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Assessment of Yield-contributing Traits and Genetic Variability in Field Pea (*Pisum sativum* L.) under Heat Stress using Half-diallel Derived Genotypes

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ABSTRACT

Background: The field pea is a vital, nutrient-dense and extremely productive cool-season legume crop that is planted all over the world and used for food, feed and fodder. Breeders can speed up the creation of robust, high-yielding cultivars by using half-diallel mating to choose superior parents and possible hybrids.

Methods: This study was conducted for analyzing the genetic variability on 55 field pea accessions, encompassing both parental line and there F_1 progeny (hybrids) which were raised in late-sown conditions using a randomized block design (RBD) at the Genetics and Plant breeding Farm of Acharya Narendra Deva University of Agriculture and Technology, Ayodhya, Uttar Pradesh, India, over two successive *Rabi* seasons of 2022-23 and 2023-24. Data for eleven quantitative traits were collected by selecting five plants per plot randomly. ANOVA, PCV and GCV, broad sense heritability (h^2b), genetic advance as a percentage of mean, path analysis and correlation coefficient were evaluated using statistical and biometrical methods to investigate the genetic diversity among the field pea genotypes.

Result: All traits showed a significant genetic variation, indicating scope for selection. All traits have higher PCV as compared to GCV, indicating environmental influences on their expression. Secondary branches/plant (27.838%) and primary branches/plant (21.005%) displayed the highest PCV values. Traits that showed significant variation across accessions had heritability ranging from 37.9% to 92.8%, suggesting low to high heritability. Seed yield per plant showed a positive correlation all traits except days to 50% flowering and days to maturity. A notable negative correlation was shown by seed yield plant^{-1} with days to 50% flowering and days to maturity. Path analysis identified biological yield, pods/plant, 100-seed weight and branches as having strong positive direct effects on yield, while days to flowering/maturity had negative direct effects. Based on these results, it is possible to enhance the yield components of late-sown peas by selecting for high biomass, pod number and seed weight.

Key words: ANOVA, Correlation, GCV, Genetic advance, Half-diallel, Heat stress, Heritability.

INTRODUCTION

Pulses are classified within the Leguminosae family and the Papilionoidea subfamily. Pulses are being produced in India's semi-arid regions from ancient times. They are inexpensive and a reliable source of fibre, protein and phytochemicals. Legumes have been recognized as an important resource of food in the diet of human, decreasing the risk of heart disease and cancer because of their composition that makes it suitable for human consumption (Carbas *et al.,* 2023). Field pea belongs to dicotyledons class with the chromosome number of 2n=14. It is extensively cultivated in cooler climates and is native to Southwestern Asia. Even though it is a self-pollinating crop, which precludes a significant amount of gene flow, the Pisum genus is the origin of many viable wild crosses, due to which there is sufficient variation within the species (Jing *et al*., 2010). Since it is primarily a cold-weather crop, it can endure light frost. Field pea and garden pea are the two types of peas grown traditionally all around the globe. One of the many uses for field peas is as a green manure, straw, immature grain, silage, haylage, forage dry matter and green fodder (Ravindran *et al.,* 2010). Field pea

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contribution in India is about 3% of the overall area used for pulses and approximately five percent of the entire quantity produced. Previous studies show that crops grown under heat stress conditions tend to reduce yield by 18 to 33 per cent (Lamichaney *et al.,* 2021). Temperature sensitivity of field pea (cold-season legumes) is greater than warm season legumes (Hall, 2001). Moreover, field peas are relatively low heat-tolerant compared to chickpeas and lentils (Siddique, 1999) and therefore their production often decreases when the day temperature at the time of flowering go beyond 25°C (Guilioni *et al.*, 2003; Sadras *et al.*, 2013). In this article, we examine the variability and correlation among F_{1s} and their parents, while analysis of heterosis and combining ability will be reported in a distinct paper. By the year 2100, the optimum temperature will increase from 2-4 degrees celsius (IPCC, 2007). The field pea cultivars which are under late-sown condition, there is a substantial loss in yield due to terminal heat stress. (Lamichaney *et al.,* 2021). Since cool-season legumes growth and development processes are greatly impacted by high ambient temperatures, it is anticipated that seed quality will be impacted as well. High temperatures can have a negative impact on seed growers, since the seed requirements of field pea are higher. This research analyses the variability, association and path coefficient analysis of yield components of the accessions of field pea under heat stress environment.

MATERIALS AND METHODS

The trial was conducted over two consecutive *Rabi* seasons. In the first year (2022-23), ten genetically diverse field pea lines were evaluated under randomized block design (RBD) and used to generate 45 F hybrids following a half-diallel mating design (Griffing *et al.*, 1956). In the following season (2023-24), these F_{1s}, along with their 10 parents, were evaluated under late-sown conditions using an RBD with three replications. The formula for crosses was:

$$P(p-1)/2$$

'p' denotes = No. of parents.

Forty five F_{1s} and ten parental lines (PANT P-347, PANT P-200, RFP 2009-2, IPFD 18-14, PANT P-243, VL-47, IPF14-13, IPF 14-16, RILHE-2 and HFP-1802) are selected based on genetic diversity and accession were grown using a randomized block design (RBD) in *Rabi season* during November 2022-23 and 2023-24 in late-sown or heat stress conditions at the Genetics and Plant Breeding Farm of Acharya Narendra Deva University of Agriculture and Technology in Ayodhya, Uttar Pradesh, India, for optimal crop growth. Genotypes were grown in 3 replications for the study of eleven traits *viz*., days to 50% flowering, days to maturity, secondary branches/plant, primary branches/plant, plant height, pods/plant, seeds/pod, harvest index (%), 100-seed weight (g), biological yield/plant (g) and seed yield/plant (g). Collection of data was done by selecting five plant/plot randomly. Different biometrical and statistical measures, including GCV and PCV (Burton, 1953), ANOVA (Panse and Sukhatme, 1954), genetic advance (Johnson *et al.*, 1955), Broad sense heritability (h^2b) (Allard, 1960), path coefficient (Dewey 1959) and trait correlation (Searle, 1961) were evaluated.

RESULTS AND DISCUSSION

Anova, GCV and PCV

The analysis of variance (ANOVA) for all 11 morpho-agronomic traits in late-sown field pea revealed highly significant differences among genotypes (both parents and half-diallel crosses), demonstrating substantial genetic variation within the experimental material (Table 1). When comparing parents versus hybrids, significant differences were observed for all traits except seed per pod, indicating that hybridization effectively enhanced most agronomic characteristics. This genetic diversity provides a solid foundation for effective selection and breeding programs. The inference drawn from Table 2 showed that PCV were higher than the GCV for all traits, showing environmental influence on the trait expression. Secondary branches/plant (27.838%) and primary branches/plant (21.005%) displayed the maximum values of PCV, trailed by seed yield $plant^{-1}$ (20.42%).

Similarly, the highest GCV values were found for secondary branches/plant at 23.85%, trailed by seed yield/plant at (19.51%) and biological yield/plant (18.52%). Days to maturity has the lowest GCV (5.198%) and PCV (7.440%,) values, respectively. Consistent with Jeberson *et al.* (2016), Afreen *et al.* (2017) and Meena *et al. (*2017). The narrow gap between GCV and PCV values for traits such as biological yield per plant and plant height suggests these characteristics are less influenced by environmental fluctuations and are primarily under genetic control. Conversely, traits showing wider GCV-PCV gaps, such as harvest index, indicate greater environmental sensitivity and may require more careful management during selection.

Heritability and genetic advance

Heritability for all traits ranges from 37.9% to 92.8%, suggesting low to high heritability. The largest heritability trait is biological yield per plant (92.8%), followed by plant height (91.6%), seed yield per plant (91.22%), pod per plant (89.4%), seed per pod (76.5%), secondary branches per plant (73.4%) and 100-seed weight (62.2%). Days to 50% flowering (55.4%) has shown moderate heritability, followed by days to maturity (48.8%) and primary branches per plant (41.04%), while harvest index (37.9%) has the lowest heritability. Higher heritability estimates suggest that genetic factors influenced these traits. Biological yield/plant had the largest genetic advance (GA), at 35.10%, followed by plant height (29.40%) and seed yield per plant (13.25%). The range of genetic advance was 0.50% to 35.10%. These results are in agreement with the findings of Afreen *et al.* (2017) and Pratap *et al.* (2024) who reported significant

variability for all traits including 100-seed weight, plant height, pods per plant and primary branches per plant in pea. Similarly, Singh *et al.* (2019) and Gebre *et al.* (2024) concluded that traits with high heritability and high genetic advance are most amenable to breeding improvement. The present study confirms that biological yield per plant, seed yield per plant and plant height possess the most favorable genetic parameters for effective selection and breeding improvement in field pea under late-sown conditions.Traits exhibiting high heritability but low genetic advance may be governed by non-additive gene effects, while traits with low heritability and low genetic advance are highly influenced by environmental factors and are difficult to improve through direct selection. For such traits, indirect selection through correlated characters or selection in controlled environments would be more effective.

Correlation coefficient and path analysis

The perusal of Table 3 and 4 showed a wide similarity among the traits. This pattern is consistent with the findings of Singh *et al.* (2017) and Iqbal *et al.* (2020). The higher genotypic correlations suggest that the true genetic relationships between traits are stronger than what appears phenotypically, emphasizing the importance of considering genetic correlations in breeding decisions. Positive correlation was found among seed yield/plant and all traits except days to 50% flowering and days to maturity. Days to 50% flowering and days to maturity were significantly negatively correlated with seed yield plant^{-1}. This relationship can be attributed to the fact that early maturing genotypes escape terminal heat stress and moisture stress commonly encountered in late-sown conditions, thereby maintaining higher productivity. Similar observations were reported by Katoch *et al.* (2016), Tasnim *et al.* (2022) and Yadav *et al.* (2024). Primary branches plant^{-1} were significantly positively associated with seed yield per plant, harvest index, plant height and 100-seed weight, showing that more primary branches increase the components of seed yield and overall yields. Secondary branches/plant were significantly positively associated with pod/plant, biological yield/plant, 100-seed weight and seed yield/plant. In the trait plant height, there is a positive and significant relationship with seeds/pod, seed yield per plant, harvest index and primary branches per plant, showing that taller plants typically produce more seeds and produce a more yield. A significant positively correlation between pods/plant and 100-seed weight, secondary branches/plant, biological yield/plant, primary branch/plant and seed yield/plant, signifying that pods/plant plays an important role in improving seed yield and overall yield.

The seed pod^{-1} was significantly correlated with plant height, biological yield/plant, seed yield/plant and harvest index, suggesting that increase in seed/pod positively affect overall seed yield. A positive correlation was found between 100-seed weight and biological yield/plant, pods/plant, primary branches/plant, number of secondary branches/ plants, harvest index and seed yield plant^{-1}, indicating that

Table 1: Anova of half-diallel crossings and parents for 11 field pea traits under late-sown condition.

Sources of variation	d.f.	Mean sum of squares										
		D50	DTM	PH (cm)	PBPP	NSBPP	Pod/ plant	Seeds/ pod	100 -SW	HI (%)	BYPP (g)	SYPP (g)
Replication	2	13.861	4.988	23.533	0.210	0.764	0.680	0.004	3.372	1.010	3.634	3.646
Genotypes	54	40.144**	104.185**	806.404**	0.361**	3.195**	56.157**	0.789**	12.198**	88.869**	1710.154**	140.513**
Parents	9	68.996**	123.500**	836.685**	0.523**	0.590	41.709**	0.972**	2.415	138.636**	326.996**	59.242**
Hybrids	44	22.242**	73.474**	814.420**	0.306*	0.938**	40.284**	0.764**	5.536**	46.676**	798.574**	85.225**
Parent vs. Hybrids	1	568.149**	1281.616**	181.216**	1.311*	125.944**	884.586**	0.283	393.360**	1497.461**	54268.090**	3304.629**
Error	108	8.490	26.982	22.308	0.194	0.344	2.121	0.073	2.051	7.766	6.868	4.341

'*' indicates significance at 5% and '**' indicates significance at 1% level of significance.
d. f.- Degree of freedom; D50- days to 50% flowering; DTM- Days to maturity; PH- Plant height; PBPP- Primary branches/plant; NSBPP- No. secondary branches per plant; BYPP- Biological yield/plant; SYPP- Seed yield/plant; 100-sw- 100-Seed weight.

increase in this trait can result in increased yield. Biological yield/plant is correlated positively with its seed yield, pod/plant, secondary branches/plant, seed pod^{-1} and 100-seed weight demonstrating that biomass enhancement can increase overall yield. Seed yield/plant, seed pod^{-1}, primary branches/plant, plant height and 100-seed weight all have positive correlations with harvest index, indicating that a higher harvest index leads to a higher total yield component. These trait associations are in agreement with the results of Ali *et al.* (2019) and Jeberson *et al.* (2016), Katoch *et al.* (2021) who reported similar correlation patterns in field pea. The consistent positive correlations observed across studies indicate the reliability of these relationships and their potential exploitation for indirect selection to improve seed yield, particularly focusing on pods per plant and 100-seed weight, as suggested by Srivastava *et al.* (2018), Georgieva *et al.* (2015) and Sharma *et al* (2023). Seed yield was strongly and significantly positively correlated with pods/plant ($r \approx 0.83$) and 100-seed weight ($r \approx 0.74$) and negatively with days to flowering/maturity. By concentrating on these traits, breeders can increase field pea production, particularly in light of changing climates. Bhuvaneswari *et al.* (2017) and Lal *et al.* (2018) had similar findings. Fig 1 demonstrate correlation heatmap of 11 traits in field pea showing relationship among variables. Correlation coefficients reveal trait relationships, without demonstrating causation. Phenotypic path coefficient analysis partitions correlation coefficients into direct and indirect effects with seed yield as the dependent variable. Table 5 shows that biological yield (0.8698) has

Table 2: Mean and range of variability of parents and half-diallel crosses for 11 characters of field pea in late sown condition.

Trait	Mean	Max	Min	GCV (%)	PCV (%)	Heritability (h^2b)	Genetic advanceas	Genetic advance 5% of mean
Days to 50% flowering	54.10	75.00	42.00	6.00	8.07	0.55	4.98	9.21
Days to maturity	97.59	119.00	80.00	**5.20**	**7.44**	0.49	7.30	7.48
Plant height	89.98	115.60	64.50	16.58	17.32	0.92	29.41	32.68
PBPP	2.86	3.80	1.20	13.46	21.01	0.41	0.51	17.76
NSBPP	4.09	6.20	1.20	**23.86**	**27.84**	0.73	1.72	42.12
Pod/plant	26.56	38.56	17.45	15.98	16.89	0.89	8.27	31.13
seeds/pod	5.07	6.60	3.80	9.64	11.02	0.77	0.88	17.38
100-seed weight	25.46	30.55	16.97	7.23	9.16	0.62	2.99	11.75
HI	36.25	45.94	27.86	6.06	9.84	**0.38**	2.79	7.69
BYPP	95.46	131.55	58.45	18.52	19.22	**0.93**	**35.10**	36.77
SYPP (g)	34.52	48.85	19.87	19.52	20.43	0.91	13.26	38.41

PBPP- Primary branches per plant; NSBPP- Number of secondary branches per plant; BYPP- Biological yield per plant; SYPP- Seed yield per plant; HI- Harvest index.

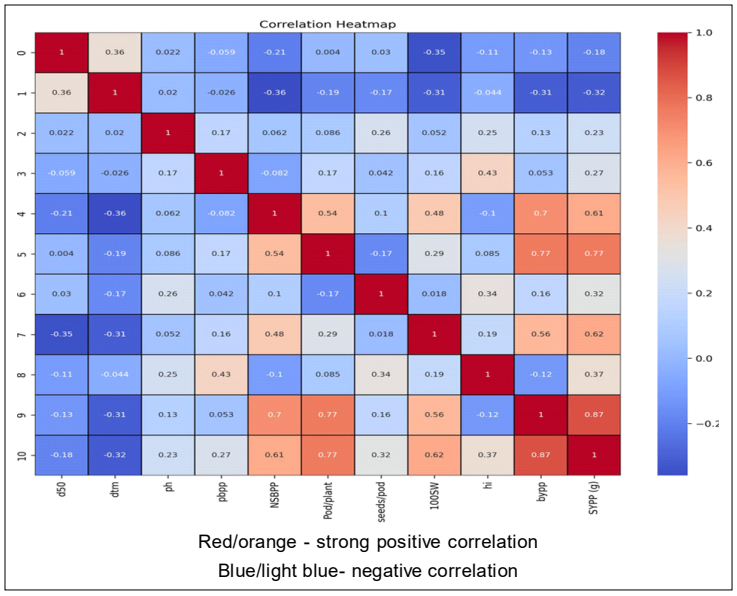


Fig 1: Correlation heatmap of 11 traits in field pea showing relationship among variables.

Table 3: Genotypic correlation of parents and their half-diallel crosses for 11 characters in field pea under late sown condition.

Traits	Days to 50% flowering	Days to maturity	Plant height (cm)	PBPP	SBPP	Pods/plant	seeds/pod	100-seed weight	HI	BYPP	SYPP
Days to 50% flowering	1	0.6609 **	0.0358	-0.1905	-0.4357 **	-0.0285	0.0277	-0.5656 **	-0.1988	-0.1669	-0.2295
Days to maturity		1	0.0514	-0.0706	-0.5031 **	-0.2787 *	-0.2673 *	-0.5802 **	0.011	-0.4986 **	-0.4776 **
Plant height (cm)			1	0.2961 *	0.0931 NS	0.1074	0.2948 *	0.0505 NS	0.3908 **	0.1406	0.2407
PBPP				1	-0.1567 NS	0.2735 *	0.1202 NS	0.3928 **	1.0832 **	0.1357	0.4791 **
SBPP					1	0.646 **	0.1109 NS	0.7184 **	-0.25	0.8466 **	0.7218 **
Pods/plant						1	-0.1282 NS	0.5009 **	0.0934	0.8391 **	0.8332 **
seeds/pod							1	0.07	0.3752 **	0.2091	0.3099 *
100- seed weight								1	0.1395	0.7323 **	0.7379 **
HI									1	-0.0033	0.3173 *
BYPP										1	0.9455 **

'*' indicates significance at 5% and '**' indicates significance at 1% level of significance.

PBPP- Primary branches per plant; NSBPP- Number of secondary branches per plant; BYPP- Biological yield per plant; SYPP- Seed yield per plant; HI- Harvest index.

Table 4: Phenotypic correlation of parents and their half-diallel crosses for 11 characters in field pea under late sown condition.

Traits	Days to 50% flowering	Days to maturity	Plant height (cm)	PBPP	SBPP	Pods/plant	seeds/pod	100-seed weight	HI	BYPP	SYPP
Days to 50% flowering	1	0.3627 **	0.0218	-0.0592	-0.2071 **	0.0036	0.03	-0.3459 **	-0.1143	-0.1316	-0.1842 *
Days to maturity		1	0.0204	-0.0264	-0.3586 **	-0.1884 *	-0.1692 *	-0.3085 **	-0.0436	-0.3082 **	-0.3148 **
Plant height (cm)			1	0.1654 *	0.0615	0.0855	0.2581 **	0.052	0.2467 **	0.1269	0.2253 **
PBPP				1	-0.0821	0.1709 *	0.0418	0.1587 *	0.4313 **	0.0525	0.2711 **
SBPP					1	0.543 **	0.1039	0.4803 **	-0.0998	0.7045 **	0.6084 **
Pods/plant						1	-0.1688 *	0.2901 **	0.0851	0.7656 **	**0.7649 ** **
seeds/pod							1	0.0184	0.3373 **	0.1634 *	0.3197 **
100- seed weight								1	0.1861 *	0.5602 **	0.6169 **
HI									1	-0.1251	0.3731 **
BYPP										1	**0.8698 ** **

'*' indicates significance at 5% and '**' indicates significance at 1% level of significance.

PBPP- Primary branches/ plant; NSBPP- Number of secondary branches/plant; BYPP- Biological yield/ plant; SYPP- Seed yield/plant; HI- Harvest index.

Table 5: Phenotypic path matrix of parents and their half-diallel crosses for 11 characters in field pea under late sown condition.

Traits	Days to 50% flowering	Days to maturity	Plant height (cm)	PBPP	SBPP	Pods/plant	Seeds/pod	100-seed weight	HI	BYPP	SYPP
Days to 50% flowering	-0.01829	0.001692	-0.00027	-0.00095	0.001712	0.000476	0.002348	-0.02087	-0.04746	-0.10259	-0.1842*
Days to maturity	-0.00664	0.004666	-0.00026	-0.00043	0.002965	-0.02491	-0.01324	-0.01861	-0.0181	-0.24025	-0.3148**
Plant height (cm)	-0.0004	.0000951	-0.01254	0.002663	-0.00051	0.011305	0.020198	0.003137	0.102425	0.098922	0.2253**
PBPP	0.001083	-0.00012	-0.00207	0.0161	0.000679	0.022597	0.003271	0.009573	0.179067	0.040925	0.2711**
NSBPP	0.003789	-0.00167	-0.00077	-0.00132	-0.00827	0.071799	0.008131	0.028974	-0.04144	0.549177	0.6084**
Pods/plant	-.000065	-0.00088	-0.00107	0.002752	-0.00449	0.132226	-0.01321	0.0175	0.035332	0.596806	0.7649**
seeds/pod	-0.00055	-0.00079	-0.00324	0.000673	-0.00086	-0.02232	0.078255	0.00111	0.14004	0.127375	0.3197**
100-seed weight	0.006328	-0.00144	-0.00065	0.002555	-0.00397	0.038359	0.00144	0.06032	0.077265	0.436691	0.6169**
HI	0.002091	-0.0002	-0.00309	0.006944	0.000825	0.011252	0.026395	0.011226	0.415181	-0.09752	0.3731**
BYPP	0.002408	-0.00144	-0.00159	0.000845	-0.00582	0.101232	0.012787	0.033794	-0.05194	0.779527	0.8698**

Residual effect = 0.0528, (bold values) indicates direct effects.

PBPP- Primary branches/ plant; NSBPP- Number of secondary branches/plant; BYPP- Biological yield/ plant; SYPP- Seed yield/plant; HI- Harvest index.

the highest direct positive effects on seed yield, suggesting that it is a primary driver of seed yield, indicating importance selecting high biomass. Pods/plant (0.7649), 100-seed weight (0.6169), secondary branches/plant (0.6084), harvest index (0.3731), seed/pod (0.3197), primary branches/plant (0.2711) and plant height (0.2253) were the next most positive direct effects on seed yield. These findings were also reported Tiwari and Lavanya (2012); Basaiwala *et al.* (2013) and Kumar *et al.* (2013). Characters' indirect contributions to seed yield were extremely minimal and detrimental. Days to 50% flowering (-0.1842) and days to maturity (-0.3148) showed a significant negative direct effect. By biological yield per plant, strong indirect impacts were observed in the no. of pods/plant (0.5968), secondary branches plant^{-1} (0.5491), 100-seed weight (0.4366) and seeds per pod (0.1273). This indicates that these traits influence seed yield through two pathways: directly through their own effects and indirectly by enhancing total biomass production, which subsequently translates to higher seed yields. The substantial indirect effects through biological yield demonstrate that traits contributing to vegetative vigor ultimately benefit seed production. This finding aligns with Tofiq *et al.* (2015), who demonstrated that biomass increase is strongly associated with higher seed yield.

CONCLUSION

Significant genetic diversity was found in the plant height, days to 50% flowering, days to maturity and number of pods per plant for late-planted field pea half-diallel crosses, according to the analysis of variance (ANOVA). More phenotypic variance than genotypic variation was discovered in the study, indicating that the environment influences how traits are expressed. High PCV and GCV values were found for the number of secondary branches plant^{-1}, which can be used to optimize the breeding program. Plant height and biological yield plant^{-1} showed high heritability coupled with high genetic advance, suggesting traits can be enhanced by breeding and selection. This implies that selection can enhance these traits and that heredity has a significant impact on them. Correlation research demonstrated the significance of variables such as harvest index, pods per plant and 100-seed weight in field pea breeding initiatives aimed at increasing output. According to path coefficient analysis, 100-seed weight, biological yield, harvest index, pods/plant and secondary branches/ plant all directly increase seed yield/plant, demonstrating their worth. The results suggest that field pea output can be increased by choosing key agronomic traits which can be helpful in increasing its productivity.

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Disclaimers

The authors present only their findings and do not represent any affiliated organizations. In the case of direct or indirect losses resulting from the use of this content, the authors accept responsibility for its accuracy and quality.

Informed consent

No animal used during the research.

Conflict of interest

Neither author has a conflict of interest. No funding or sponsorship was involved in the design or article preparation.

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