CHAPTER SIX

Summary & Conclusion
SUMMARY AND CONCLUSION

The present investigation entitled “Genetic diversity and crop improvement in *Momordica charantia* L. through use of agro-morphological characters and molecular markers.” was undertaken with the following objectives:

1. Assemblage of bitter gourd accessions available in Eastern and North Eastern India (hereby comprises the states of Odisha, West Bengal, Assam, Jharkhand, Bihar and Southern part of Sikkim).
2. Characterization & evaluation of the assembled accessions for different agro-morphological characters and tolerance to fruit fly infestation under natural epiphytotic condition.
3. Genetic divergence analysis of the assembled genotypes.
4. Differentiation of the genotypes through RAPD marker.
5. Combining ability analysis through “Line x Tester” approach.
7. Testing of the evolved lines through multi-locational trials and characterizing the selected ones followed by documentation.

To achieve the above objectives, field experiments were undertaken to study the extent of genetic variability for yield, yield contributing and biochemical characters as well as to estimate the correlations, direct and indirect effect of yield components on yield. D² analysis was also carried out to know the amount of diversity present among the accessions. The field experiments were carried out at the Agricultural Experimental Research Farm of Calcutta University at Baruipur, South 24 Parganas, West Bengal in the spring summer and rainy season during the period 2008-2011.

6.1 EVALUATION OF ACCESSIONS

A total of 35 accessions were evaluated for resistance to fruit fly as well as yield components. Analysis of variance revealed significant differences among the accessions for
all the traits studied. The magnitude of PCV was slightly higher than the GCV for all the characters thus indicating that the apparent variation is not only due to the genotype but also due to environmental influence. Highest PCV & GCV were observed for total fruit yield per vine followed by fruit weight, number of seeds per fruit, fruit length, number of fruits per vine and seed weight per fruit. Moderate GCV and PCV were observed for characters like vine length, fruit flesh thickness, node number to which first male flower appears, total number of female flowers, number of primary branches per vine, total number of male flowers and node number to which first female flower appears. Low values of PCV and GCV were noticed in days taken to first male flower appearance, days taken to first female flower appearance, days taken to first picking, fruit girth, ascorbic acid, iron, phosphorus and calcium content which indicates low variability for these traits. High to moderate heritability was observed for most of the yield, yield related traits and bio-chemical characters. Among the various characters studied, high heritability coupled with high genetic advance as percentage of mean was observed for total fruit yield per vine, fruit weight, fruit length, number of seeds per fruit and seed weight per fruit thus revealing that these traits are controlled by additive gene action and consequently a high genetic advance may be expected from selection of these traits. The traits exhibiting high heritability with low GA as percentage of mean were days taken to first male flower appearance, days taken to first female flower appearance, days taken to first picking, fruit girth, ascorbic acid content, iron content, and calcium content. This indicates that these characters are mostly controlled by non-additive gene action. Improvement can be made by intermating the superior genotypes of the segregating population to develop multiple crosses and desirable genes can be accumulated in the lines.

Total fruit yield per vine exhibited significant and positive association phenotypically and genotypically with vine length, number of primary branches per vine, fruit weight, fruit length, fruit girth, fruit flesh thickness, number of fruits per vine, number of seeds per fruit and seed weight per fruit. However, it was significantly and negatively associated with days taken to first male and female flower appearance, ascorbic acid content, iron content & calcium content. Total fruit yield per vine was directly and positively dependent on fruits per vine followed by fruit weight, days taken to first male flower appearance, total number of
female flowers, fruit length, number of seeds per fruit and fruit girth. It would be rewarding if more emphasis is laid on these characters in selection programme for increasing the yield. As per D² analysis, the thirty five accessions were grouped into 5 clusters. Cluster V consisted of 15 accessions while cluster IV & I consisted of 9 & 7 accessions respectively. Cluster II & III, each had 2 accessions. The accessions under study distributed randomly among the different clusters irrespective of their source or region. Clustering pattern did not demonstrate any relation between geographical and genetic diversity. The inter cluster distance was found to be maximum in between clusters IV & II followed by cluster IV & III. Intra cluster distances suggested that cluster IV was having the highest distance from rest of the clusters. It is desirable to select accessions from clusters having high inter cluster distance and having high yield potential as parents in the recombinant breeding programme. Cluster means were calculated for each of the traits under consideration and cluster IV was deemed best for selection of diverse accessions followed by cluster HI & II.

Field screening based on coefficient of infestation revealed that out of the 35 accessions, eleven accessions were susceptible, eleven were mildly susceptible, seven were resistant and six were highly resistant against fruit fly infestation. The coefficient of infestation ranged in between 2.95 (CUBG17) to 85.20 (CUBG19). CUBG15, CUBG17, CUBG45, CUBG48, CUBG53 and CUBG77 were found to be highly resistant against Bactrocera cucurbitae (conquilett), which mostly belonged to the type Momordica charantia var. muricata. So, accessions of muricata origin may successfully be utilized in the resistance breeding programme.

RAPD analysis was done for the 35 accessions using 22 primers, amplification profiles of which were produced by 15 primers, resulting in an output of 92 bands, of which 36 (39.13%) were polymorphic. A dendrogram was constructed based on the molecular study (RAPD analysis) by following UPGMA method. It was observed that, 35 accessions under study were grouped into 6 groups. Pairwise Jaccard’s similarity co-efficient (Jaccard 1908, Nei 1972, Nei and Li 1979) for genetic similarities was performed by using the statistical Software package SPSS 16. Similarity co-efficients based on 92 RAPD fragments
ranged from 0.661-0.982 with an average similarity value of 0.821. Though a few accessions were having similarity in grouping at both morphological and molecular level, but most of the accessions failed to show similarity in grouping under morphological and RAPD analysis. It can be inferred that the environmental effects on the performance of the morphological traits, plant's biologic characteristics were the factors behind such dissimilarities. The non coding regions are not expressed at phenotypic expression; it might be a reason for the rare similarity of the molecular and morphological markers.

6.2 LINE x TESTER ANALYSIS

Considering high yield, rich nutritive components, resistance against fruit fly infestation and diversification, sixteen accessions viz. CUBG14, CUBG15, CUBG16, CUBG18, CUBG20, CUBG21, CUBG28, CUBG46, CUBG47, CUBG72, CUBG74 as lines and CUBG12, CUBG17, CUBG19, CUBG48 and CUBG75 as testers were selected for further breeding programme. Thus a total of 55 hybrids were generated by crossing each of the eleven lines to the five testers.

Analysis of variance for “Line x Tester analysis” revealed significant differences among the entries for all the characters under study. The differences among the parents were significant for all the characters, indicating that the parents differed significantly for these characters. The mean square due to “line x tester” interaction was significant for all the characters. The relative estimates of variances due to GCA and SCA revealed that the variance due to SCA was higher indicating the predominance of non additive gene action for all the characters.

Mean performance revealed that the parents CUBG16, CUBG18 and CUBG19 were found to be superior for fruit weight, parents CUBG18, CUBG19 and CUBG14 for total fruit yield per vine, while CUBG47, CUBG19 and CUBG48 were superior for number of fruits per vine.

Among the lines CUBG18 was found to be a good combiner for fruit weight, fruit length, fruit girth and fruit yield per vine. CUBG 28 was a good combiner for number of primary branches, days taken to first male & female flower appearance, days taken to first
picking and number of seeds per fruit. For ascorbic acid, iron and calcium content CUBG47 was a good combiner. Among testers, CUBG19 was the best combiner for vine length, number of primary branches per vine, total number of male flowers, total number of female flowers, fruit weight, fruit girth, fruit flesh thickness, number of fruits per vine and fruit yield. CUBG48 exhibited maximum positive significant GCA effect for days taken to first male flower & female flower appearance, days taken to first picking, number of seeds per fruit, ascorbic acid and calcium content. CUBG75 showed maximum positive significant GCA effect for characters like fruit length, flesh thickness and phosphorus content. CUBG17 was the best combiner for iron content. Highest significant desirable SCA effects for total fruit yield per vine in order of merit were observed in CUBG72xCUBG19, CUBG46xCUBG17 and CUBG21xCUBG48. Crosses CUBG21xCUBG48, CUBG74xCUBG17 and CUBG28xCUBG48 had high SCA effect for number of fruits per vine. Estimated general and specific combining ability in bitter gourd suggests both additive and non additive gene actions were involved in the expression of yield related characters but non additive gene action had greater role.

For days taken to first female flower appearance, highest value of heterosis over mid parent in negative (desired) direction was observed in CUBG72xCUBG48 followed by CUBG21xCUBG75. Over better parent the highest heterosis in negative (desired) direction was observed in CUBG28xCUBG17, followed by CUBG21xCUBG12 and over commercial check the hybrid CUBG28xCUBG48 expressed highest heterosis. CUBG47xCUBG19 exhibited maximum positive heterosis over commercial check for total number of female flowers. The hybrid CUBG74xCUBG17 had maximum and significant positive heterosis over mid parent and better parent for number of fruits per vine and over commercial check CUBG47xCUBG19 was having the highest heterotic value. CUBG74xCUBG19 exhibited maximum positive significant heterosis followed by CUBG18xCUBG19 over commercial check for fruit weight. For total fruit yield per vine the highest positive and significant heterosis over mid parent as well as over better parent was observed in CUBG21xCUBG12. However, CUBG18xCUBG19 (905.40g/vine) was having a higher yield value over commercial check as well as over the best parent utilized in these set of crosses.
SUMMARY AND CONCLUSION

From this study, it was revealed that none of the hybrids were found to exhibit superiority for all the criteria for all the characters under study. As this study involves both *Momordica charantia* var. *charantia* & *Momordica charantia* var. *muricata*, the hybrid range is much wider and in most of the cases heterosis over mid parent, better parent and commercial check do not support the same cross combination for best performance with respect to a particular trait. Hence, it would be more appropriate to evaluate the hybrids based on mean, SCA and heterosis performance.

Screening of the generated 55 hybrids against fruit fly infestation was done of which twenty were susceptible, six were mildly susceptible, ten were resistant and nineteen were highly resistant. The coefficient of infestation ranged from 3.12 (CUBG15xCUBG17) to 85.50 (CUBG16xCUBG19), which aptly suggests that use of resistant parents in the breeding programme leads to generation of hybrids with a higher degree resistance vis a vis their parents.

6.3 MULTILOCATIONAL TESTING

Based on the heterotic potential, GCA & SCA effects and their average mean performance, best twenty one promising hybrids were selected for multilocational testing as part of stability analysis. The promising twenty one F1’s were evaluated at three locations falling under different agro-climatic Zones of West Bengal viz. Baruipur (Coastal Alluvial Zone), Gayeshpur (Gangetic Alluvial Zone) and Galsi (Laterite plains). The estimates of stability parameters following linear regression model of Eberhart and Russell (1966) revealed that total fruit yield per vine was maximum in CUBG18xCUBG19 (922.52g) with a population mean of 628.87g. The regression coefficient was non significant for all the hybrids as well as for all the traits and deviation from regression coefficient was also non significant except CUBG14xCUBG17, CUBG14xCUBG75 and CUBG18xCUBG17 hybrids for total fruit yield per vine.

For total yield per vine, hybrids CUBG14xCUBG19 and CUBG18xCUBG19 recorded regression coefficient values nearer to unity, higher mean value over population mean and non significant deviation from regression coefficient. One can safely consider these hybrids to be more stable. CUBG14xCUBG19 displayed stability for the characters viz. total number
of female flowers and number of fruits per vine. From fruit weight point of view, hybrids CUBG18xCUBG17 and CUBG18xCUBG12 were considered as stable and well adapted to all the three distinct environments. For ascorbic acid content, least variation was observed in CUBG18xCUBG48 under varied environments. CUBG46xCUBG17 and CUBG14xCUBG17 were considered to be the most stable hybrids with respect to iron content.

Using RAPD markers, polymorphism among the promising twenty one hybrids were unearthed. The amplification profiles produced by 13 primers, gave a total of 100 bands, out of which 41 (41%) were polymorphic. Similarity co-efficient based on 100 RAPD markers ranged from 0.744-0.986.

Conclusions

Based on the findings of the present investigation following conclusions may be drawn

- Sufficient variability exists among bitter gourd accessions of Eastern and North Eastern India. Most of the accessions possessed promising traits in one way or the other.

- Maximum selection gain for total fruit yield per vine must be based on characters like vine length, number of primary branches per vine, fruit weight, fruit length, fruit girth, fruit flesh thickness and number of fruits per vine,

- Clustering pattern did not demonstrate any relation between geographical and genetic diversity. Rare similarity was observed between the grouping of accessions based on molecular and morphological markers.

- A majority of the accessions falling under *Momordica charantia* var muricata were promising due to enriched nutritive components and resistance against fruit fly infestation.

- Yield performance of *Momordica charantia* var charantia was better than *Momordica charantia* var. muricata. Yield performance of the promising hybrids developed through crosses involving parents of *Momordica charantia* var charantia
outyielded the commercial check variety VMR 28. So, these hybrids may be considered as potential runners for commercial exploitation.

- Crossing between *Momordica charantia* var charantia and *Momordica charantia* var muricata was successful and heterobeltiosis was observed in F₁ generation.

- Hybrids developed through crossing involving parents from *Momordica charantia* var muricata was not so high in yield but these hybrids were highly resistant against fruit fly attack. So, wide scope exists in utilizing such types in resistance breeding programme. RAPD analysis of the hybrids will be a helpful tool in identification of resistant genes present in them.

- The parents CUBG12, CUBG18, CUBG19 and CUBG14 were promising and crosses involving these parents resulted in higher fruit length, fruit girth, fruit weight and finally higher total fruit yield per vine.

- High amount of heterosis was noticed in most of the traits related to enhancement in productivity.

- CUBG18xCUBG19 exhibited high percentage of heterotic vigour followed by CUBG14xCUBG19, CUBG18xCUBG17, CUBG18xCUBG75 and CUBG72xCUBG19 over commercial check for the trait total fruit yield per vine.

- Combining ability analysis revealed that both additive and non additive gene action was involved in the expression of characters but non additive gene action too had a greater role to play. The crosses having significant SCA and GCA effects suggests presence of transgressive segregants in the advanced generations.

- Hybrids CUBG14xCUBG19 and CUBG18xCUBG19 having high yield potential were found to be stable for total fruit yield under varied environments and may be commercially exploited.

- High level of polymorphism was noticed among the hybrids.

In future, the selected F₁’s may be advanced to F₂ and successive generations for evaluation of desirable segregates to develop more improved varieties of bitter gourd.

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