.

Author Contributions: Conceptualization, Z.Y. and C.D.; methodology, Z.Y.; software, Z.Y.; validation, Y.W., W.Z., Y.H., R.Z. and X.Z.; formal analysis, Z.Y.; investigation, Z.Y.; resources, Y.D.; data curation, S.L.; writing—original draft preparation, Z.Y.; writing—review and editing, N.L. and W.Z.; visualization, Z.Y. and C.D.; supervision, C.D. and Y.D.; project administration, Y.D., C.D. and X.S.; funding acquisition, G.L., Y.D., C.D. and X.S. All authors have read and agreed to the published version of the manuscript.

Funding: This research was funded by the National Key Research and Development Program of China (Grant No. 2021YFD2201205) and the Basic Research Fund of CAF (Grant No. CAFYBB2020SZ002).

Data Availability Statement: The data presented in this study are available on request from the corresponding author.

Conflicts of Interest: The authors declare no conflict of interest.

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