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Manasa M
Department of Tree breeding and Improvement, Forest College and Research Institute, Mulugu, Siddipet, Telangana, India

Reeja S
Department of Tree breeding and Improvement, Forest College and Research Institute, Mulugu, Siddipet, Telangana, India

Lalitha T
Department of Tree breeding and Improvement, Forest College and Research Institute, Mulugu, Siddipet, Telangana, India

Arjun Ramachandran
Department of Tree breeding and Improvement, Forest College and Research Institute, Mulugu, Siddipet, Telangana, India

Sreedhar B
Department of Basic and Social Sciences, Forest College and Research Institute, Mulugu, Siddipet, Telangana, India

Shalini M
Department of Tree breeding and Improvement, Forest College and Research Institute, Mulugu, Siddipet, Telangana, India

Chiranjeeva M
Department of Silviculture and Agroforestry, Forest College and Research Institute, Mulugu, Siddipet, Telangana, India

Kala S
Indian Institute of Soil and Water Conservation Research Centre, ICAR, Kota, Rajasthan, India

Kumaran K
Forest Biology and Tree Improvement, FC&RI, TNAU, Mettupalayam, India

Corresponding Author:
Reeja S
Department of Tree breeding and Improvement, Forest College and Research Institute, Mulugu, Siddipet, Telangana, India

Genetic variability for seed traits among *Bixa orellana* L. accessions

Manasa M, Reeja S, Lalitha T, Arjun Ramachandran, Sreedhar B, Shalini M, Chiranjeeva M, Kala S and Kumaran K

Abstract
24 accessions of *Bixa orellana* L. were gathered from Annatto gene bank at TNAU, Mettupalayam, India, and their seed trait variability was evaluated. Germination percentage, seed weight and bixin content showed significant variations. The highest percentage of germination was achieved by G7 followed by G21. The 100 seed weight was high in G7 followed by G18 and the lowest by G24. Content of bixin ranged from 1.5% to 0.48%. For all the qualities, the phenotypic coefficient of variation was larger than the corresponding genotypic coefficient of variation, revealing that the environment plays a major role in all the traits. Both seed weight (91%) and germination (71%) registered high heritability. For genetic advance as percent of mean, bixin content (37.79) recorded high followed by germination percentage (35.19). High heritability coupled with genetic advance suggest additive gene action and scope for further improvement in the species.

Keywords: *Bixa orellana*, bixin, PCV, GCV, heritability, genetic advance

Introduction

Bixa orellana L. is a multifunctional species, which has a wide range of potential qualities. The most important byproduct of the seeds was the orange dye extract, bixin. The food industry is concentrating more on the connection between food consumption and human wellness because of apprehensions about the adverse effects of synthetic food additives (Boon *et al.*, 2010) [1].

The detrimental effects of chemicals on human health highlight the value of natural substances, such as the red-orange dye produced by the seeds of the *Bixa orellana*. Among the naturally occurring colorants, annatto ranks second in economic importance (Ghiraldini, 1989) [4]. It is a tree with many uses; in addition to bixin, seed and leaf extracts have therapeutic properties such as anti-diarrheal activity (Ahmad shilpi *et al*., 2006) [15], anti-histamine activity (Keong yong *et al*., 2013) [17], anti- oxidant activity like *C. nictus* [17] etc. It has the potential to function as an agroforestry tree in addition to its therapeutic properties.

Understanding genetic variability is inevitable for establishing an efficient tree-improvement programme since it influences the species' capacity for evolution. Particularly in out-crossing species, significant changes in seed characteristics, growth, and chemical components might be anticipated in population, progeny, or provenance (Kaushik *et al*., 2007) [10]. Future programmes that can give the appropriate genotype for agroforestry systems may be able to leverage the variation present in the species as a source of genetic selection. The seedlings growth was determined by the seed traits which also reduce the time and expense associated with managing the nursery (Kaushik *et al*., 2003) [9]. In particular, the selection of genotypes with high bixin content can benefit greatly from genetic variability in seed traits. Very little is known so far on the evaluation of germplasm, variability and genetic diversity of seed and seedling parameters that would help choose superior genotypes. Research works on this species in Telangana region is very scanty. Therefore the current study was designed to understand the variability of seed traits *viz*., germination percentage, seed weight and bixin content of 24 genotypes of *Bixa orellana* L. collected from annatto germplasm of TNAU, Tamil Nādu.

Materials and methods

The experiment was conducted in Forest college and Research Institute, Mulugu to determine the variability present in the species with respect to seed traits. A total of 24 accessions were assembled and observed for their variation in seed traits.

The experimental material was collected from different genotypes established at Annatto Field Gene Bank, Mettupalayam, Tamil Nādu (11 9' N and 76 56'E). The bixin content in seeds was estimated by following Mckeown and Mark (1962) [12]. Seed weight was measured by taking 100 seeds randomly from seed lot and expressed in grams. For germination studies, three replicates of seeds each including 50 were taken and sown on mother beds. Germinated seedlings were counted after 30 days and expressed in percentage. The data recorded on all seed traits were statistically analyzed for genetic variability using R open access software

Results

The analysis of variance revealed significant differences among the twenty- four *Bixa orellana* accessions for the seed traits *viz.*, Bixin content, germination percentage and hundred seed weight indicating the presence of ample amount of genetic variability (Table 1). The mean performance of the genotypes for all the seed traits were presented in Table 2.

Table 1: Analysis of variance for seed traits

Source	d.f	Mean sum of squares		
		Germination %	Hundred seed weight	Bixin %
Treatments	23	473.84**	0.182**	0.289**
Replications	2	147.39	0.002	0.069
Error	48	55.94	0.005	0.063
	SEm	4.318	0.042	0.145

The coefficients of variation at phenotypic and genotypic levels were studied (Table 3). The seed traits such as bixin percentage (PCV= 33.83, GCV=24.91), germination percentage (PCV=23.94, GCV=20.22) exhibited highest estimates of variance at both phenotypic and genotypic level whereas hundred seed weight (PCV=8.92, GCV=8.91) recorded for low estimates. The estimates of GCV were less compared to PCV for all traits, indicating the dominant role of environment in the expression of traits.

Heritability percent was categorized into different levels for seed traits as suggested by Allard as low (<30), medium (30-60) and high (>60). The traits such as germination percentage and hundred seed weight recorded for high heritability (>60%) while bixin percentage was showing moderate heritability (54%). According to Robinson *et al.*, characters with values >20% were considered to have high genetic advance as percentage of mean. In the present study germination percentage (35.18%) and bixin percentage (37.79%) exhibited high values for genetic advance as percentage of mean, while hundred seed weight (16.88%) recorded moderate value. High heritability coupled with high genetic advance as percentage of mean was observed for germination percentage. Moderate heritability and high genetic advance as percentage of mean was observed for bixin percentage.

Table 2: Mean performance of the 24 genotypes of *Bixa orellana* for seed traits

Genotypes	Germination %	Hundred seed weight(g)	Bixin (%)
G1	64.5	2.6	0.6
G2	66.2	2.6	0.5
G3	36.7	2.9*	1.5*
G4	51.1	3.0**	1.0
G5	63.8	2.8	1.0
G6	67.3	2.6	1.1
G7	81.9*	3.4**	1.3
G8	52.2	2.8	1.4*
G9	61.1	2.8	1.4*
G10	51.4	2.9*	1.1
G11	49.2	2.9*	1.2
G12	31.3	3.0**	0.9
G13	55.4	2.7	1.3
G14	46.7	3.1**	1.4*
G15	43.6	2.8	1.2
G16	61.4	2.8	0.48
G17	67.7	2.4	1.1
G18	67.3	3.2**	1.5*
G19	69.9	2.9**	1.1
G20	81.6*	2.9*	0.5
G21	47.3	3.1**	1.4*
G22	53.2	2.8	1.3
G23	64.1	2.9*	1.1
G24	65.2	2.3	1.2
Mean	58.49	2.8	1.1
SEm	4.32	0.042	0.145
*CD (5%)	12.29	0.119	0.414
**CD (1%)	16.41	0.158	0.553

Discussion

Understanding the diversity found in the *Bixa orellana* and choosing the traits for improvement programme depend on thorough study on variability present in seed traits. The analysis of seed morphological traits in natural populations is frequently regarded as an important first step in the investigation of genetic diversity. In the present study all the seed traits *viz.*, germination percentage, 100-seed weight, and bixin percentage have shown significant variations among the genotypes.

These variations may be due to the species adoptability to a broad variety of temperatures, rainfall, and soil types in *B. orellana* with regard to their morphological characteristics (Kumaran.K,2014) [11].

The seed morphological features of *B. orellana* vary among provenances, seed sources and genotypes which was also reported for several other species *viz.*, *Prosopis juliflora* [14], *Acacia catechu* [5] and *Azadirachta indica* [8].

Type and extent of genetic variability will influence the gains from the breeding programme. High gains could be obtained for the traits that are under genetic control and have wide variability (Zobel, 1971) [18]. In the study, every trait has recorded high PCV compared to GCV demonstrating that phenotypic expression of those traits was somewhat influenced by environment which was also evident in *J.curcas* [14]. Minimum difference between PCV and GCV and high heritability (broad sense) estimates for all seed traits under study revealed the heritable nature of variability present.

Table 3: Components of variance and genetic estimates of seed traits

Seed character	Variance		PCV	GCV	Heritability (%)	Genetic advance	Genetic advance as percent of mean (%)
	PV	GV					
Germination %	195.24	139.29	23.94	20.22	71	20.54	35.19
Hundred seed weight	0.06	0.06	8.92	8.91	91	0.48	16.89
Bixin content (%)	0.14	0.07	33.83	24.91	54	0.41	37.79

Heritability (Dorman *et al.*, 1976) [6] has an important place in tree breeding as it provides an index of the relative role of heredity and environment in the expression of various traits. It also useful in ranking each trait for breeding programmes. Moderate to high estimates of heritability (>54%) for all the seed traits in the current study envisaged that selection can be reliable and effective. Strong heritability with high genetic advance as percent of mean for seed attributes showed the opportunity for improvement through direct selection which was also have been reported by Kala.S in *Bixa orellana* [7], Kaushik. K in *J.curcas* [10] and for growth parameters was reported for *Melia azaderach* [16], *Toona ciliata* [13] and *Tectona grandis* [3].

The existence of considerable diversity among characteristics provided a favorable chance for picking desirable genotypes, as well as high estimates of heritability, indicating that they were least impacted by environment and that selection based on phenotypic performance would be accurate (Ingole *et al.*, 2021) [6].

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