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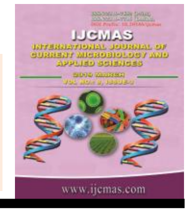

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# Genetic Variability and Correlation Analysis in Nigella (*Nigella sativum* L.) Assessed in South Eastern Rajasthan, India

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Nigella (*Nigella sativa* L.) is an important seed spice crop having high medicinal importance. Genetic variability, correlation and path analysis was carried out in thirteen nigella genotypes to work out the magnitude of variability for yield and yield contributing traits and also to understand the mutual relationship among the characters. The results revealed that primary and secondary branches per plant, seeds per plant, capsules per plant and biological yield per plant are important yield contributing traits having high heritability as well as strong correlation with seed yield. Therefore, effective selection can be exercised for these traits for realizing higher yield levels in nigella.

## Introduction

Nigella (*Nigella sativum* L.) belonging to family *Ranunculaceae* is an important minor seed spice crop of India. Here, it is mainly cultivated in states like Madhya Pradesh, Bihar, Punjab and Assam. Besides India, nigella is mainly cultivated in Pakistan, Sri Lanka, Bangladesh, Nepal, Egypt and Iraq. It is widely used medicinal plant throughout the world. The seeds contain 0.5 to 1.4% essential oil which has demand in the pharmaceutical and perfume industry (Malhotra, 2004, Dubey *et al.*, 2016).

Seed spices are cultivated in large in Rajasthan, western dry regions grow cumin and fenugreek mainly, southern parts cultivate fennel and humid south eastern plains of the state have high acreage in coriander. In the recent years, the humid south eastern plains (Zone V) comprising of districts *viz*., Kota, Baran, Bundi and Jhalawar where coriander is mainly grown are facing adverse climatic conditions and incidence of diseases like stem gall has caused significant yield loss. Therefore, the cultivators are showing increased interest towards other crops, of which nigella as an alternative seed spice crop has high potential. The area under nigella in Rajasthan and zone V has been recorded 10157 hectares and 7677 hectares respectively with maximum area of 7167 hectares in Jhalawar district of the state. The total production of nigella in Rajasthan is 8522 mt with maximum contribution of 5734 mt from Jhalawar district followed by Chittor during 2015-16. Therefore, the climate of south eastern Rajasthan seems very conducive for seed spices including nigella. Since meagre reports are available regarding the extent of genetic variability available in this crop and keeping in view the importance of this emerging crop in zone V, a study was undertaken to have an insight about the genetic parameters and mutual relationship among the various yield contributing characters for exploitation in crop improvement programme of nigella.

## Materials and Methods

The experimental material consisted of 13 diverse nigella genotypes including two checks *viz*., AN–1, KKN-Sel–9, AN-S–5, AN-S–7, AN–04, AN–06, AN–21, AN–22, AN–23, AN–20, KKN-Sel–10, Pant Krishna (C) and Azad Kalongi (C) grown in Randomized Block Design with three replication during *rabi* season at Agricultural Research Station, Kota. In each replication, genotypes were sown in a plot of 9.6 $m^2$ accommodating 8 rows of 4 m length spaced 30 cm apart with an intra row spacing of 10 cm. All the recommended package of practices was followed to raise a healthy crop. The observations were recorded for days to 50 % flowering, days to maturity, plant height (cm), primary branches per plant, secondary branches per plant, capsules per plant, seeds per plant, biological yield per plant (g), seed yield per plant (g), harvest index (%) and test weight (g). Analysis of variance was done by the method suggested by Panse and Sukhatme (1967) and genotypic coefficient of variance, heritability and genetic gain as per procedure of Burton (1952), Burton and De Vane (1953) and Johnson *et al.,* (1955), respectively. The genotypic and phenotypic correlation coefficient and the direct and indirect contribution of various characters to yield was calculated following the method suggested by Al. Jibouri *et al.,* (1958) and Dewey and Lu (1959), respectively.

## Results and Discussion

The analysis of variance revealed significant differences among all the genotypes for most of the traits studied; indicating presence of significant variability in the material thereby justifying the selection of the experimental material. The range, mean and standard error of mean, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability ($h^2$) in broad sense and genetic advance (GA) as per cent of mean for various characters are presented in Table 1. The range of characters indicated the existence of variability for all the characters. The range of variation was high for seed per plant followed by plant height and harvest index. The phenotypic coefficient of variation (PCV) were higher than genotypic coefficient of variation (GCV) for the traits studied which is an indicator of additive effect of environment on the expression of the trait. The estimates of PCV and GCV indicated the existence of fairly high degree of variability for seed yield per plant and biological yield per plant. Secondary branches per plant, harvest index, capsules per plant, primary branches per plant and test weight showed moderate estimates of GCV and PCV.

The seed yield per plant showed the higher PCV value of 52.43 per cent in comparison to GCV of 51.52 % suggesting less environmental influence on this character, which was confirmed by its high heritability. The difference between PCV and GCV was minimum for seed yield per plant, biological yield per plant, harvest index, capsule per plant suggesting that these traits were least affected by environment. This observations drawn support from the high value of heritability recorded for these traits. In corollary to high heritability estimates, high estimates of genetic advance as per cent of mean was observed for seed yield per plant, biological yield per plant, harvest index and capsule per plant indicating predominance of additive gene effects for these traits.

The highest GCV and PCV were observed for the characters biological yield and seed yield. The number of secondary branches, harvest index, capsules per plant, primary branches and test weight showed moderate estimates of GCV and PCV while the low estimates were observed for days to maturity and days to 50 percent flowering, plant height and seeds per plant.

The highest heritability estimates were found for biological yield, seed yield per plant, number of capsules per plant, harvest index, days to flowering, test weight and plant height. The characters like days to maturity, number of primary and secondary branches and seeds per plant showed moderate estimates of heritability. This implies that selection can be exercised for these traits as they are less influenced by the environment.

The genetic advance was highest for seeds per plant followed by harvest index, plant height and days to 50 percent flowering. Low estimates of genetic advance were observed for rest of the traits. Genetic gain was highest for seed yield and biological yield and lowest for days to maturity and days to 50% flowering.

The phenotypic and genotypic correlation among the yield and yield components in nigella are presented in Table 2. Significant correlation of characters suggested that there is much scope for direct and indirect selection for further improvement. In general, the estimates of genotypic correlation coefficient were higher than their corresponding phenotypic ones thereby suggesting strong inherent association among the characters studied.

In the present investigation, seed yield showed positive correlation with all the yield contributing traits but highly significant positive correlation with biological yield, capsules per plant, number of primary and secondary branches per plant and seeds per plant. Therefore, these characters should be considered while making selection for yield improvement in nigella. Similar results were reported by Salamati and Zeinali (2013), Maryam and Mohammad (2014) and Fufa (2016). With respect to the interrelationships among the different traits, plant height had significant positive correlation with primary and secondary branches per plant, capsules per plant, seeds per plant and biological yield. The days to 50 percent flowering showed significant positive correlation with days to maturity while number of primary branches showed significant positive correlation with secondary branches per plant, capsules per plant, seeds per plant and biological yield per plant. Capsules per plant had significant positive correlation with number of seeds per plant and biological yield. The correlation of seeds per plant with biological yield and harvest index was also significantly positive.

The results of present investigation on path coefficient analysis as presented in Table 3 revealed that biological yield per plant had highest direct effect on seed yield per plant. The direct effects of harvest index and primary branches per plant were also positive and high whereas, the number of capsules per plant, days to maturity and test weight had low negative direct effect.

**Table.1** Range, mean, phenotypic and genotypic coefficient of variation, heritability and genetic advance as per cent of mean for various characters in thirteen genotypes of nigella

| Characters | Range | Mean±SE | PCV (%) | GCV (%) | $h^2$(%) | GA as % of mean |
|---|---|---|---|---|---|---|
| Days to 50% flowering | 95.97-109.00 | 98.95±0.81 | 4.17 | 3.92 | 88.33 | 7.59 |
| Days to maturity | 142.67-149.00 | 145.28±0.82 | 1.52 | 1.17 | 58.81 | 1.85 |
| Plant height (cm) | 52.00-75.90 | 67.41±1.58 | 9.60 | 8.71 | 82.20 | 16.26 |
| Primary branches per plant | 2.60-4.90 | 3.62±0.34 | 24.21 | 17.74 | 53.74 | 26.80 |
| Secondary branches per plant | 1.47-6.10 | 3.76±0.56 | 37.97 | 27.96 | 54.22 | 42.41 |
| Capsules per plant | 4.20-11.20 | 7.45±0.30 | 26.10 | 25.12 | 92.68 | 49.83 |
| Seeds per plant | 194.50-297.20 | 242.89±16.71 | 16.21 | 11.00 | 46.00 | 15.36 |
| Biological yield per plant (g) | 1.39-6.24 | 2.88±0.13 | 45.18 | 44.53 | 97.15 | 90.41 |
| Seed yield per plant (g) | 0.27-1.87 | 0.77±0.04 | 52.43 | 51.52 | 96.58 | 104.30 |
| Harvest index (%) | 13.54-36.63 | 27.23±1.145 | 26.45 | 25.40 | 92.28 | 50.27 |
| Test weight (g) | 1.20-2.27 | 1.76±0.07 | 18.61 | 17.10 | 84.42 | 32.36 |
| | | | | | | |

**Table.2** Genotypic and phenotypic (rg and rp) correlation coefficients among different characters in nigella

| Character | | Days to 50% flowering | Days to maturity | Plant height | Primary branches per plant | Secondary branches per plant | Capsules per plant | Seeds per plant | Biological yield per plant | Seed yield per plant | Harvest index | Test weight |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Days to 50% flowering | $r_g$ | 1.00 | 0.97** | 0.11 | 0.02 | 0.16 | 0.11 | 0.13 | 0.04 | 0.09 | 0.13 | 0.08 |
| | $r_p$ | 1.00 | 0.72** | 0.09 | 0.06 | 0.16 | 0.1 | 0.02 | 0.04 | 0.09 | 0.12 | 0.09 |
| Days to maturity | $r_g$ | | 1.00 | 0.29 | 0.24 | 0.51 | 0.36 | 0.12 | 0.31 | 0.42 | 0.31 | 0.48 |
| | $r_p$ | | 1.00 | 0.16 | 0.21 | 0.36 | 0.35 | 0.2 | 0.27 | 0.34 | 0.19 | 0.29 |
| Plant height | $r_g$ | | | 1.00 | 0.62* | 0.66* | 0.67* | 0.59* | 0.58* | 0.51 | 0.03 | 0.38 |
| | $r_p$ | | | 1.00 | 0.33 | 0.49 | 0.59* | 0.38 | 0.49 | 0.45 | 0.05 | 0.28 |
| Primary branches per plant | $r_g$ | | | | 1.00 | 0.91** | 0.96** | 0.58* | 0.95** | 0.80** | 0.09 | 0.27 |
| | $r_p$ | | | | 1.00 | 0.79** | 0.73** | 0.63* | 0.75** | 0.63* | 0.08 | 0.3 |
| Secondary branches per plant | $r_g$ | | | | | 1.00 | 1.05 | 0.40 | 1.01 | 0.86** | 0.02 | 0.37 |
| | $r_p$ | | | | | 1.00 | 0.79** | 0.5 | 0.78** | 0.66* | 0.02 | 0.35 |
| Capsules per plant | $r_g$ | | | | | | 1.00 | 0.61* | 0.88** | 0.83** | 0.11 | 0.20 |
| | $r_p$ | | | | | | 1.00 | 0.46 | 0.84** | 0.79** | 0.08 | 0.2 |
| Seeds per plant | $r_g$ | | | | | | | 1.00 | 0.56* | 0.89** | 0.71** | 0.11 |
| | $r_p$ | | | | | | | 1.00 | 0.42 | 0.61* | 0.41 | 0.18 |
| Biological yield per plant | $r_g$ | | | | | | | | 1.00 | 0.85** | 0.14 | 0.31 |
| | $r_p$ | | | | | | | | 1.00 | 0.84** | 0.15 | 0.3 |
| Seed yield per plant | $r_g$ | | | | | | | | | 1.00 | 0.38 | 0.19 |
| | $r_p$ | | | | | | | | | 1.00 | 0.38 | 0.19 |
| Harvest index | $r_g$ | | | | | | | | | | 1.00 | 0.08 |
| | $r_p$ | | | | | | | | | | 1.00 | 0.08 |
| Test weight | $r_g$ | | | | | | | | | | | 1.00 |
| | $r_p$ | | | | | | | | | | | 1.00 |

**Table.3** Direct and indirect effect of different characters on seed yield in nigella

| Character | Days to 50% flowering | Days to maturity | Plant height | Primary branches per plant | Secondary branches per plant | Capsules per plant | Seeds per plant | Biological yield per plant | Harvest index | Test weight | R with seed yield per plant |
|---|---|---|---|---|---|---|---|---|---|---|---|
| Days to 50% flowering | 0.05 | -0.03 | 0.00 | 0.00 | 0.01 | -0.04 | -0.00 | 0.04 | 0.07 | -0.01 | 0.09 |
| Days to maturity | 0.04 | -0.03 | 0.01 | 0.03 | 0.02 | -0.12 | 0.00 | 0.32 | 0.17 | -0.03 | 0.42 |
| Plant height | 0.00 | -0.01 | 0.02 | 0.08 | 0.03 | -0.22 | 0.01 | 0.61 | 0.02 | -0.03 | 0.51 |
| Primary branches per plant | 0.00 | -0.01 | 0.01 | 0.13 | 0.04 | -0.31 | 0.01 | 1.00 | -0.05 | -0.02 | 0.80** |
| Secondary branches per plant | 0.01 | -0.02 | 0.01 | 0.11 | 0.05 | -0.34 | 0.01 | 1.07 | -0.01 | -0.03 | 0.86** |
| Capsules per plant | 0.00 | -0.01 | 0.01 | 0.12 | 0.05 | -0.33 | 0.01 | 0.93 | 0.06 | -0.01 | 0.83** |
| Seeds per plant | 0.01 | -0.00 | 0.01 | 0.07 | 0.02 | -0.20 | 0.01 | 0.60 | 0.40 | -0.01 | 0.89** |
| Biological yield per plant | 0.00 | -0.01 | 0.01 | 0.12 | 0.05 | -0.29 | 0.01 | 1.06 | -0.08 | -0.02 | 0.85** |
| Harvest index | 0.01 | -0.01 | 0.00 | -0.01 | -0.00 | -0.04 | 0.01 | -0.15 | 0.56 | 0.01 | 0.38 |
| Test weight | 0.00 | -0.02 | 0.01 | 0.03 | 0.02 | -0.07 | 0.00 | 0.33 | -0.04 | -0.07 | 0.19 |

In conclusion, the present study indicated that selection can be exercised for traits like number of primary and secondary branches, number of seeds and capsules per plant and biological yield owing to their high heritability and strong correlation with seed yield as well as significant positive inter-correlation between themselves and high positive direct effect. It is concluded that simultaneous improvement of these traits by selection will improve the seed yield of nigella. Besides this, based on their mean performance, the genotypes KKN- Sel - 9 and AN-21 can be used as suitable parents for breeding high yielding, dwarf and early maturing varieties.

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