



ISSN (E): 2277-7695
 ISSN (P): 2349-8242
 NAAS Rating: 5.23
 TPI 2023; 12(10): 650-653
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www.thepharmajournal.com
 Received: 20-07-2023
 Accepted: 26-08-2023

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Influence of source variability on morphological traits of *Salix triandra* L.: Exploring shoots, nodes and inter nodal length

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Abstract

The almond-leaved willow, scientifically classified as *Salix triandra* L. within the Salicaceae family, exhibits dioecious characteristics, occasionally assuming a small tree form, and thrives in a wide range of environmental conditions. The present study delves into the intricate aspects of nodes and inter nodal lengths in *Salix triandra* L. The present study considered the impact of source variability on the number of shoots, the count of nodes, and the length of internodes in *Salix triandra* L. A total of 15 diverse sources from the Kashmir Valley were selected based on species distribution and abundance. These sources were subjected to experimentation at a research field within the Division of Forest Biology and Tree Improvement at Sher-e-Kashmir University of Agricultural Sciences & Technology of Kashmir. The findings reported that the treatments, G₃, G₇, and G₁₄ in Ganderbal, Budgam, and Pulwama respectively had the highest number of shoots (5). No significant differences were found in the number of nodes among treatment combinations. The treatment, G₁ had the longest inter nodal length at 2.55 cm, while G₄ and G₁₄ were statistically similar at 1.35 cm each. Genotypic coefficient of variation (GCV) averaged 28.56, 21.18, and 35.59. The highest heritability (H²) was found for node count (inch⁻¹) at 0.86. Genetic advance at 5% selection intensity was 2.13 for shoot number, 0.75 for inter nodal length, and 0.08 for node count. High Genetic Advance as a Percentage of Mean (GAM), especially for shoot number and node count (inch⁻¹) at 52.81 and 50.33, highlights effective genetic diversity utilization in breeding, guiding crop enhancement strategies. The study underscores the importance of understanding node and internodal characteristics in the context of source variability, providing valuable insights into the biological processes of *Salix triandra* L. in diverse environmental conditions.

Keywords: Source, variability, *Salix triandra*, nodes, shoots, inter nodal length

Introduction

Salix triandra L., commonly known as the almond-leaved willow, is a dioecious shrub species within the Salicaceae family. This versatile species, known for its adaptability and ecological significance, often assumes a small tree form and thrives in a wide range of environmental conditions (Levensen and Gleason, 2015; Aronsson *et al.*, 2010) [6, 2]. *Salix triandra* L. has been the subject of extensive ecological and genetic studies due to its unique characteristics, including its ability to grow in diverse habitats, rapid growth, and capacity for vegetative propagation (Isebrands and Richardson, 2018; Pliura *et al.*, 2015; Trybush *et al.*, 2008) [4, 7, 11]. Morphological traits, such as the number of shoot, node count, and inter nodal length, play crucial roles in the growth and development of *Salix triandra* L. These traits are of particular interest not only for ecological understanding but also for potential applications in breeding programs aimed at harnessing the species' genetic diversity for various purposes, including bioenergy production and environmental restoration (Abdollahzadeh *et al.*, 2017; Serapiglia *et al.*, 2015; Taylor *et al.*, 2019) [1, 8, 10]. The variation in these morphological traits within and among populations of *Salix triandra* L. has been the focus of previous research, with studies indicating that environmental factors and genetic diversity can significantly influence these traits (Xiao *et al.*, 2019; Isebrands and Richardson, 2018) [12, 4]. Understanding the sources of variability in these traits is essential for effective breeding and conservation efforts.

Nodes, those discrete points along a stem from which branching twigs, buds, and leaves emanate, play pivotal roles in a plant's life cycle. These unassuming structures serve as hubs for critical biological functions, including healing, structural support, and the initiation of new growth (Kozlowski and Pallardy, 1997) [5]. Even during the harsh winter months when deciduous trees shed their leaves, nodes remain active, occasionally bearing buds that may

determine the plant's future vitality. Internodal lengths, the segments of the stem that bridge the gaps between nodes, function as conduits for the transport of essential nutrients, hormones, and water from one node to the next. In essence, they are the plant's circulatory system, facilitating the flow of life-sustaining resources (Taiz and Zeiger, 2010) [9]. These lengths are a crucial determinant of a plant's architecture and its ability to efficiently allocate resources (Givnish, 1988) [3].

The present study delves into the intricate world of nodes and inters nodal lengths in *Salix triandra* L. and their dynamic relationship with source variability. The diversity of environmental conditions across different sources of this species offers a unique opportunity to explore how these fundamental characteristics adapt and respond to varying ecological contexts. The present investigation takes place against the backdrop of the Kashmir Valley, a region known for its ecological diversity and unique environmental challenges. By selecting sources from various districts within this valley, the present study aims to capture the full spectrum of environmental conditions and genetic factors that *Salix triandra* L. encounters in its habitat. In the present study, a detailed analysis of the number of nodes, inter nodal length, and their relationship with source variability in *Salix triandra* L. is presented. The present study also examines genetic parameters, including genotypic coefficient of variation (GCV), heritability (H^2), and genetic advance, to quantify the genetic influence on these key traits. Additionally, the concept of Genetic Advance as a Percentage of Mean (GAM) is employed to assess the effectiveness of utilizing genetic diversity in breeding programs for trait enhancement. The findings of the study hold significance not only for understanding the biology of *Salix triandra* L. but also for informing breeding strategies that can optimize the performance of this species in diverse environmental conditions. Moreover, this research contributes to the broader understanding of the ecological and genetic dynamics of dioecious shrub species, which have ecological relevance beyond their immediate applications.

Materials and methods

Study area

The present study was carried out in the research field of Division of Forest Biology and Tree Improvement, Faculty of Forestry, Benhama, Ganderbal, Sher-e-Kashmir University of Agricultural Sciences & Technology of Kashmir, J&K, India, located at an elevation of 1783 m (5850 ft) above mean sea level, between latitude 34°16'44"N and longitude 74°46'31"E. Average annual precipitation is 690 mm, with average maximum and lowest temperatures of 20.13°C and 6.5°C respectively.

Experimental setup and design

For leading the experiment, the five districts of Kashmir region namely Ganderbal, Srinagar, Budgam, Baramulla, and Pulwama were chosen as the sources for the collection of experimental material. Based on the distribution and abundance of the species, three locations from each district were chosen using the purposive sampling technique. Finally, 15 sources were selected across the five districts of Kashmir Valley. At a spacing of 40 cm × 30 cm in a randomized block design, the procured stem cuttings were planted in three replicates in the research field of study area. The plant

samples were examined at the Laboratory of Forest Biology and Tree Improvement after the completion of the growing season for various morphometric, physiological, and wood characteristics.

Methodology

Number of nodes

Nodes are the places on a stem from which branching twigs, buds, and leaves emerge. They are critical locations on the plant where vital biological functions, such as healing and structural support, occur. Many plants lose their leaves in the winter, and some nodes never develop stems, yet even under these situations, buds may be seen at a node on living wood. However, occasionally the buds may die and detach at a node. When the shoots were brought to the lab for additional morphological examinations, the total number of nodes was measured on per inch basis. The total number of nodes per inch was counted when the shoots were brought to the laboratory for additional morphological examinations.

Inter nodal length

Internodes are the stem sections between nodes. If the nodes are the essential organs of the plant, the internodes are the conduits that transport nutrients, hormones, and water from one node to the next. The inter nodal length was calculated using a measuring scale as the distance between two successive leaves on the main axis at a distance of 30 cm from the base.

Results

The examination of the data presented in Table 1 reveals the highest number of shoots (5) in G₃, G₇, and G₁₄ for Ganderbal, Budgam, and Pulwama, respectively. Regarding the number of nodes, no significant differences were observed among the various treatment combinations. Specifically, treatment G₁ displayed a significantly maximum inter nodal length of 2.55 cm, whereas the minimum inter nodal length was observed in G₄, which was found to be statistically equivalent to G₁₄, with a value of 1.35 cm each.

Table 1: Effect of source variability on number of shoots, number of nodes and inter nodal length of *Salix triandra* L.

Source	Number of Shoots	Number of Nodes (inch ⁻¹)	Internodal Length (cm)	
Ganderbal	G ₁	4 ^b	1 ^b	2.55 ^a
	G ₂	4 ^b	2 ^a	1.50 ^{ef}
	G ₃	5 ^a	1 ^b	1.75 ^{def}
Srinagar	G ₄	4 ^b	2 ^a	1.35 ^f
	G ₅	4 ^b	2 ^a	1.45 ^{ef}
	G ₆	3 ^c	2 ^a	1.55 ^{ef}
Budgam	G ₇	5 ^a	1 ^b	2.20 ^{abc}
	G ₈	2 ^d	1 ^b	1.70 ^{def}
	G ₉	2 ^d	1 ^b	1.70 ^{def}
Baramulla	G ₁₀	4 ^b	1 ^b	1.85 ^{cde}
	G ₁₁	3 ^c	1 ^b	1.75 ^{def}
	G ₁₂	3 ^c	1 ^b	2.10 ^{bcd}
Pulwama	G ₁₃	3 ^c	1 ^b	2.45 ^{ab}
	G ₁₄	5 ^a	2 ^a	1.35 ^f
	G ₁₅	2 ^d	1 ^b	2.29 ^{ab}
C. D. ($p \leq 0.5$)		0.41	NS	0.69
W ($p \leq 0.05$)		0.03	0.06	0.09

Table 2: Mean, range, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability, genetic advance, genetic advance as percentage of mean of morphometric traits of *Salix triandra* L.

Characters	Mean	Range	GCV	PCV	Heritability (H ²)	Genetic advance	Genetic advance as percentage of mean
No. of shoots	4.04	1.00 - 7.00	28.56	31.82	0.80	2.13	52.81
Internodal length (cm)	2.05	0.77 - 3.81	21.18	25.25	0.70	0.75	36.58
No. of nodes (inch ⁻¹)	1.60	1.00 - 3.00	36.59	46.59	0.86	0.08	50.33

From the data presented in Table 2, it is evident that there was variation in the number of shoots, inter nodal length, and number of nodes, ranging from 1.00 to 7.00, 0.77 cm to 3.81 cm, and 1.00 inch⁻¹ to 3.00 inch⁻¹, respectively. The genotypic coefficient of variation (GCV) for these traits was approximately 28.56, 21.18, and 35.59, as shown in Table 2. Notably, for all the parameters under study, the phenotypic coefficient of variation (PCV) exceeded the GCV. Of particular interest, the highest heritability (H²) was observed in the case of node count (inch⁻¹), with a value of 0.86. This high heritability suggests that environmental factors had minimal influence on this trait, highlighting its strong genetic determination (Table 2). Genetic advance represents an increase in the mean genotypic value of selected plants compared to the parental population. We calculated the expected genetic advance at a 5 percent selection intensity and found that the greater the genetic advance, the more significant the improvement in the genotypic value over the parental population. Specifically, the genetic advance values for the number of shoots, inter nodal length, and node count were 2.13, 0.75, and 0.08, respectively. High Genetic Advance as a Percentage of Mean (GAM) values are generally positive indicators in plant breeding, as they suggest that breeding programs effectively leverage genetic variation to enhance the trait of interest. In our study, the highest GAM values were observed for the number of shoots and node count (inch⁻¹), with values of 52.81 and 50.33, respectively (Table 2).

Discussion

Number of nodes

Nodes are integral components of a plant's architecture and physiology. These discrete points along a stem serve as hubs for various biological functions, including the initiation of new growth and the production of lateral branches (Kozłowski and Pallardy, 1997) [5]. Nodes also play essential roles in healing processes and structural support (Givnish, 1988) [3]. Their significance extends to resource allocation strategies and reproductive success in plants (Pliura *et al.*, 2015) [7].

No. of nodes (inch⁻¹)

Our study's finding that node count (inch⁻¹) exhibits high heritability (0.86) suggests that this trait is primarily governed by the plant's genetic makeup. Such a high heritability value for node count underscores the stable genetic basis of this trait, making it a reliable target for selective breeding programs aimed at optimizing *Salix triandra* L.'s growth and resource allocation strategies.

Genetic Parameters

Genetic parameters, including genotypic coefficient of variation (GCV) and genetic advance, provide valuable insights into the genetic diversity within *Salix triandra* L. populations and the potential for trait improvement. The substantial GCV values for the number of shoots, inter nodal

length, and node count indicate the presence of genetic diversity that can be harnessed for crop improvement (Abdollahzadeh *et al.*, 2017) [1]. These findings corroborate the importance of conserving genetic resources in *Salix triandra* L. for future breeding efforts (Trybush *et al.*, 2008) [11]. The genetic advance values for shoot number (2.13) and inter nodal length (0.75) signify that these traits can be significantly improved through selective breeding. However, the relatively lower genetic advance value for node count (0.08) suggests that this trait may already be close to its genetic optimum. These insights guide breeding strategies by indicating which traits are more amenable to improvement.

Genetic Diversity

The concept of Genetic Advance as a Percentage of Mean (GAM) is a powerful tool in plant breeding, as it reflects the effective utilization of genetic diversity in breeding programs (Abdollahzadeh *et al.*, 2017) [1]. In our study, the exceptionally high GAM values for shoot number and node count (inch⁻¹) at 52.81 and 50.33, respectively, demonstrate that *Salix triandra* L. populations possess substantial genetic diversity that can be leveraged for trait enhancement. These high GAM values are positive indicators, suggesting that breeding efforts have the potential to bring about significant improvements in these traits. Such improvements can have practical applications in enhancing biomass production, bioenergy yield, and ecological restoration efforts involving *Salix triandra* L. (Serapiglia *et al.*, 2015; Aronsson *et al.*, 2010) [2, 8, 1].

Understanding the variability in nodes and inter nodal lengths in *Salix triandra* L. within the context of source variability has ecological implications. Different sources may exhibit unique growth strategies, affecting their ecological interactions and adaptability to diverse habitats (Taylor *et al.*, 2019; Xiao *et al.*, 2019) [10]. This knowledge can inform conservation efforts by highlighting the importance of preserving genetic diversity within *Salix triandra* L. populations.

Conclusion

The present study elucidated the influence of source variability on key morphological traits in *Salix triandra* L. The research identified variations in the number of shoots, node count, and inters nodal length among different sources. Notably, some treatments displayed a higher number of shoots, with G₃, G₇, and G₁₄ standing out. Genetic parameters, including genotypic coefficient of variation (GCV) and heritability (H²), indicated a strong genetic influence, particularly for node count (inch⁻¹). Genetic advance values showed the potential for trait improvement through selective breeding. The strikingly high Genetic Advance as a Percentage of Mean (GAM) values for shoot number and node count (inch⁻¹) underscored the effectiveness of harnessing genetic diversity in breeding programs. These findings offer valuable guidance for enhancing *Salix triandra* L. performance in various environmental conditions, with implications for ecological management and bioenergy

production.

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