

1. Genetic Analysis of Yield and Quality Traits in Tomato (*Solanum Lycopersicum L.*)

M.D SAMIYODDIN

ABSTRACT

A field experiment was conducted to study heterosis and combining ability for yield and quality traits, titled "Genetic analysis of yield and quality traits in tomato (*Solanum lycopersicum L.*)". The experiment was conducted at KRC College of Horticulture Arabhavi. Thirty FI hybrids were produced by crossing ten lines with three testers by following line x tester mating design.

Variances due to the parents were found significant for entire yield related components and quality attributes except plant height, number of fruit clusters and ascorbic acid. Variances due to crosses found significant for all the yield related components and quality attributes. The line x tester analysis revealed that no single line or tester is superior for all the traits under consideration. Significant *per se* performance and economic heterosis in desirable direction was recorded in several crosses. Maximum standard heterosis for total yield per plant was observed in the cross AR 21 x Arka Vikas followed by AR 56 x PKM 1 and AR 29 x PKM 1. All the characters expressed greater SCA variance than GCA variance indicating the predominance of non-additive gene action. Among the lines, Podlandt Pink and among the testers, Arka Vikas is good general combiner. AR 29 x PKM 1, AR 28 x Arka Vikas and AR 39 x Arka Alok crosses had significant SCA effects for yield per plant. AR 4 x PKM 1 and AR 21 x PKM 1 are good cross combinations for lycopene and ascorbic acid contents whereas AR 56 x PKM 1 and AR 21 x Arka Vikas are good cross combinations for total soluble solids. The present study revealed that heterosis breeding is useful for improvement of tomato crop through exploitation of non-additive gene action

August 2014

(Narayanaswamy, M)  
Major Advisor

## 2. Genetic Analysis of Single Cross and Double Cross Hybrids for Yield and Quality Parameters in Tomato (*Solanum lycopersicum* mill.)

**MAHANTESH L. P.**

### **ABSTRACT**

Genetic analysis of single cross and double cross hybrids for yield and quality parameters in tomato (*Solanum lycopersicum* Mill.) were undertaken during 2014-2015 at Department of Crop Improvement and Biotechnology, College of Horticulture, Mudigere. Forty five double cross hybrids were produced by crossing ten single cross hybrids following 10 x10 diallel mating design (excluding reciprocals). Association analysis revealed that total yield per plant was significantly and positively associated with number of primary branches, number of secondary branches, number of clusters per plant, number of fruits per cluster, average fruit weight and number of fruits per plant at both genotypic and phenotypic level and path analysis showed that number of clusters per plant had high direct effect on yield per plant. Maximum standard heterosis over which check for total yield per plant was observed in the cross DCH-43 followed by DCH-39. Variance due to parents versus hybrids was highly significant for number of secondary branches, average fruit weight (g), number of fruits per plant, fruit yield per plant (kg) and number of locules per fruit. In almost all the characters SCA variance was greater than GCA indicating the predominance of non-additive gene action. Among different parents, SCH-9, SCH-8 and SCH-10 were good combiner in desirable direction. Two major double cross hybrids DCH-43 followed by DCH-39 showed significant sca effects in desirable direction for yield per plant. With regard to general performance of single cross hybrids in hill zone of Karnataka SCH-9 (1.36 kg) was better performing single cross hybrid for yield per plant and among the double crosses the DCH-43 showed higher yield (1.8 kg) per plant.

June, 2015

(Narayanaswamy, M)  
Major Advisor

### 3. Genetic Diversity analysis in Tomato (*Solanum lycopersicon L.*) Germplasm

**PRIYANKA, S. M**

#### **ABSTRACT**

An investigation on “Genetic diversity analysis in tomato (*Solanum lycopersicon L.*) germplasm” was carried out in a Randomized Complete Block Design with two replications conducted at farmers’s field nearby College of Horticulture, Mudigere during the year 2015-16. Analysis of variance revealed highly significant difference among the genotypes for all the characters studied. Genetic variability studies indicated that phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) for all the traits. High heritability (>60%) coupled with high genetic advance as per cent mean (>30%) was observed for days to 50 per cent flowering, plant height, number of primary and secondary branches, chlorophyll content, number of fruits per cluster, fruit weight, fruit diameter, total soluble solids, number of locules, pericarp thickness, lycopene content and ascorbic acid indicating the prevalence of additive gene action for these traits. Correlation studies showed that significant and positive association of number of fruit clusters per plant, fruit diameter, number of fruits per plant, fruit weight and number of fruits per cluster at both phenotypic and genotypic level. Path coefficient analysis revealed that direct effect on fruit yield through plant height, number of fruits per plant and fruit diameter. Based on Mahalanobis’s  $D^2$  analysis, thirty two genotypes of tomato were grouped into six clusters, fifteen genotypes were present in cluster V followed by cluster III consisting of nine genotypes, cluster I consisting of five genotypes and clusters II, IV and VI were solitary. Lycopene content followed by fruit weight contributed maximum towards genetic diversity. Molecular characterization of tomato genotypes was done using RAPD markers. Among primers screened, all the primers *viz.*, OPA-7, OPC-4, OPC-8, OPL-5, OPK-3 gave consistent banding patterns. Based on genetic diversity generated by dendrogram analysis, thirty two genotypes were grouped into ten clusters and it is evident that cluster I with two tomato accessions AR-17 and AR-19 appears to be the most diverse among the accessions, with lowest (63%) similarity value than rest of genotypes.

July, 2016

(D. Lakshmana)  
Major Advisor

#### 4. Genetic Variability and Character Association Studies in Ridge gourd (*Luffa acutangula* L.)

**MANOJ, Y. B.**

##### **ABSTRACT**

An experiment was carried out to assess the genetic variability, heritability, diversity and character association among different yield and yield traits of ridge gourd. Thirty five germplasm lines of ridge gourd were evaluated in a randomized block design with two replications at the College of Horticulture, Mudigere during 2015-16. Analysis of variance revealed that highly significant difference was observed among the genotypes for growth, yield and quality parameters indicating existence of greater variability among the lines. The values of phenotypic coefficient of variation was higher than genotypic coefficient of variation, but narrow range of differences indicated that most of the traits were least influenced by environment. High heritability (>60%) with high genetic advance (>20%) was observed for characters *viz.*, sex ratio, days to first harvest, leaf area, leaf area index, chlorophyll content, fruit length, per cent fruit set, fruit weight, fruit yield per plant, fruit yield per hectare, rind thickness and flesh thickness indicating predominance of additive gene component. Thus, there is ample scope for improving these characters through direct selection. Fruit yield per plant had strong positive correlation with fruit weight, number of ridges per fruit, flesh thickness, per cent fruit set, fruit diameter and fruit length. High positive direct effect was recorded for traits *viz.*, number of branches per plant, fruit length, fruit diameter, fruit set per cent, flesh thickness, number of ridges per fruit, fruit weight which are important characters to be accounted for gaining improvement in fruit yield per plant. Based on Mahalanobis's  $D^2$  values, the thirty five germplasm lines were grouped into eight clusters. Cluster I was largest with eleven lines followed by cluster II with four germplasm lines. Among the traits studied flesh thickness (38.66 %), rind thickness (16.30 %), fruit weight (9.58 %) and number ridges per fruit (8.74 %) were contributed maximum to the total divergence. Genotypes Nimbegondi local-2 and Kanapur recorded higher yield and these can be utilized for further breeding programme.

July, 2016

(D. Lakshmana)  
Major Advisor

## 5. Heterosis and Combining Ability Studies for Yield and Quality Traits in Ridge Gourd [*Luffa acutangula* (L) ROXB.]

**CHANDAN, B. M.**

### **ABSTRACT**

The study on heterosis and combining ability for yield and quality traits in Ridgegourd was undertaken during 2017-18 at the Department of Crop Improvement and Biotechnology, College of Horticulture, Mudigere. Twenty hybrids derived by crossing of five parents in diallel fashion were evaluated along with parents and check (US-276) in a randomized complete block design with three replications. Variances due to genotypes varied significantly for all characters and mean performance of majority hybrids were better than parents for almost all qualitative and quantitative parameters. The magnitude of heterosis over mid parent, better parent and check was high in desirable direction for all characters studied. The estimates of heterosis over check ranged from -1.28 % (Krishna-51 × Shittahalli Local and Krishna-51 × TNAU CO-1) to 12.16% (ArkaSujath × Krishna-51 and TNAU CO-1 × Krishna-51) for days to 50% flowering and -30.92 % (Krishna-51 × TNAU CO-1) to 9.29 % (ArkaSujath × Krishna-51) for fruit yield (t/ha). Combining ability analysis revealed higher dominance variance than additive variance for majority of characters indicating preponderance of non-additive gene action. The parents PusaNasdar and Shittahalli Local were identified as good general combiners. Similarly, crosses PusaNasdar × ArkaSujath and ArkaSujath × Krishna-51 were identified as good specific combiners. Hybrids ArkaSujath × Krishna-51 (12.23 t/ha) and ArkaSujath × PusaNasdar (12.16 t/ha) were considered as the most productive hybrids and Shittahalli Local × Krishna-51 (56.01 %) and Krishna-51 × Shittahalli Local (53.26 %) as the most heterotic hybrids.

December, 2018

(D. Lakshmana)  
Major Advisor

## 6. Heterosis and Combining Ability Studies for Yield and Quality Traits in Brinjal (*Solanum melongena* L.)

**SANTOSHKUMAR PATIL**

### **ABSTRACT**

The study on heterosis and combining ability in brinjal was undertaken during 2017-2018 at the Department of Crop Improvement and Biotechnology, College of Horticulture Mudigere. Twenty hybrids derived by crossing five parents in diallele mating system were evaluated along with parents and standard check in a randomized completely block design with three replications. The variances due to genotypes varied significantly for all the characters studied. The mean performance of the majority hybrids were better than parents for almost all qualitative and quantitative parameters. The magnitude of heterosis over mid parent, better parent and standard check ArkaAnand was very high in desirable direction for characters studied. The estimates of heterosis in per cent over the standard check ranged from 11.35 % (Melavanki × Coorg) to -26.39 % (Melavanki × Malapur) for days to 50% flowering and 46.45 % (Kudchi × Malapur) to 7.37 % (Kudchi × Melavanki) for total fruit yield tonnes per hectare. The studies on combining ability revealed that dominance variance was higher than additive variance for majority of characters indicating preponderance of non-additive gene action, thus these characters could be improved through recurrent selection or heterosis breeding. The parent Mattigulla and Melavanki were identified as good general combiners for various characters studied. Similarly, the cross Melavanki × Malapur and Coorg × Mattigulla were identified as good specific combiners. Hybrid Kudchi × Melavanki (24.18 t/ha) and Mattigulla × Coorg (23.55 t/ha) were considered as the most productive hybrids and Kudchi × Melavanki (82.70 %) and Melavanki × Kudchi (43.26 %) were considered as the most heterotic hybrids.

September, 2018

(D. Lakshmana)  
Major Advisor

## 7. Assessment of Genetic Diversity in Bitter Gourd (*Momordicacharantia* L.) for Yield and its Attributing Characters

**SOWMYA, H. M.**

### **ABSTRACT**

An experiment was carried out at College of Horticulture, Mudigere during 2017-18 to assess the extent of genetic diversity for yield and its attributing characters in Bitter gourd. The experiment was laid out in a randomized complete block design with three replications including twenty four bitter gourd genotypes. Analysis of variance revealed that highly significant differences was observed among the genotypes for yield and its attributing characters indicating existence of genetic variability among the genotypes. The estimates of phenotypic coefficient of variation were higher than the genotypic coefficient of variation with narrow differences indicated most of the characters were less influenced by the environment which provides scope for improvement through simple selection. High heritability coupled with high genetic advance as per cent mean was observed for all the characters indicating predominance of additive gene action and amenability for phenotypic selection in early generations. Fruit yield per plant had significant positive correlation with fruit length and fruit weight. High positive direct effect was observed between fruit yield per plant with vine length, node at which male flower appears, number of fruits per vine, fruit weight and fruit length which are important characters to be accounted for gaining improvement in yield. Twenty four genotypes were grouped into five clusters based on Mahalanobis's  $D^2$  statistic. Twenty genotypes were included in cluster I and cluster II, cluster III, cluster IV and V were solitary in nature. Fruit weight (31.16%), flesh thickness (19.93%), node at which first female flower appear (11.59%) contributed maximum to the total divergence. Hubli local, Chickmanglore local, Chitradurga local-1 and Bidar local-1 recorded higher yield and these can be utilized for further breeding programme.

July, 2018

(Shashikala S. Kolakar)  
Major Advisor

## 8. Genetic Diversity in Okra (*Abelmoschus esculentus* L.) for Yield and Seed Quality Traits

**SUNIL GATADE**

### **ABSTRACT**

An experiment was carried out at University of Agricultural and Horticultural Sciences (UAHS), Navile, Shivamogga during the year 2017-18 to study the genetic diversity for yield and seed quality traits in okra. The experiment was laid out in a randomized completely block design with three replications including thirty five okra genotypes. Analysis of variance revealed that highly significant differences were observed among the genotypes for yield and seed quality traits indicating existence of genetic variability in the genotypes. The estimate of phenotypic coefficient of variation was higher than the genotypic coefficient of variation with narrow differences indicated most of the characters were less influenced by the environment which provides scope for improvement through simple selection. High heritability coupled with high genetic advance as per cent mean was observed for total chlorophyll content and number of branches per plant indicating predominance of additive gene action and amenability for phenotypic selection in early generations. Fruit yield per plant had significant positive correlation with plant height, number of branches, number of fruits per plant and fruit length. High positive direct effect was observed between fruit yield per plant with fruit weight, number of fruits per plant and fruit length which are important characters to be accounted for gaining improvement in yield. Based on Mahalanobis  $D^2$  analysis, 35 genotypes were grouped into three clusters and cluster I (26) consisted highest number of genotypes. Among the traits studied plant height (21.18 %), days to 50 per cent flowering (17.14 %), fruit weight (16.13 %) and number of branches (10.08 %) contributed maximum to the total genetic diversity. The present study identified three promising genotypes viz., UHSB-L9, UHSB-L26, OkraB-1, OkraB-2 and OkraB-6, for yield and OkraB-1, OkraB-3, OkraB-6, OkraB-7 for seed quality which can be utilized for further crop improvement programme.

September, 2018

(Usha, T. N.)  
Major Advisor

## **9. Genetic Diversity Studies in Vegetable Amaranthus (*Amaranthus Tricolor* L.) Genotypes for Yield and its Component Traits**

**(ANNAPOORNA H. AGADI)**

### **ABSTRACT**

An experiment was conducted to study genetic diversity in vegetable amaranthus (*Amaranthus tricolor* L.) genotypes for yield and its component traits at the Department of Crop Improvement and Biotechnology, College of Horticulture, Mudigere, during 2018-19. The experiment was laid out in Randomized Block Design with two replications including twenty amaranthus genotypes. Analysis of variance revealed that highly significant difference was observed among the genotypes for yield and its component traits indicating existence of genetic variability among the genotypes. The estimates of phenotypic coefficient of variation were higher than the genotypic coefficient of variation with narrow differences. The high estimates of heritability coupled with higher values of genetic advance as per cent mean were observed for all the parameters indicating predominance of additive gene action and amenability for phenotypic selection in early generations. Total yield per plot was significantly correlated with number of branches per plot, stem weight of plant per plot and foliage yield per plant. High positive direct effect was observed between foliage yield per plot with stem girth, number of branches per plant, leaf length, stem weight of plant per plot, which are important characters to be accounted for gaining improvement in yield. Twenty genotypes were grouped into six distinct clusters based on Mahalanobis's D<sup>2</sup> statistic. Twenty amaranthus genotypes were grouped into six distinct clusters. Cluster V was the largest cluster having five genotypes followed by cluster-III with four genotypes, cluster II, cluster I and cluster IV included three genotypes each and cluster VI included two genotypes. Number of nodes per plant (78.42 %) contributed maximum to the total genetic diversity. Arka Arunima, Chikmagalur local, IC-551486, IC-551494 and IC-551466 recorded high foliage yield per plot and these can be utilized in further breeding programme.

August, 2019

(Shashikala S. Kolakar)  
Major Advisor

## 10. Morphological and Molecular Characterization of Arecanut (*Areca catechu* L.) Germplasm

(KIRAN KUMAR, D.G.)

### ABSTRACT

The present investigation was carried out in a randomized block design and replicated twice. Significant differences among 25 arecanut accessions were observed for most of the characters under study. High heritability coupled with high genetic advance as per cent mean, high GCV and PCV were observed for number of female flowers per inflorescence per palm per year, number of nuts per inflorescence, fresh fruit weight, dry weight of nuts, dry weight of kernel, dry weight of husk and fresh nut yield indicated lesser influence of environment on expression of these traits and prevalence of additive gene action in their inheritance. Hence, these traits are amenable to selection for genetic improvement. Dry kernel yield per palm was positively and significantly correlated with palm height, husk thickness, kernel breadth and dry weight of kernel at both genotypic and phenotypic level. Path analysis revealed that positive direct effects on dry kernel yield was showed by palm height, leaf length, number of nuts per palm per year, fruit set (%), husk thickness, kernel length and kernel recovery (%). Twenty-five accessions were grouped into ten clusters based on Mahalanobis D<sup>2</sup> statistic, where Cluster I was the largest containing 9 accessions followed by Cluster III (5 accessions). The maximum inter cluster distance was observed between cluster IV and cluster IX followed by cluster III and cluster IV. Highest intra cluster distance was observed in cluster III. Dry weight of husk contributed maximum to the total genetic diversity followed by Kernel recovery (%). Molecular diversity using SSR markers revealed high genetic diversity among accessions and the dice similarity index based on SSR data ranged from 0.458 to 1.00. UPGMA dendrogram revealed 3 major clusters divergent at 72 per cent similarity level. Considering the magnitude of cluster mean and agronomic performance Boko, Amchup, Ketakibari and Kumargaon considered as promising and can be utilized for future crop improvement programmes.

August, 2019

(Lakshmana, D.)  
Major Advisor

## **11. Heterosis and Combining Ability Studies for Yield and Yield Attributes in Bitter Gourd (*Momordica charantia* L.) under Hill Zone of Karnataka**

**(SUSHMITHA J. SHETTY)**

### **ABSTRACT**

The study on heterosis and combining ability studies for yield and yield attributes in bitter gourd was undertaken during 2018-2019 at the Department of Genetics and Plant Breeding, College of Horticulture Mudigere. Twenty eight hybrids derived by crossing eight parents in half diallel mating system were evaluated along with parents and standard checks in a randomized complete block design. The variances due to genotypes varied significantly for all the characters studied. The mean performance of majority of the hybrids was better than parents for almost all qualitative and quantitative parameters. The magnitude of heterosis over mid parent, better parent and standard checks ArkaHarit and Pusa Do Mousami were in desirable direction for characters studied. The cross Hiriyur local  $\times$  Hubli local exhibited significant positive heterosis over check ArkaHarit (138.71 %) and over Pusa Do Mousami (106.95 %) for fruit yield (t/ha). The studies on combining ability revealed that, additive variance was higher than dominance variance for majority of characters indicating preponderance of additive gene action. The parents Hiriyur local and Hubli local were identified as good general combiners for overall characters studied. Similarly, crosses Chamrajpet local  $\times$  Villupuram green long and Dharwad local  $\times$  Chitradurga local were identified as good specific combiners. Hybrids Hiriyur local  $\times$  Hubli local (18.46 t/ha) and Chamrajpet local  $\times$  Villupuram green long (15.70 t/ha) were considered as most productive hybrids and Chamrajpet local  $\times$  Villupuram green long (67.20 %) and Villupuram white long  $\times$  Chamrajpet local (47.77 %) were considered as most heterotic hybrids.

August, 2019

(Shashikala S. Kolakar)  
Major Advisor

## **12. Survey and Assessment of Genetic Variability for Yield and Yellow Leaf Disease in Arecanut (*Areca catechu* L.)**

**(VIRUPAKSHI HIREMATA)**

### **ABSTRACT**

The present investigation was carried out to assess the genetic variability for yield and yellow leaf disease in eight years old arecanut plantation at AHRS, Sringeri which is located in the Western Ghats of Karnataka during Kharif and Rabi seasons of 2018-19. Ten arecanut cultivars viz., Sumangala, Sringeri Local, Mohithnagar, SAS-1, Hirehalli Dwarf, Keladi Local, Sagar Local, Thirthahalli Local, Sreemangala and Mangala were laid out in Randomized Block Design with three replications. Survey for incidence of Yellow Leaf disease on arecanut was carried out in major arecanut growing Malnad areas of Karnataka namely Sringeri and Koppa during Kharif 2018 and observed high incidence of YLD as it ranged from 86.59 to 96.20 per cent. Highest disease incidence and disease index was recorded in Muruvinakombe village followed by Talamakki and it was also recorded natural escapes for the YLD were it ranged from 2 to 5 in number and the maximum numbers were observed in the Honnavalli, Bandlapur, Kachkal, Hoskoppa. Higher PCV and GCV were observed for most of the traits and highest heritability was observed for recovery percentage. The association of fruit yield per palm was positively significant with fifteen fruit and quality characters. Path analysis revealed that nineteen of thirty eight characters showed positive direct effect on fruit yield per palm. Genetic diversity for YLD resistant and susceptible genotypes revealed that RAPD marker produced the 4 clusters, ISSR marker produced the 6 clusters and RGP marker produced the 5 clusters which indicates variability exist in studied genotypes of arecanut. These resistance plants can use in the further crop improvement and resistance breeding for YLD disease of arecanut.

August, 2019

(Narayana swamy M.)  
Major Advisor

