Postprint: Early Selection of Superior Drought-Resistant Families of Nitraria tangutorum

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Abstract

To select drought-resistant elite families of Nitraria tangutorum, this experiment measured the contents of soluble sugar (SS), soluble protein (SP), free proline (Pro), catalase (CAT), peroxidase (POD), superoxide dismutase (SOD), and chlorophyll (Chl) in 31 families from Lanzhou and Wuwei test sites in 2015, 2016, and 2018. Principal component analysis and membership function method were employed to comprehensively evaluate family drought resistance, select elite families, and conduct comparative analysis. The results showed that the coincidence rate of results from the two comprehensive evaluation methods exceeded 80%. At a 20% selection rate, four families (j3-9, jc-8, w3-15, and w3-12) from the two test sites were selected in both 2015 and 2016, and their drought resistance was significantly superior to other families in 2018. The selected families exhibited consistent drought resistance performance across different years and test sites, indicating that drought-resistant elite families of Nitraria tangutorum display stable drought resistance across different physiological stages and environments, and that early selection is reliable.

Full Text

Early Selection of Drought-Resistant Superior Families in *Nitraria tangutorum*

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Abstract

To select superior drought-resistant families of *Nitraria tangutorum*, we measured soluble sugar (SS), soluble protein (SP), free proline (Pro), peroxidase (POD), catalase (CAT), superoxide dismutase (SOD), and chlorophyll (Chl) contents in 31 families across two experimental sites (Lanzhou and Wuwei) during 2015, 2016, and 2018. Principal component analysis and membership function methods were employed for comprehensive evaluation and comparison of drought resistance. The results showed that the coincidence rate between the two evaluation methods exceeded 80%. When using a 20% selection rate to identify drought-resistant families, four families (j3-9, jc-8, w3-15, and w3-12) were selected in both 2015 and 2016, and their drought resistance in 2018 was significantly superior to unselected families. The selected families exhibited consistent drought resistance performance across different years and experimental sites, indicating stable drought resistance in superior *N. tangutorum* families under varying physiological stages and environmental conditions, thus confirming the reliability of early selection.

Keywords: *Nitraria tangutorum*; superior families; drought resistance; early selection; comprehensive evaluation

1 Materials and Methods

1.1 Study Area Overview

The *Nitraria tangutorum* family trial forests were established at two environmentally distinct locations: Yangxiaba Town, Liangzhou District, Wuwei City, Gansu Province (38°24 N, 103°9 E) and Daoshuitang Village, Zhongchuan Town, Lanzhou New District, Gansu Province (36°30 N, 103°37 E), representing the northern Hexi Corridor and northwestern Loess Plateau, respectively. The sites have elevations of 1378 m and 1947.2 m, annual precipitation of 113.2 mm and 328 mm, annual evaporation of 2604.3 mm and 1880 mm, and mean annual temperatures of 9.6°C and 6.9°C. Both locations feature alkaline sandy loam soils with precipitation as the primary water source, representing typical temperate continental desert and semi-arid continental climates.

1.2 Experimental Materials and Field Design

In October 2014, seeds were collected from multiple healthy, disease-free maternal plants across five natural *N. tangutorum* populations in Jiuquan, Zhangye, Lanzhou, and Wuwei, Gansu Province . Seeds were sown in plug trays in April 2015 and systematically numbered according to their parental origin. Seedlings were transplanted to the experimental sites in April 2016 when soil thawed and soil temperature exceeded 0°C. A randomized block design was employed with 0.5 m $\times$ 1.5 m spacing, 10 plants per family per replicate, and three replicates. Irrigation was applied after transplanting, and routine management practices including timely weeding were implemented after seedling establishment.

1.3 Measurement Indicators and Methods

In mid-July 2016 and 2018, 31 families preserved at both Wuwei and Lanzhou sites were selected as experimental materials. Based on preliminary experiments, three families each representing high, medium, and low drought resistance were selected for analysis. For each family, three individual plants were sampled, and leaves from the middle portion of upright stems were collected, immediately frozen in liquid nitrogen, and transported to the laboratory for physiological and biochemical measurements. Each sample was measured in triplicate. Soluble sugar content was determined using the anthrone colorimetric method, soluble protein by Coomassie brilliant blue G-250 staining, free proline by sulfosalicylic acid extraction, chlorophyll by acetone colorimetry, catalase activity by UV absorption, peroxidase by guaiacol method, and superoxide dismutase by nitroblue tetrazolium method.

2 Comprehensive Evaluation Methods

2.1 Principal Component Analysis

Principal component analysis is a multivariate technique that reduces data dimensionality while eliminating redundant information among variables. This method was applied to analyze seven physiological indicators of *N. tangutorum* families.

2.2 Membership Function Method

The membership function method was used to comprehensively evaluate drought resistance across different families based on their physiological responses.

3 Results

3.1 Drought Resistance Indicators Across Families

Physiological indicators varied significantly among the 31 *N. tangutorum* families at both experimental sites. Using 2016 data as an example , at the Lanzhou site, family gl-34 exhibited the highest POD content, jc-8 the highest Pro content, and j3-9 the highest CAT content. At the Wuwei site, gl-35 showed the highest POD content, j3-9 the highest CAT content, and jc-5 the highest SS content. Family w3-12 demonstrated the highest SP content, while w3-15 showed the highest SOD content at both sites. Variations and fluctuations in indicators were observed across different sites and years. Evaluating drought resistance using single indicators yielded inconsistent results due to complex relationships among indicators and varying importance of each parameter, necessitating comprehensive analysis.

3.2 Comprehensive Evaluation

3.2.1 Principal Component Analysis Principal component analysis revealed that at the Lanzhou site, the first three principal components in 2016 contributed 54.3%, 20.4%, and 11.4% of the variance, respectively, with cumulative contributions of 73.0% and 81.5% for 2016 and 2018. At the Wuwei site, the first three components contributed 53.4%, 22.7%, and 12.6% in 2016, and 49.1%, 28.0%, and 17.5% in 2018, with cumulative contributions of 83.3% and 94.6%, respectively [TABLE:3, TABLE:4]. Families w3-15, w3-12, and zl-23 consistently ranked highest across both years and sites [TABLE:5, TABLE:6]. Notably, w3-15 and w3-12 were repeatedly selected, ranking 1st and 2nd respectively in both 2016 and 2018, demonstrating superior and stable drought resistance across different environments and physiological stages.

3.2.2 Membership Function Method Using CAT, SS, SP, Pro, and Chl as evaluation indicators, average membership function values were calculated for each family. At the Lanzhou site, selected families in 2016 were w3-15, w3-12, zl-24, and jc-8, with average membership values of 0.91–0.68. In 2018, selected families were w3-15, w3-12, and zl-23, with values of 0.85–0.64. Families w3-15 and w3-12 were repeatedly selected across both years . At the Wuwei site, selected families in 2016 were w3-12, w3-15, and zl-23, with values of 0.77–0.62. In 2018, selected families were w3-12, w3-15, and lsm-28, with w3-12 and w3-15 showing repeated selection . Both evaluation methods identified w3-15 and w3-12 as superior drought-resistant families across different years and sites, with coincidence rates exceeding 80%.

4 Discussion and Conclusion

Drought resistance is a complex adaptive mechanism formed through long-term evolution in arid environments, involving multiple interacting factors. Previous studies have demonstrated that single-indicator assessments of plant resistance are incomplete. Our findings confirm that using individual indicators to evaluate *N. tangutorum* families yields inconsistent results. Therefore, comprehensive evaluation through multiple physiological indicators is essential for accurate assessment of drought resistance and stability.

The selected superior families showed consistent drought resistance performance across different years at the same site (coincidence rate >80%), indicating stable drought resistance expression at different physiological stages under consistent environmental conditions. This stability suggests that early-stage drought resistance correlates with mature-stage performance, validating the reliability of early selection based on physiological indices. Two families (w3-15 and w3-12) consistently outperformed others across different years and sites, demonstrating both superior drought resistance and high environmental adaptability.

While the coincidence rate of selected families between Wuwei and Lanzhou sites exceeded 70% within the same year, some variations existed, indicating that drought resistance in *N. tangutorum* families is influenced by environmental conditions and that adaptive capacity differs among families. This environmental sensitivity is advantageous for identifying families with stronger adaptability to specific arid conditions. The declining membership function values from 2016 to 2018 may reflect physiological adjustments to environmental changes, warranting further investigation, though family rankings remained relatively stable.

Numerous studies have established correlations between physiological-biochemical indicators at different developmental stages in forest trees, supporting the use of comprehensive physiological evaluations for early selection. Our results demonstrate that early selection of superior drought-resistant families in *N. tangutorum* is reliable, providing a theoretical foundation for breeding and popularization of drought-resistant germplasm.

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Note: Figure translations are in progress. See original paper for figures.