Studies on Genetic Diversity and Variability in Cluster Bean [*Cyamopsis tetragonoloba* (L.) Taub.] Genotypes Through Morphological and Molecular Characterization

Thesis

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Supervisor
Prof. R. B. Ram

By
Vikas Kumar
ENROLLMENT No. 633/11

**Department of Applied Plant Science (Horticulture)
School for Biosciences and Biotechnology**

**BABASAHEB BHIMRAO AMBEDKAR UNIVERSITY
(A CENTRAL UNIVERSITY)
Vidya Vihar, Rae Bareli Road, Lucknow–226 025 (U.P.), INDIA**

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SUMMARY AND CONCLUSION

CHAPTER- VI

The present investigation entitled "Studies on Genetic Diversity and Variability in Cluster Bean [*Cyamopsis tetragonoloba* (L.) Taub.] Genotypes Through Morphological and Molecular Characterization." were conducted at the Horticulture Research Farm-I, of the Department of Applied Plant Science (Horticulture), Babasaheb Bhimrao Ambedkar University, Vidya Vihar, Rae Bareli Road, Lucknow, (U.P.), India during Rabi season of 2012-13 and 2013-14. The objectives of present investigation were to study variability in the morphological and yield and yield attributing characters. The present study is focused on the following objectives:

1. To estimate the extent of genetic diversity in cluster bean germplasm.
2. To evaluate the extent of genetic variability in the germplasm of cluster bean.
3. To study the contribution towards yield by correlation and path coefficient analysis.
4. To identify potential genotypes of cluster bean on the basis of yield and yield attributes.
5. To screen out the most desirable genotypes on the basis of morphological characterization.
6. To investigate the most desirable genotypes on the basis of molecular characterization.

To determine direct and indirect effect for this study, thirty genotypes were grown with recommended cultural practices in randomized block design with three replications.

The observations recorded on 20 characters i.e., plant height (cm), germination (%), days taken for first flowering, days taken for 50% flowering, number of reproductive branches/plant, pod breadth (cm), pod length (cm), pod width (cm), number of pods/plant, number of pods/cluster, number of clusters/plant, number of branches/plant at maturity, number of seeds/pod, pod yield/plant (g), pod yield/plot (kg), 100-seed weight (g), seed yield/plant (g), days to maturity, pod yield (q/ha) and flower colour. The data were statistically analyzed for different variability parameters.

The study was carried out during 2012-2013 and 2013-2014 at the Horticulture Research Farm-I, of the Department of Applied Plant Science (Horticulture), Babasaheb Bhimrao Ambedkar University, Vidya-Vihar, Rae-Bareli Road, Lucknow, (U.P.), India. The salient experimental findings of the present investigation are summarized below:

6.1 Morphological Characterization

The analysis of variance revealed that sufficient variation existed among genotypes for all the characters under study.

1. The considerable wide range of variation was observed in germplasm for different characters like plant height (cm), germination%, number of pods/plant, number of pods/cluster, number of clusters/plant, number of branches/plant at maturity, pod yield/plant (g), pod yield/plot (kg), seed yield/plant (g), days to maturity and pod yield (q/ha).

2. High magnitude of GCV and PCV was observed for number of pods/cluster (56.77) followed by number of clusters/plant (39.80) and number of pods/cluster (58.05) followed by number of clusters/plant (40.47).

3. Highest estimates of heritability in broad sense along with high genetic advance as percent of means were recorded for number of clusters/plant, number of pods/cluster, pod yield/plant (g), plant height (cm) and seed yield/plant (g). High heritability along with moderate genetic advance were expressed by the characters like number of pods/plant, 100-seed weight (g), number of branches/plant at maturity and pod length (cm).

4. Highest genetic advance over mean was observed in the characters like pods/plant (g), days to maturity, seed yield/plant (g), number of branches/plant at maturity and pod yield (q/ha) recorded high genetic advance over mean.

5. Correlation studies revealed that pod yield exhibited highly significant and positive association with pod yield/plant and pod yield/plot at genotypic correlation

coefficient level and the character like pod yield/plant is highly significant and positive correlation on pod yield at phenotypic correlation coefficient level.

6. The genotype IC-421855 (121.49 g) produced high yield on the basis of pod yield/plant (g) in both the year. The genotypes IC-421828 (0.76 kg) produced high yield followed by IC-421855 (0.75 kg) on the basis of pod yield/plot (kg). The genotypes HG-365 (8.64 g) produced high yield on the basis of seed yield/plant (g). The genotypes IC-421855 (142.23 q/ha) produced high yield followed by HG-365 (138.15 q/ha), IC-421809 (135.48 q/ha) and IC-421806 (133.41 q/ha) on the basis of pod yield (q/ha).

7. Path analysis identified characters such as days taken for first flowering, days taken for 50% flowering, number of pods/plant, number of pods/cluster, number of clusters/plant, number of branches/plant at maturity, number of seeds/pod, pod yield/plant and pod yield/plot showed significant and positive direct effects on the pod yield (q/ha) at genotypic path coefficient analysis.

8. Path analysis identified characters such as number of reproductive branches/plant, pod length, pod width, number of pods/cluster, number of branches/plant at maturity, number of seeds/pod, pod yield/plot, 100-seed weight and seed yield/plant showed significant and positive direct effects on pod yield (q/ha) at phenotypic path coefficient analysis.

9. Thus present path analysis study in cluster bean, it may be concluded that improvement in pod yield/ha could be brought by selection for component characters like days to 50% flowering, pods/cluster, pod length, number of seeds/pod and pod yield/plant.

10. The most important characters contributing to maximum genetic divergence was pod yield per hectare followed by other main responsible characters like 100-seed weight (g), pod breadth (cm), number of pods/cluster, number of pods per plant, number of seeds/pod and number of clusters/plant (5.87).

6.2 Molecular Characterization

Morphological and molecular characterization of germplasm and identification of genetically diverse attributes specific sources are important for enhanced utilization of cluster bean genetic resources in breeding improved cultivars.

Hence, the current study was undertaken to understand the morphological and molecular genetic diversity in cluster bean germplasm, to identify trait specific germplasm and the ISSR markers associated with phenotypic variation.

For the molecular characterization of cluster bean germplasm, 21 ISSR markers were used. The results are summarized below.

1. Genetic diversity among 30 germplasm of cluster bean analyzed on following basis describe in this study. The primers UBC-841, UBC-855, ISSR-5 and ISSR-8 produced highest bands as compared to UBC-856 and UBC-829-11 primers produce lowest bands.
2. The phylogenetic study was done in 30 germplasm of cluster bean. The phylogenetic tree was constructed on the basis of phylogenetic analysis. A dendrogram is generated with the help of UPGMA Jaccard coefficient analysis. The dendrogram possess five major cluster and seven sub cluster.
3. The genome size of cluster bean is approximately 2.45 Giga Bases/Centimeter. Cross pollination is strictly prohibited due to the cleistogamous nature of flowers. There are 30 major maps and 90 sub maps of cluster bean construct in the present study.
4. The values of number of amplified fragment for ISSR marker was ranged between 6 (UBC-854) and 17 (UBC-841), 17 (UBC-855) respectively. The average number of amplified fragment in this study was 12.52.
5. The values of polymorphic fragment for ISSR marker was ranged between 4 (UBC-854) and 15 (ISSR-8), 15 (IS-7), respectively. The average polymorphic fragment in this study was 9.71.
6. The values of polymorphism percentage for ISSR marker was ranged between 58.33% (UBC-856) and 100% (UBC-820), 100% (ISSR-8) respectively. The average polymorphism percentage in this study was 77.06%.
7. The values of monomorphic fragment for ISSR marker was ranged between 1 (IS-7) and 5 (UBC-856), 5 (IS-25), respectively. The average monomorphic fragment in this study was 2.80.

8. The values of monomorphism percentage for ISSR marker was ranged between 6.25% (IS-7) and 41.66% (UBC-856). The average monomorphism percentage in this study was 22.93%.

In summary, the cluster bean germplasm is genetically diverse and possesses potential variation for morphological and yield attributing characters and hence could be extensively evaluated for greater exploitation for use in breeding programs. The superior trait specific germplasm identified could be utilized in breeding programs to improve traits and to widen the genetic base of cluster bean cultivars. Marker trait associations identified in this study using ISSR markers and association mapping approach the first effort in this crop, and will provide important information to the research community for further QTL identification, to identify candidate genes and gene cloning that underlie QTLs in cluster bean.