1.2 Genetic diversity and kinship analysis of *Platycladus orientalis*

Genetic variation among *Platycladus orientalis* populations was analyzed using seven SSR markers. Based on GenAlEx analysis, the results (Table 2) showed that at the population level, the observed number of alleles per population ranged from 2.571 to 3.571, with an average of 3.071. The effective number of alleles ranged from 1.865 to 1.987, with an average of 1.909. The Shannon information index ranged from 0.725 to 0.807, with a mean of 0.766. Observed heterozygosity ranged from 0.393 to 0.492, with an average of 0.423, while expected heterozygosity ranged from 0.431 to 0.452, with a mean of 0.439. The fixation index (Fst), which reflects the level of allelic heterozygosity among populations and is used to measure the degree of population differentiation, was 0.0371. This value falls within the range of 0–0.05, indicating a high degree of similarity among populations, small genetic distances, and very low genetic differentiation. Population A exhibited the highest values of polymorphism rate, Na, and I, indicating that this population had the highest genetic diversity. It is therefore inferred that population A represents the center of genetic diversity of *P. orientalis* among the four sampling regions.

Table 2 Genetic diversity of *Platycladus orientalis*

Population	N	*Na*	*Ne*	*I*	*Ho*	*He*	*uHe*
a	68	3.571	1.902	0.807	0.394	0.431	0.434
b	9	2.857	1.883	0.761	0.492	0.452	0.479
c	4	2.571	1.987	0.725	0.393	0.433	0.495
d	19	3.286	1.865	0.771	0.414	0.438	0.450
Mean	25	3.071	1.909	0.766	0.423	0.439	0.464

1.3 Genetic Differentiation Analysis of *Platycladus orientalis*

Analysis of variance (ANOVA) was used to assess genetic variation in *Platycladus orientalis*. The results (Table 3) showed that genetic variation in *P. orientalis* was mainly derived from within populations, accounting for 91% of the total variation, while genetic variation among populations accounted for 9%. This indicates that the genetic variation of *P. orientalis* is predominantly distributed within populations.

Table 3 Molecular variance analysis of *P. orientalis* germplasm

Sources of variation	df	SS	MS	Est. Var.	Percentage of variation
Among Pops	3	4.36	1.45	0	0%
Among Indiv	96	165.74	1.73	0.15	9%
Within Indiv	100	143	1.43	1.43	91%
Total	199	313.10		1.58	100%

1.4 Genetic structure analysis of *Platycladus orientalis*

Bayesian clustering analysis of 100 individuals from four populations was performed using STRUCTURE software. The number of subpopulations (K) was preset from 2 to 10, with 10 independent runs for each K value. The value of LnP(D) continuously decreased with increasing K. When K=3, ΔK reached its maximum peak, indicating that division of the experimental materials into three clusters was the most appropriate (Figure 1; Figure 2).

The distribution of individuals among the three clusters (Table 4) showed a relatively even composition, with mean Q values of 0.619, 0.476, and 0.461, respectively. When Q≥0.6, the genetic background of a sample is considered relatively pure, whereas when Q<0.6, the genetic background is considered complex (Falush et al., 2003). In this study, the Q value of Subpopulation 1 was≥0.6, indicating a relatively homogeneous genetic background. In contrast, Subpopulations 2 and 3 had Q values<0.6, suggesting that these two subpopulations integrated genetic components from multiple clusters and exhibited evident gene flow.

The first cluster contained 39 individuals, including 27 from Shanting District, 2 from Yicheng District, 2 from Shizhong District, and 7 from Tengzhou City. The second cluster comprised 28 individuals, including 18 from Shanting District, 2 from Yicheng District, and 5 from Tengzhou City. The third cluster contained 23 individuals,