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Genetic variability in spinach genotypes for yield and yield components under north Indian conditions

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ABSTRACT

The present study was conducted to assess the genetic variability, heritability and genetic advance for yield and yield-attributing traits in twenty diverse spinach genotypes under the environmental conditions of the north Indian plains (Jalandhar, Punjab). A randomized block design with three replications was employed. Analysis of variance revealed significant differences among genotypes for all fifteen studied traits, indicating the presence of substantial genetic variability. Phenotypic coefficient of variation was generally higher than genotypic coefficient of variation, with high estimates (>25%) observed for phosphorus and number of leaves per plant. High broad-sense heritability (>50%) was recorded for most traits, including phosphorus, leaf area, first cutting yield and number of leaves per plant. Similarly, high genetic advance as a percentage of the mean (>20%) was observed for phosphorus, number of leaves per plant, petiole length and leaf area. The combination of high heritability and high genetic advance for these traits suggests the potential for substantial genetic improvement through direct selection. The findings of this study provide valuable information for spinach breeding programmes aimed at enhancing productivity and selecting desirable traits adapted to the north Indian agro-ecological zone.

Keywords: Spinach; genetic variability; heritability; genetic advance; yield components

INTRODUCTION

Spinach (*Spinacia oleracea* L) also known as Palak, is one of the most nutritious vegetables consumed throughout the world as salad or as cooked vegetable. It is a leafy cool season vegetable belonging to the family Chenopodiaceae. Spinach is a dioecious plant (Gyawali et al 2021) with higher pigment and carbohydrate content in females as compared to males. Cross pollination in spinach is generally assisted by wind. Being a highly cross-pollinated crop, huge amount of variability is observed in its population. It is native to central and western Asia (Jain et al 2022). China is the largest producer of spinach followed by USA and Japan (Turkiewicz et al 2025).

In India, spinach is mostly cultivated in tropical and sub-tropical regions like Uttar Pradesh, West Bengal, Maharashtra, Rajasthan, Punjab, Haryana and Gujrat (Nasrabadi et al 2022). It has significant amount of beta-carotene (Alhasnawi et al 2024), folate, vitamin C and calcium along with considerable amount of phosphorus, sodium and potassium. Spinach is a rich source of antioxidants and is among the vegetables with highest ORAC (oxygen radical absorbance capacity) (Gupta and Wagle 1998). Genetic variability is the cornerstone of any crop improvement programme, as it provides the raw material for selection and breeding (Asadi and Hasandokht 2007).

Assessing the extent of genetic diversity among available germplasm is essential to identify promising genotypes and traits that can be targeted for enhancement (Anandhinatchiar et al 2024). In spinach, traits such as leaf size, number of leaves, plant biomass, chlorophyll content and yield potential are crucial indicators of performance and market value (Gerrano et al 2015, Reddy et al 2014). A systematic evaluation of genetic variability for these traits under specific environmental conditions can significantly aid in the development of high-yielding and climate-resilient cultivars.

Despite its importance, limited studies have focused on the genetic variability of spinach genotypes in the context of the north Indian plains. Given the region's unique agro-ecological profile, it is essential to characterize and utilize local and introduced genetic resources effectively (Sabaghnia et al 2014). The present study aims to assess the magnitude of genetic variability, heritability and genetic advance in a diverse set of spinach genotypes under the environmental conditions of the north Indian plains. The findings will contribute to a more efficient selection strategy for spinach improvement programmes tailored to this region.

MATERIAL and METHODS

The present investigations were carried out at the experimental farm of the Department Agricultural Science, DAV University, Jalandhar, Punjab from October 2019. The experiment was laid out in randomized block design with three replications; the plot size was kept 5.4 m × 3 m, with row to row spacing of 20 cm. The genotypes were raised in three rows in each plot as per recommended package of practices. The material for the present study comprised twenty genotypes of diverse origin viz Green star, Palak Harit Shobha, Super All Green, Evergreen, Supriya, All Green, Palak Harita, Komal Spinach, Palak All Green, Spinach Solan Harit, Green Flavour, Ananya Green, Samag Star, Spinach Green Hara Sona, Palak Beej, Pusa Harit (check variety recommended for the area), All Green Composite, Local Selection 1, Local Selection 2 and Local Selection 3. The material was planted during winter 2019-2020. Observations were recorded in each replication on five randomly selected competitive plants and mean values were calculated. Days to emergence were counted from sowing till emergence. Leaf length and width were measured with the help of scale. Petiole length was measured from base of plant to tip of petiole with the help of scale and petiole diameter with the help of digital Vernier calliper. Number of leaves in selected plants was counted after cutting fresh plants. Leaf area was calculated by grid method. Days to first cutting were counted from sowing till harvesting and cutting yield was calculated by weighing the fresh plants. For bolting initiation, the days were counted from sowing till 10 per cent of plants had 5 cm high stems. The quantity of chlorophyll 'a' and 'b' was calculated according to chlorophyll extraction protocol (Hiscox and Israelstam 1979) adopted by Richardson et al (2002) and thus total chlorophyll content was calculated. Phosphorus was estimated as per Kitson and Mellon (1944). Phenols were estimated by the method described by Sadasivam and Manickam (1997).

RESULTS and DISCUSSION

Analysis of variance

Perusal of data in Table 1 reveal significant differences among the genotypes for all the traits viz days to emergence, leaf length, leaf width, petiole length, petiole diameter, number of leaves per plant, leaf area, days to first cutting, first cutting yield, bolting, chlorophyll 'a', chlorophyll 'b', total chlorophyll, phenolics and phosphorus, indicating the prevalence of wide range of genetic variability in the material under study. The analysis of variance revealed significant mean sum of squares for all the 15 traits, whereas, replication sum of squares were insignificant throughout indicating low environmental effect on the variability expressed by the genotypes. Significant variability in spinach genotypes has also been reported by Singh et al (2008), Eftekhari et al (2010), Reddy et al (2014), Ebadi-Segheloo et al (2015), Sabaghnia et al (2014) and Wu et al (2000) and Kanthaswamy (2006) in other leafy vegetables (amaranthus).

Parameters of variability

The estimates of parameters of variability viz phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability in broad sense (h^2bs) and genetic advance (GA) expressed as percentage of mean for different traits are presented in Table 2.

Phenotypic and genotypic coefficients of variation: The knowledge of PCV and GCV are helpful in predicting the amount of variation present in the genetic stock. The estimates of PCV were higher than the corresponding estimates of GCV for all fifteen characters under study, indicating that the apparent variation is also contributed by the environmental factors. Therefore, caution has to be exercised in making selection for these characters on the basis of phenotype alone, keeping in mind the unpredictable nature of environmental variations. However, the

Table 1. Analysis of variance for various quantitative traits of spinach genotypes

Character	Mean sum of squares (replications) (df = 2)	Mean sum of squares (genotypes) (df = 38)	Error (df = 76)
Days to emergence	00.12	03.05*	00.50
Leaf length	00.17	00.92*	00.49
Leaf width	00.25	01.07*	00.45
Petiole length	00.17	06.92*	00.24
Petiole diameter	00.02	00.42*	00.01
Leaves/plant	00.22	23.94*	00.76
Leaf area	07.14	159.89*	03.31
Days to first cutting	08.02	14.09*	02.88
First cutting yield	00.69	98.28*	03.03
Bolting	33.45	124.75*	14.31
Chlorophyll 'a'	00.01	04.28*	00.59
Chlorophyll 'b'	00.09	02.99*	00.23
Total chlorophyll	00.12	12.94*	00.44
Phenolics	00.04	00.35*	00.02
Phosphorus	00.00	0.007*	0.0001

*Significant at 0.05% LoS

Table 2. Parameters of variability of various quantitative traits in twenty spinach genotypes

Character	GCV	PCV	(h^2bs) (%)	GA (%)
Days to emergence	17.29	21.81	62.84	28.23
Leaf length (cm)	5.06	10.68	22.46	4.95
Leaf width (cm)	9.89	17.76	31.01	11.34
Petiole length (cm)	30.15	31.79	89.96	58.91
Petiole diameter (mm)	18.37	19.32	90.39	35.98
Leaves/plant	33.16	34.75	91.04	65.17
Leaf area (cm^2)	27.47	28.32	94.05	54.88
Days to first cutting	4.53	6.02	56.51	7.01
First cutting yield (g)	17.98	18.82	91.29	35.39
Bolting	6.98	8.22	72.01	12.19
Chlorophyll 'a' (mg/g)	18.51	22.53	67.53	31.34
Chlorophyll 'b' (mg/g)	28.85	32.31	79.72	53.06
Total chlorophyll (mg/g)	21.99	23.11	90.51	43.09
Phenolics	17.20	18.71	84.54	32.58
Phosphorus	70.53	71.36	97.68	73.59

GCV: Genotypic coefficient of variation; PCV: Phenotypic coefficient of variation; h^2bs: Broad sense heritability; GA (%): Genetic advance as per cent of mean

differences between these values were not very high indicating that the maximum amount of variation present can be attributed to the genotypic component. Highest estimates of PCV and GCV (>25%) were observed in phosphorus (71.36 and 70.53 respectively) and leaves per plant (34.75 and 33.16 respectively) followed by chlorophyll 'b' (32.31 and 28.85 respectively), petiole length (31.79 and 30.15 respectively) and leaf area (28.32 and 27.47 respectively); moderate (20-25%) in total chlorophyll (23.11 and 21.99 respectively); moderate PCV with low GCV in chlorophyll 'a' (22.53 and 18.51 respectively), days to emergence (21.81 and 17.29 respectively) and low PCV and GCV (<20%) in petiole diameter (19.32 and 18.37 respectively), first cutting yield (18.82 and 17.98 respectively), phenolics (18.71 and 17.20 respectively), leaf width (17.76 and 9.89 respectively), leaf length (10.68 and 5.06 respectively), bolting (8.22 and 6.98 respectively) and days to first cutting (6.02 and 4.53 respectively).

Heritability: High PCV or GCV do not provide true estimates of extent of genetic gain that can be achieved from selection until the heritable fraction of the trait is known (Kumari et al 2018). Estimation of heritability is, therefore, important. High estimates of heritability increase the possibility of fixing the characters through selection.

Therefore, heritability studies play an important role in judging whether the observed variation for a particular character is due to genotype or due to environmental factors. The estimates of broad sense heritability varied from 22.46 to 97.68 per cent for different traits under study. Heritability estimates were found to be high (>50%) for phosphorus (97.68%), leaf area (94.05%), first cutting yield (91.29%), leaves per plant (91.04%), total chlorophyll (90.51%), petiole diameter (90.39%), petiole length (89.96%), phenolics (84.54%), chlorophyll 'b' (79.72%), bolting (72.01%), chlorophyll 'a' (67.53%), days to emergence (62.84%) and days to first cutting (56.51%) and low (<35%) in leaf width (31.01%) and leaf length (22.46%).

Genetic advance: Genetic advance as percentage of mean, also known as genetic gain, can be used to estimate the amount of improvement that can be achieved through selection in the breeding material.

As per Johnson et al (1955), estimates of heritability coupled with genetic advance during selection are more effective as compared to heritability alone. High (>20%) genetic advance was observed in phosphorus (73.59%), leaves per plant (65.17%), petiole length (58.91%), leaf area (54.88%), chlorophyll 'b' (53.06%), total chlorophyll (43.09%), petiole diameter (35.98%), first cutting yield (35.39%), phenolics (32.58%), chlorophyll 'a' (31.34%) and days to emergence (28.23%) while low (<15%) estimates of genetic gain were observed in bolting (12.19%), leaf width (11.34%), days to first cutting (7.01%) and leaf length (4.95%).

High heritability coupled with high genetic advance was observed in all the traits except leaf length, leaf width, days to first cutting and bolting. Among these traits petiole length, number of leaves per plant, leaf area, chlorophyll 'b' and phosphorus content also showed high genotypic coefficient of variance. Therefore, high genetic improvement can be expected through direct selection for these traits. However, in traits with either low heritability or genetic advance or both should be selected indirectly through the correlated traits with high estimates of heritability and genetic advance.

Singh et al (2008) also reported higher PCV and heritability estimates for most of the traits including yield in spinach. Varalakshmi and Devaraju (2010) and Reddy et al (2014) reported higher PCV estimates as compared to the GCV and moderate to high heritability for traits like petiole length, leaf weight, leaf length and leaf width. Similar results have been reported by Madalgeri (1998), Shukla et al (2006), Ahuja and Mohideen (2007) and Khurana et al (2009) in other leafy vegetables.

CONCLUSION

The analysis of variance revealed significant genetic variability among the twenty spinach genotypes for all fifteen studied traits under the north Indian plains conditions, indicating a substantial potential for genetic improvement. The phenotypic coefficient of variation was generally higher than the genotypic coefficient of variation, suggesting the influence of environmental factors, although the differences were not substantial. High estimates of heritability in broad sense were observed for most traits, including phosphorus, leaf area, first cutting yield, number of leaves per plant and chlorophyll content, indicating that a significant portion of the phenotypic variation is due to genetic factors and these traits can be effectively improved through selection.

Furthermore, high genetic advance as a percentage of the mean was also recorded for several traits such as phosphorus, number of leaves per plant, petiole length, leaf area and chlorophyll 'b', suggesting considerable potential for genetic gain through direct selection. The combination of high heritability and high genetic advance for these traits suggests that direct selection would be an effective strategy for enhancing these desirable characteristics in spinach breeding programmes tailored for the north Indian plains.

Conversely, traits exhibiting low heritability and limited genetic advance, such as leaf length, leaf width, days to first cutting and bolting, may necessitate the implementation of indirect selection strategies. These approaches would involve focusing on other, correlated traits that possess more favourable genetic parameters, thereby, offering a more effective pathway for improvement. The findings offer valuable and actionable insights for plant breeders to strategically prioritize key traits and to develop highly efficient selection strategies specifically tailored for enhancing the overall productivity and nutritional quality of spinach within the distinct north Indian agro-ecological zone.

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