

**Genetic Divergence and Selection Indices for Yield and its
Attributing Traits in Fenugreek (*Trigonella foenum-graecum* L.)**

सर्वप्रथम प्रस्तुत की गई है, यह एक वैज्ञानिक शोध कार्य है, जिसमें
वैज्ञानिकों द्वारा प्रयोग किए गए हैं।

HIMANSHI JHALORA

Thesis

Master of Science in Agriculture
(Genetics and Plant Breeding)



2024

**DEPARTMENT OF GENETICS AND PLANT BREEDING
RAJASTHAN COLLEGE OF AGRICULTURE
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UDAIPUR – 313 001 (RAJASTHAN)**

**Genetic Divergence and Selection Indices for Yield and its
Attributing Traits in Fenugreek (*Trigonella foenum-graecum* L.)**

सर्वप्रथम प्रस्तुत की गई है, यह एक वैज्ञानिक शोध कार्य है, जिसका उद्देश्य फेनूग्रीक (*Trigonella foenum-graecum* L.) में आनुवंशिक विचलन और चयन सूचकांक को उत्पादन और इसके संबंधित लक्षणों के लिए निर्धारित करना है।

Thesis

Submitted to the

Maharana Pratap University of Agriculture and Technology, Udaipur

In partial fulfillment of the requirements for the Degree of

Master of Science in Agriculture
(Genetics and Plant Breeding)



By

HIMANSHI JHALORA

2024

CERTIFICATE-I

CERTIFICATE OF ORIGINALITY

The research work embodied in the thesis titled “**Genetic Divergence and Selection Indices for Yield and its Attributing Traits in Fenugreek (*Trigonella foenum-graecum* L.)**” was submitted for the award of the degree of M.Sc. (Ag.) Genetics and Plant Breeding to Maharana Pratap University of Agriculture and Technology, Udaipur (Rajasthan), is an original and bonafide record of research work carried out by me under the supervision of Dr. Abhay Dashora, Assistant Professor, Department of Genetics and Plant Breeding, Rajasthan College of Agriculture, Udaipur. The contents of the thesis, either partially or fully, have not been submitted or will not be submitted to any other institute or university for the award of any degree or diploma.

The work embodied in the thesis represents my ideas in my own words and where the ideas or words of others have been included; I have adequately cited and referenced the original sources. I also declare that I have adhered to all principles of academic honesty and integrity and have not misrepresented or fabricated or falsified any idea/data/fact/source in my submission. I understand that any violation of the above will be a cause for disciplinary action by the university and can also evoke panel action from the sources which have thus not been properly cited or from whom proper permission has not been taken when needed.

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Dated: / /2024

This is to certify that the thesis entitled “**Genetic Divergence and Selection Indices for Yield and its Attributing Traits in Fenugreek (*Trigonella foenum-graecum* L.)**” submitted for the degree of **Master of Science in Agriculture** in the subject of **Genetics and Plant Breeding**, embodies bonafide research work carried out by Miss HIMANSHI JHALORA under my guidance and supervision and that no part of this thesis has been submitted for any other degree. The assistance and help received during the course of the investigation have been fully acknowledged. The draft of this thesis was also approved by the advisory committee on / /2024.

The manuscript has been subjected to plagiarism checked by the software DrillBit. It is certified that as per the check, the similarity index of the content is 9% and is within the permissible limit as per the MPUAT guidelines on checking Plagiarism.

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This is to certify that **Miss HIMANSHI JHALORA** student of Master of Science in Agriculture, **Department of Genetics and Plant Breeding**, Rajasthan College of Agriculture, Udaipur has made all the corrections/ modifications in the thesis entitled **“Genetic Divergence and Selection Indices for Yield and its Attributing Traits in Fenugreek (*Trigonella foenum-graecum* L.)”** which were suggested by the external examiner and the advisory committee in the oral examination held on / /2024. The final copies of the thesis duly bound and corrected were submitted on / /2024, are enclosed herewith for approval.

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ACKNOWLEDGEMENT

First of all, I express my infinite indebtedness and deep sense of gratitude to the God for the continuous inspiration and providing me spiritual energy which has enabled me to reach at this level. It has still great at this juncture to recall all the faces and spirit in the form of teachers, friends, near and dear ones. I would consider this work nothing more than incomplete, without attending to the task of acknowledging the overwhelming help I received during this endeavor of mine.

*I express my feelings of profound gratitude towards my Major Advisor **Dr. Abhay Dashora**, Assistant Professor, Department of Genetics and Plant Breeding, Rajasthan College of Agriculture, MPUAT, Udaipur, for his selfless assistance, precise guidance, propelling encouragement and constructive comments during the course of investigation. I am indebted for his generosity, constant counsel and genuine interest which induced self confidence in me. It was my pleasure and privilege to be associated with him and work under his close guidance and supervision. His unwavering support and belief in my abilities have been invaluable.*

*I am privileged to express a sincere and deep sense of gratitude to **Dr. Hemlata Sharma**, Associate Professor and Head, Department of Genetics and Plant Breeding, Rajasthan College of Agriculture, Udaipur for her kind cooperation and help as and when needed.*

*I am also indebted to **Dr. R.B. Dubey**, Dean, Rajasthan College of Agriculture, Udaipur for his due attention and encouragement during the study period and also for providing me with the necessary facilities during my research.*

*I am deeply grateful to **Dr. B.L. Baheti**, DRI, MPUAT for constant supervision and also for his support in completing this endeavour.*

*I am gratified to acknowledge my thanks to the members of the advisory committee, **Dr. Pratap Bhan Singh**, Assistant Professor, Department of Genetics and Plant Breeding, **Dr. Devendra Jain**, Assistant. Professor, Department of Molecular Biology and Biotechnology, and DRI nominee **Dr. Pokhar Rawal**, Associate Professor, Department Pathology, RCA, Udaipur for their generous gestures and valuable suggestion in planning and execution of this study.*

*I especially want to thank all staff members of Department of Genetics and Plant Breeding, **Dr. R. B. Dubey**, **Dr. Amit Dadheech**, **Dr. Urmila**, **Sh. Parbat Singh Rathore** and **Sh. Amar Singh Solanki** for their encouragement and help in numerous ways.*

*I am extremely thankful to Director, NRCSS, Tabiji, Ajmer, **Dr. Shailesh Marker**, PI AICRP on Seed Spices, SKNCOA, Jobner, **Dr. S.S. Meena**, PS (GPB), NRCSS, Ajmer and **Dr. Mahesh Mahatma** PS (Plant Biochemistry) NRCSS, Tabiji, Ajmer for providing research materials and lab facilities for quality parameter analysis.*

*I want to express my deep special thanks **Dr. Bhavendra Tiwari, Dr. Dharmesh Bhatt, Sh. K. D. Bhimawat, Sh. Dinesh Regar, Sh. Yogesh Salvi, Sh. Gheesu Meghwal and Sh. Bhagwan** for the help and cooperation in numerous ways.*

*I feel fortunate to express my deep sense of gratefulness and indebtedness to my seniors **Himansuman, Parul, Hariram, Jitendra, Naveen and Avadhoot** for their invaluable moral support, technical guidance, valuable suggestions, motivation and judicious direction rendered during the course of this investigation. I am beholden by the assistance provided by my friends **Radhika, Harshita, Dishita, Nishakar, Sohail, Aamir, Ajay, Pulkit, Pawan and Rishi** indebted by their love, support and faith, they showed me in every possible way. I would also extend my heartiest thanks to my juniors **Deepak, Rahul, Mohit, and Lekhraj** for their joyful company and help, they rendered during the course of study.*

*I am very fortunate and lucky to have the ceaseless encouragement and love from my family. No words in this mortal world can suffice, to express my feelings towards my father **Shri Sunil Jhalora** and my mother **Smt. Leela Jhalora**, and my brother **Rhythm Jhalora** for their constant encouragement, blessings and moral support for completion of my goal. I am overwhelmed with the love, care and affection showered on me by my family members who had done a lot to bring me to this level are inexpressible in words.*

My sincere gratitude towards MPUAT, Udaipur for providing me the opportunity of higher studies and such a great environment for social development. Finally, I extend my apologies and gratitude to everyone who had helped me directly or indirectly in this endeavor and I was unable to mention them herein.

Place: Udaipur

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Date: / /2024

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1. INTRODUCTION

Fenugreek (*Trigonella foenum-graecum* L; 2n=16), belongs to family Fabaceae, is an annual and self-pollinated seed spices (Frayer, 1930) that is popularly known as “Methi”. Fenugreek is one of the oldest cultivated seed spice crops in the world. It was named, *Trigonella*, from Latin language that means “*little triangle*” due to its yellowish-white triangular flowers (Flammang *et al.*, 2004). The species name, *foenum-graecum*, means Greek hays, (Sinskaja, 1961) which indicates that historically it was being used as a forage crop. Fenugreek is believed to be originated from South-Eastern Europe and Western Asia. It is largely grown in India during *Rabi* season. The cultivation of this crop is confined to areas with moderate or low rainfall and a cool growing season without extreme temperatures. It can tolerate 10-15°C of frost (Duke, 1986).

Fenugreek is primarily grown in India, Pakistan, France, Argentina and North Africa (Singh and Thamburaj, 2003). India occupies prime position in the world in both production and consumption of fenugreek. India is one of the major producers and exporters of fenugreek. In India, it is cultivated on an area of 1.67 lakh ha with an annual production and productivity of 2.48 lakh tones and 1482 kg/ha, respectively (2021-22). Among the major producing states of fenugreek seeds, Rajasthan ranks first followed by Madhya Pradesh and Gujarat. It is cultivated to the limited extent in Andhra Pradesh, Tamil Nadu, Haryana, Maharashtra and Punjab. In the state of Rajasthan, it is mainly grown in the districts of Sikar, Chittorgarh, Jaipur, Nagaur and Kota covering an area of 68652 ha with a production of 73421 tons and productivity of 807 kg/ha. (Anonymous, 2023)

Fenugreek is a dicotyledonous crop with light green, pinnately trifoliate leaves and yellow-white papilionaceous flowers (Srinivasan, 2006). Fenugreek has two species of economic importance viz., *T. foenum graecum*, the common methi and *T. corniculata*, the Kasuri methi. *Trigonella foenum-graecum* plants are semi-erect, tall and moderately branched, with bold, yellow seeds. Fenugreek is extensively used as fresh leaves as green leafy vegetable, chopped leaves as flavoring agent, sprouts as salad, micro greens as salad, pot herbs as decoration and most importantly the seeds are used as spices and condiment to improve the flavor and nutritive value of food. Fenugreek seed contains carbohydrate (48%) followed by proteins (25.5%),

mucilaginous matter (20%), fat (7.9%) and saponins (4.8%) (Rao and Sharma, 1987). Due to its mucilaginous, demulcent, diuretic, carminative, astringent, emollient and aphrodisiac properties of seeds, its powders and extracts are also used in preparation of several ayurvedic medicines. Besides young green tender plant and leaves are also used as nutritionally rich vegetable. Fenugreek which forms the actual spice is rich source of vitamin A, vitamin C, vitamin B₂ (Aykroyd, 1963) and protein (Rao and Sharma, 1987). The seeds of fenugreek contain *diosgenin* which is used in the preparation of oral contraceptive pills. Fenugreek seeds are a source of minerals such as copper, potassium, calcium, iron, selenium, zinc, manganese and magnesium.

In spite of gaining a prime position among the seed spices grown in Rajasthan, its productivity is low due to non-availability of suitable high yielding varieties for various agro-climatic regions. In order to make this crop more productive and resistant to diseases and insect-pests, breeders have to launch an intensive breeding programme for releasing array of variability.

Yield is a complex quantitative character highly influenced by environmental conditions, resulting in difficulty to determine whether the observed variability is heritable or not, for this, heritability is a suitable measure to estimate the heritable genetic portion of the total variability. The estimation of heritability along with genetic advances is generally more useful to provide a clear prediction of the breeding value. Correlation reveals only the direction and magnitude of association between any two traits however the path coefficient analysis partition the correlation into direct and indirect effects of various components on yield and serves as a powerful tool in the selection procedure accordingly.

The assessment of genetic diversity using quantitative traits is very important for differentiating well-defined populations. Several methods of divergence analysis based on quantitative traits have been proposed to suit various objectives, of which Mahalanobis's (1936) generalized distance occupies a unique place and is an efficient method to gauge the extent of diversity among genotypes, which quantify the differences among several quantitative traits.

Seed yield in fenugreek is determined by a polygenic system and is highly susceptible to environmental fluctuations. Consequently, direct selection of plants based solely on seed yield may not yield reliable results in many cases. Therefore, it is essential to study the relative contributions of each component and assign appropriate

weights to them. Constructing selection indices based on genotypic worth offers a comprehensive and effective approach. By utilizing a discriminant function, developed by Smith (1936), it becomes possible to identify important combinations of seed yield components that are useful for selection and formulate suitable selection indices. These indices allow for the integration of multiple sources of information from the experimental units, enabling selection based on a combination of economically important variables.

Keeping these in view, the present investigation entitled “**Genetic Divergence and Selection Indices for Yield and its Attributing Traits in Fenugreek (*Trigonella foenum-graecum* L.)**” had conducted during *Rabi*, 2023-24 to obtain the information on following aspects:

- i. To estimate genetic variability parameters for yield and its attributing traits in fenugreek.
- ii. To work out character association and path coefficient analysis for yield and its attributing traits in fenugreek.
- iii. To assess the extent of genetic divergence (D^2) among the fenugreek genotypes.
- iv. To construct the selection indices.

2. REVIEW OF LITERATURE

The present research was undertaken to study the genetic divergence and selection indices for various quantitative and qualitative traits in 25 genotypes of fenugreek. The available relevant literature on the present research in fenugreek (*Trigonella foenum-graecum* L.) has been reviewed under the following heads:

2.1 Genetic variability

2.2 Character association and path coefficient analysis

2.3 Genetic divergence

2.4 Discriminant function and selection indices

2.1 GENETIC VARIABILITY PARAMETERS

Maloo and Dashora (2011) studied 48 fenugreek genotypes/varieties in context to the genetic variability, character association and path analysis between yield and its component traits and concluded highly significant variations between genotypes for all of the traits under study. Higher estimates of phenotypic coefficient of variance and genotypic coefficient of variance along with high heritability and high genetic advance as a percent of mean were recorded for pods per plant.

Meena *et al.* (2011) observed that there was a significant difference between genotypes for most of the characters under study. High estimates of GCV were recorded for plant height, number of branches, yield per plant and test weight.

Naik *et al.* (2012) conducted an experiment on 31 fenugreek genotypes and the results revealed that the seed yield per plant had high PCV and GCV followed a similar pattern. Number of pods per plant, number of branches per plant, number of seeds per pod and plant height all showed high heritability and genetic advance as percent of mean. Apart from this, the genetic advance for pods per plant and seed yield was higher while the genetic advance for test weight, seeds per pod and branches per plant was lower.

Pushpa *et al.* (2012) evaluated 25 genotypes of fenugreek and observed that number of branches per plant at 30 DAS, number of branches and plant distribution at harvest had the highest genotypic and phenotypic coefficients of variation. High

estimates of heritability and genetic advance were observed for all the characters except plant height, number of branches, plant spread at 30 days after sowing, pod weight and harvest index.

Jain *et al.* (2013) studied 50 genotypes of fenugreek along with five standard checks and revealed that the high estimates of phenotypic coefficient of variance, genotypic coefficient of variance, broad sense heritability, genetic advance and genetic advance as percentage of mean were observed for number of pods on main axis and seed yield per plant. High heritability with moderate genetic advance was shown by total number of pods per plant. The traits *viz.*, primary branches per plant, secondary branches per plant and test weight showed the moderate to high estimates of heritability along with moderate to high genetic advance.

Phom *et al.* (2014) evaluated 7 genotypes and observed that in terms of growth, yield and quality characteristics, all of the genotypes showed considerable variation. They were found that RMT-1 had the highest plant height, number of branches per plant, leaves per plant, longest pods, pods per plant, seeds per pod, highest test weight and highest seed yield per plant.

Singh *et al.* (2016) conducted an experiment on 30 genotypes of fenugreek and found that the traits like seed protein content, days to 50% flowering, number of pods per plant and dry weight at flowering stage were found to have the least variation between phenotypic coefficient of variance and genotypic coefficient variance level. The high estimates of heritability were observed for protein content (96.9%) and number of pods per plant (96.7%).

Verma *et al.* (2016) tested a set of 16 fenugreek genotypes and concluded high estimates of GCV and PCV values for the pods per plant, number of secondary branches per plant, seeds per pod and seed output. High to moderate heritability and genetic advance were shown by pods per plant, secondary branches per plant, seeds per pod and test weight.

Wojo *et al.* (2016) studied 36 fenugreek genotypes and the results indicated that the high GCV was observed for number of secondary branches per plant. High magnitude of PCV was showed by number of primary and secondary branches per plant, 1000-seed weight, number of seeds per pod. Heritability values were high for the traits *viz.*, the number of seed per pod (63.1%), plant height (65.3%), biological

yield per plot (80.1%), seed yield per plot (89.0%), day to maturity (80.8%) and day to flowering (71.4%). High genetic advance was showed by days to maturity, number of pods per plant, number of secondary branches per plant, biological yield and seed yield per plot.

Hosamath *et al.* (2017) evaluated 35 germplasm of fenugreek and result revealed that the high GCV and PCV coupled with high heritability and genetic advance as per cent of mean were observed for the plant height, number of branches per plant, number of leaves, number of pods per plant and seed index.

Mamatha *et al.* (2017) conducted an experiment on 150 fenugreek genotypes and observed that primary branches per plant, secondary branches per plant, number of pods per axis, number of pods per plant, yield per plant and test weight had high PCV and GCV value, it showed that there was a wide range of genetic variability in yield and yield attributing traits in the genotypes under study. A narrow difference between PCV and GCV values was recorded for the number of pods per plant and yield per plant.

Panwar *et al.* (2018) studied 17 fenugreek genotypes and found that the high phenotypic coefficient of variance was recorded for the characters such as number of branches per plant, number of pods per plant, test weight, number of nodules per plant, plant height and seed yield per plant. High estimates of heritability and genetic advance were recorded for test weight and plant height.

Sindhu *et al.* (2018) studied 90 fenugreek genotypes and result revealed that yield per plant showed highest PCV and GCV estimates followed by days to field emergence, pods per plant, seeds per pod, plant height and branches per plant. A low estimate of PCV and GCV was observed for days to 50 percent flowering and days to maturity. Yield per plant had the maximum genetic advance as percent of mean, while days to 50 percent flowering showed the lowest value. High estimates of heritability as well as genetic advance were also observed for pods per plant, plant height, yield per plant and seeds per pods. The traits having high heritability and genetic advance showed medium to high GCV and PCV estimates. Low GCV and PCV estimate with high heritability value was reported for days to 50 percent flowering and days to maturity.

Yadav *et al.* (2018) examined 60 genotypes of fenugreek and concluded that the highest GCV and PCV was observed for seed yield, number of pods per plant and seed vigor index-II. High heritability was observed for seed yield and number of pods per plant.

Yadav *et al.* (2018) examined 21 genotypes of fenugreek and found that the characters *viz.*, seed yield per plot, number of pods on main axis and number of pods per plant showed highest GCV and PCV values. Moderate to high GCV and PCV were recorded for number of primary branches per plant, number of secondary branches per plant, plant height and seed yield. The remaining characters *viz.*, pod length, number of seeds per pod and test weight had low estimate of GCV and PCV. High heritability was observed for seed yield per plot and number of pods on main axis while days to 50 percent flowering showed low heritability values.

Bhatt *et al.* (2019) examined 37 genotypes of fenugreek and found that the traits *viz.*, number of leaves plant at 45 days after sowing (DAS), number of leaves at 60 DAS, leaf yield per plant, number of pods per plant, seed yield per plant and test weight were having higher GCV, PCV, heritability and genetic advance as a percent of mean which showed that these characters were governed by additive gene action and selection would be significantly effective for these polygenic characters.

Singh *et al.* (2019) conducted an experiment on 120 fenugreek genotypes along with three checks and found that the magnitude of PCV was higher than GCV. The number of branches per plant and plant height had high genotypic and phenotypic coefficient of variation. Plant height and number of branches per plant showed higher genetic advance as percent of mean.

Gaikwad *et al.* (2020) conducted an experiment on 24 fenugreek genotypes and revealed that both GCV and PCV were found highest for copper content in fenugreek followed by zinc content, iron content and chlorophyll content in leaves. For the days to harvesting, both the components *i.e.*, GCV and PCV were found lowest. In case of broad sense heritability, higher estimates were recorded for the traits such as copper content, iron content, total chlorophyll content, number of leaves, number of secondary roots, leaf area, biological yield. For manganese content, number of root nodules and zinc content, moderate heritability percentage were recorded. Days to harvesting showed the lowest heritability.

Kumar *et al.* (2020) examined 123 genotypes of fenugreek and revealed that days to 50 percent flowering showed highest broad sense heritability followed by seeds per pod and pod length. Heritability and genetic advance had high estimates of both days to 50 percent flowering and pod length.

Prakash *et al.* (2020) evaluated 122 fenugreek genotypes and result indicated that high estimates of PCV, GCV and heritability was recorded for number of branches per plant and seed yield. Seed yield followed by branches per plant had high heritability estimates.

Upadhyay *et al.* (2020) examined 28 fenugreek genotypes for 14 characters and result revealed that high estimates of GCV and PCV was observed for number of pods per plant, number of branches at 60 DAS and 90 DAS, seed yield per plant, test weight and number of leaves per plant at 30DAS. High heritability estimates was notes for plant height at 60 DAS, number of leaves at 30 DAS and 90 DAS, number of pods per plant, seed yield per plant and number of branches per plant.

Krishnaveni *et al.* (2021) studied 18 genotypes of fenugreek including 2 check varieties and result revealed that high GCV and PCV was recorded for the number of primary and secondary branches per plant, number of pods per plant and seed yield per plant.

Maurya *et al.* (2021) studied 72 genotypes of fenugreek for 11 quantitative characters. The analysis of variance indicated highly significant differences among the genotypes for all the characters under study. Length of pod and primary branches per plant showed the high magnitude of variability based on the mean performance of seed yield and yield components, the genotypes NDM-97, NDM-116, NDM-1, NDM-37, NDM-137, NDM-20, NDM-57, NDM-76, NDM-14 and NDM-132 were identified as most promising genotypes for yield and major component characters.

Meena *et al.* (2021) evaluated 17 fenugreek genotypes and found that the seed yield per plot and test weight had high estimates of GCV and PCV Seed yield per plot and plant height showed high estimates of genetic advance. The highest heritability was recorded for seed yield followed by plant height and number of primary branches.

Mishra *et al.* (2021) studied 30 fenugreek genotypes and result revealed that number of pods showed highest GCV and PCV followed by seed yield per plant, biological yield per plant, number of branches per plant and harvest index. High estimates of heritability and genetic gain were high for the traits such as protein percent, number of branches per plant and 1000-seed weight.

Patel *et al.* (2021) studied 40 genotypes of fenugreek. High estimates of GCV was observed for seed yield per plant, number of branches per plant, number of pods per plant and harvest index. High heritability along with high genetic advance as percent of mean (genetic gain) was observed for seed yield per plant, number of branches per plant, number of pods per plant, pod length and harvest index.

Kumari *et al.* (2022) evaluated 36 diverse genotypes of fenugreek and results revealed that high estimates of PCV and GCV were observed for fat content, seed yield per plant, harvest index, biological yield per plant and number of branches per plant. High heritability coupled with a high genetic gain was observed for the traits *viz.*, fat content, seed protein content, 1000-seed weight and seed yield per plant.

2.2 CHARACTER ASSOCIATION AND PATH COEFFICIENT ANALYSIS

Dashora *et al.* (2011) evaluated 48 fenugreek genotypes and result revealed that harvest index and biological yield showed a positive and significant correlation with seed yield while days to 50 percent blooming showed a negative and significant association with seed yield. The path analysis indicated that biological yield per plot had highest positive direct effect on seed yield followed by pod length, number of branches plant and test weight.

Naik *et al.* (2011) conducted research on 31 genotypes of fenugreek and estimated path coefficients at the genotypic and phenotypic levels. At the phenotypic level, number of branches per plant, length of branches per plant, length of pod, plant height, number of grains per pod, days to 50% blooming and number of pods per plant showed a positive direct influence on seed yield per plant.

Fikreselassie *et al.* (2012) conducted study on 143 random genotypes of fenugreek and observed that the number of seeds per plant and 1000-seed weight contributed the most significant positive direct effects on seed yield per plant for the path analysis at genotypic level.

Jain *et al.* (2013) studied 50 fenugreek genotypes along with five standard checks and revealed that seed yield per plant had a positive and significant correlation with plant height, total number of pods per plant, number of pods on main axis and 1000-seed weight while seed yield per plant exhibited a positive but non-significant association with secondary branches per plant and number of seeds per pod.

Singh *et al.* (2013) conducted research experiment on 102 genotypes of fenugreek and found that seed yield per plant had a positive and significant association with 50 percent flowering, days to 75 percent maturity, number of primary branches per plant and petiole length. Chlorophyll content at 60 DAS, 1000-seed weight, plant height at maturity and days to 50% flowering showed a positive and significant correlation with vegetable yield. Number of primary branches per plant and days to 50 percent flowering had a positive and significant association with nodulation at 60 DAS. Number of primary branches per plant had a significant and positive association with number of pods per plant, days to 50 percent flowering, days to 75 percent maturity and seed yield per plant. Number of seeds per pod had a positive and significant association with 1000-seed weight.

Patahk *et al.* (2014) conducted an experiment on 40 fenugreek genotypes and found that seed yield per plant showed a positive and significant correlation with plant height, number of pods per plant, number of seeds per pod, pod length and protein content. Plant height showed highest direct positive effect on seed yield per plant followed by the number of seeds per pod and protein content. It was also observed that the characters like plant height, pod length, number of pods per plant and 100-seed weight significantly increased the seed yield.

Singh (2014) evaluated 30 diverse fenugreek genotypes and found that pod number, stem weight, husk weight and harvest index exhibited a positive and significant genotypic and phenotypic correlation with the seed yield. Most of the traits except days to flowering and test weight showed a positive and significant correlation with seed yield in all environments except in E₃. In case of path analysis, the positive direct effects were recorded for seeds per pod, test weight and pod number.

Lodhi *et al.* (2015) conducted an experiment on 28 genotypes of fenugreek and found that a positive and significant correlation with the seed yield per plant was exhibited by the biological yield per plant, plant height, number of pods per plant, dry

weight at flowering initiation, dry matter content and 1000-seed weight. Highest direct effect on seed yield was expressed by dry matter content followed by plant height and number of seeds per pod.

Maurya *et al.* (2015) conducted research with 100 selection germplasm lines of fenugreek in augmented design and found that at phenotypic level days to maturity followed by days to 50 percent flowering showed the highest positive direct effect on seed yield per plant. Along with this, number of seed per pod, length of pod, number of pods per plant and 1000-seed weight exhibited a negative direct effect on seed yield per plant.

Gurjar *et al.* (2016) conducted research on 30 fenugreek genotypes and results of path coefficient analysis indicated that highest positive direct effect of seed yield per plant was exerted by biological yield followed by dry matter content per plant and number of seeds per pod. It was also revealed that improvement in seed yield of fenugreek is possible through the selection of dry weight per plant at flower initiation, biological yield per plant, protein content, number of seeds per pod and 1000-seed weight.

Singh *et al.* (2016) conducted an experiment on the 30 genotypes of fenugreek and the results indicated that the biological yield had a positive and significant correlation with chlorophyll content of the leaves, straw yield per plant, number of pods per plant, test weight, dry matter content of the plant and seed yield per plant and had a negative correlation with the harvest index at both phenotypic and genotypic levels. Path coefficient analysis showed that biological yield per plant, harvest index, chlorophyll content, dry weight at flower initiation, number of branches per plant and 1000-seed weight were the most important traits which contributed towards seed yield.

Wojo *et al.* (2016) conducted an experiment on 36 diverse fenugreek genotypes and found that the seed yield per plot had a positive and significant genotypic correlation with all the characters except days to 50 percent flowering and plant height. Seed yield per plot showed a positive and significant phenotypic association with number of primary branches and plant height.

Kumar *et al.* (2018) evaluated 124 genotypes of fenugreek and concluded that secondary branches per plant, pod length, primary branches and pods per plant exhibited a positive and significant correlation with seed yield per plant. The most beneficial positive direct effect on seed yield was shown by the pods per plant followed by secondary branches per plant.

Panwar *et al.* (2018) studied 17 fenugreek genotypes and the results of the experiment showed that there was highly significant and positive correlation and high direct effect of test weight, number of pods per plant and plant height on seed yield.

Sindhu *et al.* (2018) conducted an experiment on 90 genotypes of fenugreek and found that pod length had a positive and significant genotypic and phenotypic association with seeds per pod. Number of branches per plant showed a positive and significant correlation with number of pods per plant and number of seeds per pod. Yield per plant had a positive correlation with number of pods per plant. Pods per plant were found to be positively associated with number of seeds per pod and plant height showed a positive association with seed yield per plant. Days to field emergence had a negative and significant correlation with number of seeds per pod. Results of path coefficient analysis indicated that seeds per pod showed highest positive effect on yield per plant followed by pods per plant, branches per plant, plant height and days to 50 percent flowering.

Singh *et al.* (2019) studied 120 genotypes of fenugreek and observed that seed yield had a positive and highly significant correlation association with pods per plant. The results of path coefficient analysis showed that pods per plant, seeds per pod and 1000-seed weight had direct effect on seed yield per plant at both genotypic and phenotypic levels.

Ali abteu and Abate (2020) conducted research experiment on 62 genotypes along with standard and local checks and revealed that seed yield per plot had positive and significant correlation with biomass yield and harvest index at genotypic level. Also seed yield was positively correlated with harvest index. Results of path coefficient analysis indicated that biomass, harvest index and pod length had contributed the maximum a positive and negative direct effect on seed yield, respectively at phenotypic level. Biomass yield per plant and harvest index had a strong positive direct effect and plant height contributed weak negative direct effect.

Krishnaveni *et al.* (2021) studied 18 Fenugreek genotypes including 2 check varieties and observed that the seed yield had a positive and significant correlation with pod length and the number of pods per plant both at genotypic and phenotypic levels. The highest positive direct effect on seed yield per plant was observed for the number of pods per plant followed by the number of primary and secondary branches per plant, number of seeds per pod and pod length.

Singh *et al.* (2022) evaluated 30 Fenugreek genotypes and observed that the seed yield per plant had a positive and significant correlation with number of pods per plant, number of seeds per pod, and pod length in both the environments *i.e.*, E₁ and E₂. The highest direct effect on seed yield per plant was observed for the number of pods per plant, number of seeds per pod and test weight at genotypic and phenotypic levels in E₁ and E₂.

2.3 GENETIC DIVERGENCE

Patahk *et al.* (2014) conducted research on 40 genotypes of fenugreek (*Trigonella foenum graecum* L.) and observed that all the genotypes were grouped into nine clusters. Cluster III, followed by clusters IV and II has the largest intra cluster distance. The greatest inter-cluster distance was noted for Cluster IV and V, followed by I and IV. Among the eleven variables analysed protein content contributed the most to genetic divergence, accounting for 53.85 percent of total of the divergence, followed by days to 50 percent flowering (16.41%) and seed yield per plant (15.90%).

Kole *et al.* (2015) examined 30 genotypes of fenugreek and concluded that all the genotypes were grouped into nine clusters of which four were mono- genotypic. The clustering pattern of genotypes showed that genetic divergence had a little effect on geographical differentiation. Cluster-V had the highest average intra- cluster distance (12.66) and Cluster III and VII had the highest and maximum inter- cluster distance 455.22.

Miraj *et al.* (2017) investigated 21 genotypes of fenugreek to analyse the genetic divergence using SDS-PAGE. At a similarity level of 1.8, four groups were found using cluster analysis. Overall, the grouping pattern of *Trigonella foenum graecum* was mainly congruent with their species status based on the total seed protein. genotypes belonging to the same species were clustered together and *vice versa*.

Tariyal *et al.* (2017) investigated 20 genotypes of fenugreek and found that the genotypes under study were grouped into four clusters. Hybridization between the genotypes from the cluster III and cluster IV for these traits can produce better segregants in the segregating populations according to cluster analysis of all the genotypes.

Asati *et al.* (2018) studied 40 genotypes of fenugreek and found that the genotype grouped into 6 clusters. Cluster VI and V had the maximum inter-cluster distance, followed by Cluster VI and V. Cluster V and IV were shown to had the minimum inter-cluster distance. Cluster I had an intra-cluster distance of 8.40, while the remaining clusters have only one genotype. As a result, genotypes from these clusters could be used in a hybridization programme to produce better segregants. Total oil content, protein content, green biomass per plant, secondary branches per plant, days to 50 percent flowering, length of pod and main branches per plant all contributed the most to the expression of genetic divergence, according to the analysis.

Panwar *et al.* (2018) evaluated 17 varieties of fenugreek for analysing the diversity and grouped the set of 17 varieties into two clusters and found that there was lack of parallelism between genetic and geographical diversities. Cluster I had the highest intra-cluster distance followed by Cluster II. The test weight made the highest contribution to the overall divergence followed by plant height.

Sulochna *et al.* (2018) studied a total of 34 fenugreek genotypes for genetic divergence analysis using Mahalanobis D^2 analysis and concluded that 34 genotypes were grouped into three different clusters. The cluster I showed maximum (241.03) intra-cluster distance. Inter-cluster distance showed the maximum divergence between clusters III and cluster II ($D^2 = 3067.42$) followed by the cluster III and cluster I ($D^2=1905.37$). Among all the 26 productivity characters studied, 100-seed weight, pod number, seed yield per plot, days to fruit maturity, pod weight, pod length and seed yield per plant showed greater contribution towards divergence. These characters maybe given more importance in selecting the genotypes. The genotype Kasuri methi (*Trigonella corniculata*) in cluster II recorded the highest cluster mean.

Yadav *et al.* (2018) evaluated 60 genotypes of fenugreek. Following the Tocher's method, sixty genotypes were grouped into a total of eight separate clusters based on their similarity in their D^2 values. The geographical distribution of the genotypes evaluated do not always match the clustering pattern. A lot of diversity was observed within and between the eight clusters. Cluster V had the highest number of genotypes (16), followed by cluster III (12), cluster I (9) and VII (7), clusters VI (6), cluster IV (5), cluster II (4) and cluster VIII, which were mono-genotypic. The greatest intra-cluster distance was recorded for the cluster IV, followed by Cluster

VII. Cluster IV and VIII showed the highest inter-cluster distance, followed by Cluster II and VIII and Cluster I and III. Cluster VIII and V can be deemed to be better for picking superior genotypes for most of the characters, based on cluster mean performance.

Bhatt *et al.* (2021) evaluated 36 genotypes of fenugreek and analysis of diversity leads to formation of nine different clusters and maximum intra-cluster distance was observed in cluster IV (21.07) while highest inter-cluster distance was recorded between cluster VII and IV (46.07). These clusters indicated various heterotic pools and heterosis and transgressive segregants can be produced by crossing genotypes from different pools.

Meena *et al.* (2021) examined 17 genotype of fenugreek and they were grouped into six clusters. Clusters IV and VI had the maximum inter-cluster distance, followed by III and VI and clusters II and IV had the minimum. Cluster I had the greatest intra-cluster distance. The seed yield of 5 plants contributed the most to genetic divergence, accounting for 46.32 percent of total divergence followed by number of primary branches (16.9%) and plant height (12.5%).

Choudhary *et al.* (2022) conducted an experiment for the study of genetic divergence on 48 fenugreek genotypes and revealed that the genotypes were best separated into five clusters. The maximum numbers of genotypes were included into cluster I (21) and minimum number of genotypes in cluster V (1). The inter cluster distance was maximum between clusters II and V ($D^2=8.115$) followed by IV and V ($D^2=7.856$) showing that the genotypes of these clusters were highly diverse from others and can be used as divergent parents for hybridization and selection programmes, while maximum intra-cluster distance was shown by cluster IV ($D^2=4.679$) showed maximum difference among the genotypes within this cluster. Total divergence was highly contributed by seeds per pod accounting for 22.78% of the total divergence followed by pods per plant (20.39%) and plant height (16.13%). The result of PCA showed that all the three principal components *viz.* PC-I, PC-II and PC-III contributed 66.62% of the total variability.

Maurya *et al.* (2023) estimated 75 genotypes of fenugreek to assess genetic diversity. Genotypes were grouped into 8 clusters with cluster VI comprising maximum genotypes. Maximum intra-cluster distance was observed in cluster V followed by cluster IV. Similarly maximum inter-cluster distance was recorded between the cluster V and VIII followed by cluster III and VIII respectively.

2.4 DISCRIMINANT FUNCTION AND SELECTION INDICES

Adsul *et al.* (2014) evaluated 100 germplasm of soybean. Discriminant function analysis indicated that almost all the selection indices were found to be more efficient than straight selection based on seed yield alone. Selection efficiency of the function was improved by increasing number of characters in the index. The index consisting of all the six traits gave the highest genetic gain and selection efficiency. Inclusion of pods per plant in selection index appears to increase its relative efficiency.

Kachhadia *et al.* (2014) evaluated 61 soybean genotypes in a Randomized Block Design with three replications to study selection indices. Discriminant function analysis indicated that selection efficiency of the function was improved by increasing number of characters in the index. Among the single character index, biological yield per plant exhibited higher genetic advance and relative efficiency over straight selection for seed yield. The index based on five characters *viz.*, seed yield per plant, 100 seed weight, biological yield per plant, harvest index and days to maturity recorded the highest genetic advance as well as relative efficiency and selection efficiency.

Mori *et al.* (2016) studied the performance of 40 genotypes of fenugreek. Discriminant function analysis indicated that almost all the selection indices were found more efficient than straight selection based on seed yield per plant (100%) alone. The index consisting of five traits gave the highest genetic gain and selection efficiency under timely sown conditions (846.24) and all the six traits gave the highest genetic gain and selection efficiency under late sown conditions (1724.68).

Hadiya *et al.* (2019) evaluated 30 genotypes of chickpea for construction of selection indices. Thirty-one selection indices, involving seed yield and four yield components characters, were constructed using the discriminant function technique. The efficiency of selection increased with the inclusion of more number of characters in the index. The selection index based on five characters *viz.* seed yield per plant, plant height, number of pods per plant, biological yield per plant and harvest index possessed highest genetic gain and relative efficiency.

Debnath *et al.* (2021) studied 21 chickpea genotypes for determination of the selection indices in chickpea. The study consisted of for 13 characters. The results revealed the direct effect and significantly positive total effect of biological yield of plant, harvest index, total seeds per plant and seed index on seed yield. This indicated the maximum contribution of these characters to the genotypes yield and thus, considered as vital selection indices for increasing the plant yield.

Parmar *et al.* (2022) evaluated 19 F₃S and 1 check variety of chickpea. Discriminant function technique was used to create 31 selection indices involving seed yield and four yield components. The inclusion of more characters in the index increased the efficiency of selection. The selection index based on four characters *viz.*, seed yield per plant, number of branches per plant, number of pods per plant and harvest index exhibited maximum relative efficiency.

Garde *et al.* (2023) evaluated 55 progenies of Indian bean with checks GNIB-21 and GNIB-22 in Randomized Block Design (RBD) with 3 replications. An attempt was made to build a selection index by taking 3 different types of economic weights *viz.* equal weight [W₁], genotypic correlation coefficients [W₂] and genotypic path coefficients (Direct effect) [W₃]. It was seen that genetic gain of Indian bean of selected progenies observed higher with equal weight method as compared to weight assigned method with genotypic correlation coefficients and genotypic path coefficients (Direct effect). It has been concluded that the selection of progeny based on seed yield per plant, plant height, pod width and days to maturity provide higher genetic gain in Indian bean.

3. MATERIALS AND METHODS

The present investigation entitled “**Genetic Divergence and Selection Indices for Yield and its Attributing Traits in Fenugreek (*Trigonella foenum-graecum* L.)**” was conducted during *Rabi*, 2023-24. The details of materials and techniques adopted during the course of investigation are presented in this chapter with following heads: -

3.1 SITE OF EXPERIMENT

The experiment was carried out at Rajasthan College of Agriculture, Maharana Pratap University of Agriculture and Technology, Udaipur. It is located at an elevation of 579.5 meters above mean sea level in the south-east Rajasthan on latitude of 24° 35 North and longitude of 70° 42 East. The meteorological data recorded during the crop period are appended in Appendix I and Fig. 3.1.

3.2 MATERIALS USED FOR EXPERIMENT

The experimental materials used for present investigation comprised of 25 fenugreek genotypes, were collected from various seed spices research centres which include National Research Centre on Seed Spices (NRCSS), Tabiji, Ajmer, Rajasthan, CCSHAU, Hisar, Haryana, AICRP on Seed Spices, SKNCOA, Jobner and Deptt. of GPB, RCA, Udaipur. The name of genotypes/varieties and their sources are given in Table 3.1.

3.3 EXPERIMENTAL DESIGN

All the 25 genotypes were grown in Randomized Block Design (RBD) with 3 replications. In each replication, genotypes were sown in 2 rows of 2.5 meter length with row to row and plant to plant spacing of 30 cm and 10 cm, respectively. The date of sowing of the experiment was November 07, 2023. All the recommended package of practices was adopted to raise a good and healthy crop.

3.1 OBSERVATIONS RECORDED

The observations for all the characters, except days to 50 percent flowering and days to maturity were recorded on five randomly selected competitive plants for

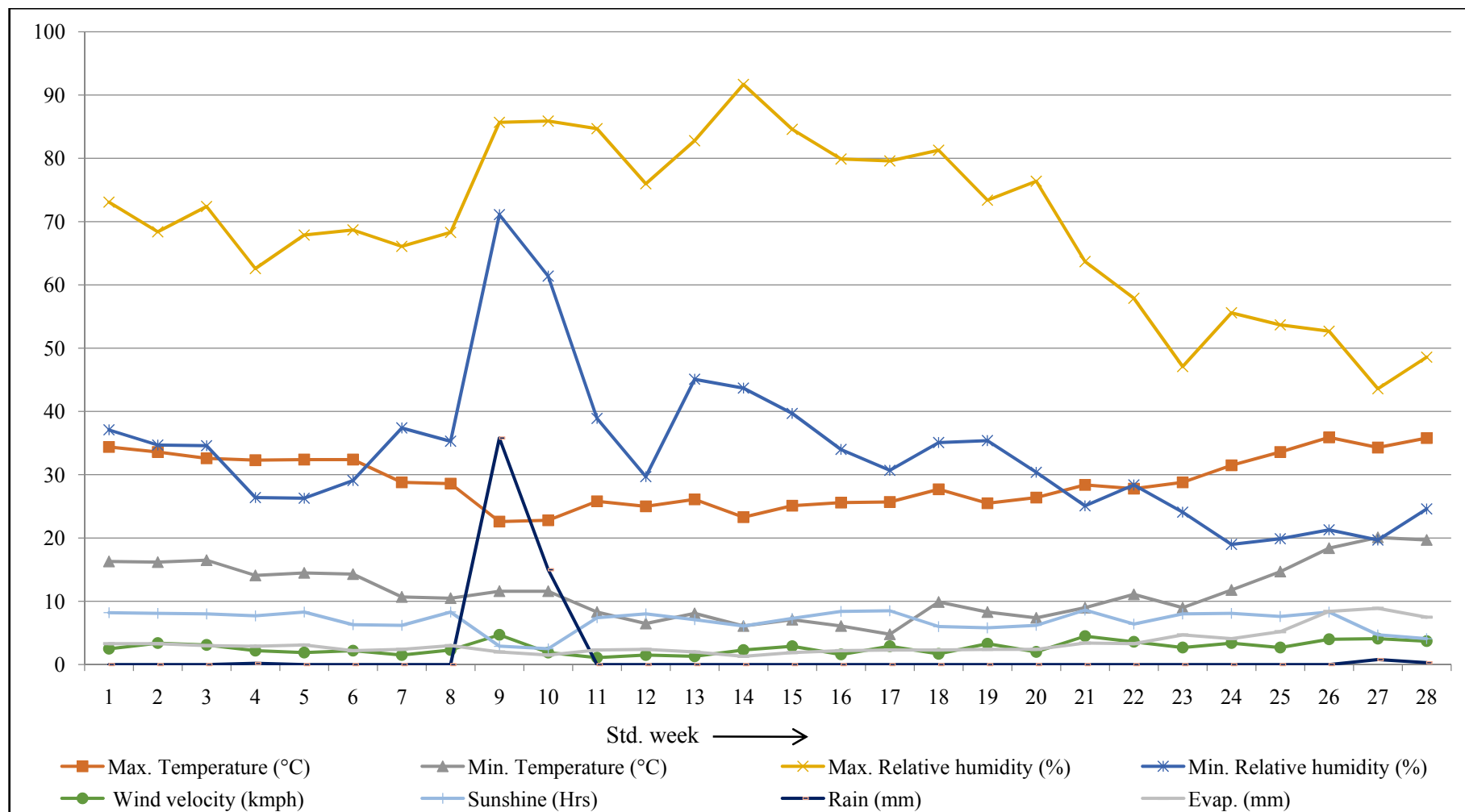


Figure 3.1: Mean weekly data on meteorological parameters during the crop growth period for *Rabi*, 2023-24



Figure 3.2: A field view of Fenugreek Research Experiment at Instructional Farm, RCA, Udaipur

each genotype in each replication. The observations for days to 50 percent flowering and days to maturity were recorded on the whole plot basis. A brief description of the procedure adopted for recording observations for characters under study are as under:

Table 3.1: Name and source of fenugreek of genotypes/varieties

S. No.	Name of genotypes	Source
1.	AM-31-30-5	NRCSS, Tabiji, Ajmer, Rajasthan
2.	AM-45-20-4	NRCSS, Tabiji, Ajmer, Rajasthan
3.	AM-6-1-27	NRCSS, Tabiji, Ajmer, Rajasthan
4.	AM-6-2-28	NRCSS, Tabiji, Ajmer, Rajasthan
5.	Afg-3-300-160	NRCSS, Tabiji, Ajmer, Rajasthan
6.	Afg-3-350-273	NRCSS, Tabiji, Ajmer, Rajasthan
7.	Afg-3-350-48	NRCSS, Tabiji, Ajmer, Rajasthan
8.	Afg-1	NRCSS, Tabiji, Ajmer, Rajasthan
9.	Afg-2	NRCSS, Tabiji, Ajmer, Rajasthan
10.	Afg-3	NRCSS, Tabiji, Ajmer, Rajasthan
11.	Afg-4	NRCSS, Tabiji, Ajmer, Rajasthan
12.	Afg-5	NRCSS, Tabiji, Ajmer, Rajasthan
13.	IC-397506	NRCSS, Tabiji, Ajmer, Rajasthan
14.	RMt-354	SKNCOA, Jobner, Jaipur, Rajasthan
15.	RMt-303	SKNCOA, Jobner, Jaipur, Rajasthan
16.	RMt-143	SKNCOA, Jobner, Jaipur, Rajasthan
17.	RMt-361	SKNCOA, Jobner, Jaipur, Rajasthan
18.	RMt-351	SKNCOA, Jobner, Jaipur, Rajasthan
19.	RMt-1	SKNCOA, Jobner, Jaipur, Rajasthan
20.	RMt-305	SKNCOA, Jobner, Jaipur, Rajasthan
21.	PRM-45	MPUAT, Udaipur
22.	Hisar suvarna	AICRP on Spices, CCSHAU, Hisar
23.	Hisar sonali	AICRP on Spices, CCSHAU, Hisar
24.	Pant Ragini	GBPUAT, Pantnagar
25.	JFg-244	Jagudan, Gujarat

1. Days to 50 percent flowering

Number of days taken from sowing to 50 percent of plants completed their opening of first flower was recorded on plot basis.

2. Days to maturity

The number of days recorded from date of sowing to date when 75% plants achieve physiological maturity.

3. Plant height (cm)

Height was measured in centimeters (cm) from the ground level to the apex of the main stem at maturity.

4. Number of branches per plant

The total numbers of primary and secondary branches were counted in each randomly selected plant.

5. Number of pods per plant

The total number of pods were counted in each randomly selected plant.

6. Pod length (cm)

Length in centimeters (cm) of five randomly selected pods from each randomly selected plant was measured and averaged.

7. Number of seeds per pod

Total number of seeds were counted from five randomly selected pods in each randomly selected plant and averaged.

8. 1000-seed weight (g)

It was measured by counting the 1000-seeds taken randomly from the bulk of genotype in each replication and weighed in grams.

9. Biological yield per plant (g)

The five randomly selected plants from each plot were harvested separately. These plants were sun dried, weighted in grams (g) and average value was worked out to obtain biological yield per plant.

10. Seed yield per plant (g)

Total seeds obtained from five randomly selected plants of each entry from each replication were weighted separately and their average was recorded in grams.

11. Harvest index (%)

Harvest index was computed by using following formula:

$$\text{Harvest Index (\%)} = \frac{\text{Grain yield per plant (g)}}{\text{Biological yield per plant (g)}} \times 100$$

12. Seed protein content (%)

Protein content in the seeds was determined by the Micro Kjeldahl's as per the method suggested by Linder (1944). Detailed procedure of seed protein content estimation is given in Appendix II.

13. Fat content (%)

Fat content in the seeds was determined by the Soxhlet Extraction Method. Detailed procedure of fat content estimation is given in Appendix III.

3.5 STATISTICAL METHODOLOGY

The data collected for each character on an individual plant basis for five competitive plants were analysed with the help of standard statistical procedures.

3.5.1 Analysis of Variance

The analysis of variance was worked out separately for each character as per the method suggested by Panse and Sukhatme (1985) in order to test the difference among the genotypes. The mean values for various characters were subjected to statistical analysis for various parameters viz., genotypic and phenotypic correlation as per details given below:

Table 3.2: Analysis of variance (ANOVA)

Source of variation	D.F.	Sum of squares	Mean sum of squares	Expected meansum of squares
Replications	(r-1)	SS _r	MS _r	$\sigma^2_e + g\sigma^2_r$
Genotypes	(g-1)	SS _g	MS _g	$\sigma^2_e + r\sigma^2_g$
Error	(r-1) (g-1)	SS _e	MS _e	σ^2_e
Total	(rg-1)			

Where,

r = Number of replications

g = Number of genotypes

d.f. = Degree of freedom

SS_r = Sum of squares due to replications

SS_g = Sum of squares due to genotypes

SS_e = Sum of squares due to error

MS_r = Mean sum of squares due to replications

MS_g = Mean sum of squares due to genotypes

MS_e = Mean sum of squares due to error

Standard Error of Mean (S. E. M.): It was calculated as follows: -

$$S. E. M. \pm = \sqrt{MSE / r}$$

MSE = Mean sum of squares due to error

r = Number of replications

Standard Error of Difference (S. E. D.): It was calculated as follows: -

$$S.E.D. = \sqrt{\frac{2MSE}{r}}$$

Critical difference (C. D.): It was estimated as follows: -

$$C. D. = S. E. D. \times t_{value}$$

t_{value} = t_{value} at 5% or 1% probability level at error degree of freedom

Coefficient of variance (C.V.)

CV is the ratio of the standard deviation to the arithmetic mean. It is expressed as percentage.

$$CV = \frac{SD}{\bar{X}} \times 100$$

Where,

SD = Standard deviation

$\bar{X}$ = Mean

Analysis of variance components

The genotypic, phenotypic and error variance were estimated as follows: -

3.5.1.1 Genotypic variance (σ^2g)

The genotypic variance is due to the differences among genotypes included in the study. It was calculated by the following formula described by Burton and Devane (1953).

$$\text{Genotypic variance } \sigma^2g = \frac{MSg - MSe}{r}$$

Where,

σ^2g = Genotypic variance

MSg = Mean sum of squares due to genotypes

MSe = Mean sum of squares due to error

r = Number of replications

3.5.1.2 Phenotypic variance (σ^2p)

It is sum of the variance contributed by genetic cause and environmental factors. It was calculated by the following formula described by Burton and Devane (1953).

$$\text{Phenotypic variance } (\sigma^2p) = \sigma^2g + \sigma^2e$$

Where,

σ^2p = Phenotypic variance

σ^2g = Genotypic variance

σ^2e = Error variance *i.e.* MSe

3.5.1.3 Error variance (σ^2e)

It is the mean sum of squares of error represented by the variation attributed to environmental causes.

$$\text{Error variance } (\sigma^2e) = MSe$$

3.5.2 Variability Parameters

The following parameters were calculated for the characters having significant mean squares due to the genotypes.

3.5.2.1 Range

The range of each character was determined by taking the minimum and maximum values for each trait within population.

$$\text{Range} = \text{Highest value} - \text{Lowest value}$$

3.5.2.2 Mean ($\bar{X}$)

It was calculated by dividing the sum of all observations in a sample by their number.

$$\bar{X} = \sum X_i / n$$

Where,

$\bar{X}$ = General mean

n = Number of observations

$\sum X_i$ = Summation of all observations

3.5.2.3 Standard Error of Mean (S.E.M.): It was calculated as follows: -

$$\text{S. E. M. } \pm = \sqrt{MSE/r}$$

Where,

MSE = error variance

r = Number of replications

3.5.2.4 Coefficient of variation (C.V.)

The coefficient of genotypic and phenotypic variation was calculated by using the formula suggested by Burton (1952)

a) Genotypic coefficient of variation (GCV)

$$\text{GCV}(\%) = \frac{\sqrt{\sigma^2 g}}{\bar{X}} \times 100$$

Where,

$\sigma^2 g$ = Genotypic variance

$\bar{X}$ = General mean

b) Phenotypic coefficient of variation (PCV)

$$PCV (\%) = \frac{\sqrt{\sigma^2 p}}{\bar{X}} \times 100$$

Where,

$\sigma^2 p$ = Phenotypic variance

$\bar{X}$ = General mean

3.5.2.5 Heritability in broad sense (H_{bs})

It is the ratio of total genotypic variance to total genotypic variance to total phenotypic variance. It was calculated as per the formula suggested by Burton and Devane (1953).

$$H_{(bs)} = \frac{\sigma^2 g}{\sigma^2 p} \times 100$$

Where,

$H_{(bs)}$ = Heritability in broad sense

$\sigma^2 g$ = Genotypic variance

$\sigma^2 p$ = Phenotypic variance

The heritability was divided into following three groups proposed by Johnson *et al.* (1955).

0 – 30% = Low

30 – 60% = Moderate

> 60% = High

3.5.2.6 Genetic Advance

It represents the shift in a population mean towards the superior side under selection pressure after a single generation of selection. It was computed as per the formula described by Johnson *et al.* (1955).

$$GA = H_{(bs)} \times k \times \sigma_p$$

Where,

GA = Genetic advance

$H_{(bs)}$ = Heritability in broad sense

k = Selection intensity ($k= 2.06$ at 5% selection intensity)

σ_p = Phenotypic standard deviation

3.5.2.7 Genetic advance as per cent of mean (Genetic Gain)

It was calculated by the following formula described by Johnson *et al.* (1955).

$$\text{Genetic advance as per cent of mean} = \frac{G.A.}{\bar{X}} \times 100$$

Genetic advance was categorized as follows:

Low = < 10 percent

Moderate = 10–20 percent

High = > 20 percent

3.5.3 Correlation Coefficient Analysis

The correlation coefficient was used to measure the degree of association of the characters with yield and its contributing traits. Genotypic and phenotypic correlation coefficient was computed as per the formula suggested by Al-Jibouri *et al.* (1958).

Genotypic correlation coefficient (r_g)

$$r_{xy}(g) = \frac{Cov.xy(g)}{\sqrt{V_x(g) \cdot V_y(g)}}$$

Phenotypic correlation coefficient (r_p)

$$r_{xy}(p) = \frac{Cov.xy(p)}{\sqrt{V_x(p) \cdot V_y(p)}}$$

Where,

$r_{xy}(g)$ = Genotypic correlation coefficient between x and y characters

$r_{xy}(p)$ = Phenotypic correlation coefficient between x and y characters

$V_x(g)$ = Genotypic variance of x character

$V_y(g)$ = Genotypic variance of y character

$V_x(p)$ = Phenotypic variance of x character

$V_y(p)$ = Phenotypic variance of y character

$Cov_{xy}(g)$ = Genotypic covariance between x and y characters

$Cov_{xy}(p)$ = Phenotypic covariance between x and y characters

Test of Significance

The significance of correlation coefficient was tested by the 't' test given by W. S. Gosset (1908).

$$t = \frac{r\sqrt{n-2}}{\sqrt{1-r^2}}$$

Where,

r = Correlation coefficient

n = Total number of observations

This t value is tested against the table value of 't' for n-2 degree of freedom.

3.5.4 Path analysis

The cause and effect relationships are well defined in path analysis. It is simply a standard partial regression coefficient which divides the correlation coefficient into the measures of direct and indirect effects. The method suggested by Wright (1921) and elaborated by Dewey and Lu (1959).

Direct effect

$$r_{(x_1,y)} = P_{1y} + r_{(x,x_2)}P_{2y} + r_{(x,x_3)}P_{3y} + \dots r_{(x_1,x_{15})}P_{15y}$$

$$r_{(x_1,y)} = \text{Correlation coefficient between } x_1 \text{ and } y$$

$$P_{1y} = \text{Direct effect of } x_1 \text{ on } y$$

$$R_{(x_1,x_2)}P_{2y} = \text{Indirect effect of } x_1 \text{ on } y \text{ via } x_2$$

$$r_{(x_1,x_{13})}P_{13y} = \text{Indirect effect of } x_1 \text{ on } y \text{ via } x_{13}$$

Similar procedure used for $r_{(x_2,y)}$ to $r_{(x_{13},y)}$.

Residual effect

$$R = \sqrt{1 - (\sum P_{iy} - r_{iy})}$$

Where,

R = Residual effect

P_{iy} = Direct effect of x_i on y

r_{iy} = Correlation coefficient between x_i and y

The direct and indirect effects are rated as follows by Lenka and Misra (1973).

0.00-0.09 = Negligible

0.10-0.19 = Low

0.20-0.29 = Moderate

0.30-1.00 = High

>1.00 = Very high

3.5.5 Genetic Divergence Analysis

The genetic divergence amongst different genotypes is determined based on the estimated inter-se genetic distances amongst the genotypes. The D^2 statistics proposed by Mahalanobis in 1936, is one of the most efficient tools for determining genetic divergence. The D^2 statistics technique measures the differentiation forces at two levels, namely intra-cluster and inter-cluster, and thus facilitates the identification of genetically divergent parents for exploitation in hybridization programmes.

3.5.5.1 Clustering of genotypes using the D^2 values

The genotypes were clustered into different groups using Tocher's method (Rao, 1952). The idea behind this type of clustering was that any two varieties belonging to the same cluster would have lower D^2 values than those belonging to two distinct clusters. This approach began with two closely related populations in order to identify a third population with the smallest average D^2 value. In the same manner, the fourth one was selected because it had the lowest average of D^2 values from the first three, and so on. This procedure was repeated until D^2 values of all the genotypes were exhausted except for those genotypes that were used in the previous cluster.

3.5.5.2 Testing differences in the population

A dispersion table was created from the variance analysis when the null hypothesis of no treatment differences failed in respect of individual characters. A simultaneous test of differences between mean values of a number of correlated variable was performed using the V statistic, which in turn used Wilk's criteria (Δ)(Rao, 1952).

$$\text{Wilk's criterion}(\Delta) = \frac{\text{Determinants of error variance and covariance matrix (E)}}{\text{Determinants of genotypic + error variance and covariance matrix}}$$

$$V \text{ statistic} = -m \log_e \Lambda = -n \left(n - \frac{p + q + 1}{2} \right) \log \Lambda$$

Where,

$$m = \left(n - \frac{p + q + 1}{2} \right)$$

p = Number of variables or characters

q = Degree of freedom for population (*i.e.*, number of genotypes -1)

n = Degrees of freedom for error + genotypes

$\log_e \Lambda = 2.3026 \log_{10} \Lambda$

‘V’ statistic is distributed as χ^2 with pq degrees of freedom. The test of significance of ‘V’ statistic showed that the differences between the means value in terms of the pooled effect of p characters between different populations were significant. Hence, further analyses were made to estimate D^2 values.

3.5.5.3 Mahalanobis D^2 statistics

The genetic divergence in this study was estimated using Mahalanobis generalized distance as defined by Rao (1952). The pivotal condensation method of inversion matrix transformation was used to convert original variable means to uncorrelated variables. The D^2 values between the genotypes were obtained as the sum of squares of differences of the values of the corresponding transformed variables. For each pair of combinations, the mean deviation *i.e.*, $d_i = Y_i^1 - Y_i^2$, where Y_i denotes the transformed variables ($i = 1, 2, 3, 4, 5, \dots, p$) were calculated and the D^2 was then calculated as sum of the squares of those deviations, *i.e.*

$$D^2 = \sum (Y_i^1 - Y_i^2)^2$$

Where,

p = Number of characters

The significance of D^2 values was tested by treating them as chi-square (χ^2) at p degrees of freedom where p is the number of characters considered.

3.5.5.4 Grouping of genotypes by Tocher's method

After arranging the D^2 values of all combinations of one genotype with the others in ascending order of magnitudes, the genotypes were grouped into a number

of clusters by Tocher's method described by Rao (1952). The criterion used in this method was that any two varieties belonging to the same cluster, at least on an average, show a smaller D^2 value than those belonging to two different clusters. Then inter and intra-cluster distances were calculated and their relationships were diagrammatically represented.

3.5.6 Selection Indices

Application of discriminant function as a basis for making selection on several characters simultaneously is aimed at discriminating the desirable genotypes from undesirable ones on the basis of their phenotypic performance. The concept of selection index was first proposed by Smith (1936) on the basis of discriminant function of Fisher (1936). The model suggested by Robinson *et al.* (1951) was used for the construction of selection indices and development of a required discriminant function. Smith (1936) defined the genetic worth (H) of an individual as,

$$H = a_1G_1 + a_2G_2 + \dots + a_nG_n$$

Where, $G_1, G_2, \dots, G_n$ are the genotypic values of individual characters and $a_1, a_2, \dots, a_n$ signify their relative economic importance.

Another function (I), based on phenotypic performance of various characters was defined as:

$$I = b_1p_1 + b_2p_2 + \dots + b_np_n$$

Where, $b_1, b_2, \dots, b_n$ are to be estimated such that the correlation between H and I *i.e.*, $r(H, I)$ becomes maximum. Once such function is obtained, discrimination of good genotypes/characters from the undesirable ones could be possible on the basis of phenotypic performance *i.e.*, $p_1, p_2, \dots, p_n$ directly.

The maximization of $r(H, I)$ leads to a set of simultaneous equations which upon solving give the desired estimate of "bi" values. Considering three characters as an example, the simultaneous equations look like as follows.

$$b_1X_{11} + b_2X_{12} + b_3X_{13} = a_1G_{11} + a_2G_{12} + a_3G_{13}$$

$$b_1X_{21} + b_2X_{22} + b_3X_{23} = a_1G_{21} + a_2G_{22} + a_3G_{23}$$

$$b_1X_{31} + b_2X_{32} + b_3X_{33} = a_1G_{31} + a_2G_{32} + a_3G_{33}$$

The matrix form of above simultaneous equations is as under:-

$$\begin{bmatrix} X_{11} & X_{12} & X_{13} \\ X_{21} & X_{22} & X_{23} \\ X_{31} & X_{32} & X_{33} \end{bmatrix} \begin{bmatrix} b_1 \\ b_2 \\ b_3 \end{bmatrix} = \begin{bmatrix} G_{11} & G_{12} & G_{13} \\ G_{21} & G_{22} & G_{23} \\ G_{31} & G_{32} & G_{33} \end{bmatrix} \begin{bmatrix} a_1 \\ a_2 \\ a_3 \end{bmatrix}$$

Where,

X = Phenotypic variance-covariance

b = Discriminant function coefficient

G = Genotypic variance-covariance

a = Economic weightage

The solution of these equations gives the estimate of 'bi' values in the following manner.

$$b_i = X^{-1} \cdot G \cdot a.$$

Where,

X^{-1} = Inverse matrix of X

G = Genotypic variance-covariance matrix

a = Economic weightage matrix

The mathematical description of the function (I) is known as selection index.

$$I = b_1p_1 + b_2p_2 + \dots + b_np_n$$

Using this function, it is possible to discriminate among the superior and inferior plants or combination of characters. Selection index or score is calculated for all the plants or combination of characters and those with the highest values are considered.

4. EXPERIMENTAL RESULTS

The aim of this study was to determine the nature and magnitude of variability parameters, correlation, path coefficient analysis, genetic divergence and selection indices among 25 fenugreek genotypes for 13 different characters. The experiment was laid out in Randomized Block Design (RBD) with three replications during *Rabi*, 2023-24. The experimental data obtained was statistically analysed. The experimental results are well explained under the following sub-heads.

4.1 Analysis of variance

4.2 Mean performance of the genotypes and range

4.3 Genetic variability parameters

4.4 Correlation coefficient analysis

4.5 Path analysis

4.6 Genetic divergence

4.7 Discriminant function and selection indices

4.1 ANALYSIS OF VARIANCE (ANOVA)

The analysis of variance (ANOVA) indicated that the mean sum of squares due to genotypes were highly significant for all the traits under study *viz.*, days to 50 percent flowering, days to maturity, plant height(cm), number of branches per plant, number of pods per plant, pod length (cm), number of seeds per pod, 1000-seed weight (g) biological yield per plant (g), seed yield per plant (g), harvest index (%), seed protein content (%) and fat content (%) indicating the presence of adequate genetic variability in the existing material. The mean sum of squares due to replication showed no significant differences for all the characters under study indicating that there was high homogeneity among the replications. Mean sum of square from analysis of variance for various characters are given in Table 4.1.

4.2 MEAN PERFORMANCE OF THE GENOTYPES AND RANGE

Per se performance and the range for all the 13 characters for different genotypes are presented in Appendix IV and V.

4.2.1 Days to 50 percent flowering

The Days to 50 percent flowering ranged from 45.67 days to 51 days, with a mean value of 49.11 days. The genotype RMt-305 was first to flower (45.67)

4.2.2 Days to maturity

The days to maturity ranged from 120 days to 124 days with a mean value of 121.96 days. The genotype AM-31-30-5 was first to mature (120) while genotype Pant Ragini was last to mature (124 days).

4.2.3 Plant height (cm)

The plant height ranged from 63.89 cm to 99.78 cm with a mean value of 86.9 cm. Amongst genotypes, RMt-305 had lowest plant height (63.89 cm) while Afg-5 had maximum plant height *i.e.*, 99.78 cm.

4.2.4 Number of branches per plant

The mean value for number of branches per plant was noted as 4.51 with a range from 3.53 to 5.33. Amongst genotypes, IC-397506 had maximum number of branches per plant *i.e.*, 5.33.

4.2.5 Number of pods per plant

The number of pods per plant ranged from 54.33 to 108.27 with a mean value of 73.93 was recorded. The genotype Hisar Suvarna exhibited maximum number of pods per plant (108.27) among all genotypes.

4.2.6 Pod length (cm)

The pod length ranged from 8.93 cm to 11.8 cm with a mean value of 10.32 cm. amongst genotypes, Afg-3-350-48 had highest pod length *i.e.*, 11.8cm.

4.2.7 Number of seeds per pod

The number of seeds per pod ranged from 16.33 to 19.89 with a mean value of 17.8. The genotype Afg-1 had highest number of seeds per pod *i.e.*, 19.89.

4.2.8 1000-seed weight (g)

The 1000-seed weight ranged from 7.98 g to 13.57 g with a mean value of 11.01 g. The genotype PRM-45 had highest 1000-seed weight *i.e.*, 13.57g among all genotypes.

4.2.9 Biological yield per plant (g)

The biological yield per plant ranged from 23.53 g to 40.03 g with a mean value of 31.46 g. Amongst genotypes, Agf-3-350-48 had highest biological yield per plant *i.e.*, 40.03g

4.2.10 Seed yield per plant (g)

The seed yield per plant ranged from 6.7 g to 11.31 g with a mean value of 8.05 g. The genotype Jfg-244 exhibited highest seed yield per plant (11.31g) among all the genotypes

4.2.11 Harvest index (%)

The mean value for harvest index was 25.97% and it ranged from 20.19% (Afg-3-350-48) to 30.86% (Afg-1). Amongst genotypes, Afg-1 had highest harvest index *i.e.*, 30.86%.

4.2.12 Seed protein content (%)

The mean value for seed protein content was 23.84% and it ranged from 20.54% to 26.3%. The genotype AM-6-1-27 had highest seed protein content (26.30%) among all genotypes.

4.2.13 Fat content (%)

The fat content showed a range from 3.29% to 6.33%, with a mean of 4.84%. Amongst genotypes, Afg-3-300-160 had highest fat content (6.33%).

4.3 GENETIC VARIABILITY PARAMETERS

The various parameters of genetic variability such as mean, range, phenotypic and genotypic coefficient of variation (%), heritability (%) in broad sense, genetic advance and genetic advance as percent of mean genetic gain for each of the character have been shown in Table 4.2.

4.3.1 Genotypic Coefficient of Variation (GCV)

The magnitude of the Genotypic Coefficient of Variation (GCV) varied from 0.70% to 19.52%. Genotypic coefficient of variation (GCV) was highest for number of pods per plant (19.52%), 1000-seed weight (15.36%), fat content (14.69%), harvest

index (14.17%), biological yield per plant (14.13%), and seed yield per plant (12.72%). Days to maturity (0.70%) and days to percent flowering (2.63%) exhibited a low genotypic coefficient of variation.

4.3.2 Phenotypic Coefficient of Variation (PCV)

For all of the characters under study, the phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV). The highest value of PCV was recorded for number of pods per plant (21.20%) followed by harvest index (16.64%), biological yield per plant (15.95%), 1000-seed weight (15.78%) and seed yield per plant (15.71%). The lowest phenotypic coefficient of variation was observed for days to maturity (1.36%) followed by days to 50 percent flowering (3.59%).

4.3.3 Heritability (h^2)

The broad sense heritability was estimated for all the characters under study. High estimates of heritability were observed for most of the traits and it was noted highest for fat content (99.11%) followed by 1000-seed weight (94.72%), seed protein content (92.55%) and number of pods per plant (84.78%). However, plant height (56.00%), days to 50 percent flowering (53.52%) and number of branches per plant (51.88%) exhibited moderate heritability.

4.3.4 Genetic Advance (GA)

The high genetic advance was recorded for number of pods per plant (27.37) followed by plant height (10.73) and biological yield per plant (8.11) while number of branches per plant (0.52) and number of seeds per pod (0.57) showed lower genetic advance.

4.3.5 Genetic Gain (GG)

The highest genetic advance as per cent of mean (genetic gain) was recorded for number of pods per plant (37.02%) followed by 1000 seed-weight (30.79%), fat content (30.13%), biological yield per plant (25.77%) and harvest index (24.85%). However, the lowest value of genetic gain was recorded by days to maturity (0.75%) followed by number of seeds per pod (3.18%).

4.4 CORRELATION COEFFICIENT ANALYSIS

When a breeder is trying to combine high yield potential with desirable agronomical and quality parameters, knowledge of genetic correlation for yield, its components and various quality characters becomes important. The type, extent and direction of selection may all be determined using association studies. The degree of mutual relationship between yield and their component traits was worked out by estimating the correlation coefficient at the phenotypic and genotypic levels using 25 genotypes of fenugreek and estimates are presented in Table 4.3. Perusal of results revealed that the estimates of genotypic correlation coefficients were higher in magnitude than their respective phenotypic correlation coefficients for all the character pairs under study. The correlations between different characters are being presented as under:

The days to 50 percent flowering expressed a negative and significant correlation with seed yield per plant ($r_g = -0.48^*$ and $r_p = -0.36^*$) at both genotypic and phenotypic levels.

The days to maturity expressed a negative and significant correlation with plant height ($r_g = -0.53^{**}$ and $r_p = -0.26^*$) at both genotypic and phenotypic levels. It showed a positive and significant correlation with pod length ($r_p = 0.24^*$) at phenotypic level only and with number of seeds per pod ($r_g = 0.93^*$) at genotypic levels only. However, it exhibited a negative and significant correlation with seed protein content ($r_p = -0.36^*$) at phenotypic level only.

The plant height expressed a positive and significant correlation with biological yield per plant ($r_g = 0.72^{**}$ and $r_p = 0.46^{**}$) and seed yield per plant ($r_g = 0.54^{**}$ and $r_p = 0.31^*$) at both genotypic and phenotypic levels.

The number of branches per plant showed a positive and significant correlation with number of pods per plant ($r_g = 0.63^{**}$ and $r_p = 0.49^{**}$) at both phenotypic and genotypic levels. However, it exhibited a negative and significant correlation with harvest index ($r_p = -0.47^*$ and $r_g = -0.30^*$) at both genotypic and phenotypic levels.

The number of pods per plant showed a positive and significant correlation with 1000-seed weight ($r_g = 0.52^{**}$ and $r_p = 0.47^{**}$) at both genotypic and phenotypic levels.

The 1000-seed weight showed a positive and significant correlation with biological yield per plant ($r_g = 0.39^*$ and $r_p = 0.35^*$) and seed yield per plant ($r_g = 0.52^{**}$ and $r_p = 0.54^{**}$) at both genotypic and phenotypic levels.

The biological yield per plant exhibited a positive and significant correlation with seed yield per plant ($r_g = 0.39^*$ and $r_p = 0.44^{**}$) at both genotypic and phenotypic levels. However, it showed a negative and significant correlation with harvest index ($r_g = -0.68^{**}$ and $r_p = 0.58^{**}$) at both genotypic and phenotypic levels.

The harvest index showed a positive and significant correlation with seed yield per plant ($r_g = 0.46^{**}$ and $r_p = 0.40^*$) at both phenotypic and genotypic levels.

4.5 PATH COEFFICIENT ANALYSIS

The amount of contribution of various yield contributing characters to yield in the form of cause and effect was determined using path coefficient analysis.

In the present study, seed yield per plant was taken as dependent variable where as other traits *viz.*, days to 50 percent flowering, days to maturity, plant height, number of branches per plant, number of pods per plant, pod length, number of seeds per pod, 1000-seed weight, biological yield per plant, seed protein content and fat content were taken as independent variables. It revealed whether the association of these independent traits with seed yield is due to their direct effect on yield or is consequence of their indirect effect *via* other component traits. The estimates of path coefficient analysis using genotypic and phenotypic correlation are presented in Table 4.4.

4.5.1 Direct Effect

The impact of characters can be measured by the magnitude of direct effect irrespective of its direction. The maximum positive direct effect on seed yield per plant was exhibited by number of seeds per pod (1.3770) followed by days to 50 percent flowering (0.5501), fat content (0.3648), number of pods per plant (0.3369), plant height (0.2514), 1000-seed weight (0.1440), number of branches per plant (0.0564), seed protein content (0.0171) and biological yield per plant (0.0132).

Maximum negative direct effect on seed yield per plant was exhibited by days to maturity (-1.0822) and pod length (-0.5533).

4.5.2 Indirect Effect

The indirect effect on seed yield per plant was estimated at genotypic level *via* different characters are presented in Table 4.4.

4.5.2.1 Positive indirect effect

The maximum positive indirect effect was recorded by days to maturity *via* number of seeds per pod (1.2784), pod length *via* number of seeds per pod (0.6786) plant height *via* days to maturity (0.5763), biological yield per plant *via* days to maturity (0.5184), 1000-seed weight *via* days to maturity (0.2401), number of branches per plant *via* number of pods per plant (0.2128), plant height *via* days to 50 percent flowering (0.1882), number of pods per plant *via* days to 50 percent flowering (0.1846), biological yield per plant *via* plant height (0.1805), 1000-seed weight *via* number of pods per plant (0.1765), pod length *via* days to 50 percent flowering (0.1715), seed protein content *via* number of seeds per pod (0.1698), fat content *via* days to maturity (0.1408), plant height *via* fat content (0.1236) and days to 50 percent flowering *via* number of pods per plant (0.1131).

4.5.2.2 Negative indirect effect

The maximum negative indirect effect was recorded for number of seeds per pod *via* days to maturity (-1.0099), plant height *via* number of seeds per pod (-0.6243), biological yield per plant *via* number of seeds per pod (-0.4714), pod length *via* days to maturity (-0.4221), number of branches per plant *via* number of seeds per pod (-0.4200), fat content *via* number of seeds per pod (-0.2986), number of seeds per pod *via* pod length (-0.2741), seed protein content *via* days to 50 percent flowering (-0.2614), number of pods per plant *via* number of seeds per pod (-0.2495), days to maturity *via* pod length (-0.2158), 1000-seed weight *via* number of seeds per pod (-0.2089), days to 50 percent flowering *via* days to maturity (-0.2064) days to 50 percent flowering *via* pod length (-0.1725), number pods per plant *via* days to maturity (-0.1571), number of branches per plant *via* pod length (-0.1417), days to maturity *via* plant height (-0.1339) and number of seeds per pod *via* plant height (-0.1146)

Path coefficient analysis was demonstrated at genotypic level for seed yield per plant for 11 traits out of them only traits *viz.*, plant height and 1000-seed weight showed a positive and significant correlation to seed yield per plant are explained: -

4.5.3.1 Plant height

Plant height had a positive and significant direct effect (0.2514) on seed yield per plant. It showed a positive and indirect effect *via* days to maturity (0.5763), days to 50 percent flowering (0.1882), fat content (0.1236), number of pods per plant (0.0716), 1000-seed weight (0.0447), biological yield per plant (0.0094) and number of branches per plant (0.0033). Negative indirect effect was observed *via* number of seeds per pod (-0.6243), pod length (-0.0957), and seed protein content (-0.0038).

4.5.3.2 1000-seed weight

1000-seed weight showed a positive and direct effect (0.1440) on seed yield per plant. It manifested a positive indirect effect *via* days to maturity (0.2401), number of pods per plant (0.1765), plant height (0.0780) and days to 50 percent flowering (0.0584), fat content (0.0302), number of branches per plant (0.0090) and biological yield per plant (0.0051). It exhibited a negative and indirect effect *via* number of seeds per pod (-0.2089), pod length (-0.0150) and seed protein content (-0.0004).

4.5.4 Residual Effect

The residual effect ($R = 0.7519$) showed that 24.81 per cent variability was demonstrated by the characters considered for path study.

4.6 GENETIC DIVERGENCE

To estimate the genetic divergence between two genotypes/lines or a group of genotypes/ lines, Tocher's method (Rao, 1952) was used to grouping genotypes into different clusters using Mahalanobis D^2 statistics (1936), as described by Rao (1952).

4.6.1 Genotypes grouping into clusters

Twenty-five fenugreek genotypes were classified into seven clusters based on their relative magnitude of D^2 values. The result of the genotype grouping into clusters is displayed in Table 4.5. Cluster I was the largest one with 18 genotypes followed by cluster II with 2 genotypes and remaining clusters *viz.*, III, IV, V, VI, VII were smallest with a single genotype in each.

4.6.2 Average intra and inter-cluster distance

Average inter and intra-cluster distance among 7 clusters was displayed in Table 4.6. The mean intra-cluster distance ranged from 0.00 (cluster III to cluster VII) to 7.91 (cluster II). The cluster II had maximum intra-cluster distance (7.91) followed by cluster I (7.01)

Maximum inter-cluster distance was exhibited by cluster IV and VII (15.26), followed by cluster III and V (14.72), cluster V and VII (13.31), cluster VI and VII (13.25), cluster IV and VI (12.48), cluster II and VII (12.37), cluster IV and V (12.35), cluster II and cluster VI (12.25), cluster II and cluster V (12.20), cluster II and cluster III (11.8) and cluster II and IV (11.53) while the minimum inter-cluster distance was exhibited by cluster I and VI (9.08) followed by cluster I and II (9.23).

4.6.3 Cluster mean

The cluster means of various characters are shown in Table 4.7. The extent of difference among cluster means for different characters was found to be prominent. The variation for days to 50 percent flowering was ranged from 46.67 days (cluster IV) to 51.00 days (cluster VII), days to maturity from 121 days (cluster VII) to 124 days (cluster V), plant height from 82.33 cm (cluster V) to 97.56 cm (cluster III), number of branches per plant from 3.53 (cluster VII) to 4.93 (cluster III), number of pods per plant from 54.33 (cluster VI) to 90.6 (cluster V), pod length from 8.93 cm (cluster V) to 11.8 cm (cluster IV), number of seeds per pod from 17.13 (cluster III) to 18.8 (cluster VI), 1000-seed weight from 8.73 g (cluster VI) to 12.37 g (cluster VII), biological yield per plant from 26.43 g (cluster V) to 40.03 g (cluster IV), seed yield per plant from 6.97 g (cluster VI) to 11.31 g (cluster VII), harvest index from 20.19% (cluster IV) to 30.85% (cluster VII), seed protein content from 21.45% (cluster II) to 25.39% (cluster IV) and fat content was recorded from 4.32% (cluster VII) to 6.09% (cluster IV).

4.6.4 Relative contribution of different character towards total divergence

The percent contribution of independent characters in the direction of total divergence has been presented in Table 4.8. The character number of pods per plant was found to be the most important character in contributing to the total divergence, accounting for 66.24% followed by plant height (23.97%), biological yield per plant

(4.96%), days to 50 percent flowering (1.10%), seed protein content (1.02%), 1000-seed weight (0.89%), days to maturity (0.71%), number of seeds per pod (0.29%), seed yield per plant (0.28%), fat content (0.20%), Pod length (0.18%), Number of branches per plant (0.08%) and harvest index (0.07%).

4.7 DISCRIMINANT FUNCTION AND SELECTION INDICES

For the construction of selection indices, the character, which had desirable correlation on seed yield per plant were considered. In this context, seed yield per plant (X_1) along with its four components *viz.*, days to 50 percent flowering (X_2), Plant height (cm) (X_3), number of pods per plant (X_4) number of seeds per pod (X_5) fat content (X_6) were identified and considered for the construction of selection indices.

Twenty-eight selection indices were constructed in all possible combinations of the five yield contributing characters and seed yield per plant. Their respective genetic advances were calculated and relative efficiency of different discriminant functions in relation to the straight selection for seed yield per plant were compared. The data on selection indices, discriminant functions, genetic gain, relative efficiency and relative efficiency per character are given in Table 4.9, assuming the efficiency of straight selection for seed yield per plant as 100%. The results suggested that the selection efficiency was higher, in general, over straight selection when the selection was based on component character, which further increased with the inclusion of two or more characters. The highest efficiency was noted when all six characters were considered together.

When the relative efficiency of single character index was measured, it was noted that the maximum efficiency of 1603.12% was exhibited by number of pods per plant followed by plant height (628.55%) compared to 100% relative efficiency of seed yield per plant. Among the combination involving two characters, relative efficiency was noted maximum for the combination of seed yield per plant and number of pods per plant [(X_1+X_4) , 1656.29%] followed by seed yield per plant and plant height [(X_1+X_3) , 711.56%], seed yield per plant and days to 50 percent flowering [(X_1+X_2) , 193.21%], seed yield per plant and fat content [(X_1+X_6) , 151.19%], seed yield per plant and number of seeds per pod [(X_1+X_5) , 96.00%].

The combination of three characters with the highest relative efficiency which found to be the most effective, was seed yield per plant, plant height and number of pods per plant $[(X_1+X_3+X_4), 1913.20\%]$ followed by seed yield per plant, days to 50 percent flowering, and number of pods per plant $[(X_1+X_2+X_4), 1713.14\%]$, seed yield per plant, number of pods per plant and number of seeds per pod $[(X_1+X_4+X_5), 1642.55\%]$, seed yield per plant, number of pods per plant and fat content $[(X_1+X_4+X_6), 1641.70\%]$, seed yield per plant, days to 50 percent flowering and , plant height $[(X_1+X_2+X_3), 778.72\%]$ seed yield per plant, plant height and number of seeds per pod $[(X_1+X_3+X_5), 679.97\%]$, seed yield per plant, plant height and fat content $[(X_1+X_3+X_6), 672.83\%]$, seed yield per plant, days to 50 percent flowering and fat content $[(X_1+X_2+X_6), 222.47\%]$, seed yield per plant, plant height and number of seeds per pod $[(X_1+X_2+X_5), 187.32\%]$ seed yield per plant, number of seeds per pod and fat content $[(X_1+X_5+X_6), 139.3\%]$ and days to 50 percent flowering, plant height, and number of pods per plant $[(X_2+X_3+X_4), 265.36\%]$.

The selection index based on four characters combination indicated that a discriminant function with seed yield per plant, days to 50 percent flowering, plant height and number of pods per plant $[(X_1+X_2+X_3+X_4), 1980.01\%]$ has highest relative efficiency followed seed yield per plant, days to 50 percent flowering, plant height and number of seeds per pod $[(X_1+X_2+X_3+X_5), 747.82\%]$, and seed yield per plant, days to 50 percent flowering, plant height and fat content $[(X_1+X_2+X_3+X_6), 719.25\%]$.

The selection index based on five characters combinations indicated that a discriminant function with seed yield per plant, days to 50 percent flowering, plant height, number of pods per plant and number of seeds per pod $(X_1+X_2+X_3+X_4+X_5)$ exerted 1957.88% relative efficiency followed by seed yield per plant, days to 50 percent flowering, plant height, number of pods per plant and fat content $[(X_1+X_2+X_3+X_4+X_6), 1831.67\%]$ and seed yield per plant, days to 50 percent flowering, plant height, number of seeds per pod and fat content $[(X_1+X_2+X_3+X_5+X_6), 789.27\%]$.

The selection index based on six characters combinations indicated that a discriminant function with seed yield per plant, days to 50 percent flowering, plant height, number of pods per plant, number of seeds per pod and fat content $(X_1+X_2+X_3+X_4+X_5+X_6)$ exerted 1983.01% relative efficiency.

Among all 28 selection indices (Table 4.9), the index based on six characters *viz.*, seed yield per plant, days to 50 percent flowering, plant height, number of pods per plant, number of seeds per pod and fat content ($X_1+X_2+X_3+X_4+X_5+X_6$) possessed the highest genetic advance and relative efficiency (33.86% and 1983.01%) as compared to straight selection for seed yield per plant. Among the indices based on five characters, the index based on characters *viz.*, seed yield per plant, days to 50 percent flowering, plant height, number of pods per plant and number of seeds per pod ($X_1+X_2+X_3+X_4+X_5$) possessed the highest genetic advance and relative efficiency (33.43% and 1957.88%). Among the indices based on four characters, the index based on characters *viz.*, seed yield per plant, days to 50 percent flowering, plant height and number of pods per plant ($X_1+X_2+X_3+X_4$) possessed the highest genetic advance and relative efficiency (33.81% and 1980.01%). Similarly for three-character combinations seed yield per plant, plant height and number of pods per plant ($X_1+X_3+X_4$) possessed the highest genetic advance and relative efficiency (32.66% and 1913.20%).

While calculating relative efficiency per character, it was observed that maximum relative efficiency was recorded by direct selection of number of pods per plant (1603.12%). Likewise, the highest relative efficiency per character of 828.15% was exhibited by a selection index involving two component characters *viz.*, seed yield per plant and number of pods per plant (X_1+X_4). The selection index based on three characters *viz.*, seed yield per plant, plant height and number of pods per plant ($X_1+X_3+X_4$) exerted 637.73% relative efficiency per character. In four-character selection index, a function involving seed yield per plant, plant height, days to 50 percent flowering and number of pods per plant ($X_1+X_2+X_3+X_4$) exerted 495.00% relative efficiency per character. In five-character selection index, a function involving seed yield per plant, plant height, days to 50 percent flowering, number of pods per plant and number of seeds per pod ($X_1+X_2+X_3+X_4+X_5$) exerted 391.58% relative efficiency per character. Similarly, seed yield per plant, plant height, days to 50 percent flowering, number of pods per plant, number of seeds per pod and fat content ($X_1+X_2+X_3+X_4+X_5+X_6$) possessed relative efficiency per character of 330.50% in respect of six component combination.

Selection based on yield alone may be often misleading due to high environmental influence and multiple traits selection can improve selection efficiency and can attain largest economic gain. Therefore, utilizing the best selection index (seed yield per plant + days to 50 percent flowering + plant height + number of pods per plant + number of seeds per pod and fat content), the relative genetic score of each genotype was determined [Table 4.10]. It was found that the genotypes Hisar Suvarna, IC-397506, Hisar Sonali, Afg-4, PRM-45 and Pant Ragini were superior among all genotypes tested, having the optimal contribution of attributes.

Table 4.1: Analysis of variance for yield and yield contributing traits in fenugreek

S. No.	Characters	Replication [2]	Genotype [24]	Error [48]
1	Days to 50% flowering	1.65	6.44**	1.45
2	Days to maturity	0.84	4.20*	2.01
3	Plant height (cm)	81.39	183.45**	38.07
4	Number of branches per plant	0.34	0.49**	0.12
5	Number of pods per plant	98.07	662.06**	37.38
6	Pod length (cm)	0.07	1.49**	0.50
7	Number of seeds per pod	3.11	2.07*	1.09
8	1000-Seed weight (g)	0.23	8.73**	0.16
9	Biological (g) yield per plant	16.82	64.69**	5.44
10	Seed yield per plant (g)	0.94	3.69**	0.55
11	Harvest index (%)	8.42	45.78**	5.14
12	Protein content (%)	0.68	8.90**	0.23
13	Fat content (%)	0.00	1.52**	0.00

*, ** Significant at 5% and 1% respectively
[] figure in parenthesis is degree of freedom

Table 4.2: Genetic variability parameters for yield and its contributing traits in fenugreek

Characters	Mean	Range		GCV (%)	PCV (%)	H ² (%)	GA	GG (%)
		Min.	Max.					
Days to 50 percent flowering	49.11	45.67	51.00	2.63	3.59	53.52	1.94	3.96
Days to maturity	121.96	120.00	124.00	0.70	1.36	26.73	0.91	0.75
Plant height (cm)	86.90	63.89	99.78	8.01	10.70	56.00	10.73	12.35
Number of branches per plant	4.51	3.53	5.33	7.83	10.87	51.88	0.52	11.61
Number of pods per plant	73.93	54.33	108.27	19.52	21.20	84.78	27.37	37.02
Pod length (cm)	10.32	8.93	11.80	5.55	8.82	39.58	0.74	7.19
Number of seeds per pod	17.80	16.33	19.89	3.21	6.68	23.08	0.57	3.18
1000 seed weight (g)	11.01	7.98	13.57	15.36	15.78	94.72	3.39	30.79
Biological yield per plant (g)	31.46	23.53	40.03	14.13	15.95	78.42	8.11	25.77
Seed yield per plant (g)	8.05	6.70	11.31	12.72	15.71	65.55	1.71	21.22
Harvest index (%)	25.97	20.19	30.86	14.17	16.64	72.49	6.46	24.85
Seed protein content (%)	23.84	20.54	26.30	7.13	7.41	92.55	3.37	14.13
Fat content (%)	4.84	3.29	6.33	14.69	14.76	99.11	1.46	30.13

Table 4.3: Estimation of genotypic (rg) and phenotypic (rp) correlation coefficient for different characters in fenugreek

S. Character No.	r	Days to 50 percent flowering	Days to maturity	Plant height	Number of branches per plant	Number of pods per plant	Pod length	Number of seeds per pod	1000-seed weight	Biological yield per plant	Harvest index	Seed protein content	Fat content	Seed yield per plant
1. Days to 50 percent flowering	rg		0.19	0.34	0.04	0.34	0.31	-0.01	0.11	0.02	0.24	-0.48*	-0.02	0.37
	rp		0.04	0.21	-0.01	0.24	0.02	0.13	0.06	-0.01	0.10	-0.36*	-0.01	0.15
2. Days to maturity	rg			-0.53*	0.01	0.15	0.39	0.93*	-0.22	-0.48	0.45	-0.01	-0.13	-0.09
	rp			-0.26*	0.03	0.04	0.24*	0.06	-0.44	-0.01	0.10	-0.36*	-0.06	0.15
3. Plant height	rg				0.06	0.21	0.17	-0.46	0.31	0.72**	-0.43	-0.22	0.34	0.54**
	rp				0.15	0.22	0.06	-0.02	0.24	0.46**	-0.16	-0.19	0.25	0.31*
4. Number of branches per plant	rg					0.63**	0.26	-0.31	0.16	0.30	-0.47*	0.02	0.13	-0.19
	rp					0.49**	0.17	-0.01	0.11	0.20	-0.30*	-0.00	0.10	-0.13
5. Number of pods per plant	rg						-0.08	-0.18	0.52**	0.11	0.16	-0.28	0.14	0.37
	rp						-0.07	-0.02	0.47**	0.06	0.12	-0.27	0.13	0.23
6. Pod length	rg							0.50	0.03	0.13	-0.11	-0.09	0.16	-0.03
	rp							0.04	0.02	0.22	-0.16	-0.04	0.11	0.02
7. Number of seeds per pod	rg								-0.15	-0.34	0.23	0.12	-0.22	-0.21
	rp								-0.05	-0.22	0.03	-0.02	-0.01	-0.21
8. 1000-seed weight	rg									0.39*	0.04	-0.02	0.08	0.52**
	rp									0.35*	0.04	-0.03	0.09	0.44**
9. Biological yield per plant	rg										-0.68**	0.09	0.29	0.39*
	rp										-0.58**	0.09	0.25	0.44**
10. Harvest index	rg											-0.26	-0.07	0.46**
	rp											-0.23	-0.06	0.40*
11. Seed protein content	rg												-0.27	-0.19
	rp												-0.25	-0.26
12. Fat content	rg													0.20
	rp													0.26
13. Seedyield perplant	rg													
	rp													

*, ** Significant at 5% and 1% respectively

Table 4.4: Genotypic path analysis for seed yield per plant in fenugreek

S. No.	Character	Days to 50 percent flowering	Days to maturity	Plant height	Number of branches per plant	Number of pods per plant	Pod length	Number of seeds per pod	1000-seed weight	Biological yield per plant	Seed protein content	Fat content	r with seed yield per plant
1.	Days to 50 percent flowering	0.5501	-0.2064	0.0860	0.0025	0.1131	-0.1725	-0.0086	0.0153	0.0002	-0.0081	-0.0061	0.3654
2.	Days to maturity	0.1049	-1.0822	-0.1339	0.0004	0.0489	-0.2158	1.2784	-0.0319	-0.0063	-0.0003	-0.0475	-0.0852
3.	Plant height	0.1882	0.5763	0.2514	0.0033	0.0716	-0.0957	-0.6243	0.0447	0.0094	-0.0038	0.1236	0.5445**
4.	Number of branches per plant	0.0242	-0.0086	0.0145	0.0564	0.2128	-0.1417	-0.4200	0.0229	0.0039	0.0003	0.0490	-0.1864
5.	Number of pods per plant	0.1846	-0.1571	0.0534	0.0356	0.3369	0.0418	-0.2495	0.0754	0.0014	-0.0047	0.0493	0.3671
6.	Pod length	0.1715	-0.4221	0.0435	0.0144	-0.0254	-0.5533	0.6786	0.0039	0.0018	-0.0015	0.0593	-0.0293
7.	Number of seeds per pod	-0.0034	-1.0099	-0.1146	-0.0173	-0.0614	-0.2741	1.3700	-0.0220	-0.0045	0.0021	-0.0795	-0.2144
8.	1000-seed weight	0.0584	0.2401	0.0780	0.0090	0.1765	-0.0150	-0.2089	0.1440	0.0051	-0.0004	0.0302	0.5169**
9.	Biological yield per plant	0.0099	0.5184	0.1805	0.0168	0.0371	-0.0743	-0.4714	0.0560	0.0132	0.0015	0.1040	0.3916
10.	Seed protein content	-0.2614	0.0161	-0.0559	0.0009	-0.0932	0.0484	0.1698	-0.0035	0.0011	0.0171	-0.0968	-0.2573
11.	Fat content	-0.0091	0.1408	0.0852	0.0076	0.0455	-0.0900	-0.2986	0.0119	0.0038	-0.0045	0.3648	0.2573

Residual = 0.7519

** Significant correlation with dependent character at 1%

Table 4.5: Grouping of 25 fenugreek genotypes into seven clusters (by Tocher's method)

Cluster No.	Name of genotype	Number of genotype
I	AM-31-30-5, AM-6-1-27, AM-6-2-28, Afg-3-300-160, Afg-1, Afg-2, Afg-3,Afg-5, IC-397506, RMt-354, RMt-143, RMt-361, RMt-351, RMt-1, RMt-305, PRM-45, Hisar Suvarna, Hisar sonali	18
II	AM-45-20-4, RMt303	2
III	Afg-4	1
IV	Afg-3-350-48	1
V	Pant Ragini	1
VI	Afg-3-350-273	1
VII	JFg-244	1

Table 4.6: Average inter and intra-cluster distance based on corresponding D^2 values in fenugreek

Clusters	I	II	III	IV	V	VI	VII
I	7.09	9.23	10.12	10.14	10.77	9.08	10.76
II		7.91	11.80	11.53	12.20	12.25	12.37
III			0.00	10.79	14.72	11.45	11.49
IV				0.00	12.35	12.48	15.26
V					0.00	11.39	13.31
VI						0.00	13.25
VII							0.00

Table 4.7: Mean values of different characters for 25 fenugreek genotypes grouped into seven clusters

Cluster	Days to 50 percent flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of pods per plant	Pod length (cm)	Number of seeds per pod	1000-seed weight (g)	Biological yield per plant (g)	Seed yield per plant (g)	Harvest index (%)	Seed protein content (%)	Fat content (%)
I	49.04	121.89	86.33	4.56	75.18	10.33	17.93	10.90	30.39	7.72	25.85	24.22	4.72
II	49.83	121.17	84.56	4.30	60.70	11.13	17.20	12.17	32.60	8.24	25.76	21.45	5.01
III	50.00	122.67	97.56	4.93	84.60	10.80	17.13	11.28	36.63	11.27	30.80	22.05	5.72
IV	46.67	123.33	93.22	4.67	62.93	11.80	17.46	9.98	40.03	8.10	20.19	25.39	6.09
V	49.33	124.00	82.33	4.27	90.60	8.93	17.20	12.30	26.43	8.04	30.40	21.99	5.42
VI	48.33	121.67	83.00	4.60	54.33	9.07	18.80	8.73	34.40	6.97	20.20	24.51	4.54
VII	51.00	121.00	93.33	3.53	80.97	9.33	17.20	12.37	36.73	11.31	30.85	23.14	4.32

Table 4.8: Percent contribution of different characters towards total genetic divergence in fenugreek

Character	Per cent contribution
Days to 50 per cent flowering	1.10
Days to maturity	0.71
Plant height	23.97
Number of branches per plant	0.08
Number of pods per plant	66.24
Pod length	0.18
Number of seeds per pod	0.29
1000-seed weight	0.89
Biological yield per plant	4.96
Seed yield per plant	0.28
Harvest index	0.07
Seed protein content	1.02
Fat content	0.20

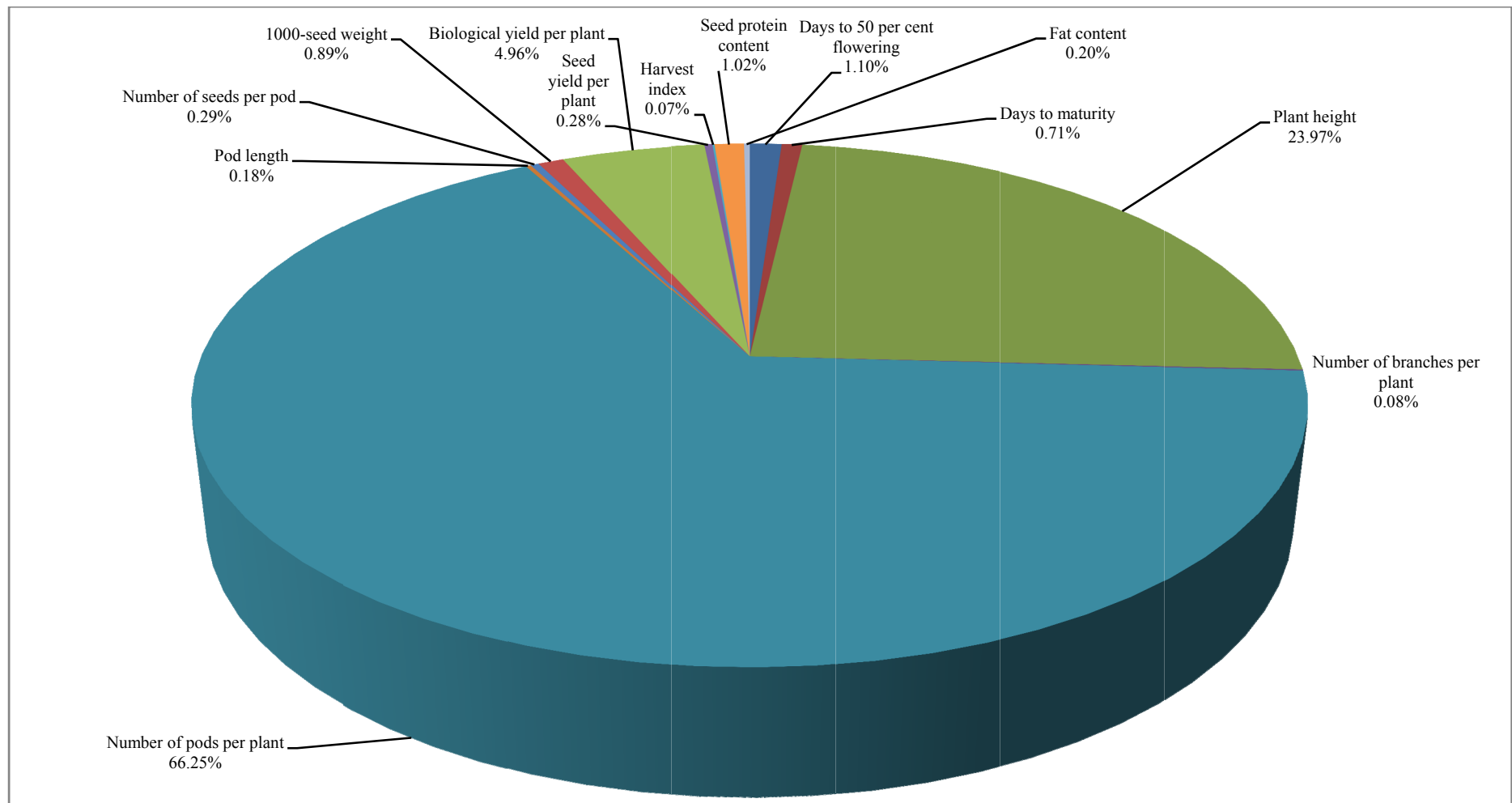


Figure 3.3: Percent contribution of different characters towards total genetic divergence in fenugreek

Table 4.9: Selection index, discriminant function, expected genetic advance in yield and relative efficiency from the use of different selection indices in fenugreek

S.No.	Selection index	Discriminant function	Expected genetic advance (Gs)	Relative efficiency (%)	Relative efficiency per character
1	X ₁	0.66X ₁ [X ₁ = seed yield per plant]	1.71	100.00	100.00
2	X ₂	0.54X ₂ [X ₂ = Days to 50 percent flowering]	1.94	113.86	113.86
3	X ₃	0.56X ₃ [X ₃ = Plant height]	10.73	628.55	628.55
4	X ₄	0.85X ₄ [X ₄ = number of pods per plant]	27.37	1603.12	1603.12
5	X ₅	0.23X ₅ [X ₅ = number of seeds per pod]	0.57	33.11	33.11
6	X ₆	0.99X ₆ [X ₆ = Fat content]	1.46	85.48	85.48
7	X ₁ +X ₂	0.64X ₁ +0.51X ₂	3.30	193.21	96.61
8	X ₁ +X ₃	0.61X ₁ +0.51X ₃	12.15	711.56	355.78
9	X ₁ +X ₄	0.63X ₁ +0.83X ₄	28.28	1656.29	828.15
10	X ₁ +X ₅	0.67X ₁ +0.22X ₅	1.64	96.00	48.00
11	X ₁ +X ₆	0.64X ₁ +0.99X ₆	2.58	151.19	75.60
12	X ₁ +X ₂ +X ₃	0.60X ₁ +0.51X ₂ +0.50X ₃	13.30	778.72	259.57
13	X ₁ +X ₂ +X ₄	0.62X ₁ +0.50X ₂ +0.83X ₄	29.25	1713.14	571.05
14	X ₁ +X ₂ +X ₅	0.65X ₁ +0.52X ₂ +0.23X ₅	3.20	187.32	62.44
15	X ₁ +X ₂ +X ₆	0.62X ₁ +0.51X ₂ +0.99X ₆	3.80	222.47	74.16
16	X ₁ +X ₃ +X ₄	0.59X ₁ +0.51X ₃ +0.84X ₄	32.66	1913.20	637.73
17	X ₁ +X ₃ +X ₅	0.62X ₁ +0.51X ₃ +0.23X ₅	11.61	679.97	226.66
18	X ₁ +X ₃ +X ₆	-3.75X ₁ +5.04X ₃ +0.99X ₆	11.49	672.83	224.28
19	X ₁ +X ₄ +X ₅	0.64X ₁ +0.83X ₄ +0.22X ₅	28.04	1642.55	547.52
20	X ₁ +X ₄ +X ₆	-6.70X ₁ +11.05X ₄ +0.90X ₆	28.03	1641.70	547.23
21	X ₁ +X ₅ +X ₆	0.65X ₁ +0.22X ₅ +0.99X ₆	2.38	139.30	46.43
22	X ₁ +X ₂ +X ₃ +X ₄	0.59X ₁ +0.49X ₂ +0.50X ₃ +0.84X ₄	33.81	1980.01	495.00
23	X ₁ +X ₂ +X ₃ +X ₅	0.61X ₁ +0.51X ₂ +0.50X ₃ +0.23X ₅	12.77	747.82	186.96
24	X ₁ +X ₂ +X ₃ +X ₆	-2.98X ₁ +0.67X ₂ +4.49X ₃ +0.99X ₆	12.28	719.25	179.81
25	X ₁ +X ₂ +X ₃ +X ₄ +X ₅	0.60X ₁ +0.50X ₂ +0.50X ₃ +0.83X ₄ +0.23X ₅	33.43	1957.88	391.58
26	X ₁ +X ₂ +X ₃ +X ₄ +X ₆	-8.68X ₁ +1.01X ₂ -0.20X ₃ +13.55X ₄ +0.88X ₆	31.27	1831.67	366.33
27	X ₁ +X ₂ +X ₃ +X ₅ +X ₆	0.60X ₁ +0.51X ₂ +0.48X ₃ +0.23X ₅ +0.99X ₆	13.48	789.27	157.85
28	X ₁ +X ₂ +X ₃ +X ₄ +X ₅ +X ₆	0.59X ₁ +0.50X ₂ +0.48X ₃ +0.83X ₄ +0.23X ₅ +0.99X ₆	33.86	1983.01	330.50

Table 4.10: Relative genetic score of 25 fenugreek genotypes based on the best selection index (seed yield per plant, days to 50 percent flowering, plant height, number of pods per plant, number of seeds per pod and fat content)

Rank	Genotypes	Selection Index (selection score)
1.	Hisar Suvarna	170.95
2.	IC-397506	163.28
3.	Hisar sonali	161.01
4.	Afg-4	158.35
5.	PRM-45	153.70
6.	Pant Ragini	153.54
7.	Jfg-244	152.44
8.	Afg-5	152.28
9.	Afg-3	150.74
10.	Afg-2	143.61
11.	RMt-354	141.62
12.	Afg-1	140.46
13.	AM-31-30-5	139.87
14.	AM-45-20-4	138.33
15.	RMt-143	137.80
16.	Afg-3-350-48	135.12
17.	Afg-3-300-160	133.09
18.	AM-6-2-28	132.58
19.	RMt-1	132.18
20.	AM-6-1-27	129.40
21.	RMt-361	127.96
22.	Afg-3-350-273	121.97
23.	RMt-303	120.90
24.	RMt-305	120.66
25.	RMt-351	119.97

5. DISCUSSION

The importance of breeding programme of fenugreek is to develop a variety combining high yielding and better quality attributes. An effective breeding programme can be formulated only if information regarding the magnitude and nature of variability for different characters and their association with each other and with seed yield is available.

Keeping in view, the present investigation entitled “**Genetic Divergence and Selection Indices for Yield and its Attributing Traits in Fenugreek (*Trigonella foenum-graecum* L.)**” was undertaken at the Instructional Farm, RCA, Udaipur during *Rabi*, 2023-24. The available information on various aspects of the investigation from 25 fenugreek genotypes has been discussed under the following heads:

5.1 Analysis of variance

5.2 Genetic variability parameters

5.3 Correlation coefficient analysis

5.4 Path coefficient analysis

5.5 Genetic diversity (D^2) analysis

5.6 Discriminant function and selection indices

5.1 ANALYSIS OF VARIANCE

The analysis of variance (ANOVA) revealed highly significant differences among the genotypes for all the characters under study indicating the presence of sufficient variability among the genotypes for the characters *viz.*, days to 50 percent flowering, days to maturity, plant height (cm), number of branches per plant, number of pods per plant, pod length (cm), number of seeds per pod, 1000-seed weight (g), biological yield per plant (g), seed yield per plant (g), harvest index (%), seed protein content (%) and fat content (%). Similar inferences for all yield and its related traits have been reported by Dashora *et al.* (2011), Gangopadhyay *et al.* (2009), Meena *et al.* (2011) and Kumari *et al.* (2022).

5.2 GENETIC VARIABILITY PARAMETERS

The presence of sufficient genetic variability is needed and its evaluation, in combination with heritability (broad sense), can help to determine the relative contributions of genetic and non-genetic (environmental) variables to the overall phenotypic variation present in a population. The variability can be further partitioned into two groups viz. genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) to obtain a more defined conclusion of the variability in all the genotypes under study. In the present study, the phenotypic coefficient of variation (PCV) was found to be slightly higher than that of the genotypic coefficient of variation (GCV) for all the characters included in the study showing the environmental (non-genetic variable) changes have little effect on the characters. The estimates of Genotypic coefficient of variation and phenotypic coefficient of variation was high for the number of pods per plant, 1000-seed weight, fat content, harvest index, biological yield per plant, and seed yield per plant. These observations are in agreement with Balai *et al.* (2006). A low estimate of genotypic coefficient of variation and phenotypic coefficient of variation was found for the characters like days to maturity and days to 50 percent flowering. These findings were found to be similar to the earlier reports of Pushpa *et al.* (2012), Panwar *et al.* (2018), Singh *et al.* (2019) and Prakash *et al.* (2020).

The genotypic and phenotypic coefficient of variation gives an idea about the level of variability for different characters, but it does not provide information about the heritable portion of that variability. Selection can be effective only if there is a high or moderate amount of heritability and a high or moderate genetic advance. It clearly states that the additive gene action is involved in the inheritance of any character in concern. In the present study, the heritability estimates were moderate to high for most of the characters showing a greater contribution of genetic nature for all the characters examined. Selection for most of the characters may be effective in these genotypes because of the high heritability. The high heritability estimates along with high genetic gain for number of pods per plant, 1000-seed weight and fat content indicated that all the traits are governed by additive gene action and are expected to contribute to the improvement of genotypes by direct selection. These findings are in agreement with the earlier reports of Balai *et al.* (2006), Upadhyay *et al.* (2020) and Mishra *et al.* (2021).

5.3 CORRELATION COEFFICIENT ANALYSIS

The study of inter-relationship among various traits in the form of correlation is, in fact, one of the most important aspects of the selection programme for the breeder to make an effective selection based on the uncorrelated and correlated response. Indirect selection is useful when the desired traits have low heritability. Knowledge of correlation is required when selection is to be made on several traits at a time even if the objective is to make the selection on a single character only, the knowledge of interrelationship is essential to avoid the undesirable correlated changes in other traits.

The study of correlation coefficient indicated the degree of association between the dependent variable *i.e.* yield and its contributing component traits. In the present study, thirteen characters were studied to find out the genotypic and phenotypic correlations with seed yield. It was found that the value of the genotypic correlation coefficient was higher than the phenotypic correlation coefficient value for all the characters under study. This indicated how much of the phenotypic correlation coefficient is influenced by the environment. The seed yield per plant had a positive and significant association with plant height, 1000-seed weight, harvest index and biological yield per plant at both phenotypic and genotypic levels. These results were found in agreement with an earlier report by Dashora *et al.* (2011), where biological yield per plant and harvest index showed a positive correlation with seed yield. Yadav *et al.* (2018) and Singh *et al.* (2019) also found that 1000-seed weight had a positive and significant correlation with seed yield.

5.4 PATH ANALYSIS

The correlation coefficient indicated the relationship existing between pair of characters but a dependent trait is an interaction of the product of many mutually associated component traits and change in any one component will disturb the whole network of cause and effect system. Path coefficient analysis is a statistical method invented by Wright (1921). It considers the cause and the effect of correlations between variables and is unique in partitioning the association into direct and indirect effects through other dependent variables. Path coefficient analysis also helps to work out the relative relevance of the causal factors involved.

In the present study, the path coefficient was estimated for seed yield per plant at the genotypic level taking yield as a dependent variable. The result of a path analysis revealed that the number of seeds per pod, followed by days to 50 percent flowering, fat content, number of pods per plant, plant height, 1000-seed weight, number of branches per plant, biological yield per plant, seed protein content exhibited a positive direct effect on seed yield per plant. These results were in an agreement with the results by Singh *et al.* (2018), Dashora *et al.* (2011) and Mishra *et al.* (2021) for biological yield per plant, number of branches per plant, and 1000-seed weight, by Jain *et al.* (2013) for 1000-seed weight and secondary branches per plant. The characters *viz.*, plant height, number of pods per plant, days to maturity, pod length, days to 50 percent flowering and number of seeds per pod showed a negative direct effect on seed yield per plant. Similar results were reported by Mishra *et al.* (2021) for plant height, days to 50 percent flowering, number of pods per plant and pod length.

The plant height and 1000-seed weight showed the direct effect on seed yield per plant with a positive correlation coefficient so selection of this trait for seed yield per plant is useful. Hence, the addition of these characters in the selection criteria could be effective to get increased seed yield. Similar results were reported by Jain *et al.* (2013), Lodhi *et al.* (2015), and Panwar *et al.* (2018) The maximum positive indirect effect on seed yield was exerted by days to maturity through number of seeds per pod, pod length through number of seeds per pod, biological yield per plant through days to maturity and 1000 seed weight through days to maturity. The maximum negative indirect effect was exerted by number of seeds per pod through days to maturity, plant height through number of seeds per pod, biological yield per plant through number of seeds per pod and pod length through days to maturity. These findings were similar to the results of Gangopadhyay *et al.* (2009), where number of pods per plant and 1000-seed weight exerted positive and high direct effects on seed yield per plant and Krishnaveni *et al.* (2021) reported that the highest positive direct effect on seed yield per plant was observed on the number of pods per plant followed by the number of secondary branches per plant, the number of seeds per pod and pod length.

5.5 GENETIC DIVERGENCE

The genetic diversity of parents is of uttermost importance for any successful breeding programme. In plant breeding, genetic diversity plays a very important and indispensable role, because the hybrids between the parents of diverse origin, generally exhibit a greater hybrid vigor and lead to the development of more recombinants than those between the closely related parents. For the fulfilment of this objective, it is recommended to select more divergent genotypes from the available germplasm. The method used for estimating genetic diversity is the D^2 statistic, introduced by Mahalanobis in 1936. The D^2 statistic assesses the relative contribution of each of the characters to the overall divergence by measuring the degree of diversification.

Twenty-five fenugreek genotypes were classified into 7 clusters based on their relative magnitude of the D^2 values. Cluster I was the largest one with 18 genotypes. Clusters II with 2 genotypes and remaining clusters III, IV, V, VI and cluster VII with single genotype in each. The present findings are in accordance with reports of Pathak *et al.* (2014) where the fenugreek genotypes were grouped into 9 clusters, Wojo *et al.* (2015) grouped fenugreek genotypes into 6 clusters and Tariyal *et al.* (2017) grouped fenugreek genotypes into 4 clusters.

In the genetic divergence studies, diversity is measured on the basis of the relative inter and intra-cluster distances. Inter-cluster distance is demonstrated in terms of the genetic distance between two clusters, while the intra-cluster distance measures the extent of genetic diversity between genotypes of the same cluster. The measure of inter-cluster distance was higher than the intra-cluster distance indicating wide genetic diversity among the genotypes. In the present study, the inter-cluster distance ranged from clusters I and VI (9.08) to IV and VII (15.26). Some other remarkable inter-cluster distances were observed between clusters cluster III and V cluster V and VII and cluster VI and VII, claiming that the genotypes involved in these clusters have a great genetic diversity and incorporation of these genotypes in the fenugreek hybridization programme will lead a significant improvement in the seed yield. The high intra-cluster distance among the genotypes of these clusters was mainly due to the wide genetic diversity in these genotypes. Cluster II had maximum intra-cluster distance. Similar findings of intra and inter cluster distances were observed by Kole and Goswami (2015) where maximum inter-cluster distance was found in between Cluster III and VII, Wojo *et al.* (2015) where maximum intra-

cluster distance was found in cluster I followed by cluster II, Tariyal *et al.* (2017) where Cluster analysis of the genotypes indicated hybridization between genotypes from cluster III and cluster IV, Panwar *et al.* (2018) where intra cluster distance was the highest in cluster I than cluster II and Yadav *et al.* (2018) found that intra-cluster distance was highest in cluster IV followed by cluster VII and inter cluster distance was observed maximum in cluster IV and VIII followed by cluster II and VIII.

The traits contributing maximum to the divergence give greater emphasis to deciding the cluster type for the purpose of further use in selection and the choice of parents for the hybridization programme. The results revealed that the traits *viz.*, number of pods per plant and plant height contributed more towards the total genetic divergence among 25 fenugreek genotypes so that the direct selection for these traits would be effective as evident from the number of times these traits appeared or ranked first during contribution to diversity. Similarly plant height by Jain *et al.* (2006), test weight and plant height by Panwar *et al.* (2018) and protein content followed by days to 50 percent flowering Patahak *et al.* (2014) were reported as main contributing characters towards the total genetic divergence.

Cluster III had genotypes having higher mean values for plant height, number of branches per plant and harvest index. Similar findings were reported by Yadav *et al.* (2018) where cluster VIII showed higher mean values for plant height, number of branches per plant. Cluster IV had genotypes having higher mean values for the pod length, biological yield per plant, seed protein content and fat content. Cluster V had genotypes having higher values for days to maturity and pod length. Cluster VI had genotypes having higher mean values for number of seeds per pod and. Cluster VII had genotypes having higher mean values for days to 50 percent, 1000-seed weight and seed yield per plant. Therefore, hybridization between selected genotypes from divergent clusters is desired to sparingly combine all of the targeted traits.

5.6 DISCRIMINANT FUNCTION AND SELECTION INDICES

The plant breeders have certain desired plant characteristics in their mind while selecting for particular genotypes and for this they apply various weights to different traits for arriving on decisions. The better way of exploiting genetic correlations with several traits having high heritability is to construct an index which combines information on all the characters associated with seed yield. This suggests the use of selection index, which gives proper weight to each of the two or more characters to be considered.

Hazel and Lush (1943) showed that the selection based on such an index was more efficient than selecting individually for the various characters. The basis for the development of the selection indices has been provided by Smith (1936), Hazel and Lush (1943) and Robinson *et al.* (1951). In the present study also, the genetic advance and relative efficiency assessed for different indices increased considerably when selection was based on two or more characters.

The maximum genetic advance (Gs) and relative efficiency (RI) in single character discriminant function were 27.37% and 1603.12% respectively; which however, increased to 28.28% and 1656.29%, in two character combinations respectively; 32.66% and 1913.20%, in three character combinations, respectively; 33.81% and 1980.01%, in four character combinations, respectively; 33.43% and 1957.88%, in five character combinations, respectively. Thus, there was an increase in the genetic gain as well as relative efficiency with inclusion of an additional trait in the character combination.

In six character combinations, the highest relative efficiency of 1983.01% was observed for combination of characters $X_1+X_2+X_3+X_4+X_5+X_6$ (seed yield per plant, days to 50 percent flowering, plant height, number of pods per plant, number of seeds per pod and fat content). Adsul *et al.* (2014), Mori *et al.* (2016) and Kachhadia *et al.* (2014) were also with the similar opinion that an increase in characters resulted in an increase in genetic gain and that the selection indices improve the efficiency that the straight selection for seed yield alone.

The present study also revealed that the method of discriminant function for making selections in plants appears to be the most useful than the straight selection for seed yield alone and hence, due weightage should be given to the important selection indices while making selection for seed yield advancement in fenugreek crop.

6. SUMMARY AND CONCLUSION

The present investigation entitled “**Genetic Divergence and Selection Indices for Yield and its Attributing Traits in Fenugreek [*Trigonella foenum-graecum* L.]**” was conducted during *Rabi*, 2023-24 at Instructional Farm, RCA, Udaipur.

The experimental material, comprised of 25 fenugreek genotypes, was evaluated in Randomized Block Design with three replications. The observations were recorded on five randomly selected competitive plants for each genotype in each replication for plant height (cm), number of branches per plant, number of pods per plant, pod length (cm), number of seeds per pod, biological yield per plant (g), seed yield per plant (g), 1000-seed weight (g), harvest index (%), seed protein content (%) and fat content (%) while days to 50 percent flowering and days to maturity were recorded on whole plot basis. The data so obtained were subjected to statistical analysis. The significant results obtained on field and laboratory studies are briefly summarized as under:

1. The mean sum of squares due to genotypes was found significant for all the characters under study, indicating presence of enough variability among the genotypes for different traits.
2. In general, estimates of phenotypic coefficient of variation (PCV) were slightly higher than their corresponding genotypic coefficient of variation (GCV) indicating a little effect of the environment on the expression of the characters. High value of (GCV) was observed for number of pods per plant, 1000-seed weight, fat content, harvest index, biological yield per plant, and seed yield per plant, whereas a low estimates of genotypic coefficient of variation was observed for days to maturity and days to 50 percent flowering.
3. The highest value of PCV was recorded for number of pods per plant followed by harvest index, biological yield per plant, 1000-seed weight, seed yield per plant and fat content, whereas lowest phenotypic coefficient of variation was recorded for the character days to maturity followed by days to 50 percent flowering.

4. High estimates of heritability were observed for most of the traits and it was noted highest for fat content followed by 1000-seed weight, seed protein content, number of pods per plant, biological yield per plant, and harvest index. However, plant height, days to 50 percent flowering and number of branches per plant exhibited moderate heritability.
5. The high genetic advance was recorded for number of pods per plant followed by plant height and biological yield per plant while the characters number of branches per plant and number of seeds per pod showed a low level of genetic advance.
6. The highest genetic advance as percent of mean (genetic gain) was recorded for number of pods per plant followed by 1000-seed weight, fat content, biological yield per plant and harvest index. All these characters are governed by additive gene action and as such are expected to exhibit improvement for such traits by direct selection in the fenugreek improvement programme. However, days to maturity and number of seeds per pod had a low genetic gain.
7. The higher heritability implied that selection for most of the traits might be effective in this set of genotypes. The high heritability estimates coupled with high genetic gain for number of pods per plant, 1000-seed weight and fat content indicated that all these traits are governed by additive gene action; hence direct selection for these traits may be effective.
8. The correlation of different traits with seed yield per plant was examined both at phenotypic and genotypic levels and the study showed that genotypic correlation coefficient values were higher than the phenotypic correlation coefficient values. The seed yield per plant exhibited a positive and significant correlation with plant height, 1000-seed weight, harvest index and biological yield per plant at both genotypic and phenotypic levels.
9. The genotypic path coefficient analysis of different traits on seed yield per plant revealed that number of seeds per pod exhibited maximum direct positive effect on seed yield per plant followed by days to 50 percent flowering and fat content. Maximum negative direct effect on seed yield per plant was observed for days to maturity and pod length. The residual effect ($R = 0.7591$) indicated that 24.09 percent variability was explained by the traits considered for path study.

10. Twenty-five fenugreek genotypes were classified into seven clusters based on their relative magnitude of D^2 values. Cluster I was the largest one with 18 genotypes followed by cluster II with 2 genotypes and remaining clusters *viz.*, III, IV, V, VI and cluster VII have single genotype. The cluster II had maximum intra-cluster distance followed by cluster I. Maximum inter-cluster distance was observed by cluster IV and VII followed by cluster III and V, cluster V and VII and cluster VI and VII indicating wide diversity between genotypes. The greater the distance between two clusters, wider is the expected genetic diversity. Minimum inter-cluster distance was exhibited by cluster I and VI.
11. Cluster III had genotypes having higher mean values for plant height, number of branches per plant and harvest index. Cluster IV had genotypes having higher mean values for number of pod length, biological yield per plant, seed protein content and fat content. Cluster V had genotypes having higher values days to maturity and number of pods per plant. Cluster VI had genotypes having higher mean values for number of seeds per pod. Cluster VII had genotypes having higher mean values for days to 50 percent flowering, 1000-seed weight and seed yield per plant.
12. The characters *viz.*, number of pods per plant and plant height contributed the most towards the total divergence in the 25 fenugreek genotypes.
13. The results of the present study revealed that the discriminant function method of making selection in plants appeared to be the most useful than the straight selection for seed yield per plant and hence, due weightage should be given to the important selection indices while making selection for yield improvement in fenugreek.
14. Among all the 28 selection indices, the index based on all six characters under study *viz.*, seed yield per plant, days to 50 percent flowering, plant height, number of pods per plant, number of seeds per pod and fat content possessed the highest genetic gain and relative efficiency as compared to straight selection for seed yield per plant. The result thus, indicated that the maximum weightage should be given to these functions while making selection for high yielding genotypes in fenugreek.

15. In the present investigation, genotypes *viz.*, PRM-45, AM-6-2-28, AFg-4, AM-45-20-4, JFg-244 and Hisar Suvana were superior not only in terms of seed yield per plant but also in terms of traits like 1000-seed weight, number of pods per plant, number of seeds per pod, number of branches per plant, pod length, harvest index and biological yield per plant. These diverse genotypes could be used in the future for the genetic improvement of fenugreek.

LITERATURE CITED

- Adsul, H. R. and Monpara, B. A. 2014. Genetic variability and selection indices for improving seed yield in soybean (*Glycine max* L. Merrill). *Electronic Journal of Plant Breeding*, **5**: 807-811.
- Ali Abteu, Y. and Abate, A., 2020. Association of traits in Ethiopian fenugreek (*Trigonella foenum-graecum* L.) genotypes regarding to seed yield by using phenotypic data. *Acta agriculturae Slovenica*, 115/1, 161-169.
- Al-Jibouri, H. A., Miller, P. A. and Robinson, H. F. 1958. Genotypic and environmental variance in upland cotton of interspecific origin. *Agronomy Journal*, **50**: 633-663.
- Anonymous, 2022. Rajasthan Agricultural Statistics at A Glance 2021-2022, Commissionerate of Agriculture, (CSO cell) Rajasthan, Jaipur (GOR), pp: 1-234.
- Anonymous, 2023. Rajasthan Agricultural Statistics at A Glance 2022-2023, Commissionerate of Agriculture, (CSO cell) Rajasthan, Jaipur (GOR), pp: 1-234.
- Asati, J., Desai, P. and Patel, R. K., 2018. Genetic diversity analysis for seed yield and its attributes in Fenugreek (*Trigonella foenum-graecum* L.). *International Journal of Current Microbiology and Applied Sciences*, **7**: 1988-1993.
- Aykroyd, W.R. 1963. The nutritive value of Indian foods and planning for satisfactory diets. ICMR Special Report, Series No. **42**: 1-255.
- Balai, O. P., Singh, D. and Jain, U. K. 2006. Genetic variation and character association among yield and yield related traits in fenugreek. *Indian Journal of Agricultural Research*, **40**: 35-39.
- Bhatt, B., Raghav, M., Jeena, A. S., Agrawal, S. and Gaur, A. K. 2019. Assessment of genetic variability of fenugreek (*Trigonella foenum-graecum* L.) genotypes under Tarai conditions of Uttarakhand. *International Journal of Chemical Studies*, **7**: 484-487.
- Bhatt, B., Raghav, M., Singh, A., Jeena, A. S., Agrawal, S. and Bhardwaj, S. B. 2021. Designing selection criteria by using association studies and estimation of genetic diversity in fenugreek (*Trigonella foenum-graecum* L.) germplasm. *Legume Research: An International Journal*, **44**: LR-4233 (1-8).

- Burton, G. W. 1952. Quantitative Inheritance in Grasses. *Proceeding 6th International Grassland Congress*, **1**: 277-283.
- Burton, G. W. and Devane, D. E. 1953. Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. *Agronomy Journal*, **45**: 478-481.
- Choudhary, M., Gothwal, D. K., Kumawat, K. R., R Kumawat, R., Kumar, O. and Bajya, M., 2022. Cluster and principal component analysis in fenugreek (*Trigonella foenum-graecum* L.) genotypes based on yield and yield related traits. *The Pharma Innovation Journal*, **11**: 1723-1728.
- Dashora, A., Maloo, S. R. and Dashora, L. K. 2011. Variability, correlation and path coefficient analysis in fenugreek (*Trigonella foenum-graecum* L.) under water limited conditions. *Journal of Spices and Aromatic Crops*, **20**: 38-42.
- Debnath, S., Lal, G. M. and Xalxo, B. 2021. Determination of Selection Indices and Path Coefficient Analysis of yield and its contributing characters in chickpea (*Cicer arietinum* L.). *International Journal of Agricultural Science and Research*, **11**: 169-174.
- Dewey, D. R., and K. H. Lu. 1959. A Correlation and path-coefficient analysis of components of crested wheat grass seed production. *Agronomy Journal*, **51**: 515-518.
- Duke, A. J. 1986. Handbook of legumes of world economic importance. New York: Plenum Press. Diversity in exotic fenugreek (*Trigonella foenum-graecum* L.) Germplasm Using Sds-Page Analysis. *Middle East Journal of Agriculture Research*, **6**: 1285-1294.
- Fikreselassie, M., Zeleke, H. and Alemayehu, N. 2012. Genetic variability of Ethiopian fenugreek (*Trigonella foenum-graecum* L.) landraces. *Journal of Plant Breeding and Crop Science*, **4**: 39-48.
- Fisher, R. A. 1954. Statistical methods for research workers. 12th Edition. *Biological Monograph and Manuals*, **5**: 130-131.
- Flammang, A. M., Cifone, M. A., Erexson, G. L. and Stankowski Jr, L. F. 2004. Genotoxicity testing of a fenugreek extract. *Food and chemical toxicology*, **42**, 1769-1775.

- Frayer, J. K. 1930. Chromosome atlas of flowering plant. *Georg Allen and Urwin London*, 519.
- Gaikwad, S. P., Dhumal, S. S., Bhagat, A. A. and Sagbhor, D. A. 2020. Genetic variability in fenugreek genotypes. *Indian Journal of Pure & Applied Bioscience*, **8**: 199-203.
- Gangopadhyay, K. K., Yadav, S. K., Kumar, G., Meena, B. L., Mahajan, R. K., Mishra, S. K. and Sharma, S. K. 2009. Correlation, path-coefficient and genetic diversity pattern in fenugreek. *Indian Journal of Agricultural Science*, **79**: 521-526.
- Garde, Y. A., Chaudhary, A. P., Bhimani, P. C., Modha, K. G., Shrivastava, A., & Varshney, N. (2023). Construction of Selection Indices by using Different Economic Coefficients in Indian Bean [*Lablab purpureus* (L.) Sweet]. *Legume Research*, **46**: 1155-1161.
- Gosset, W. S. 1908. The probable error of a mean. *Biometrika*, **6**: pp. 1-25.
- Gurjar, M., Naruka, I. S. and Shaktawat, R. P. S. 2016. Variability and correlation analysis in fenugreek (*Trigonella foenum-graecum* L.). *Legume Research-An International Journal*, **39**: 459-465.
- Hadiya, G., Sharma, L. K., & Rawat, A. K. 2019. Study of Selection Indices in Chickpea (*Cicer arietinum* L.). *Frontiers in Crop Improvement*, **6** (2): 63.
- Hanson, C. H., Robinson, H. F. and Comstock, R. E. 1956. Biometrical studies on yield in segregating generation in Korean lespedeza. *Agronomy Journal*, **48**: 268-272.
- Hazel, L. N. and Lush, J. L. 1943. The efficiency of three methods of selection. *Journal of Heredity*, **33**: 393-399.
- Hosamath, J. V., Hegde, R. V., Venugopal, C. K., Vijayakumar, A. G. and Hegde, M. G. 2017. Studies on Genetic variability, heritability and genetic advance in fenugreek (*Trigonella foenum-graecum* L.). *International Journal of Current Microbiology and Applied Sciences*, **6**: 4020-4036.
- Jain, A., Singh, B., Solanki, R. K., Saxena, S. N., Kakani, R. K., 2013. Genetic variability and character association in fenugreek (*Trigonella foenum graecum* L.). *International Journal of Seed Spices*, **3**: 22-28.

- Johnson, H. W., Robinson, H. F. and Comstock, R. E. 1955. Estimates of genetic and environmental variability in soybean. *Agronomy Journal*, **47**: 14-318.
- Kachhadia, V. H., Baraskar, V. V., Vachhani, J. H., Barad, H. R., Patel, M. B., & Darwankar, M. S. 2014. Selection indices for improvement of seed yield in Soybean [*Glycine max* (L.) Merrill]. *Electronic Journal of Plant Breeding*, **5**: 268-271.
- Kole, P. C. and Goswami, T. 2015. Genetic divergence in fenugreek grown under sub-humid sub-tropical red lateritic belt of eastern India. *International Journal of Bio-resource, Environment and Agricultural Sciences*, **1**: 97-102.
- Krishnaveni, B., Irene Vethamoni, P., Senthamizh Selvi, B., and Raveendran, M. 2021. Studies on genetic variability, correlation and path coefficient analysis in Fenugreek *Trigonella foenum graecum* L. genotypes. *Electronic Journal of Plant Breeding*, **12**: 835-840.
- Kumar, A., Pandey, V. P., Maurya, V. K., Tiwari, D. and Sriom. 2018. Genetic variability, heritability & genetic advance in fenugreek (*Trigonella foenum-graecum* L.). *International Journal of Chemical Studies*, **6**: 153-156.
- Kumar, A., Pandey, V. P., Maurya, V. K., Tiwari, D. and Yadav, G. C. 2018. Correlation coefficient and path analysis for yield and its component traits in Fenugreek (*Trigonella foenum-graecum* L.). *Quarterly Research Journal of Plant & Animal Sciences/Bhartiya Krishi Anusandhan Patrika*, **33**: 209-211.
- Kumar, S., Ram, C. N., Nath, S., Kumar, S., Kumari, M. and Singh, V., 2020. Studies on genetic variability, heritability and genetic advances in fenugreek (*Trigonella foenum-graecum* L.). *Journal of Pharmacognosy and Phytochemistry*, **9**: 1358-1361.
- Kumari, N., Dashora A., Urmila., Regar, H., Mariyam, A., Sharma, A., and Choudhary, S., 2022. Assessment of Genetic Variability, Heritability and Genetic Advance in Fenugreek [*Trigonella foenum-graecum* L.] Genotypes. *Frontiers in Crop Improvement*, **10**: 1544-1546.
- Lenka, D. and Misra, B. 1973. Path co-efficient analysis of yield in rice varieties. *Indian Journal of Agricultural Science*, **43**: 376-379.
- Lindner, R. C. (1944). Rapid analytical methods for some of the more common inorganic constituents of plant tissues. *Plant physiology*, **19**, 76.

- Lodhi, P. S., Singh, P. P., Naruka, I. S., Kushwah, S. S. and Singh, A. K., 2015. Genetic variability, correlation and path analysis in fenugreek (*Trigonella foenum-graecum* L.). *Indian Journal of Horticulture*, **72**: 429-433.
- Mahalanobis, P. C. 1936. On the general distance in statistics. *Proceeding of Nation Academy of Science (India)*, **12**: 49-55.
- Maloo, A. D. and Dashora, L. K. 2011. Variability, correlation and path coefficient analysis in fenugreek (*Trigonella foenum-graecum* L.) under water limited conditions. *Journal of Spices and Aromatic Crops*, **20**: 38- 42.
- Mamatha, N. C., Tehlan, S. K., Srikanth, M., Ravikumar, T., Batra, V. K., Reddy, K. P. and Kumar, M. 2017. Variability studies for yield and its attributing traits in fenugreek (*Trigonella foenum-graecum* L.) genotypes. *International Journal of Pure & Applied Bioscience*, **5**: 1075-1079.
- Maurya, H. K., Mishra, D. P., Singh, H. and Singh, A. V. 2021. Studies on genetic variability in fenugreek (*Trigonella foenum-graecum* L.). *The Pharma Innovation*, **10**: 1893-1897.
- Meena, R. S., Choudhary, S., Verma, A. K., Meena, N. K. and Mali, S. C. 2021. Estimates of genetic variability, divergence, correlation and path coefficient for morphological traits in fenugreek (*Trigonella foenum-graecum* L.) genotypes. *Legume Research: An International Journal*, **44**.
- Meena, R. S., Kakani, R. K., Anwer, M. M., Panwar, A., Choudhary, S. and Meena, S. R. 2011. Variability studies in fenugreek (*Trigonella foenum-graecum* L.). *International Journal of Seed Spices*, **1**: 44-46.
- Miraj, M., Durrishahwar, S., Anjum, M. M., Ali, N. and Islam, S. 2017. Assessment of genetic diversity in exotic fenugreek (*Trigonella foenum-graecum* L.) Germplasm Using Sds-Page Analysis. *Middle East Journal of Agriculture Research*, **6**: 1285-1294.
- Mishra, A., Dodiya N. S., Dashora A., Meena B. S., Deora N. S. and Dave Mayur 2021. Assessment of genetic variability, heritability and genetic advance in Fenugreek (*Trigonella foenum-graecum* L.). *The Pharma Innovation Journal* 2021, **10**: 1038-1040.

- Mori, K., Sharma, L. K., Mori, V., & Kulkarni, G. U. 2016. Study of variability and association analysis in fenugreek (*Trigonella foenum-Graecum* L.) under timely and late sown conditions. *Progressive Research – An International Journal*, **10**: 567-569.
- Naik, A., Akhtar, S. and Pandey, V. P. 2012. Variability in growth, yield attributes and yields in different genotypes of fenugreek (*Trigonella foenum-graecum* L.) grown during winter season. *Environment and Ecology*, **30**: 1366-1368.
- Naik, A., Akhtar, S., Bhuniam, P. and Pandey, V. P. 2011. Correlation coefficient and path analysis studies in fenugreek (*Trigonella foenum-graecum* L.). *Environment and Ecology*, **29**: 1546-1549.
- Panse, V. G., and Sukhatme, P. V. 1985. Statistical Methods for Agricultural Workers, ICAR New Delhi.
- Panwar, A., Sharma, Y. K., Meena, R. S., Solanki, R. K., Aishwath, O. P., Singh, R. and Choudhary, S. 2018. Genetic variability, association studies and genetic divergence in Indian fenugreek (*Trigonella foenum-graecum* L.) varieties. *Legume Research-An International Journal*, **41**: 816-821.
- Parmar, B. R., Monpara, B. A. and Bhut, N. M. 2022 Selection indices in F3 generation of chickpea (*Cicer arietinum* L.). *Pharma Innovation*; **11**: 1834-1836.
- Patahk, A. R., Patel, A. I., Joshi, H. K. and Patel, D. A. 2014. Genetic divergence in fenugreek (*Trigonella foenum-graecum* L.) germplasm. *Trends in Biosciences*, **7**: 295-297.
- Patahk, A. R., Patel, A. I., Joshi, H. K. and Patel, D. A. 2014. Genetic variability, correlation and path coefficient analysis in fenugreek (*Trigonella foenum-graecum* L.). *Trends in Biosciences*, **7**: 234-237.
- Patel, D. K., A. M. Patel and Sundesha, D. L. 2021. Genetic variability, heritability and genetic advance for seed yield in Fenugreek [*Trigonella foenum-graecum* (L.)]. *International Journal of Current Microbiology and Applied Sciences*, **10**: 3233-3237.
- Phom, M. Alen, Kanaujia, S. P. and Chaturvedi, H. P. 2014. Performance of fenugreek genotypes under foot hill condition of Nagaland. *Annals of Horticulture*, **7**: 115-118.

- Prakash, S., Pandey, V. P., Gautam, D. K., Bhargava, A. K. and Nath, T. 2020. Evaluation of germplasm genetic variability, heritability and genetic advance in fenugreek (*Trigonella foenum-graecum* L.). *International Journal of Current Microbiology and Applied Sciences*, **9**: 303-308.
- Pushpa, T. N., Chandregowda, M., Srikantaprasad, D. and Gowda, A.P., 2012. Evaluation of fenugreek (*Trigonella foenum-graecum* L.) genotypes for growth and seed yield. *CropResearch*, **43**: 238-244.
- Rao, C. H. 1952. Advanced Statistical Methods in Biometric Research. John Wiley & Sons, New York.
- Rao, P. U. and Sharma, R. D. 1987. An evaluation of protein quality of fenugreek seed (*Trigonella foenum-graecum* L.) and their supplementary effect. *Food Chemistry*, **24**: 1-9.
- Robinson, H. F., Comstock, R. E. and Harvey, P. H. 1951. Genotypic and phenotypic correlations in corn and their implications in selection. *Agronomy Journal*, **43**: 282-287.
- Satish Kumar Gautam, Ram, C. N., Rao, O. P. and Shiva Nath. 2021. Appraisal studies on genetic variability, heritability and genetic advance in fenugreek (*Trigonella foenum-graecum* L.). *Pharma Innovation*, **10**: 1573-1576.
- Sindhu, A., Tehlan, S. K. and Chaudhury, A. (2018). Effect of morphological trait variance on plant yield in different *Trigonella foenum-graecum* L. varieties. *Australian Journal of Crop Science*, **12**: 1-10.
- Singh, A., Pandey, V. P., Singh, A. P., Singh, A. K., Yadav, S. and Verma, M. 2019. To estimate genetic variability analysis among different characters in germplasm of fenugreek [*Trigonella foenum-graecum* L.]. *Journal of Pharmacognosy and Phytochemistry*, **8**: 1073-1076.
- Singh, J., 2014. Correlation coefficient of component characters with seed yield and their effect in path analysis in fenugreek grown under six environmental conditions. *Global Journal of Wood Science, Forestry and Wildlife*, **2**: 034-037.
- Singh, N. and Thamburaj, S. 2003. *Textbook of Vegetables, Tuber crops and Spices*, ICAR, New Delhi.

- Singh, P. P., Gujar, M., Naruka, I. S., 2016. Association and path analysis in fenugreek (*Trigonella foenum-graecum* L.). *The Indian Journal of Agricultural Sciences*, **7**: 951-955.
- Singh, P. S., Nair, B., Jain, P. K., Sengupta, S. K. 2013. Correlation studies in fenugreek (*Trigonella foenum-graecum* L.) *African Journal of Agricultural Research*, **8**: 4773-4779.
- Singh, S., & Singh, B. 2022. Character Association and Path Coefficient Analysis of Certain Biometrical Traits among Fenugreek Genotypes under Different Environmental Conditions. *Agricultural Science Digest-A Research Journal*, **42**: 420-425.
- Singh A. K., Singh D. R., Singh A., Maurya J. K., Pandey V. P. and Sriom 2019. Studies on character association and path analysis of yield with important yield contributing traits in Fenugreek (*Trigonella foenum-graecum* L.). *Journal of Pharmacognosy and Phytochemistry* 2019, **8**: 4616-4619.
- Sinskaja, E. 1961. Flora of the cultivated plants of the U.S.S.R. XIII. In Perennial leguminous plants. Part I: Medicago, sweet clover, fenugreek. Jerusalem: Israel Program for Scientific Translations.
- Smith, H. F. 1936. A discriminant function for plant selection. *Annals of Eugenics*, **7**: 240-250.
- Srinivasan, K. 2006. Fenugreek (*Trigonella foenum-graecum* L.) A review of health beneficial physiological effects. *Food Reviews International*, **2**: 203-224.
- Sulochana, J., Masuthi, J. D., Naika, B. N., M., Tatagar, M. H. and Koulagi, S., 2018. Estimation of genetic diversity in fenugreek (*Trigonella foenum-graceum* L.) genotypes for productivity traits. *International journal of chemical studies*, **6**: 2701-2703.
- Tariyal, Y. S., Bisht, S. S., Pant, S. C. and Chauhan, R. S. 2017. Study of genetic divergence in fenugreek (*Trigonella foenum-graecum* L.). *Journal of Pharmacognosy and Phytochemistry*, **6**: 1551-1552.
- Upadhyay, R., Naidu, A. K. and Dhakhariya, T. 2020. Studies on genetic variability among yield attributing traits of fenugreek genotypes. *International Journal of Chemical Studies*, **8**: 1821-1825.

- Verma, P., Solanki, R. K., Dhasora, A. and Kakani, R. K. 2016. Genetic variability in Fenugreek (*Trigonella foenum-graecum* L.) as expressed under South Eastern region of Rajasthan State. *International Journal of Seed Spices*, **6**: 93-95.
- Wojo, A. A., Alamerew, S., Nebiyu, A. and Menamo, T. 2016. Genotype and phenotype variability studies in fenugreek (*Trigonella foenum-graecum* L.) accessions in Kaffa Zone, South West Ethiopia. *Journal of Spices and Aromatic Crops*, **25**: 159-168.
- Wright, S. 1921. Correlation and causation. *Journal of Agricultural Research*, **20**: 555-586.
- Yadav, P., Tehlan, S. K. and Deswal, S. 2018. Assessment of genetic divergence in fenugreek (*Trigonella foenum-graecum* L.) based on biological characters. *Journal of Pharmacognosy and Phytochemistry*, **7**: 1257-1260.
- Yadav, P., Tehlan, S. K. and Kumar, M., 2018. Genetic variability and association analysis for seed yield and its components in fenugreek (*Trigonella foenum-graecum* L.). *Indian Journal of Genetics and Plant Breeding*, **78**: 275-278.
- Yadav, T. C., Meena, R. S. and Dhakar, L. 2018. Genetic variability analysis in Fenugreek (*Trigonella foenum-graecum* L.) genotypes. *International Journal of Current Microbiology and Applied Sciences*, **7**: 2998-3003.

Genetic Divergence and Selection Indices for Yield and its Attributing Traits in Fenugreek (*Trigonella foenum-graecum* L.)

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ABSTRACT

The Present investigation entitled “**Genetic Divergence and Selection Indices for Yield and its Attributing Traits in Fenugreek (*Trigonella foenum-graecum* L.)**” was carried out using 25 fenugreek genotypes at Instructional Farm, Rajasthan College of Agriculture, Udaipur during *Rabi*, 2023-24. The genotypes were evaluated in Randomized Block Design with three replications.

The observations were recorded on five randomly selected competitive plants for each genotype for the characters *viz.*, plant height (cm), number of branches per plants, number of pods per plant, pod length (cm), number of seeds per pod, biological yield per plant (g), seed yield per plant (g), 1000-seed weight (g), harvest index (%), seed protein content (%) and fat content (%) while for days to 50 percent flowering and days to maturity, the observations were noted on plot basis.

Analysis of variance demonstrated a significant difference among genotypes for all the traits showing that the experimental materials under investigation have an ample amount of variability.

High estimates of Genotypic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV) were recorded for number of pods per plant, 1000-seed weight, harvest index, biological yield per plant and seed yield per plant indicating the presence of genetic variability for these traits.

High heritability coupled with high genetic gain was observed for the traits *viz.*, number of pods per plant, 1000 seed weight and fat content indicating that all these traits are regulated by additive gene action and the direct selection of these traits is expected to show improvement.

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The association study revealed that the seed yield per plant exhibited a positive and significant correlation with plant height, 1000-seed weight, harvest index and biological yield per plant at both genotypic and phenotypic levels.

Path coefficient analysis showed that the maximum positive direct effect on seed yield per plant was exerted by number of seeds per pod, days to 50 percent flowering and fat content. So, these characters can be considered as selection criteria for improving the seed yield.

Based on multivariate hierarchical cluster analysis 25 genotypes were classified into seven clusters the maximum numbers of genotypes were grouped into cluster I which had 18 genotypes followed by cluster II having 2 genotypes while the clusters *viz.*, III, IV, V, VI, and VII had single genotype. The cluster II had maximum intra-cluster distance followed by cluster I. Maximum inter-cluster distance was observed by cluster IV and VII, followed by cluster III and V, cluster V and VII and cluster VI and VII indicating wide diversity between genotypes and these genotypes could be used in the future for fenugreek crop improvement programme.

The characters *viz.*, number of pods per plant and plant height contributed the most towards the total divergence in the 25 fenugreek genotypes.

Among all the 28 selection indices, the index based on all six characters under study *viz.*, seed yield per plant, days to 50 percent flowering, plant height, number of pods per plant, number of seeds per pod and fat content possessed the highest genetic gain and relative efficiency as compared to straight selection for seed yield per plant. The result thus, indicated that the maximum weightage should be given to these functions while making selection for high yielding genotypes in fenugreek.

In the present investigation, genotypes *viz.*, PRM-45, AM-6-2-28, AFg-4, AM-45-20-4, JFg-244 and Hisar Suvarna were superior not only in terms of seed yield per plant but also in terms of traits like 1000-seed weight, number of pods per plant, number of seeds per pod, number of branches per plant, pod length, harvest index and biological yield per plant. These diverse genotypes could be used in the future for the genetic improvement of fenugreek.

eFkh ¼fvxkuyk Qk,ue&xide ,y-½ e mit ,o bld x.kk d fy,
vkuof'kd fopyu vkj p;u lpdkd

fgek'kh >kykj^{*}
शोधकर्ता

Mk- vHk; n'kkjk^{**}
मुख्य सलाहकार

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वर्तमान अध्ययन ^MeFkh ¼Vkbxkuyk Qkue&xide ,y-½ e mit vkj mld: x.kdkjh x.kk d fy, vkuof'kd fopyu vkj p;u lpdkd^{**} शीर्षक के अन्तर्गत मेथी के 25 समपैत्रकों का रबी, 2023–24 के दौरान निर्देशात्मक प्रक्षेत्र, राजस्थान कृषि महाविद्यालय, उदयपुर में किया गया।

प्रत्येक समपैत्रको का मूल्यांकन यादृच्छिक खण्डक अभिकल्पना में तीन प्रतिकृतिओं के साथ सम्पन्न किया गया था।

प्रत्येक समपैत्रक के लिए पांच यादृच्छिक रूप से चयनित प्रतिस्पर्धी पौधों पर पौधे की ऊंचाई (सेमी), प्रति पौधे शाखाओं की संख्या, प्रति पौधे फली की संख्या, फली की लंबाई (सेमी), प्रति फली बीज की संख्या, जैविक प्रति पौधा उपज (ग्राम), प्रति पौधा बीज उपज (ग्राम), 1000–बीज वजन (ग्राम), फसल सूचकांक (प्रतिशत), बीज प्रोटीन सामग्री और वसा सामग्री (प्रतिशत) जबकि 50 प्रतिशत पुष्पावस्था एवं परिपक्वता में लगे दिन, लक्षणों का अवलोकन सम्पूर्ण प्रक्षेत्र भूखण्ड के आधार पर किया गया।

विचरण के विश्लेषण से ज्ञात हुआ कि समपैत्रकों में प्रायः सभी लक्षणों के लिए अर्थपूर्ण अन्तर है जो यह दर्शाता है कि जांच के तहत प्रयोगात्मक सामग्री में पर्याप्त मात्रा में विविधता है।

प्रति पौधा फलियों की संख्या, 1000–बीज वजन, फसल सूचकांक, प्रति पौधा जैविक उपज और प्रति पौधा बीज उपज के लिए जीन प्ररूपी गुणांक के भिन्नता का प्रतिशत (जीसीवी) और लक्षण प्ररूपी गुणांक के भिन्नता का प्रतिशत (पीसीवी) के उच्च अनुमानों ने इन लक्षणों के लिए व्यापक आनुवंशिक विविधता की उपस्थिति को इंगित किया है।

उच्च आनुवंशिक लाभ के साथ युग्मित उच्च आनुवंशिकता के अनुमानों का अवसादन मूल्य, प्रति पौधे फलियों की संख्या, 1000–बीज का वजन और वसा की मात्रा जैसे लक्षणों के लिए अधिक पाया गया जो कि यह दर्शाता है कि ये सभी लक्षण योज्य जीन क्रिया द्वारा नियंत्रित होते हैं और प्रत्यक्ष चयन की उम्मीद ऐसे लक्षणों में सुधार के लिए की जाती है।

* शोधकर्ता, आनुवंशिकी एवं पादप प्रजनन विभाग, राजस्थान कृषि महाविद्यालय, महाराणा प्रताप कृषि एवं प्रौद्योगिकी विश्वविद्यालय, उदयपुर

** सहायक आचार्य, आनुवंशिकी एवं पादप प्रजनन विभाग, राजस्थान कृषि महाविद्यालय, महाराणा प्रताप कृषि एवं प्रौद्योगिकी विश्वविद्यालय, उदयपुर

सहसंबंध विश्लेषण के अध्ययन से ज्ञात हुआ कि प्रति पौधा बीज उपज का प्रति पौधे जैविक उपज द्वारा पौधे की ऊँचाई, 1000-बीज वजन, फसल सूचकांक और प्रति पौधा जैविक उपज का जीन प्ररूपी और लक्षण प्ररूपी दोनों स्तरों पर सकारात्मक और सार्थक सहसंबंध प्रदर्शित किया।

पथ गुणांक विश्लेषण से पता चला कि प्रति पौधे बीज उपज पर अधिकतम सकारात्मक प्रत्यक्ष प्रभाव प्रति फली में बीज की संख्या, 50 प्रतिशत पुष्पावस्था और वसा की मात्रा ने उच्च प्रत्यक्ष सकारात्मक प्रभाव दिखाया। इसलिए, इन लक्षणों को बीज उपज में सुधार के लिए चयन मानदंड माना जा सकता है।

बहुभिन्नरूपी पदानुक्रमित समूह विश्लेषण के आधार पर मेथी के 25 समपैत्रकों को 7 समूहों में बांटा गया। समूह विश्लेषण के आधार पर समपैत्रकों की अधिकतम संख्या को समूह I में समूहीकृत किया गया था, जिसमें 18 समपैत्रक थे, इसके बाद समूह II में 2 समपैत्रक थे, जबकि समूह अर्थात्, III, IV, V, VI और VII में एक-एक समपैत्रक थे। समूह II के बाद समूह I में अधिकतम अंतरा-समूह दूरी दर्ज की गई थी। समूह IV और VII, समूह III और V, समूह V और VII एवं समूह VI और VII के द्वारा प्रदर्शित अधिकतम अन्तर-समूह दूरी ने संकेत दिया कि इन समूहों से जुड़े समपैत्रकों का उपयोग बीज की उपज में सुधार के लिए मेथी के संकरण कार्यक्रम के लिए किया जा सकता है।

25 मेथी समपैत्रकों में कुल विचलन में लक्षण जैसे, प्रति पौधा फलियों की संख्या और पौधे की ऊँचाई ने सबसे अधिक योगदान दिया।

सभी 28 चयन सूचकांकों में से, अध्ययन के तहत सभी छह लक्षणों पर आधारित सूचकांक, प्रति पौधा बीज उपज, 50 प्रतिशत पुष्पावस्था, पौधे की ऊँचाई, प्रति पौधे फलियों की संख्या, प्रति फली में बीजों की संख्या और वसा की मात्रा शामिल किये गये थे। प्रति पौधा बीज उपज के लिए सीधे चयन की तुलना में उच्चतम आनुवंशिक लाभ और सापेक्ष दक्षता थी। इस प्रकार, परिणाम से संकेत मिलता है कि मेथी में उच्च उपज देने वाले समपैत्रकों का चयन करते समय इन लक्षणों को अधिकतम महत्व दिया जाना चाहिए।

वर्तमान शोध में, समपैत्रक जैसे, पी.आर.एम-45, ए.एम-6-2-28, ए.एफजी.-4, ए.एम-45-20-4, जे.एफजी.-244 और हिसार सुवर्णा न केवल प्रति पौधा बीज उपज के संदर्भ, अपितु 1000-बीज वजन, प्रति पौधा फलियों की संख्या, प्रति फली बीजों की संख्या, प्रति पौधा शाखाओं की संख्या, फली की लंबाई, फसल सूचकांक और प्रति पौधा जैविक उपज जैसे लक्षणों के संदर्भ में भी बेहतर थे। इन विशिष्ट समपैत्रकों का उपयोग भविष्य में मेथी के आनुवंशिक सुधार के लिए किया जा सकता है।

APPENDIX-I
Mean weekly data on meteorological parameters during the crop growth
period *Rabi* 2023-24

Std. week	Period	Temperature (°C)		Relative humidity (%)		Wind velocity (kmph)	Sunshine (Hrs)	Rain (mm)	Evap. (mm)
		Max.	Min.	Max.	Min.				
40	1 Oct-7 Oct	34.4	16.3	73.1	37.1	2.5	8.2	0.0	3.3
41	8 Oct-14 Oct	33.6	16.2	68.4	34.7	3.4	8.1	0.0	3.3
42	15 Oct-21 Oct	32.6	16.5	72.4	34.6	3.1	8.0	0.0	3.0
43	22 Oct-28 Oct	32.3	14.1	62.6	26.4	2.2	7.7	0.2	2.9
44	29 Oct-4 Nov	32.4	14.5	67.9	26.3	1.9	8.3	0.0	3.1
45	5 Nov-11 Nov	32.4	14.3	68.7	29.1	2.2	6.3	0.0	2.2
46	12 Nov-18 Nov	28.8	10.7	66.1	37.4	1.5	6.2	0.0	2.4
47	19 Nov-25 Nov	28.6	10.5	68.3	35.3	2.3	8.3	0.0	3.0
48	26 Nov-2 Dec	22.6	11.6	85.7	71.1	4.7	2.9	35.8	2.0
49	3 Dec-9 Dec	22.8	11.6	85.9	61.4	1.9	2.5	15.0	1.5
50	10 Dec-16 Dec	25.8	8.3	84.7	38.9	1.1	7.4	0.0	2.3
51	17 Dec-23 Dec	25.0	6.5	76.0	29.7	1.5	8.0	0.0	2.4
52	24 Dec-31 Dec	26.1	8.1	82.8	45.1	1.3	7.1	0.0	2.0
1	1 Jan-7 Jan	23.3	6.1	91.7	43.7	2.3	6.1	0.0	1.3
2	8 Jan-14 Jan	25.1	7.1	84.6	39.7	2.9	7.3	0.0	1.9
3	15 Jan-21 Jan	25.6	6.1	79.9	34.0	1.6	8.4	0.0	2.2
4	22 Jan-28 Jan	25.7	4.8	79.6	30.7	2.9	8.5	0.0	2.3
5	29 Jan- 4 Feb	27.7	9.9	81.3	35.1	1.7	6.0	0.0	2.3
6	5 Feb-11 Feb	25.5	8.3	73.4	35.4	3.3	5.8	0.0	2.4
7	12 Feb - 18 Feb	26.4	7.4	76.4	30.4	2.0	6.2	0.0	2.4
8	19 Feb -25 Feb	28.4	9.0	63.7	25.1	4.5	8.6	0.0	3.4
9	26 Feb - 4 Mar	27.8	11.1	57.9	28.4	3.6	6.4	0.0	3.3
10	5 Mar -11 Mar	28.8	9.0	47.1	24.1	2.7	8.0	0.0	4.7
11	12 Mar - 18 Mar	31.5	11.8	55.6	19.0	3.4	8.1	0.0	4.1
12	19 Mar - 25 Mar	33.6	14.7	53.7	19.9	2.7	7.6	0.0	5.2
13	26 Mar - 1 Apr	35.9	18.4	52.7	21.3	4.0	8.3	0.0	8.4
14	2 Apr- 8 Apr	34.3	20.1	43.6	19.7	4.1	4.7	0.8	8.9
15	9 Apr- 15 Apr	35.8	19.7	48.6	24.6	3.7	4.1	0.3	7.5

APPENDIX-II

Estimation of Protein Content by Micro Kjeldahl's Method, Linder (1944)

Principle

Samples are digested with H_2SO_4 and then with H_2O_2 till it become colorless. The intensity of the color developed by Nessler's reagent in the presence of sodium hydroxide (NaOH) and sodium silicate (Na_2SiO_3) is measured on a spectrophotometer at 420- 650 nm. (For more sensitivity, shorter wavelength should be taken).

Procedure

- Put 0.1 g (100 mg) well- ground and dried seed sample into a 100 ml dry Kjeldahl's flask.
- Add 2 ml of concentrated H_2SO_4 to the Kjeldahl's flask, mix the contents of the flasks place on the digestion assembly (hotplate) and heat it till the sample is digested (for 1:30 hour).
- Cool the flask and add 0.5 ml (8- 10 drops) of 30% H_2O_2 and again heat the contents till it become clear and colorless.
- Transfer the digested contents of Kjeldahl's flask into 100 ml of volumetric flask by washing it 2-3 times with distilled water and make the volume.
- Take 5 ml of digested solution into 50 ml volumetric flask and add few ml distilled water. Then add 2ml of 10% sodium hydroxide and 1 ml of 10% sodium silicate solutions respectively and then add some distilled water.
- Mix the contents and 1.6 ml of Nessler's reagent to the flask while shaking. After this, make its volume and allow 10 minutes for color development.
- Run a control with distilled water by the same procedure.
- Take the reading of standard working solutions by adjusting the spectrophotometer at wave length of 420-650 nm. (In this experiment readings were taken at 420 nm)
- Plot the concentration of N on X- axis and the spectrophotometer reading on Y- axis and prepare a standard curve.
- Now take the reading of plant sample and calculate the ppm N with the help of standard curve.

Standard Curve

Dissolve 0.118 g of AR grade in water and make the volume one litre in volumetric flask. This solution contains 25 ppm N. For working standards, take 1, 2, 3, 4, 5, 6, 7, 8 ml of 25 ppm N solution in 50 ml volumetric flasks. Add 2 ml 10% NaOH and 1 ml 10% sodium silicate solution in 50 ml volumetric flasks. Add some water and shake the contents. Now add 1.6 ml Nessler's reagent slowly drop while shaking and make the volume. The flasks will contain 0.5, 1.0, 1.5, 2.0, 2.5, 3.0, 3.5 and 4.0 ppm N, respectively.

Estimation of Protein

Determine the nitrogen content using the standard curve. Then calculate the crude protein contents by multiplying the N contents with 6.25.

APPENDIX–III

Estimation of Fat Content by Soxhlet Extraction Method

Methanol (99% purity), n-hexane (99% purity), 2, 2-diphenylpicrylhydrazyl (DPPH), sodium carbonate, Folin-Ciocateu reagent and gallic acid (GA) were obtained from Sigma Aldrich (M) Sdn. Bhd, Selangore, Malaysia. All chemicals used for the extraction process were analytical grade with high purity.

Extraction Process

A 100 g of crushed fenugreek seed was extracted using hexane (600 mL) and a Soxhlet extractor for 3 h at (65-70 C). Then, the mixture of solvent-oil was filtered through a No.1 paper filter (Whatman). The extract was transferred into a round flask and solvent was evaporated using rotary evaporator, (Rotavapor R-200, Büchi, Germany) at 40 C. Finally, the oil extract was stored at 4°C to prevent degradation of the compounds for further analysis. The yield of extraction was calculated using following formula:

$$\text{Extraction yield} \left(\frac{v}{w} \% \right) = \frac{\text{Amount of oil extracted (ml)}}{\text{Weight of dry sample used (g)}} \times 100$$

APPENDIX-IV

Mean values for Days to 50 percent flowering, Days to maturity, Plant height (cm), Number branches per plant, Number of pods per plant, Pod length (cm) and Number of seeds per pod

S. No.	Genotype	Days to 50 percent flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of pods per plant	Pod length (cm)	Number of seeds per pod
1.	AM-31-30-5	48.33	120.00	95.11	4.47	67.57	10.40	18.67
2.	AM-45-20-4	51.00	121.00	94.11	4.53	65.80	11.40	16.73
3.	AM-6-1-27	47.00	120.33	89.00	4.47	61.73	9.73	16.33
4.	AM-6-2-28	46.33	120.33	91.67	4.30	62.53	9.33	17.20
5.	Afg-3-300-160	50.00	121.00	94.78	3.97	57.61	9.80	17.53
6.	Afg-3-350-273	48.33	121.67	83.00	4.60	54.33	9.07	18.80
7.	Afg-3-350-48	46.67	123.33	93.22	4.67	62.93	11.80	17.46
8.	Afg-1	51.00	123.67	86.89	4.13	72.13	11.00	19.89
9.	Afg-2	50.67	122.67	86.55	4.67	77.40	10.40	17.53
10.	Afg-3	50.67	121.33	86.78	4.87	83.13	10.60	18.67
11.	Afg-4	50.00	122.67	97.56	4.93	84.60	10.80	17.13
12.	Afg-5	48.67	121.33	99.78	4.33	79.53	10.53	18.53
13.	IC-397506	49.67	121.00	85.33	5.33	101.00	9.93	17.47
14.	RMt-354	49.67	122.67	88.22	4.60	75.00	10.80	18.33
15.	RMt-303	48.67	121.33	75.00	4.07	55.60	10.87	17.67
16.	RMt-143	49.67	121.00	81.56	4.73	73.40	10.20	16.80
17.	RMt-361	48.67	122.00	79.33	4.20	62.60	10.53	18.00
18.	RMt-351	49.67	123.00	79.00	4.20	54.53	10.33	18.00
19.	RMt-1	49.33	123.33	81.44	4.80	66.93	10.53	17.47
20.	RMt-305	45.67	123.33	63.89	4.20	65.73	10.20	18.80
21.	PRM-45	49.67	123.33	86.67	4.63	87.80	11.07	18.33
22.	Hisar suvarna	48.33	121.00	89.33	5.13	108.27	9.87	16.87
23.	Hisar sonali	49.67	122.67	88.55	5.07	96.40	10.60	18.33
24.	Pant Ragini	49.33	124.00	82.33	4.27	90.60	8.93	17.20
25.	JFg-244	51.00	121.00	93.33	3.53	80.97	9.33	17.20
	GM	49.11	121.96	86.90	4.51	73.93	10.32	17.80
	Min	45.67	120	63.89	3.53	54.33	8.93	16.33
	Max	51	124	99.78	5.33	108.27	11.8	19.89
	SEM±	0.69	0.82	3.56	0.20	3.53	0.41	0.60
	CD(5%)	1.97	2.33	10.13	0.56	10.04	1.16	1.71
	CD(1%)	2.63	3.10	13.52	0.74	13.40	1.55	2.28
	CV(%)	2.45	1.16	7.10	7.54	8.27	6.86	5.86

APPENDIX-V

Mean values for 1000-seed weight (g), Biological yield per plant (g), Seed yield per plant (g), Harvest index (%), Seed protein content (%) and Fat content (%)

S. No.	Genotype	1000-seed weight (g)	Biological yield per plant (g)	Seed yield per plant (g)	Harvest index (%)	Seed protein content (%)	Fat content (%)
1.	AM-31-30-5	12.48	38.50	8.11	21.02	26.04	4.95
2.	AM-45-20-4	13.43	37.33	8.31	22.24	22.36	4.36
3.	AM-6-1-27	10.50	33.57	6.99	20.85	26.30	4.12
4.	AM-6-2-28	13.08	32.03	8.29	25.89	25.38	4.73
5.	Afg-3-300-160	7.98	30.03	7.69	25.84	23.09	6.33
6.	Afg-3-350-273	8.73	34.40	6.97	20.20	24.51	4.54
7.	Afg-3-350-48	9.98	40.03	8.10	20.19	25.39	6.09
8.	Afg-1	11.61	25.87	7.97	30.86	25.25	4.15
9.	Afg-2	10.03	27.93	6.70	24.15	22.61	4.53
10.	Afg-3	12.08	33.53	7.97	23.74	23.05	5.77
11.	Afg-4	11.28	36.63	11.27	30.80	22.05	5.72
12.	Afg-5	11.51	27.77	8.31	30.03	20.81	4.89
13.	IC-397506	12.76	34.33	8.11	23.58	23.00	4.79
14.	RMt-354	8.16	32.43	6.71	20.68	21.34	4.04
15.	RMt-303	10.92	27.87	8.17	29.29	20.54	5.65
16.	RMt-143	8.11	24.77	7.21	29.36	25.05	4.82
17.	RMt-361	10.56	27.80	7.51	27.09	25.31	5.10
18.	RMt-351	9.32	25.97	7.83	30.43	25.25	3.29
19.	RMt-1	10.48	32.67	7.53	22.99	25.71	4.47
20.	RMt-305	9.85	23.53	7.24	30.74	25.25	4.05
21.	PRM-45	13.57	34.50	8.43	24.54	25.22	5.19
22.	Hisar suvarna	13.17	33.93	8.44	24.88	24.41	5.08
23.	Hisar sonali	10.90	27.87	7.97	28.67	22.96	4.68
24.	Pant Ragini	12.30	26.43	8.04	30.40	21.99	5.42
25.	JFg-244	12.37	36.73	11.31	30.85	23.14	4.32
	GM	11.01	31.46	8.05	25.97	23.84	4.84
	Min	7.98	23.53	6.7	20.19	20.54	3.29
	Max	13.57	40.03	11.31	30.86	26.3	6.33
	SEM±	0.23	1.35	0.43	1.31	0.28	0.04
	CD(5%)	0.66	3.83	1.22	3.72	0.79	0.11
	CD(1%)	0.87	5.11	1.63	4.97	1.06	0.15
	CV (%)	3.63	7.41	9.22	8.73	2.02	1.39

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