



ISSN Print: 2663-1067
 ISSN Online: 2663-1075
 NAAS Rating (2026): 4.74
 IJHFS 2026; 8(9): 123-126
www.hortijournal.com
 Received: 15-07-2026
 Accepted: 21-08-2026
 Published: 30-09-2026

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Genetic variability, heritability and genetic advance for growth and yield parameters in *Helichrysum* (*Xerochrysum bracteatum* (Vent.) Tzvelev)

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DOI: <https://www.doi.org/10.33545/26631067.2026.v8.i9b.866>

ABSTRACT

Twenty-five genotypes of *Helichrysum* (*Xerochrysum bracteatum* (Vent.) Tzvelev) were evaluated in a Randomized Block Design with two replications during Rabi, 2025–26 at the AICRP on Floriculture, Zonal Agricultural Research Station, Ganeshkhind, Pune, to assess the magnitude of genetic variability, heritability and genetic advance for twelve growth, flowering and yield characters. Analysis of variance revealed highly significant differences among genotypes for all the characters studied, indicating the presence of considerable genetic diversity. The phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for all the characters, suggesting some environmental influence on their expression; however, the differences between PCV and GCV were narrow for most traits. The highest GCV and PCV were recorded for weight of single flower (24.713% and 25.350%, respectively), followed by flower yield per plant, while the lowest were recorded for days to 50 per cent flowering. High heritability (>60%) was observed for nine of the twelve characters, with the maximum for number of whorls (97.024%), followed by weight of single flower, flower yield per plant, number of branches, flower yield per square metre, flower diameter, plant height, number of flowers and plant spread. High genetic advance as per cent of mean, coupled with high heritability, was recorded for weight of single flower (49.630%), flower yield per plant (48.234%), number of whorls (44.994%), flower yield per square metre (35.295%), number of flowers (34.976%), number of branches (33.456%), plant spread (23.240%) and flower diameter (20.274%), indicating the predominance of additive gene action and good scope for improvement of these traits through direct phenotypic selection.

Keywords: *Helichrysum*, *Xerochrysum bracteatum*, Genetic variability, GCV, PCV, Heritability, Genetic advance

Introduction

Helichrysum, commonly known as strawflower, everlasting flower or paper flower, is an attractive annual ornamental crop belonging to the family Asteraceae and is native to Australia. The species traditionally described as *Helichrysum bracteatum* is currently accepted botanically as *Xerochrysum bracteatum* (Vent.) Tzvelev. The crop is characterized by terminal flower heads surrounded by numerous colourful, stiff and papery involucral bracts that retain their colour and shape even after drying, making the crop particularly suitable for loose flower, cut flower and dried flower use. Despite its considerable ornamental and commercial potential, *Helichrysum* remains relatively less studied than major flower crops, and information on the extent of genetic variability available for important growth, flowering and yield attributes is comparatively limited. Genetic variability is the basic prerequisite for any crop improvement programme, since the effectiveness of selection depends upon the presence of adequate heritable variation among genotypes for economically important traits. Burton *et al.* (1953) [1] emphasized the usefulness of genotypic and phenotypic coefficients of variation for assessing the extent of variability in quantitative characters. However, variability alone does not establish whether a character can be improved effectively through selection; heritability, which represents the proportion of the observed variation attributable to genetic causes, must also be considered. Johnson *et al.* (1955) [2] recommended that heritability be interpreted together with genetic advance, since this combination provides a more reliable indication of the expected response to selection than heritability estimates alone. Characters exhibiting high heritability coupled with high genetic advance are generally governed by additive gene action and are therefore more amenable to improvement through direct phenotypic selection. The present investigation was therefore undertaken to evaluate twenty-five genotypes of *Helichrysum* for twelve growth, flowering and yield characters, with the objective of assessing the genetic variability, heritability and genetic advance present in the available germplasm, so as to identify characters and genotypes with the greatest potential for genetic improvement of this relatively under-exploited ornamental crop.

Materials and Methods

The present investigation was carried out during Rabi, 2025–26 at the AICRP on Floriculture, Zonal Agricultural Research Station, Ganeshkhind, Pune (18.32° N latitude, 73.85° E longitude; 557.74 m above mean sea level), Maharashtra, under the jurisdiction of Mahatma Phule Krishi Vidyapeeth, Rahuri. The experimental site is situated in the Western Maharashtra Plain Zone and experiences a tropical climate with mild winters and moderate humidity; the temperature during the crop growth period ranged from about 11 °C to 36 °C. The soil of the experimental plot was red laterite soil of medium texture with good drainage.

The experimental material comprised twenty-five genotypes of *Helichrysum* (GKHS-25-1 to GKHS-25-25) collected from farmers in and around Pune district, the Parks and Gardens of Pune University campus, the AICRP on Floriculture, ZARS, Pune, and from fields at Ooty, Tamil Nadu. The experiment was laid out in a Randomized Block Design with two replications, at a spacing of 45 cm × 30 cm on a ridges-and-furrows layout, with a plot size of 2.7 m × 0.9 m accommodating eighteen plants per plot. Seeds were sown on 13 October 2025 and thirty-day-old seedlings were transplanted on 14 November 2025. A basal dose of compost @ 10 t/ha and N:P₂O₅:K₂O @ 150:75:75 kg/ha was applied, and cultural and plant-protection practices were followed uniformly for all the genotypes.

Observations were recorded on five randomly selected and tagged plants per treatment for twelve quantitative characters, viz., plant

height (cm), plant spread (cm), number of branches per plant, days to 50 per cent flowering, days to flower bud initiation, number of whorls of ray florets, flower diameter (mm), flowering duration (days), number of flowers per plant, weight of single flower (g), flower yield per plant (g) and flower yield per square metre (g). The data were subjected to analysis of variance as per the method described by Panse *et al.* (1985) [3] for a Randomized Block Design. Genotypic and phenotypic variances and their respective coefficients of variation (GCV and PCV) were computed following Burton (1952) [4] and categorized as low, moderate or high following the scale of Sivasubramanian *et al.* (1973) [5]. Broad-sense heritability was estimated as per Allard (1960) [6] and categorized following Robinson *et al.* (1949) [7]. Expected genetic advance at 5 per cent selection intensity ($K = 2.06$) and genetic advance expressed as a percentage of the mean (genetic gain) were computed following the methods of Allard (1960) [6] and Johnson *et al.* (1955) [2], respectively, and categorized as low, moderate or high following Johnson *et al.* (1955) [2].

Results and Discussion

Analysis of variance

The analysis of variance (Table 1) revealed highly significant differences among the twenty-five genotypes for all twelve characters studied, indicating the presence of appreciable genetic diversity in the experimental material and confirming the suitability of the genotypes for further genetic analysis.

Table 1. Analysis of variance (mean sum of squares) for twelve characters in *Helichrysum* genotypes

Character	Replication MS (df = 1)	Treatments MS (df = 24)	Error MS (df = 24)
Plant height (cm)	196.02	365.536**	29.392
Plant spread (cm)	2.785	72.811**	7.568
Number of branches	0.289	3.053**	0.175
Days to 50% flowering	30.42	29.905**	8.545
Days to flower bud initiation	62.72	30.395**	11.262
Number of whorls	0.003	3.633**	0.055
Flower diameter (mm)	25.319	24.669**	1.760
Flowering duration (days)	10.58	30.845**	12.372
Number of flowers	2.943	334.350**	32.886
Weight of single flower (g)	0.002	0.611**	0.016
Flower yield per plant (g)	31.49	2,377.520**	105.934
Flower yield per m ² (g)	1,030.58	44,901.240**	2,952.410

** Significant at 1 per cent level of significance.

Genetic variability, heritability and genetic advance

The estimates of range, mean, GCV, PCV, broad-sense heritability and genetic advance as *per cent* of mean for the twelve characters studied are presented in Table 2.

Coefficient of variation

The genotypic coefficient of variation (GCV) was consistently lower than the corresponding phenotypic coefficient of variation (PCV) for all twelve characters, indicating that the observed phenotypic variation, although predominantly genetic in nature, was also influenced to some extent by environmental factors. The lowest GCV (3.906%) and PCV (5.241%) were recorded for days to 50 *per cent* flowering, fol-

lowed by days to flower bud initiation and flowering duration, indicating comparatively low variability for these phenological traits. In contrast, the highest GCV (24.713%) and PCV (25.350%) were recorded for weight of single flower, followed closely by flower yield per plant (GCV = 24.482%, PCV = 25.598%), number of whorls, flower yield per square metre and number of flowers, indicating the presence of considerable exploitable variability among the genotypes for these yield-related characters. These findings are in agreement with those of Baskaran *et al.* (2009) [8], Prakash *et al.* (2017) [9], Telem *et al.* (2017) [10] and Gaikwad *et al.* (2020) [11] in chrysanthemum, and Rai *et al.* (2017) [12] and Naikwad *et al.* (2018) [13] in China aster, all of whom reported higher PCV than GCV together with high variability for yield and yield-attributing characters.

Table 2. Estimates of range, mean, genetic parameters and genetic advance for twelve characters in *Helichrysum* genotypes

Character	Range	Mean	GCV (%)	PCV (%)	Heritability (h ² bs) (%)	Genetic advance (5%)	GA as % of mean
Plant height (cm)	90.60 – 148.00	131.99	9.822	10.646	85.115	24.639	18.666
Plant spread (cm)	24.20 – 56.20	45.61	12.522	13.899	81.169	10.60	23.240

(continued on next page)

Character	Range	Mean	GCV (%)	PCV (%)	Heritability (h^2 bs) (%)	Genetic advance (5%)	GA as % of mean
Number of branches	5.10 – 9.90	6.97	17.203	18.222	89.128	2.333	33.456
Days to 50% flowering	73.50 – 89.50	83.66	3.906	5.241	55.553	5.018	5.998
Days to flower bud initiation	58.50 – 75.50	68.52	4.514	6.661	45.931	4.318	6.302
Number of whorls	3.10 – 8.00	6.03	22.174	22.511	97.024	2.714	44.994
Flower diameter (mm)	24.48 – 40.58	32.02	10.571	11.354	86.680	6.491	20.274
Flowering duration (days)	53.50 – 70.50	61.38	4.951	7.573	42.746	4.093	6.669
Number of flowers	48.30 – 109.00	65.51	18.740	20.683	82.090	22.915	34.976
Weight of single flower (g)	0.83 – 3.91	2.210	24.713	25.350	95.036	1.096	49.630
Flower yield per plant (g)	84.90 – 243.89	137.66	24.482	25.598	91.469	66.398	48.234
Flower yield per m ² (g)	485.50 – 1110.00	791.42	18.299	19.545	87.661	279.328	35.295

Heritability (broad sense)

Heritability estimates in the present study ranged from 42.746 *per cent* (flowering duration) to 97.024 *per cent* (number of whorls). High heritability (>60%) was recorded for number of whorls (97.024%), weight of single flower (95.036%), flower yield per plant (91.469%), number of branches (89.128%), flower yield per square metre (87.661%), flower diameter (86.680%), plant height (85.115%), number of flowers (82.090%) and plant spread (81.169%), whereas moderate heritability was recorded for days to 50 *per cent* flowering (55.553%), days to flower bud initiation (45.931%) and flowering duration (42.746%). None of the characters exhibited low heritability. The consistently high heritability observed for most of the growth, flowering and yield characters indicated a substantial genetic contribution to their phenotypic expression, comparable to the high heritability estimates reported by Ghimiray *et al.* (2015) [14] in gerbera, Gobade *et al.* (2018) [15] and Latha *et al.* (2018) [16] in marigold, and Sushma Patil *et al.* (2019) [17] and Shingala *et al.* (2022) [18] in chrysanthemum.

Genetic advance as per cent of mean

High genetic advance as per cent of mean (> 20%) was recorded for weight of single flower (49.630%), flower yield per plant (48.234%), number of whorls (44.994%), flower yield per square metre (35.295%), number of flowers (34.976%), number of branches (33.456%), plant spread (23.240%) and flower diameter (20.274%). Plant height recorded a moderate genetic advance as *per cent* of mean (18.666%), while comparatively low values were recorded for flowering duration (6.669%), days to flower bud initiation (6.302%) and days to 50 *per cent* flowering (5.998%).

High heritability coupled with high genetic advance as per cent of mean, observed for weight of single flower, flower yield per plant, number of whorls, flower yield per square metre, number of flowers, number of branches, plant spread and flower diameter, indicated the predominance of additive gene action in the inheritance of these characters, suggesting that these traits could be effectively improved through simple phenotypic selection. Plant height, which exhibited high heritability but only moderate genetic advance, was likely influenced jointly by additive and non-additive gene effects, and improvement in this trait may therefore require a few generations of recombination followed by selection. In contrast, the comparatively low genetic advance recorded for days to 50 *per cent* flowering, days to flower bud initiation and flowering duration, despite their moderate heritability, indicated a greater relative influence of non-additive gene action and environment on these phenological characters, limiting the scope for improvement through direct selection alone. These results are broadly in agreement with the findings of Kumar *et al.* (2017)

[19], Reshma Negi *et al.* (2020a) [20], Sharma *et al.* (2024) [21] and Kavana *et al.* (2025) [22] in chrysanthemum, and Modagi *et al.* (2024) [23] and Menkarani *et al.* (2025) [24] in China aster, all of whom reported high heritability coupled with high genetic advance for flower yield and its major component characters.

Conclusion

The present investigation revealed that the twenty-five *Helichrysum* genotypes evaluated possessed considerable genetic variability for growth, flowering and yield characters. Weight of single flower, flower yield per plant, number of whorls, flower yield per square metre, number of flowers, number of branches, plant spread and flower diameter exhibited high heritability together with high genetic advance as per cent of mean, indicating the predominance of additive gene action and good scope for their improvement through simple phenotypic selection. These characters may therefore be considered as reliable selection criteria for the genetic improvement of flower yield in *Helichrysum*, whereas improvement of phenological characters such as days to flowering and flowering duration may require more elaborate breeding strategies. The genotype GKHS-25-5 recorded superior mean performance for branching, flower diameter, single flower weight and flower yield per plant, and along with other high-performing genotypes identified in this study, merits further evaluation for potential use in future breeding programmes and commercial cultivation.

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How to cite this article: Jadhav A, Pawar R, Bhalekar S, Gaikwad S, Jadhav S, Chavan S. Genetic variability, heritability and genetic advance for growth and yield parameters in *Helichrysum* (*Xerochrysum bracteatum* (Vent.) Tzvelev). *International Journal of Horticulture and Food Science*. 2026;8(9):123–126. doi: <https://www.doi.org/10.33545/26631067.2026.v8.i9b.866>