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Estimation of correlation of different mutant lines of lentil (*Lens culinaris Medik. L.*)

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Abstract

Lentil is also used as nitrogen fixing crop. According to FAO statistical report, 2014 world lentil production 2012 in totaled to 4,557,972 tonnes from 4,206,024 ha area harvested. India alone produces 20.84% of world production. Lentil is self-pollinated crop ($2n=14$) and large genome size 41063Mbp. Seed of 9 induced mutant lines of lentil (*Lens culinaris Medik. L.*) were used for the experimental purpose. These mutants were isolated from variety K-75 with gamma ray and EMS treatment. The self-seeds of all mutants were sown in randomized block designed in three replications at Agricultural Research Farm, Institute of Agricultural sciences, B.H.U, Varanasi, during Rabi 2017-18. Distance between row to row and plant to plant was maintained 30cm and 5cm respectively. In phenotypic correlation, number of pods per plant (0.8504), number of secondary branches per plant (0.6395) showed positive and highly significant correlation with grain yield per plant. Number of pods per plant exhibited positive and highly significant correlation with number of secondary branches per plant (0.7758). In genotypic correlation, positive and significant correlation were exhibited by number of pods per plant with number of secondary branches, grain yield with number of secondary branches, grain yield with number of pods per plant, days to maturity with 100% flowering and days to 50% flowering with grain yield. So that from above interrelationship could be cleared that improving yield in lentil and ideal plant type would be expected to have more number of pods per plant and number of secondary branches per plant. In selection program me, inter-relationship of a number of characters with grain yield and among themselves studied.

Keywords: Phenotypic correlation, genotypic correlation, mutant line, lentil

1. Introduction

Lentil plays an important role in the farming system. Lentil was first domesticated in about 9000 years ago from *L. culinaris subsp orientalis* (Boiss). Lentil is the source of high-quality protein (26%). Lentil is used as dhal and residue for fodder purpose. Lentil is also used as nitrogen fixing crop. According to FAO statistical report, 2014 world lentil production 2012 in totaled to 4,557,972 tonnes from 4,206,024 ha area harvested. India alone produce 20.84% of world production. Lentil is self-pollinated crop ($2n=14$) and large genome size 41063Mbp. Mutation breeding is feasible and sustainable technique to create a gene pool of numerous desirable traits of economic importance. Lentil is responsive to both chemical and physical mutagens. The frequency of getting chlorophyll mutants like viridis, xantha and chlorina is high with NEU (N-ethyl-N-nitrosourea) than EI (ethylene imine) and Gamma rays (Solanki and Sharma, 2001, Sarker and Sharma, 1987) ^[32, 30]. The EMS induced mutants varies more for growth habit and foliage types, whereas SA treatments generates more of mutants for flowering behaviour, maturity duration and plant height in lentil (Solanki *et. al.*, 2004, Khan *et. al.*, 2006 Solanki, 2005, Solanki and Phogat, 2005) ^[33, 34]. The SA is found to be more effective than EMS to induce sterility in lentil (Solanki 2005) ^[33]. The NMU treatment induces sterile mutants (Sharma and Sharma, 1979) ^[79] it also generates mutants with tendrils in place of top two three terminal leaflets (Sharma and Sharma, 1978) ^[21] in some cases elongated peduncles and multi-floret inflorescences with sterile plant types in lentil have also been observed (Sharma and Sharma, 1981) ^[24]. Mutation is also found to be effective in generating disease resistant lines as gamma ray's induction produced resistant plants against wilt in lentil. Treatment with nitrosoguanidine increased nodule dry weight and nitrogenase activity of root nodules in lentil (Rai, 1985) ^[18]. Among the various mutagens EMS is found to be more effective than SA, genotypes response also varies for mutation rates as per the mutagen used (Gaikwad and Kothekar, 2004) ^[10].

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Wild Lens species are a significant source of genetic variation for improving the relatively narrow genetic base of this crop. The wild species possess many diverse traits including disease resistances and abiotic stress tolerances. The above-mentioned *L. nigricans* and *L. orientalis* possess morphological similarities to the cultivated *L. culinaris*. But only *L. culinaris* and *L. culinaris* subsp. *orientalis* are crossable and produce fully fertile seed. Between the different related species hybridization barriers exist. According to their inter-cross ability Lens species can be divided into three gene pools.

1. Primary gene pool: *L. culinaris* (and *L. culinaris* subsp. *orientalis*) and *L. odemensis*
2. Secondary gene pool: *L. ervoides* and *L. nigricans*
3. Tertiary gene pool: *L. lamottei* and *L. tomentosus*

Crosses generally fail between members of different gene pools. However, plant growth regulators and/or embryo rescue allows the growth of viable hybrids between groups. Even if crosses are successful, many undesired genes may be introduced as well in addition to the desired ones. This can be resolved by using a backcrossing program. Thus, mutagenesis is crucial to create new and desirable varieties. According to Yadav *et al.* other biotechnology techniques which may impact on lentil breeding are micro-propagation using meristematic explants, callus culture and regeneration, protoplast culture and doubled haploid production.

High yield, number of pods seed weight, etc. are the important objectives for lentil improvement. During evolutionary selection history, lentil has acquired a number of traits, which do confer the kind of ideotype which is required under conditions of improvement of agronomy. For this reason, mutation breeding appears to offer a greater scope and promise to generating useful variability in lentil crop.

2. Material and methods

2.1 Seed material

Seed of 9 induced mutant lines of lentil (*Lens culinaris* Medik L.) were used for the experimental purpose. These mutants were isolated from variety K-75 with gamma ray and EMS treatment.

2.2 Methods

The self-seeds of all mutants were sown in randomized block designed in three replications at Agricultural Research Farm, Institute of Agricultural sciences, B.H.U, Varanasi, during Rabi 2017-18. Distance between row to row and plant to plant was maintained 30cm and 5cm respectively. All the recommended agronomic and cultural practices were adopted for raising good plant population.

2.3 Observation

The observation on following characters was taken for the present study.

- **Days to 50% flowering:** Days from sowing date to the stage when 50% of the plants have started flowering per pot.
- **Days to 100% flowering:** Days from sowing date to the stage when 100% of the plants have started flowering per pot.
- **Plant height:** The plant height was measured in cm at time of harvesting from tip to the base of the largest branch.

- **Number of primary branches:** Number of primary branches coming out of base of each plant was recorded.
- **Number of secondary branches:** Number of secondary branches coming out from the primary branches is recorded.
- **Number of pods per plant:** Total number of pods was counted of each plant at time of maturity.
- **Day to maturity:** Number of days has been calculated from sowing to maturity date.
- **Grain yield per plant:** pods were detached from each plant and then pods were threshed and then weight was taken on weighing machine.
- **100 Seed weight:** Weight was taken of the selected 100 seeds on the electronic balance and recorded in gram. On 5 randomly selected plants in each Observation were recorded treatments in each replication.

2.4 Phenotypic and Genotypic correlation coefficients

Genotypic (r_g) and phenotypic correlation coefficients (r_{ph}) were computed using genotypic and phenotypic variances and co-variances according to (AlJibouri *et al.*, 1958):

$$r_g = \frac{\text{cov}_{g_{xy}}}{\sqrt{v_{g_x}v_{g_y}}} \quad r_{ph} = \frac{\text{cov}_{ph_{xy}}}{\sqrt{v_{ph_x}v_{ph_y}}}$$

Where,

$\text{cov}_{g_{xy}}, \text{cov}_{ph_{xy}}, v_{g_x}, v_{g_y}, v_{ph_x}, v_{ph_y}$ is genotypic co-variance of the two characters x and y, phenotypic co-variance of the two characters x and y, genotypic variance of the character x, genotypic variance of the character y, phenotypic variance of the character x, phenotypic variance of the character y, respectively

Simple correlation coefficients were calculated at genotypic and phenotypic levels for pairs of traits by using following formula:

$$r_{12}(g) = \sigma_g^2(X_1X_2) / \sqrt{\sigma_{g1}^2 \times \sigma_{g2}^2}$$

Phenotypic correlation between traits X_1 and $X_2 = r_{12}(p)$

$$r_{12}(p) = \sigma_p^2(X_1X_2) / \sqrt{\sigma_{p1}^2 \times \sigma_{p2}^2}$$

Where,

σ_{g1}^2 And σ_{g2}^2 = Are the genotypic variance of traits X_1 and X_2 respectively.

σ_{p1}^2 And σ_{p2}^2 = are the phenotypic variance for traits X_1 and X_2 , respectively.

Test of the significance of correlation coefficient at phenotypic level

is calculated values were compared with the table value (statistical table given by Fisher and Yates, 1967) at (n-2) degree of freedom at 1% and 5% level of significance, respectively.

3. Result and Discussion

Breeding approach has been suggested for yield improvement, where selection is made for traits having positive correlation with yield. The investigation was designed to obtain precise information about various genetic parameters viz., coefficient of variation, phenotypic and genotypic correlation, genetic advance, correlation coefficient, path coefficient and yield traits utilizing 9 diverse genotypes of lentil.

3.1 Correlation Coefficient between yield and yield contributing traits and within the characters themselves

Correlation coefficient explained the association between variables, but it did not explain about complex association and complementary effect of one component character over another.

Path analysis proposed by wright (1921) [40] which explained correlation with seed yield into direct and indirect effect of character. Yield is a quantitative character which is affected by integrated function of action of a number of factors. In biological system of plant these characters (factors) are usually independent. So, the precise knowledge of these characters interrelationship is very necessary for a breeder. So, it is useful in selecting character which not easily

observed. Now there is ample evidence to show that selection, directly for yield in plants which is very complex character may be difficult and effective. Any morphological traits associated with higher expression of yield or makes a significant contribution to yielding ability, it would be sound breeding policy to select for that distinct characters. But sometimes selection for a trait may give positive gain in one but a negative effect in another gain. So, it has also to be kept in mind so as to optimize genetic gain in selection process.

The mutual relationship among various characters is usually evaluated by estimating the correlation existing between them both at genotypic and phenotypic level. The correlation existing in 9 mutant lines of lentil has been studied and analyzed.

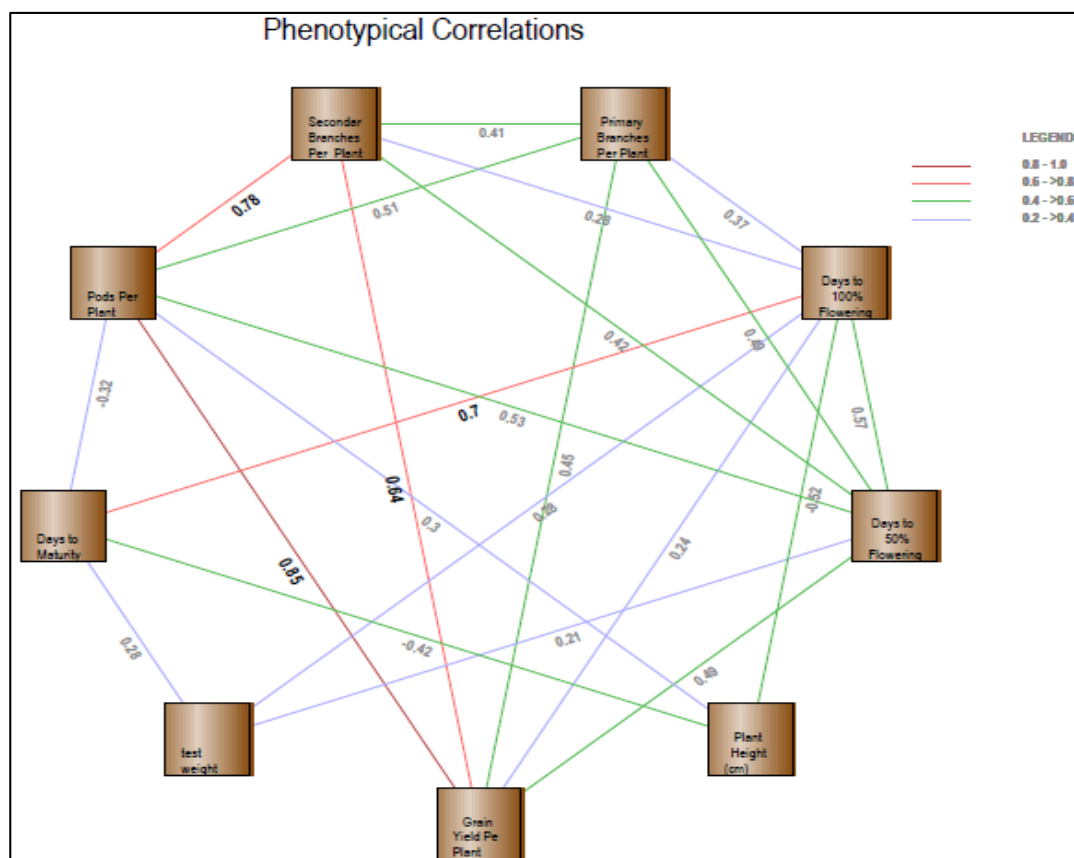


Fig 1: Diagrammatic representation of correlation between yield and various yield contributing characters induced mutants of Lentil at phenotypic level

Table 1: Estimates of phenotypic correlation coefficient between yield and its component characters in induced mutants of lentil

Character	Plant Height (cm)	Days to 50% Flowering	Days to 100% Flowering	Primary Branches Per Plant	Secondary Branches Per Plant	Pods Per Plant	Days to Maturity	Test Weight
Plant Height (cm)	1.0000	-0.1665	-0.5192**	-0.0426	0.1978	0.2961	-0.4235*	0.0581
Days to 50% Flowering		1.0000	0.5704**	0.4936**	0.4167*	0.5294**	0.1552	0.2116
Days to 100% Flowering			1.0000	0.3672	0.2807	0.1298	0.6972***	0.2835
Primary Branches Per Plant				1.0000	0.4051*	0.5065**	0.0069	0.1290
Secondary Branches Per Plant					1.0000	0.7758***	-0.1990	-0.0647
Pods Per Plant						1.0000	-0.3155	-0.0694
Days to Maturity							1.0000	0.2769
Test weight								1.0000
Grain Yield Per Plant	0.0526	0.4914*	0.2403	0.4505*	0.6395***	0.8504***	-0.1758	-0.0417

*** Values highly significant

In phenotypic correlation, number of pods per plant (0.8504), number of secondary branches per plant (0.6395) showed positive and highly significant correlation with grain yield per plant. Similar result shown by Dalbeer *et al.* (2013) [8]. Days

to 50% flowering (0.4914), number of primary branches per plant (0.4505) showed positive and significant association with yield trait. Days to 100% flowering (0.2403) and plant height (0.0526) showed positive and non-significant

correlation with grain yield. Similar result was reported by Basant *et al.*, (1983)^[1], Singh *et al.* (2007)^[36] and Tyagi and Khan (2010)^[39] for correlation of number of pods with grain yield. Similar result was reported by Chauhan and Singh (2001)^[5] for number of secondary branches and number of

Pods with grain yield. Number of pods per plant exhibited positive and highly significant correlation with number of secondary branches per plant (0.7758), same result was reported by Singh and Singh (1969)^[19].

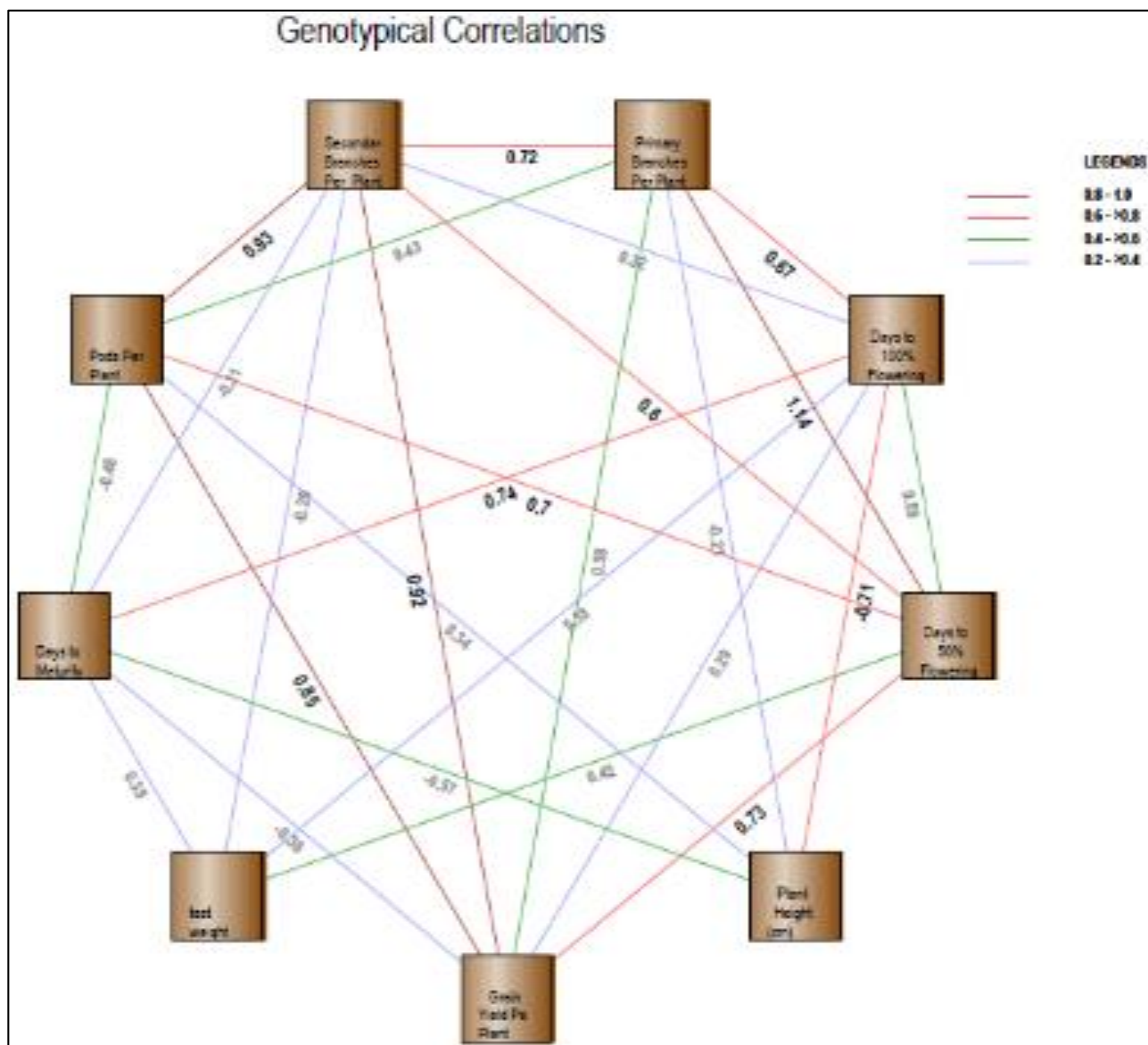


Fig 2: Diagrammatic representation of correlation between yield and various yield contributing characters induced mutants of Lentil at Genotypic level

Table 2: Estimates of genotypic correlation coefficient between yield and its component characters in induced mutants of lentil

Character	Plant Height (cm)	Days to 50% Flowering	Days to 100% Flowering	Primary Branches Per Plant	Secondary Branches Per Plant	Pods Per Plant	Days to Maturity	Test Weight
Plant Height (cm)	1.0000	-0.1401	-0.7074	-0.2060	-0.1763	0.3382	-0.5699	0.1034
Days to 50% Flowering		1.0000	0.5854*	1.1408	0.6026**	0.6952**	0.1804	0.4231
Days to 100% Flowering			1.0000	0.6711**	0.3244	0.0619	0.7412**	0.3336
Primary Branches Per Plant				1.0000	0.7187**	0.4289	-0.0768	0.1353
Secondary Branches Per Plant					1.0000	0.9342***	-0.3144	-0.2858
Pods Per Plant						1.0000	-0.4767	-0.1369
Days to Maturity							1.0000	0.3913
Test Weight								1.0000
Grain Yield Per Plant	-0.1020	0.7266**	0.2913	0.5805*	0.9169***	0.8499***	-0.3774	0.1656

So that from above interrelationship could be cleared that improving yield in lentil and ideal plant type would be expected to have more number of pods per plant and number of secondary branches per plant. In selection program me,

inter-relationship of a number of characters with grain yield and among themselves studied. In such case, path coefficient analysis is useful for clarifying the role of particular trait in determining the final grain yield.

Conclusion

In phenotypic correlation, number of pods per plant, number of secondary branches per plant showed high positive and significant correlation with grain yield per plant. Days to 50% flowering and number of primary branches per plant were exhibited positive and significant correlation with yield.

In genotypic correlation, positive and significant correlation were exhibited by number of pods per plant with number of secondary branches, grain yield with number of secondary branches, grain yield with number of pods per plant, days to maturity with 100% flowering and days to 50% flowering with grain yield.

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