

PowerMarker V3.25 software was used to analyze the genotype data, including the number of alleles, number of genotypes, heterozygosity, and polymorphic information content (PIC) for different sample combinations. Genetic distances among varieties were also calculated, and clustering was performed using the unweighted pair-group method with arithmetic means (UPGMA) (Liu, 2005).

### Author Contributions

Zhou Jilei and Li Jingtao were responsible for the experimental design and the execution of the experimental research. Zhou Jilei and Zhang Liudong carried out data analysis and prepared the first draft of the manuscript. Fu Yinyin completed the experimental design and analysis of the experimental results. Chen Yong participated in sample collection for the study. Li Jingtao conceived and led the project and provided guidance on experimental design, data analysis, and manuscript writing and revision. All authors read and approved the final manuscript.

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### References

- Barbara T., Palma-Silva C., GECELE M. Paggi G.M., Bered F., Fay M.F., and Lexer C., 2007, Cross-species transfer of nuclear microsatellite markers: potential and limitations, *Molecular Ecology*, 16(18): 3759-3767.  
<https://doi.org/10.1111/j.1365-294X.2007.03439.x>
- Falush D., Wirth T., Linz B., Pritchard J.K., Stephens M., Kidd M., Blaser M.J., Graham D.Y., Vacher S., Perez-Perez G., Yamaoka Y., Me'graud F., Otto K., Reichard U., Katzwitsch E., Wang X., Achtman M., and Suerbaum S., 2003, Traces of human migrations in *Helicobacter pylori* populations, *Science*, 299(5612): 1582-1585.  
<https://doi.org/10.1126/science.1080857>
- Guichoux E., Lagache L., Wagner S., Chaumeil P., LÉGER P., Lepais O., Lepoittevin C., Malausa T., Revardel E., Salin F., and Petit R.J., 2011, Current trends in microsatellite genotyping, *Molecular Ecology Resources*, 11(4): 591-611.  
<https://doi.org/10.1111/j.1755-0998.2011.03014.x>
- Huang L.S., Song J., and Sun Y.Q., 2018, Pollination dynamics in a *Platycladus orientalis* seed orchard as revealed by partial pedigree reconstruction, *Canadian Journal of Forest Research*, 48: 952-957.  
<https://doi.org/10.1139/cjfr-2018-0077>
- Jin Y., 2020, Genetic evaluation of the breeding population of *Platycladus orientalis* and management strategies, Beijing Forestry University, Supervisors: Wang X. and Mao J., pp.79-80.
- Jing D., Luo X., Chen L., Li H., Tang L., and Cao S., 2020, Genetic diversity analysis of 78 walnuts based on SSR molecular marker, *Acta Agriculturae Jiangxi*, 32(6): 11-16.
- Kalia R.K., Rai R.K., Kalia S., Singh R., and Dhawan A.K., 2011, Microsatellite markers: an overview of the recent progress in plants, *Euphytica*, 177(3): 309-334.  
<https://doi.org/10.1007/s10681-010-0286-9>
- Lei A.A. 2018, Genetic diversity of ancient *Platycladus orientalis* population in Qiao Mountain and DNA fingerprint of the old tree planted by Huang Di, Northwest A&F University, Supervisor: Li Z., pp.17-18.
- Lexer C., Welch M.E., Raymond O., and Rieseberg L.H., 2003, The origin of ecological divergence in *Helianthus paradoxus* (Asteraceae): selection on transgressive characters in a novel hybrid habitat, *Evolution*, 57(9): 1989-2000.  
<https://doi.org/10.1111/j.0014-3820.2003.tb00379.x>
- Lin Z., Anru L., and Vendramin G.G., 2013, Old-growth *Platycladus orientalis* as a resource for reproductive capacity and genetic diversity, *PLoS One*, 8(2): e56489.  
<https://doi.org/10.1371/journal.pone.0056489>
- Liu K., and Muse S.V., 2005, PowerMarker: an integrated analysis environment for genetic marker analysis, *Bioinformatics*, 21(9): 2128-2129.  
<https://doi.org/10.1093/bioinformatics/bti282>
- Liu Y., Yang S.X., Ji P.Z., and Gao L.Z., 2012, Phylogeography of *Camellia taliensis* (Theaceae) inferred from chloroplast and nuclear DNA: insights into evolutionary history and conservation, *BMC Evolutionary Biology*, 12(1): 92.  
<https://doi.org/10.1186/1471-2148-12-92>
- Miao H., 2018, Studies on the chemical constituents and pharmacological activities of *Platycladi cacumen*, Jilin Agricultural University, Supervisor: Bao H., pp.49-51.
- Reisch C., Mayer F., Ruther C., and Nelle O., 2007, Forest history affects genetic diversity-molecular variation of *Dryopteris dilatata* (Dryopteridaceae) in ancient and recent forests, *Nordic Journal of Botany*, 25(5-6): 366-371.  
<https://doi.org/10.1111/j.0107-055X.2008.00188.x>
- Rieseberg L.H., 1995, The role of hybridization in evolution: old wine in new skins, *American Journal of Botany*, 82(7): 944-953.  
<https://doi.org/10.1002/j.1537-2197.1995.tb15711.x>