and evolutionary relationships, and evaluating its genetic potential and value, a theoretical foundation can be established for the construction of core germplasm collections and the screening of superior genes. This is of great significance for the selection and utilization of elite germplasm.

With continuous advances in science and technology, methods for studying genetic diversity have also been constantly updated. Molecular marker techniques, owing to their advantages of being unaffected by environmental factors, developmental stage, or gene expression, have become important tools in genetic research (Liu et al., 2012). Geographic population variation in *P. orientalis* has shown significant effects on population selection and improvement (Jin, 2020). There is an urgent need to improve the genetic quality and adaptability of superior *P. orientalis* varieties through molecular marker technologies and to carry out research on the genetic basis of breeding populations. Among these methods, microsatellite markers (simple sequence repeats, SSRs), because of their high level of genetic information, good reproducibility and stability, and codominant inheritance (Maroof et al., 1994; Guichoux, 2011), have been widely used in studies of genetic diversity and phylogenetic relationships in forest trees (Reisch et al., 2007; Kalia, 2011; Lin et al., 2013; Huang et al., 2018). At present, sequenced genomes are mainly concentrated in cultivated plants and species with important economic value. Meanwhile, the development of new microsatellite primers is difficult and costly. However, species derived from a common ancestor often exhibit high sequence homology. Therefore, screening SSR primers required for the target species from closely related species with well-developed microsatellite primers has been widely adopted (Barbara, 2007).

In this study, SSR molecular markers were used to analyze the genetic diversity and kinship relationships of 100 *P. orientalis* samples collected from four regions. Through preliminary screening and repeated validation, seven pairs of microsatellite primers were selected from all synthesized SSR primers. These primers produced clear gel electrophoresis patterns, could be stably amplified in each population, showed relatively ideal performance, and were easy to score and statistically analyze, and were thus used for subsequent analyses.

1 Results and Analysis

1.1 PCR amplification and primer polymorphism

Through primer screening and repeated validation, seven polymorphic microsatellite primers were successfully selected from 45 pairs of SSR primers. These primers produced clear gel electrophoresis profiles, could be stably amplified in all populations, showed relatively ideal performance, and were easy to score and statistically analyze. A total of 26 allelic loci were detected by the seven SSR primers, mainly distributed in the range of 125–309 bp (Table 1). On average, each SSR primer detected 3.714 alleles. The number of effective alleles (Ne) ranged from a minimum of 1.317 for primer 18 to a maximum of 2.819 for primer SF13, with a mean of 1.9. The observed heterozygosity (Ho) of *Platycladus orientalis* populations ranged from 0.140 to 0.610, with an average of 0.406. The expected heterozygosity (He) varied from 0.241 to 0.645, with a mean value of 0.440. The polymorphic information content (PIC) ranged from 0.212 to 0.579. Highly polymorphic primers (PIC>0.5) accounted for 28.6% of the total, primers with moderate polymorphism (0.25<PIC<0.5) accounted for 57.1%, and primers with low polymorphism (PIC<0.25) accounted for 14.3%, with an average PIC value of 0.398. The Shannon information index (I) ranged from 0.405~1.194, with an average of 0.818, indicating that the genetic diversity of the population of 100 *P. orientalis* accessions was relatively low.

Table 1 Genetic diversity characteristics of different SSR loci

Locus	Genotype No.	*Na*	*Ne*	*I*	*Ho*	*He*	u*He*	*PIC*
4	3	2	1.688	0.598	0.350	0.408	0.410	0.325
18	3	2	1.317	0.405	0.140	0.241	0.242	0.212
SF3	5	3	1.595	0.685	0.380	0.373	0.375	0.341
SF14	12	5	2.441	1.194	0.610	0.590	0.593	0.557
SF4	7	5	1.894	0.955	0.490	0.472	0.475	0.441
SF12	6	4	1.551	0.703	0.370	0.355	0.357	0.330
SF13	10	5	2.819	1.188	0.505	0.645	0.649	0.579
Mean	6.571	3.714	1.900	0.818	0.406	0.440	0.442	0.398