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Prahlad Kumar
Department of Genetics and
Plant Breeding, Govind Ballabh
Pant University of Agriculture
and Technology (G.B.P.U.A&T),
Pantnagar, Uttarakhand, India

Birendra Prasad
Department of Genetics and
Plant Breeding, Govind Ballabh
Pant University of Agriculture
and Technology (G.B.P.U.A&T),
Pantnagar, Uttarakhand, India

Shivani Ramola
Department of Genetics and
Plant Breeding, Govind Ballabh
Pant University of Agriculture
and Technology (G.B.P.U.A&T),
Pantnagar, Uttarakhand, India

Akriti Ballabh
Department of Animal Nutrition,
College of Veterinary and Animal
Sciences, Govind Ballabh Pant
University of Agriculture and
Technology (G.B.P.U.A&T),
Pantnagar, Uttarakhand, India

Anumay Singh Bhandari
College of Veterinary and Animal
Sciences, Govind Ballabh Pant
University of Agriculture and
Technology (G.B.P.U.A&T),
Pantnagar, Uttarakhand, India

Dipanjali Raj
Nalanda College of Horticulture,
Bihar Agricultural University,
Sabour, Bhagalpur, Bihar, India

Corresponding Author:
Akriti Ballabh
Department of Animal Nutrition,
College of Veterinary and Animal
Sciences, Govind Ballabh Pant
University of Agriculture and
Technology (G.B.P.U.A&T),
Pantnagar, Uttarakhand, India

Quantification of genetic variability, selection efficiency and seed quality traits in forage cowpea (*Vigna unguiculata* L. Walp.)

Prahlad Kumar, Birendra Prasad, Shivani Ramola, Akriti Ballabh, Anumay Singh Bhandari and Dipanjali Raj

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Abstract

Cowpea (*Vigna unguiculata* (L.) Walp.) is an important multipurpose legume valued for its forage, grain and soil-improving properties. The present investigation was undertaken to assess genetic variability, heritability and genetic advance among fifteen cowpea genotypes, including twelve advanced breeding lines and three check varieties, for forage yield, seed yield and seed quality traits. The experiment was conducted during the Kharif season of 2024 at the Instructional Dairy Farm, Nagla, Govind Ballabh Pant University of Agriculture and Technology, Pantnagar, Uttarakhand, using a Randomised Block Design with three replications. Observations were recorded on twenty-two morphological, yield and seed quality characters. Analysis of variance revealed highly significant differences among genotypes for all the traits studied, indicating the presence of substantial genetic variability. Considerable variation was observed for important economic traits such as green fodder yield, dry matter yield, seed yield and seed quality parameters. Green fodder yield ranged from 445.43 to 544.90 q ha⁻¹, while dry matter yield varied from 57.57 to 86.80 q ha⁻¹. Seed yield per plot ranged from 0.72 to 1.07 kg. Among the evaluated genotypes, PFC-6 recorded the highest green fodder yield (544.90 q ha⁻¹), dry matter yield (86.80 q ha⁻¹) and seed yield per plot (1.07 kg), whereas PFC-12 exhibited superior performance for hundred-seed weight (17.13 g), germination percentage (92.70%) and forage productivity. The phenotypic coefficient of variation was slightly higher than the corresponding genotypic coefficient of variation for all traits, indicating a relatively low environmental influence on character expression. High GCV and PCV values were observed for seedling root length, seedling vigour index-I, germination percentage at first count, pod length and dry matter yield. High heritability coupled with high genetic advance as a percentage of the mean was recorded for seedling root length, pod length, dry matter yield, germination percentage at first count, seedling vigour index-I and green fodder yield, suggesting the predominance of additive gene action and the effectiveness of direct selection for these traits. Heritability estimates were particularly high for the number of seeds per pod (98.6%), plant height (96.1%), seed yield per plot (95.6%) and pod length (93.6%). The study demonstrated the existence of ample genetic variability among the tested cowpea genotypes and identified PFC-6 and PFC-12 as promising genotypes for forage yield, seed yield and seed quality improvement. These genotypes may serve as valuable parental sources in future cowpea breeding programmes aimed at developing high-yielding and nutritionally superior forage cultivars.

Keywords: Cowpea, *Vigna unguiculata*, genetic variability, heritability, genetic advance, green fodder yield, dry matter yield, seed quality, seedling vigour, forage breeding

1. Introduction

Cowpea (*Vigna unguiculata* (L.) Walp.) is one of the most important multipurpose leguminous crops cultivated in tropical and subtropical regions of the world. It is grown for grain, vegetables, fodder, green manure and cover crop purposes owing to its high adaptability, nutritional value and ability to thrive under adverse environmental conditions (Baudoin and Maréchal, 1985; Boukar *et al.*, 2019) [21, 22]. The crop plays a significant role in ensuring food, nutritional and fodder security, particularly in developing countries where livestock farming is an integral component of agricultural production systems.

India possesses one of the largest livestock populations in the world; however, the availability of quality fodder remains a major challenge. The shortage of nutritious green fodder often limits animal productivity, resulting in reduced milk and meat production.

Under such circumstances, forage legumes such as cowpea assume considerable importance because they provide high-quality fodder rich in protein, minerals and vitamins. Cowpea fodder contains approximately 16–20 per cent crude protein and exhibits high palatability and digestibility, making it an excellent feed resource for dairy animals.

In addition to providing nutritious fodder, cowpea improves soil fertility through biological nitrogen fixation and contributes to sustainable agricultural production systems (Singh *et al.*, 1997; Boukar *et al.*, 2019) [23, 22].

The development of superior cowpea cultivars depends largely on the availability and utilisation of genetic variability present in the germplasm. Genetic variability is the basic prerequisite for crop improvement because it provides opportunities for selection and recombination of desirable traits. The magnitude of genetic variation available in a breeding population determines the effectiveness of selection and the extent of genetic improvement that can be achieved. Several researchers have reported substantial variability in cowpea for forage yield, seed yield and associated characters, indicating considerable scope for genetic improvement (Dahiya *et al.*, 2007; Devi and Jayamani, 2018; Sharma *et al.*, 2017) [24, 4, 17].

Assessment of genetic variability through genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) provides useful information regarding the extent of genetic and environmental influences on trait expression. Heritability estimates indicate the proportion of observed variation that is genetically inherited, while genetic advance predicts the expected progress from selection. High heritability coupled with high genetic advance generally suggests the predominance of additive gene action and the effectiveness of direct selection (Burton and DeVane, 1952; Johnson *et al.*, 1955) [3, 10]. Therefore, estimation of variability parameters is essential for identifying suitable selection criteria and designing effective breeding strategies.

Forage yield is a complex quantitative trait governed by several interrelated morphological and physiological characters. Direct selection based solely on yield may not always be effective because yield is strongly influenced by environmental factors and the interaction among component traits. Therefore, understanding the relationships among yield and its contributing characters becomes important for developing efficient breeding programmes. Correlation analysis helps in identifying characters associated with yield, whereas path coefficient analysis provides information on the direct and indirect contributions of various traits towards yield improvement (Venkatesan *et al.*, 2003; Kumar *et al.*, 2016; Walle *et al.*, 2018) [25, 11, 26].

Genetic divergence analysis is another important tool in plant breeding because it assists in identifying genetically diverse parents for hybridisation programmes. Crosses involving genetically divergent parents often produce superior segregants and desirable recombinants in subsequent generations. Several workers have successfully utilised Mahalanobis D^2 statistics to assess genetic divergence and identify promising parental combinations in cowpea (Backlyarani *et al.*, 2000; Bertini *et al.*, 2009; Udensi *et al.*, 2015) [27, 28, 29].

The present investigation was conducted during Kharif 2024 under the All India Coordinated Research Project on Forage Crops and Utilisation at the Instructional Dairy Farm, Nagla,

Pantnagar. Fifteen cowpea genotypes, including twelve advanced breeding lines and three standard checks, were evaluated for twenty-two forage yield, seed yield and seed quality traits. Considerable variation was observed among the genotypes for all the characters studied. Green fodder yield varied from 445.43 to 544.90 q ha⁻¹, dry matter yield ranged from 57.57 to 86.80 q ha⁻¹ and seed yield per plot ranged from 0.72 to 1.07 kg, indicating the existence of substantial genetic variability among the experimental materials. Notably, genotype PFC-6 recorded the highest green fodder yield (544.90 q ha⁻¹), dry matter yield (86.80 q ha⁻¹) and seed yield per plot (1.07 kg), whereas PFC-12 exhibited superior performance for seed weight, germination and forage productivity. These observations highlight the potential of the evaluated genotypes for future breeding programmes aimed at improving forage yield and quality.

In view of the economic importance of cowpea as a forage and seed crop and the need for identifying superior genotypes, the present study was undertaken to evaluate the performance of elite cowpea genotypes, estimate genetic variability, heritability and genetic advance, examine the association among important traits and identify promising genotypes for forage yield, seed yield and seed quality improvement.

2. Materials and Methods

The present investigation was conducted during the Kharif season of 2024 at the Instructional Dairy Farm, Nagla, Govind Ballabh Pant University of Agriculture and Technology (GBPUA&T), Pantnagar, Uttarakhand, under the All India Coordinated Research Project on Forage Crops and Utilisation. The experimental material comprised fifteen cowpea [*Vigna unguiculata* (L.) Walp.] genotypes, including twelve advanced breeding lines (PFC-1 to PFC-12) and three check varieties, namely UPC-622, UPC-5286 and UPC-9202. The experiment was laid out in a Randomised Block Design (RBD) with three replications. Each genotype was grown in plots consisting of ten rows of 5 m length with a row spacing of 40 cm, and all recommended agronomic practices were followed uniformly throughout the crop growth period. Observations were recorded on five randomly selected competitive plants from each replication for twenty-two morphological, yield and seed quality traits, viz., days to 50 per cent flowering, leaf stem ratio, plant height, terminal leaflet length, terminal leaflet width, pod length, number of seeds per pod, 100-seed weight, seed yield per plot, green fodder yield, dry matter yield, germination percentage, seedling shoot length, seedling root length, total seedling length, seedling fresh weight, seedling dry weight, first count germination percentage, seedling vigour index-I, seedling vigour index-II, relative growth index and mean daily germination. Green fodder yield was recorded at harvest and converted into quintals per hectare, while dry matter yield was estimated based on dry matter percentage. Seed quality parameters were evaluated under laboratory conditions following standard seed testing procedures. Relative Growth Index (RGI) was calculated as the ratio of first count germination to final germination multiplied by 100, Seedling Vigour Index-I (SVI-I) as germination percentage multiplied by seedling length, Seedling Vigour Index-II (SVI-II) as germination percentage multiplied by seedling dry weight and Mean Daily Germination (MDG) as final germination

percentage divided by the number of days taken for germination. The recorded data were subjected to statistical analysis using analysis of variance (ANOVA) as described by Panse and Sukhatme (1985) [30]. Genotypic and phenotypic coefficients of variation were estimated following Burton and DeVane (1952), while broad-sense heritability and genetic advance were computed according to Johnson, Robinson and Comstock (1955) [3, 10]. These analyses were undertaken to assess the magnitude of genetic variability, the extent of heritable variation and the potential for genetic improvement through selection among the evaluated cowpea genotypes.

3. Results and Discussion

The assessment of mean performance is an important step in identifying superior genotypes for utilization in breeding programmes. In the present investigation, fifteen cowpea genotypes, including twelve advanced breeding lines and three checks, were evaluated for twenty-two forage, seed yield and seed quality traits. The mean performance of the genotypes revealed considerable variation for all the characters studied, indicating the presence of substantial genetic diversity among the experimental materials (Table 1).

Days to 50 per cent flowering exhibited a wide range of variation from 76.00 days in PFC-4 to 91.67 days in PFC-11, with an overall mean of 83.82 days (Table 1). Early flowering genotypes such as PFC-4, PFC-5, PFC-2, PFC-3 and PFC-12 flowered earlier than the best check UPC-9202. Similar variability for flowering behaviour has been reported by Patel *et al.* (2020) [32].

Leaf stem ratio varied from 0.42 in PFC-8 to 0.64 in UPC-9202, with a population mean of 0.55 (Table 1). The highest leaf stem ratio was recorded in UPC-9202 followed by PFC-10 and PFC-12, indicating their potential usefulness in forage quality improvement programmes.

Plant height ranged from 163.67 cm in PFC-11 to 244.17 cm in PFC-6, with an overall mean of 196.69 cm (Table 1). The superior performance of PFC-6 for plant height was reflected in its higher green fodder yield and dry matter production, suggesting a positive association between vegetative growth and forage productivity.

Similarly, substantial variation was observed for terminal leaflet length, terminal leaflet width, pod length, number of seeds per pod, hundred-seed weight, seed yield per plot, green fodder yield, dry matter yield and seed quality parameters (Table 1). Genotype PFC-6 recorded the highest green fodder yield (544.90 q ha⁻¹), dry matter yield (86.80 q ha⁻¹) and seed yield per plot (1.07 kg), while PFC-12 exhibited superior performance for hundred-seed weight and germination percentage. These results indicate the existence of considerable variability among the evaluated genotypes for economically important traits.

4. Analysis of Variance

Analysis of variance was carried out to determine the significance of differences among the genotypes for the traits studied. The ANOVA revealed highly significant differences among genotypes for all twenty-two characters, indicating the existence of substantial genetic variability within the experimental material (Table 2).

The treatment mean squares were highly significant for plant height (1404.081), green fodder yield (3659.99), dry matter yield (177.975), pod length (27.275), number of seeds per pod (4.879), seed yield per plot (0.036), germination percentage (109.222) and seedling vigour index-I (940116.5), demonstrating the presence of ample genetic variation for these traits (Table 2). Similar findings have been reported by Kumar *et al.* (2019), Meena *et al.* (2021) and Yadav *et al.* (2020) [33, 34, 35].

5. Genetic Variability, Heritability and Genetic Advance

The magnitude of genetic variability present in a population determines the effectiveness of selection. Estimates of GCV, PCV, heritability and genetic advance were computed to assess the nature and extent of variability among the genotypes (Table 3).

For all traits, PCV values were slightly higher than the corresponding GCV values, indicating a minor influence of environmental factors on trait expression (Table 3). However, the narrow differences between PCV and GCV for most characters suggested that the majority of the observed variation was genetic in nature.

High GCV and PCV values were recorded for seedling root length (22.57 and 24.97%), seedling vigour index-I (18.95 and 22.87%), germination percentage at first count (18.67 and 19.61%), pod length (16.68 and 17.24%) and dry matter yield (16.47 and 18.16%), indicating substantial genetic variability and greater scope for improvement through selection (Table 3).

Heritability estimates ranged from 31.6% for seedling shoot length to 98.6% for number of seeds per pod (Table 3). High heritability was observed for number of seeds per pod (98.6%), plant height (96.1%), seed yield per plot (95.6%), pod length (93.6%) and germination percentage at first count (90.6%). These results indicate that phenotypic performance is a reliable indicator of genotypic potential.

High heritability coupled with high genetic advance as per cent of mean was observed for seedling root length (42.03%), germination percentage at first count (36.61%), pod length (33.25%), seedling vigour index-I (32.34%), dry matter yield (30.79%) and green fodder yield (21.66%), suggesting the predominance of additive gene action and the effectiveness of direct phenotypic selection (Table 3).

6. Conclusion

The present investigation conducted on fifteen cowpea genotypes revealed the existence of substantial genetic variability for all twenty-two forage, seed yield and seed quality traits studied. Analysis of variance showed highly significant differences among genotypes for all characters, indicating the presence of sufficient genetic diversity and providing ample scope for selection and genetic improvement. Among the evaluated genotypes, PFC-6 emerged as the most promising entry owing to its superior performance for plant height (244.17 cm), green fodder yield (544.90 q ha⁻¹), dry matter yield (86.80 q ha⁻¹) and seed yield per plot (1.07 kg). Genotype PFC-12 also exhibited outstanding performance for green fodder yield (535.63 q ha⁻¹), dry matter yield (71.70 q ha⁻¹), hundred-seed weight (17.13 g) and germination percentage (92.70%). These genotypes consistently outperformed the standard checks for several economically important traits and may

therefore be considered potential candidates for varietal development and future breeding programmes. The estimates of genetic parameters revealed that the phenotypic coefficient of variation (PCV) was slightly higher than the genotypic coefficient of variation (GCV) for all characters, indicating a relatively low environmental influence on trait expression. High GCV and PCV values were recorded for seedling root length, seedling vigour index-I, germination percentage at first count, pod length and dry matter yield, suggesting the presence of considerable genetic variability for these traits. High heritability coupled with high genetic advance as a percentage of the mean was observed for seedling root length, pod length, dry matter yield, germination percentage at first count, seedling vigour index-I and green fodder yield. This indicates the predominance of additive gene action and suggests that direct phenotypic selection would be effective for improving these traits. The high heritability estimates observed for the number of seeds per pod (98.6%), plant height (96.1%), seed yield per plot

(95.6%), pod length (93.6%), and germination percentage at first count (90.6%) further confirmed that these traits are largely governed by genetic factors and can be reliably improved through selection. Overall, the study identified PFC-6 and PFC-12 as superior genotypes combining high forage productivity, dry matter accumulation, seed yield and desirable seed quality attributes. These genotypes may be recommended for multilocation testing and can serve as valuable parental sources in cowpea improvement programmes aimed at developing high-yielding and nutritionally superior forage cultivars. The results of the present investigation demonstrate that significant progress in cowpea improvement can be achieved through selection for plant height, pod length, seed yield, dry matter yield and green fodder yield owing to their high variability, heritability and genetic advance. Therefore, these traits should receive greater emphasis in future breeding programmes targeting enhanced forage production and seed quality in cowpea.

Table 1: Mean, coefficient of variation, and range of quantitative and qualitative characters

S. No.	Treatments	GP%	SL	RL	SL+RL	SFW	SDW	G%1	SVI1	SVI2	RGI	MDG
1	PFC -1	80.33	11.67	14.20	25.87	3.12	0.43	62.00	2080.17	34.87	77.17	10.07
2	PFC -2	76.28	12.30	15.80	28.10	4.15	0.48	44.00	2141.77	36.70	57.77	9.57
3	PFC-3	75.12	18.97	24.60	43.57	5.87	0.68	41.00	3272.13	50.53	54.57	9.40
4	PFC-4	79.34	18.33	28.30	46.63	3.35	0.42	60.00	3701.80	33.03	75.63	9.90
5	PFC-5	76.75	12.10	13.20	25.30	4.68	0.50	56.67	1932.37	38.57	74.00	9.57
6	PFC-6	91.83	14.67	18.30	32.97	3.95	0.47	76.33	3030.93	42.80	83.17	11.50
7	PFC -7	78.50	15.13	16.60	31.73	3.51	0.44	57.67	2485.93	34.57	73.47	9.83
8	PFC -8	82.88	16.63	18.70	35.33	4.94	0.57	65.00	2930.63	47.20	78.43	10.37
9	PFC -9	81.20	17.83	22.00	39.83	4.45	0.51	62.67	3243.00	41.27	77.23	10.17
10	PFC -10	76.03	19.27	15.80	35.07	4.58	0.54	47.33	2658.80	40.93	62.10	9.50
11	PFC -11	78.25	18.33	20.00	38.33	5.42	0.61	44.33	2994.23	47.63	56.57	9.77
12	PFC -12	92.70	15.47	22.40	37.87	3.69	0.46	76.33	3504.43	42.67	82.37	11.60
13	UPC-622	79.63	15.10	19.30	34.40	5.07	0.55	58.67	2732.50	43.63	73.90	9.97
14	UPC-5286	92.71	12.87	15.50	28.37	3.92	0.49	71.67	2631.00	45.60	77.33	11.60
15	UPC-9202	81.01	10.67	13.40	24.07	4.75	0.53	56.00	1946.47	42.53	69.13	10.13
	Mean	81.50	15.29	18.54	33.83	4.36	0.51	58.64	2752.41	41.50	71.52	10.20
	Range Min.	75.12	10.67	13.20	24.07	3.12	0.42	41.00	1932.37	33.03	54.57	9.40
	Range Max.	92.71	19.27	28.30	46.63	5.87	0.68	76.33	3701.80	50.53	83.17	11.60
	C.V.	2.95	12.20	10.68	12.66	12.60	7.74	6.00	12.80	8.65	6.62	2.95
	F ratio	18.87	2.39	14.41	7.41	6.17	9.47	30.04	7.57	6.20	11.72	19.03
	F Prob.	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	S.E.	1.39	1.86	1.14	2.47	0.32	0.02	2.03	203.44	2.07	2.73	0.17
	C.D. 5%	4.02	5.40	3.31	7.17	0.92	0.07	5.88	589.35	6.00	7.92	0.50
	C.D. 1%	5.43	7.28	4.47	9.67	1.24	0.09	7.94	795.03	8.10	10.69	0.68

GP- Germination%, SL-Seedling Shoot Length, RL- Seedling Root Length, SL+RL – Seedling length, SFW- Seedling Fresh Weight, SDW- Seedling Dry Weight, G%1 – Germination Percentage at 1 Count, SVI I- Seedling Vigour Index I, SVI II- Seedling Vigour Index II, RGI – Relative Growth Index, MDG- Mean Daily Germination

Table 2: ANOVA of 22 different yield and quality attributing traits

S. No.	Characters	Source of variation (Mean sum of squares)		
		Replication	Treatment	Error
1.	Days to 50% flowering	1.088	77.517**	4.612
2.	Leaf: Stem ratio	0.003	0.015**	0.001
3.	Plant height	19.104	1404.081**	18.729
4.	Terminal leaflet length	0.039	1.586**	0.077
5.	Terminal leaflet width	0.112	1.399**	0.127
6.	Green fodder yield	423.831	3659.99**	263.341
7.	Dry matter yield	44.728	177.975**	11.899
8.	Pod length	0.356	27.275**	0.605
9.	Number of seeds/pods	0.022	4.879**	0.022
10.	Seed Yield/plot	0.001	0.036**	0.0005
11.	100- Seed weight	2.16	11.187**	0.534
12.	Germination percentage	13.192	109.222**	5.789

13.	Seedling shoot length	2.363	24.878**	10.424
14.	Seedling root length	2.712	56.451**	3.918
15.	Seedling length	7.904	136.029**	18.355
16.	Seedling Fresh weight	0.272	1.863**	0.302
17.	Seedling dry weight	0.001	0.014**	0.001
18.	Germination percentage 1 st count	34.688	371.879**	12.379
19.	Seedling Vigour Index I	11618.73	940116.5**	124168.4
20.	Seedling Vigour Index II	6.244	79.921**	12.882
21.	Relative Growth Index	20.768	262.829**	22.43
22.	Mean Daily Germination	0.169	1.72**	0.09

** Significance at 1% probability level.

Table 3: Variability Parameters of 22 different yield and quality-attributing traits

S. No.	Characters	GCV	PCV	h ²	Gen Adv @5%	Gen. Adv as % of Mean 5%
1.	Days to 50% flowering	5.881	6.415	84	9.31	11.107
2.	Leaf: Stem Ratio	12.493	14.266	76.7	0.124	22.537
3.	Plant height	10.925	11.145	96.1	43.396	22.063
4.	Terminal leaflet length	8.002	8.594	86.7	1.361	15.348
5.	Terminal leaflet width	9.119	10.398	76.9	1.176	16.472
6.	Pod length	16.681	17.24	93.6	5.943	33.248
7.	No. of seed/pods	12.209	12.292	98.6	2.603	24.979
8.	100-seed weight	13.019	13.965	86.9	3.619	25.002
9.	Seed Yield/plot	12.028	12.299	95.6	0.219	24.232
10.	Green Fodder Yield	11.675	12.962	81.1	62.434	21.662
11.	Dry Matter Yield	16.473	18.157	82.3	0.823	30.787
12.	Seed Germination%	7.204	7.786	85.6	0.856	13.733
13.	Seedling shoot length	14.357	25.536	31.6	0.316	16.628
14.	Seedling Root Length	22.571	24.968	81.7	0.817	42.03
15.	Seedling length (SL+RL)	18.514	22.431	68.1	0.681	31.478
16.	Seedling fresh weight	16.535	20.786	63.3	0.633	27.095
17.	Seedling dry weight	12.997	15.124	73.8	0.738	23.006
18.	Germination% (1 count)	18.666	19.607	90.6	0.906	36.608
19.	Seedling Vigour Index 1	18.948	22.867	68.7	0.687	32.342
20.	Seedling Vigour Index 2	11.39	14.301	63.4	0.634	18.688
21.	Relative Growth Index	12.516	14.16	78.1	0.781	22.79
22.	Mean Daily Germination	7.244	7.823	85.7	0.857	13.817

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