

Research Report

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Genetic Diversity and Genetic Relationship Analysis of *Platycladus orientalis* Germplasm Based on SSR Markers

Jilei Zhou¹, Liudong Zhang¹, Yinyin Fu², Yong Chen³, Jingtao Li¹ ✉¹ Forestry Protection and Development Service Center of Shandong Province, Ji'nan, 250014, Shandong, China² Shandong Academy of Forestry Sciences/ Key Laboratory for Genetics and Breeding in Forest Trees of Shandong, Ji'nan, 250014, Shandong, China³ Ji'nan Forestry and Fruit Technology Promotion and Industrial Service Center, Ji'nan, 250102, Shandong, China✉ Corresponding email: lzh529@163.comPlant Gene and Trait, 2026, Vol.17, No.1 doi: [10.5376/pgt.2026.17.0001](https://doi.org/10.5376/pgt.2026.17.0001)

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Abstract To investigate the genetic diversity and phylogenetic relationships among *Platycladus orientalis* germplasm resources in Zaozhuang City, simple sequence repeat (SSR) molecular markers were used to analyze genetic diversity and relatedness in 100 *P. orientalis* accessions collected from four regions. The results showed that a total of 32 allelic loci were detected using seven pairs of SSR primers, with an average of 6.571 alleles per primer pair. The mean number of alleles (N_a) was 3.714, the mean effective number of alleles (N_e) was 1.900, the mean Shannon's information index (I) was 0.818, and the mean expected heterozygosity (H_e) was 0.440, indicating relatively high genetic diversity among the 100 sampled *P. orientalis* accessions. The F_{st} value was 0.0371, suggesting a high degree of similarity among populations, small genetic distances, and low genetic differentiation. Cluster analysis based on the estimation of the optimal K value showed that the maximum ΔK occurred at $K=3$, indicating that the 100 *P. orientalis* accessions could be divided into three groups rather than clustering strictly according to geographic origin, which implies the existence of gene flow among the sampled populations. Through preliminary screening and repeated validation, seven pairs of SSR primers with clear gel electrophoresis profiles were obtained, which showed stable amplification across all populations and yielded reliable, easily interpretable results. These microsatellite markers provide a useful reference for future studies on the origin and evolution of *P. orientalis* varieties, molecular identification and classification, hybrid breeding, and parental selection for genetic mapping.

Keywords *Platycladus orientalis*; SSR; Fingerprinting; Cluster analysis

1 Introduction

Platycladus orientalis, belonging to the family Cupressaceae, subfamily Cupressoideae, genus *Platycladus* (Fu, 1982), is the coniferous tree species with the widest natural distribution in China. It has a broad ecological amplitude, strong tolerance to drought and poor soils, vigorous vitality, and a long lifespan. It is one of the most commonly used pioneer tree species for afforestation of barren mountains in northern China, possessing extremely high economic and medicinal value, and it is also an important component of historical and cultural landscapes (Wu, 1986; Yang et al., 2014a). With global climate change, under the combined effects of natural disasters, deterioration of site conditions, pests and diseases, as well as subjective factors such as human disturbance and poor management, *P. orientalis* populations have shown varying degrees of decline, including weakened growth and even near death. The conservation and utilization of *P. orientalis* germplasm resources are facing great challenges, and its ecological value has not been effectively utilized (Su, 2003; Wang et al., 2004; Yang et al., 2014b).

Since the 1970s, extensive provenance trials have been carried out for *P. orientalis*, making it one of the earliest tree species in China to undergo such trials. In recent years, many scholars have conducted substantial research on provenance testing and patterns of genetic variation in *P. orientalis* (Wang, 2011). Numerous studies have also investigated and discussed the pharmacologically active components in different parts of *P. orientalis* (Miao Hui, 2018). During cultivation, a number of regional cultivars have been formed. Due to its wide distribution, wild populations of *P. orientalis* possess rich genetic resources. By studying the genetic variation and distribution patterns of *P. orientalis*, analyzing its genetic diversity and phylogenetic relationships, further revealing kinship