University of Agricultural and Horticultural Sciences, Shivamogga

M. Sc. (Agri.) theses abstracts produced in the

Department of Genetics & Plant Breeding

1. **Assessment of Genetic Variability, Diversity for Yield and Yield Components and Morphological Characterization of Traditional Rice (*Oryza sativa* L.) Genotypes**

SRIDHAR T C

ABSTRACT

Rice (*Oryza sativa* L.) is one of the most important food crop grown worldwide. It is the staple food for half of the world's population, being primary centre of origin it posses huge diversity of rice genotypes of both wild and cultivated. The present study was undertaken to evaluate sixty four traditional rice genotypes for variability and diversity in yield and its components and morphologically characterise the genotypes according to DUS guidelines. ANOVA revealed significant difference among the genotypes studied for all the characters. High range of variation, PCV, GCV and high heritability coupled with high GAM was observed for number of tillers per plant, number of spikelets, grains per panicle, straw yield per plant, harvest index and grain yield per plant. Yield components such as plant height and test weight exhibited highly significant association with grain yield at phenotypic level. Days to maturity followed by harvest index and number of tillers per plant had the highest positive direct effect on grain yield. Using Mahalanobis' D^2 statistic, genotypes were grouped into fourteen clusters. Based on cluster distance, highest inter cluster distance between cluster X and XIV. Among all the characters, days to maturity followed by straw yield per plant had highest contribution towards the genetic diversity.

Morphological characterization inferred the existence of distinct and uniform genotypes for the characters specified for rice by DUS guidelines, *viz.,* anthocynin coloration, intensity and its distribution on coleoptile, basal leaf sheath, leaves, nodes, internodes and spikelets. Angular characters like attitude of flag leaf, culm and panicle. Grain characters *viz.,* awns, length, breadth, grain colour, and shape of both hulled and non hulled grains. Quantitative characters like days to flowering and maturity, length and breadth of leaf blade, plant height and test weight. Two genotypes (Naare kela and Navile sanna) were found entirely distinct by presence of multi spikelets per pedicel. This present study identified five promising genotypes viz., Kempakki, Navara, Chammpakali, Solari and Kaase bhai over check variety (Jyothi and JGL-1798) for yield and its components. Thus these local genotypes may be utilised in further crop improvement programme.

May, 2015 (Dushyantha kumar, B. M)

Major Advisor

2. Genetic Investigation of Yield and its Attributing Characters in Okra [*Abelmosches Esulentus* (L.) Moench]

ASHA. I. S

ABSTRACT

The genetic variability is the pre-requisite for any plant breeding programme. Forty nine Okra germplasm accessionswere evaluated in a simple lattice design with two replications during *kharif* 2014 at College of Agriculture, UAHS, Shivamogga. Data were collected on 13 quantitative traits and were subjected to variability, association and diversity studies. The results of the investigation revealed that, there were significant variation among the lines for yield and yield contributing traits. Broad sense heritability as well as expected GAM was higher for plant height, inter-nodal length, first flowering node, number of branches per plant, number of flowering nodes on main stem, fruit length, fruit diameter, number of fruits per plant, average fruit weight and fruit yield per plant.

Plant height, intermodal length, first flowering nodes, number of branches per plant, number of flowering nodes in main stem, fruit length, number of fruits per plant and average fruit weight had high significant positive association with fruit yield per plant. Direct and indirect association analysis revealed that number of fruits per plant had highest direct effect followed by average fruit weight on fruit yield per plant.

Based on Mahalonobis' D^2 values these genotypes were grouped into 8 clusters. Cluster I had maximum number of 35 genotypes followed by Cluster IV with 5 genotypes. Fruit diameter contributed maximum towards genetic divergence followed by number of flowering nodes on main stem. Pusa Makhmalli, EC 693224 and VRO-109 genotypes which are most diverse could be involved in hybridization among promising combinations to develop productive segregants.

May, 2015   (Ganga Prasad, S.)
                                                                                      Major Advisor

3. **Assessment of Genetic Variability, Association and Diversity in French bean (*Phaseolus Vulgaris*L.)**

BHAGANNA HARALAYYA

ABSTRACT

Success of any crop improvement programme depends on the extent of genetic variability present inthepopulation forthetraits forwhich the improvement isaimed at breeding. Thirty sixgermplasm collections were evaluated inasimple latticedesign with tworeplications during*summer* 2014atCollege of Agriculture, UAHS, Shivamogga. Data were collected on 13quantitative traits and were subjected tovariability, association and diversity studies.The genotypes revealed that high significant variability forallthetested characters such asgreen pod yield, plant height, number of primary branches, number of secondary branches, number of pods per plant, pod length, number of seeds per pod and 100seedweight. The high PCV and GCV values were recorded by number of pods per plant, plant height, number of secondary branches and test weight. Heritability inbroad sense and genetic advance asper cent mean were higher for plant height, number of primary branches, number ofsecondary branches, number ofpods per plant, number of seeds per pod, pod length and 100seedweight.

Association analysis revealed significant positive correlation of green pod yield with plant height, number of pods per plant, number of seeds per pod and pod length (cm). Positive direct effects were recorded by pod length, plant height, days to50 per cent flowering and flower to pod set rati oto green pod yield. The number of seeds per pod,number of pods per plant and plant height recorded high positive indirect effect with green pod yield. Based on D2 values thirty six genotypes were grouped into 6clusters. Cluster I was the biggest with19 genotypes followed by cluster VI and Cluster II&III. The maximum contribution for the diversity wasobserved in green pod yield followed by plant height. The genotypes like, IIHR-47, Arka Komal, IIHR-99, IIHR-90, IIHR-81A, IIHR-23 and IIHR-I03 are identified as high yielding and most diverse genotypes. These genotypes could be involved in hybridization among promising combinations to develop productive segregants.

May, 2015

(Ganga Prasad, S.)
Major Advisor

4. Studies on Genetic Variability in Eggplant (*Solanum Melongena* L.) Genotypes for Drought Tolerance and Yield

GOBU R

ABSTRACT

The present investigation was initiated by conducting a survey among eggplant growers of central dry zone (Zone-4) and southern transitional zone (Zone-7) of Karnataka to know their varietal preference and then a study was conducted in eggplant genotypes to assess the genetic variability for drought tolerance and yield under three experiments by imposing water stress at germination stage (73 genotypes), seedling stage (65 genotypes) and reproductive stage (62 genotypes). The survey results revealed that farmers in Zone-4 prefer local cultivars followed by private varieties/hybrids. Whereas in Zone-7, private varieties are more preferred than local cultivars. The analysis of variation revealed the existence of highly significant differences among the genotypes for all the traits recorded under moisture stressed and non-stressed condition. A high range of variation and high heritability coupled with high genetic advance was recorded for most of the traits.

The association studies revealed that fruit yield per plant showed significant positive association with plant height, number of fruits per plant, fruit circumference and average fruit weight. Path analysis revealed that average fruit weight had highest direct positive effect on fruit yield, while fruit circumference showed high indirect positive effect on fruit yield through average fruit weight. Based on Mahalanobis' D^2 analysis, the genotypes were grouped into 11 clusters. Based on cluster mean scoring, cluster II ranked first, which includes Punjab Barsati, IC104083, IVBL-9, Lal Gulab, IC90785, IC333527, Arka Abilash, IIHR-7and Arka Kranti. Out of twelve characters studied, number of primary branches per plant contributed maximum towards total genetic divergence.Based on the results of each experiment, better drought tolerant and susceptible genotypes for moisture stress at different growth stages were identified. The genotype, Jawahar Brinjal-69 has been identified as drought tolerant line at all the three stages *viz.,* germination, seedling and reproductive stage.

June, 2015

(Harish Babu B.N.)
Major Advisor

5. **Genetic Divergence and Correlation Studies for Yield and Yield Traits in Rice (*Oryza Sativa* L.) Germplasm Lines**

IRAPPA B MAMADAPUR

ABSTRACT

A field investigation was carried out involving 150 germplasm of rice at Zonal Agricultural and Horticultural Research Station, Mudigere, during *kharif* 2014, to assess genetic variability and divergence of different yield and yield contributing traits, to estimate correlation coefficients of yield attributes on yield and to estimate direct and indirect effects of yield attributes on yield. The analysis of variance revealed highly significant variability among the lines for different traits. The estimates of PCV and GCV were high for panicle exertion, number of spikelet's per panicle and number of grains per panicle.

The difference between PCV and GCV were less for these characters, indicated low environmental influence. The characters *viz*., plant height, panicle exertion, number of spikelet per panicle, number of grains per panicle, test weight, L/B ratio and grain yield per plant exhibited high heritability coupled with high predicted genetic advance as per cent of mean. The characters like days to 50 per cent flowering, days to maturity, plant height and test weight showed highly significant positive correlation with grain yield at both genotypic and phenotypic level. Plant height had highest positive direct effect on grain yield followed by number of grains per panicle and 1000-grain weight. In order to assess the divergence among 150 lines, Mahalanobis' D^2 statistics and Tocher method was applied.

The 150 lines were grouped into 8 clusters, where cluster III and IV were the largest containing fourteen and seventeen lines respectively,were the most divergent group with maximum inter-cluster distance (26389.99). Among the thirteen characters studied number of spikelet's per panicle and number of grains per panicle contributed most towards divergence. Nine different grain colour groups were observed among 150 germplasm lines. In the study 10 germplasm were found superior over two checks namely, Tunga and KHP-2 with respect to yield and yield characters.

June, 2015 (Lakshmana D)

Major Advisor

6. Assessment of Genetic Variability and Diversity Analysis for Yield and Yield Components in Traditional Rice (*Oryza Sativa* L.) Genotypes.

VIDYACHARAN D.N

ABSTRACT

Rice (*Oryza sativa*. L) is the prime, most essential and important food crop of the world. Land race plays an important role in the local food security and sustainable development in agriculture. The present study was undertaken to evaluate 100 traditional genotypes for variability and genetic divergence. The investigation was carried out at Agricultural and Horticultural Research Station (AHRS), Kathalagere. The crop for the present investigation was raised during *Kharif* of 2014.Genotypes were evaluated for extent of variability, character association, path analysis, genetic divergence for 12 traits and variability studies in 100 traditional rice genotypes for the reaction to blast disease. ANOVA revealed highly significant difference among the genotypes for all the quantitative traits. High PCV and GCV estimates for all the characters except days to 50 per cent flowering and days to maturity showed low values, High heritability and high genetic advance were recorded for all the 12 characters.

Yield component characters number of grains per panicle and test weight exhibited highly significant association with grain yield. Phenotypic path coefficient analysis revealed that Number of grains per panicle had the highest positive direct effect on grain yield. Using Mahalanobis' D^2 statistic, 100 traditional rice genotypes were grouped into twelve divergent clusters. Wide genetic variability was indicated by the intra and inter cluster distances. Based on cluster means, cluster XI ranked first. It was also found that among all the characters, Days to 50 per cent flowering had highest contribution towards the genetic diversity. Screening of the traditional rice genotypes for field resistance against leaf blast disease revealed that the disease has not been affected severely, compared with the Susceptible genotype Intan, in four out of 100 genotypes were resistant, 67 genotypes showed moderately resistant and 28 genotypes are moderately susceptible.

July, 2015   (T.H. Gowda)
                                                                   Major Advisor

7. **"Genetic Variability, *Per Se* Performance and Combining Ability Study in Maize (*Zea Mays* L.)"**

REKHA

ABSTRACT

The present investigation was carried out to elucidate the information on genetic variability and diversity, character association and path analysis among the inbred lines, and to estimate the combining ability in forty five single cross hybrids.Forty three inbreed lines of maize were evaluated at ZAHRS, Shivamogga during *kharif* 2014, observations were recorded for twenty one characters. Analysis of variance revealed significant differences among all inbred lines. High PCV, GCV, high heritability coupled with high genetic advance was noticed for leaf area at 40 days after sowing, cob weight, grain yield per plant and 100 grain weight. Mahalanobis D^2 analysis revealed that 43 inbred lines were grouped into 10 clusters, indicating the presence of diversity. The maximum inter cluster distance was observed between clusters VI and X (838.65) and highest intra cluster distance was in cluster VI. Cob weight, leaf area index and days to 50 per cent brown husk maturity contributed more towards genetic divergence.

Correlation studies revealed significant association of grain yield with most of the characters under study. The maximum positive direct effect on grain yield was exhibited by cob weight followed by 100 grain weight, shelling percentage, cob length, cob girth and number of rows per cob. In the second experiment forty five hybrids were evaluated at ZAHRS, Shivamogga during late *rabi* 2014-15. The Observations were recorded for twenty one characters. There was higher dominance variance than additive variance for most of the characters. Among five females, 18704, 18832 and 18838were the best general combiners for all characters except number of rows per cob. Among nine testers 18328, 18337, 18342, 18627 and 18850 were the best general combiners for all characters. Out of forty five hybrids, hybrids18838x18850, 18838x18627, 18495x18337, 18838x18342 and 18495x18494 with desirable significant sca effects were identified as best hybrids in respect of grain yield.

June, 2015   (H. D. Mohan Kumar)
                                                                            Major Advisor

8. Assessment of Genetic Variabilty and Diversity in Tomato (*Lycopersicon Esculentum Mill.*) Germplasm

SHWETA

ABSTRACT

Present investigation was carried out during Summer and Late *kharif* seasons of 2014 at College of Agriculture, University of Agricultural and Horticultural Sciences, Shivamogga to study the genetic variability, correlation, path coefficient analysis and genetic diversity for quantitative traits in tomato (*Lycopersicon esculentum* Mill**.**) with 36 genotypes in randomized block design. Considerable amount of variability was noticed for the sixteen and nineteen quantitative characters in summer and late *kharif* seasons respectively as indicated by the analysis of variance. High GCV and PCV, high heritability with high genetic advance as per cent mean was observed for most of the yield attributing characters in both seasons.

Fruit yield per plant had highly significant positive association with fruit length, fruit equatorial diameter, fruit volume and average fruit weight in both summer and late *kharif* seasons and number. Similarly, path coefficient analysis revealed that number of clusters per plant, number of flowers per plant and average fruit weight had high direct and indirect effect on fruit yield per plant in both summer and late *kharif* seasons.

Apart from these fruit length, fruit volume, number of fruits per plant and Total soluble solids had high effect in late *kharif* season. Mahalanobis D^2 analysis revealed that thirty six genotypes are divided into seven groups in both seasons. In summer cluster-I (21genotypes) and in late *kharif* Cluster-II had highest number of genotypes. Fruit volume and lycopene content contributed more towards total genetic divergence in summer and late *kharif* seasons respectively. Maximum score was recorded by Cluster V with two genotypes (AR-50 and AR-14) and Cluster VI with single genotype respectively in both the seasons. It appears to be containing most potential genotypes and these can be utilized in further crop improvement programme.

June 2015   (Dhushyanthakumar B. M)
                                                          Major Advisor

9. Analysis of Genetic Divergence in Groundnut (*Arachis Hypogaea* L.) Genotypes

SANJEEVAKUMAR PATIL

ABSTRACT

The genetic variability is the pre-requisite for any plant breeding programme. Fourty nine groundnut genotypes accessions were evaluated in a Simple Lattice Design with two replications during *Kharif* 2014 at college of Agriculture, UAHS, Shivamogga. Data were collected on 15 quantitative traits and subjected to variability, association and diversity studies. The results of the investigation revealed that, there were significant variation among the genotypes for yield and yield contributing traits.

The high PCV and GCV values were recorded by secondary branches per plant, immature pods per plant, mature pods per plant, pod bearing nodes per plant and pod yield per plant. Broad sense heritability as well as expected GAM was higher for matured pods per plant, days to 50 per cent flowering, kernel weight per plant, 100 kernel weight, pod bearing nodes, immature pods per plant, plant height and secondary branches per plant. Association analysis revealed significant positive correlation of pod yield per plant with number of pod bearing nodes, number of matured pods per plant, kernel weight per plant and days to 50 per cent flowering. Positive direct effects were recorded by number of matured pods per plant, pod yield per plant, kernel weight per plant, 100 kernel weight, number of secondary branches and number of primary branches per plant.

Based on D^2 values fourty nine genotypes were grouped into fourteen clusters. Cluster I was the biggest with 21 genotypes followed by cluster IV, VI and III. The maximum contribution for the diversity was observed in pod yield per plant followed by days to 50 per cent flowering. The genotypes like GPBD-5, SB-T$_1$, SB-T$_{21}$ and VB-T$_{35}$ are identified as high yielding and most diverse genotypes, the genotypes SB-T$_1$ and VB-T$_{14}$ are identified as resistant to root knot nematode disease. These genotypes could be utilizing in hybridization among promising combinations to develop productive segregants.

August, 2015   (Shivanna. S)
                                                          Major Advisor

10. Studies on Genetic Variability for Grain Yield and its Component Traits in F_3 Population of Rice (*Oryza Sativa* L.)

POOJA B.

ABSTRACT

The present investigation was undertaken during kharif 2015 at the College of Agriculture, Shivamogga, Karnataka to study the variability parameters, correlation, path analysis and identification of superior segregants in F_3 generation of two crosses of rice *viz.*, 'JGL-1798 X KHP-2 and 'KHP-2 X MO_4'.The descriptive statistical parameters viz., mean, range, skewness and kurtosis with respect to all the twelve quantitative characters in F_3 population of two crosses of rice were recorded. Out of two crosses the best performance is exhibited by KHP-2 X MO_4 in terms of range followed by JGL-1798 X KHP-2 for yield and its related traits. Platykurtic and positively skewed distribution recorded for most of the traits in both the crosses. The magnitude of PCV was more than GCV in general for most of the characters indicating that characters are invariably influenced by environment.

High heritability coupled with high genetic advance as per cent of mean is being observed for plant height, number of tillers, number of productive tillers, panicle length, number of spikelet per panicle, number of grains per panicle, grain yield per plant and harvest index indicating that the characters are controlled by additive gene action and can be transferred to next generation through selection. Grain yield per plant exhibited significant and positive association with important yield components like total tillers per plant, productive tillers per plant, spikelets per panicle, grains per panicle, spikelet fertility and harvest index. Path analysis in F_3 generation of both the crosses indicated maximum positive direct effect of productive tillers per plant, spikelet per panicle, grains per panicle and harvest index, panicle length on grain yield. Top ten superior segregants in desirable direction for grain yield, productive tillers per plant and grains per panicle were identified in both the crosses for advancing to next generations.

July, 2016   (B. M. Dushyantha Kumar)
                                                                          Major Advisor

11. Studies on Genetic Variability Diversity and Stability in Advanced Breeding Lines of Rice (*Oryza Sativa* **L.**)

RASHMI K P

ABSTRACT

Rice is the staple food crop of India. It posses huge diversity of both wild and cultivated species. The present study was undertaken to evaluate twenty two advanced breeding lines in a Randomized complete block design with two replications during *kharif* 2015 at three locations *viz,* ZAHRS Mudigere, ZAHRS Bramhavara and College of Agriculture (CoA) Shivamogga for variability, diversity and stability for yield and its components. ANOVA revealed significant differences among all the advanced breeding lines for all the characters studied. High range of variation, PCV, GCV and high heritability coupled with high GAM was observed for number of tillers per plant, number of productive tillers per plant, number of spikelets per tillers, number of grains per panicle, grain yield (kg/ha), straw yield (kg/ha) and harvest index.

Days to maturity, straw yield (kg/ha) and harvest index had significant positive association with grain yield at phenotypic level. Straw yield (kg/ha) followed by harvest index had the highest positive direct effect on grain yield, whereas highest positive indirect effect on grain yield by the trait straw yield (kg/ha) via days to maturity. Using Mahalanobis' D^2 statistics, advanced breeding lines were grouped into five clusters, cluster I (18) consists highest number of advanced breeding lines. Highest intra cluster distance were recorded in the cluster I (3.48) and highest inter cluster distance between cluster III and IV based on cluster distance. Cluster mean analysis reveals that cluster I received the first rank. Number of spikelets per panicle and number of grains per panicle had highest contribution towards the genetic diversity. The advanced breeding line JB 15-2 is identified as the stable variety for grain yield in all the three locations, whereas JM 15-4 (Mudigere), JK2 15-7 (Bramhavara) and JK 15-1 (Shivamogga) are identified as stable lines for specific locations for grain yield.

June, 2016   (DushyanthaKumar. B. M.)

                                                                                      Major Advisor

12. Genetic Variability for Grain Yield and its Component Traits in F_2 Populations of Rice (*Oryza sativa* L.)

PRADEEP, P.

ABSTRACT

The present investigation in rice (*Oryza sativa* L.) was undertaken during *Kharif*, 2015 at AHRS, Kathalagere, to study variability parameters, character association and path analysis and identification of transgressive segregants in respect of grain yield and its component traits as well as blast reaction in F_2 population of 'BPT5204 $\times$ IET21075' and 'BPT5204 $\times$ IET21214' crosses. The distribution pattern of two F_2 populations indicated large number of genes with dominance based complementary interaction in the inheritance of total tillers per plant, number of panicles per plant, number of grains per panicle, grain yield per plant and L:B ratio in both crosses but duplicate type of interaction was noticed for days to 50 per cent flowering, panicle length, number of spikelets per panicle, spikelets fertility, test weight, grain length and grain breadth in 'BPT5204 $\times$ IET21075'.

Similarly for panicle length and harvest index in 'BPT5204 $\times$ IET21214'. GCV and PCV values were relatively higher with high heritability coupled with high genetic advance for total tillers per plant, productive tillers per plant, grains per panicle and grain yield per plant in both the crosses indicating additive gene action in their genetic control. Grain yield per plant was exhibited significant positive correlation with plant height, total tillers per plant, number of panicles per plant, panicle length, number of spikelets per panicle, number of grains per plant and spikelet fertility in both the crosses. Path analysis in F_2 generation of both crosses indicated the positive direct effect of total tillers per plant, number of panicles per plant, grains per panicle, panicle length and harvest index on grain yield. Superior desirable transgressive segregants were identified in both the crosses for advancing to next generation. The maximum plants showed resistance to leaf blast for disease reaction as compared to their parent under natural field condition in both crosses.

July, 2016

(Malleshappa, C.)
Major Advisor

13. **Studies on Heterosis and Combining Ability in Okra (*Abelmoschus Esculentus* (L.) Moench)**

DARSHINI, T. K

ABSTRACT

The present investigation was undertaken with the objective of estimatingheterosis and combining ability through line x tester mating design. The experiment was conducted in College of Agriculture, Shivamogga by involving nine lines and three testers as parents and their twenty seven F_1 hybrids, generated and evaluated during 2015-16. Heterosis was recorded for fruit and its fifteen component characters, the crosses which had significant heterosis over standard check areVarshaUpahar x KashiKiranthifor plant height and days to 50% flowering, 307-10-01 x Arka Anamikafor number of leaves, ParbhaniKranthix ZARS for internodal length, VarshaUpahar x ZARS for number of branches per plant, PusaMakhmali x ZARS for number of nodes on main stem,PhuleUtkarshix KashiKiranthi for stem diameter, Punjab Padmini x ZARS for fruit length, PusaMakhmali x KashiKiranthifor fruit Diameter,VRU-109x Arka Anamika for number of fruits per plant,Punjab Padmini x ZARS for average fruit weight per plant and for total fruit yield per plant was maximum in the hybrid VRU-109 x ArkaAanamika, followed by PhuleUtkarshi xKashiKiranthiwere these hybrids may be used for exploitation of hybrid vigour on commercial scale.

Combining ability analysis was carried out for fruit yield and its components in okra. Both general a combining ability (GCA) and specific combining ability (SCA) variances were highly significant for almost all the characters indicating the importance of both additive and non additive gene actions. Parents and F_1 hybrids differed significantly for general combining ability and specific combining ability effects for all the characters respectively.The highest gca effect for total fruit yield per plant recorded in Punjab Padmini.The highest significant positive sca effect was observed in the cross VRU-109 x Arka Anamika. Among the parentsPunjab Padmini, VRU-109, VarshaUpaharproved to be the good general combiner and VRU-109 x Arka Anamikawas the good specific combiner for most of the yield and yield attributing traits followed byPunjab Padmini x ZARS.

August, 2016   (Gangaprasad, S.)
                                                                          Major Advisor

14. Genetic Investigation in Two F_2 Populations of Flue-Cured Virginia (FCV) Tobacco (*Nicotianatabacum* L.)

SAMPURNA D

ABSTRACT

The present investigation was carried out to elucidate the information on genetic variability, heritability, genetic advance, character association and path analysis in two F_2 populations and three parental cultivars of Flue cured virgina (FCV) tobacco.Two F_2 populations of the crosses, TB-70 × TB-102 and TB-100 × TB-102 and three parental cultivars *viz*., TB-70, TB-100 and TB-102 were evaluated at ZAHRS, Shivamogga during *kharif* 2015. Observations were recorded on fifteen characters. Descriptive statistical parameters were estimated which revealed wider range values for all the characters. High PCV, GCV were observed for the traits like specific leaf weight, leaf area per plant and total sugars in both the crosses. High heritability estimates were observed for all the characters investigated.

The expected genetic gain expressed as per cent of mean was high for stem girth, chlorophyll content, specific leaf weight, number of leaves per plant, leaf area per plant and days to flowering in both the crosses. High heritability coupled with high genetic advance was noticed for stem girth, chlorophyll content, specific leaf weight, number of leaves per plant, leaf area per plant and days to flowering in both the crosses, indicating additive gene action in their genetic control. Correlation studies revealed significant correlation of green leaf yield with cured leaf yield followed by top grade equivalent, leaf area per plant and number of number of leaves per plant in both the crosses. The maximum possible direct effect on green leaf yield was exhibited by cured leaf yield in both the crosses. It can be concluded that selection of green leaf yield along with its component traits, particularly cured leaf yield, top grade equivalent, leaf area per plant and number of number of leaves per plant will be highly reliable for developing high yielding genotypes in further generations.

July, 2016

(H. D. Mohan Kumar)
Major Advisor

15. Variability and Genetic Divergence Studies for Yield and Yield Component Traits in Rice (*Oryza sativa* L.) Genotypes in Hill Zone

HARISH, D.

ABSTRACT

Rice (*Oryza sativa* L.) is one of the most important food crop grown worldwide. It is the staple food for half of the world's population, India being primary centre of origin it posses huge diversity of rice genotypes of both wild and cultivated. The present study was undertaken to evaluate 100 rice genotypes for variability and divergence studies for yield and its component traits and field screening of genotypes to blast disease according to IRRI scale. ANOVA revealed significant difference among the genotypes studied for all the characters except days to maturity. High range of variation, PCV, GCV and high heritability coupled with high GAM was observed for panicle length, number of spikelets per panicle and number of grains per panicle.

All the yield component traits except plant height, panicle length, per cent spikelet fertility and test weight exhibited significant association with grain yield at phenotypic level. Straw yield per plant followed by harvest index, number of grains per panicle and days to 50 per cent flowering had the highest positive direct effect on grain yield where as highest positive indirect effect on grain yield by the trait straw yield per plant via number of tillers per plant. Using Mahalanobis' D^2 statistics, genotypes were grouped into eleven clusters the cluster IX (20) consists of highest number of genotypes. Based on cluster distance, highest intra cluster distance were recorded in the cluster VII and highest inter cluster distance between cluster IX and XI. Cluster mean analysis reveals that cluster IX received the first rank. Among all the characters, grain yield per plant followed by days to 50 per cent flowering had highest contribution towards the genetic diversity. Rice genotypes screening to blast disease shows that the genotypes IET-25147, IET-24414 shows resistance to blast disease and the genotype IET-25147 had recorded the highest yield per plant.

June, 2016

(T. H. Gowda)
Major Advisor

16. Genetic Variability and Divergence Studies in Black Gram (*Vignamungo* [L].Hepper)

BASAVARAJESHWARI B SAJJANAR

ABSTRACT

Black gram is the major pulse crop of India. It posses huge diversity of both wild and cultivated species. The present study was undertaken to evaluate sixty four germplasmlines in a simple lattice with two replications during *kharif, Rabi*, and *summer*for variability, diversity and stability for yield and its components. Analysis of variancerevealed that the treatment (genotypes) under the study differed significantly even at 1 *per cent* level of significance for all the character *viz.*, plant height, pod length, number of primary branches, number of secondary branches, number of seeds per pod, number of cluster per pod, number of pods per plant, test weight, days to 50 per cent flowering and days to 50 per cent pod maturity.

ThehigherestimatesofPCVandGCV were observed among theaccessionsfor the characters, suggesting that these characters were under the influence of genetic control. Using Mahalanobis' D^2 statistics, germplasmlineswere grouped in 9 clusters, where in cluster I had highest number of genotypes. The highestintra cluster distances showed by clusterV and intra cluster distance was observed between cluster IV and V. Genotypes M-375 and M-39 had high mean values than the population mean, regression coefficient less than one and least deviation from regression for seed yield per plant indicating that their stability over wide range of environments. Genotypes like COBG-653,M-278 and M-147 were found stable for the seed yield during *kharif, rabi* and *summer* respectively.

July, 2016   (T. H. Gowda)
                                                                                              Major Advisor

17. Assessment of Genetic Variability in Segregating Generation (F2) of Rice (*Oryza sativa* L.)

ASHWINI, K. H.

ABSTRACT

The present investigation in rice (*Oryza sativa* L.) was undertaken during *Kharif*, 2016 at College of Agriculture, Navile, UAHS, Shivamogga, to study variability parameters, character association, path analysis, and identification of transgressive segregants in respect of grain yield and its component traits in F_2 population of MO_4 x Puttabatta cross. The distribution pattern indicated large number of genes with dominance based complementary interaction in the inheritance of plant height, number of tillers per plant, number of productive tillers per plant, number of filled grains per panicle, spikelet fertility, grain yield per plant and L:B ratio and duplicate type of interaction was noticed for panicle length, test weight and harvest index. GCV and PCV values were relatively higher for grain yield per plant, number of productive tillers per plant, number of tillers per plant, harvest index and grain breadth. High heritability coupled with high genetic advance as per cent mean for spikelet fertility, test weight, plant height, harvest index, grain yield per plant, grain length, number of productive tillers per plant, number of tillers per plant and L:B ratio indicating additive gene action in their genetic control. Grain yield per plant was exhibited positive significant correlation with test weight, harvest index, number of productive tillers per plant, number of grains per panicle, plant height, spikelet fertility and panicle length. Path analysis in F_2 generation indicated the positive direct effect for number of grains per panicle, number of productive tillers per plant, harvest index, test weight, grain length, days to 50 per cent flowering, number of tillers per plant and plant height. Superior desirable transgressive segregants (MP-312, MP-319, MP-299, MP-243, MP-238, MP-291, MP-200, MP-242, MP-237 and MP-215) were identified in the cross for advancing to the next generation.

July, 2017   (Dushyantha Kumar, B. M)

Major Advisor

18. Genetic Investigation on End-of Season Drought Stress in Advanced Breeding Lines of Groundnut (*Arachishypogaea* L.)

CHANDRASHEKHARA, G.

ABSTRACT

The present investigation focused on the study of morphological, physiological and biochemical response of forty groundnut genotypes under both managed drought stress (end season drought stress) and normal moisture conditions was conducted at College of Horticulture, Hiriyur using randomized complete block design with two replications. The analysis of variance revealed the existence of highly significant differences among the genotypes under study for all the traits studied. A wide range of variability and high heritability coupled with high genetic advance were recorded for most of the yield contributing traits. The association studies revealed that, pod yield per plant showed significant positive correlation with number of mature pods per plant, number of immature pods per plant, number of pods per plant, number of kernels per plant, kernel yield per plant, fresh seedling weight, harvest index, oil content and root to shoot ratio. The results of path analysis reflected that, the yield related traits *viz.,* relative water content, phenolic content of leaves, oil content, root to shoot ratio, plant height, number of secondary branches per plant, number of mature pods per plant, number of immature pods per plant, number of kernels per plant, test weight, kernel yield per plant, fresh seedling weight, harvest index and days to maturity had direct positive effect on pod yield under moisture stressed field condition. The genotypes Dh - 234, R - 2001 - 3, ICGV - 15151, ICGV - 15138, SB - 14, ICGV - 15145, ICGV - 15154, ICGV - 15146, ICGV - 15159 and ICGV - 15158 have been identified as drought tolerant genotypes in view of their better drought tolerance ability and these can be used as donor parents to develop drought tolerant varieties in further breeding programme.

August, 2017   (Harish Babu, B. N.)
                                                                                                          Major Advisor

19. Studies on Variability, Diversity and Characterization of Genotypes in Brinjal (*Solanum melongena* L.)

JYOTI PRABHULINGA JIRANKALI

ABSTRACT

The present investigation in brinjal (*Solanum melongena* L.) was undertaken during *kharif* season of 2016. Hundred brinjal genotypes along with two checks were evaluated in Augmented design in University of Horticultural and Agricultural Sciences, Shivamogga. Analysis of variance revealed high significant differences among genotypes for fifteen out of nineteen characters studied. High estimates of PCV, GCV, heritability coupled with high genetic advance were observed for fruit weight, number of fruits per cluster and shoot borer infestation. Hence indicating high variability for these traits and selection for these traits may be effective.

Correlation studies revealed significant and positive association for total yield per plant with fruit weight, number of primary branches, fruit length, number of fruits per cluster, fruit diameter. Path analysis studies revealed high direct effects for fruit weight, number of primary branches, fruit length, number of fruits per cluster and fruit diameter on total yield per plant.

Mahalanobis D^2 analysis grouped 100 genotypes of brinjal into four clusters. The cluster III showed maximum intra-cluster distance and maximum inter-cluster distance was observed between clusters II and III, these genotypes can be chosen for further breeding programme through hybridization. Yield contributed maximum to the genetic diversity followed by leaf area, fruit borer infestation, fruit weight, Plant spread, days to first fruit maturity. Characterization for qualitative and quantitative characters showed high variability among the genotypes, based on different characters related to spines, flower, stem, leaf and fruit. The genotypes performing well can be released as a variety or it can be put to further use in the breeding programme as a breeding line by the breeder.

July, 2017   (Gangaprasad S)
                                                                                                   Major Advisor

20. Assessment of Genetic Diversity of Rice Genotypes for Submergence Tolerance in Rainfed Lowlands

LAHARI, G.

ABSTRACT

The present investigation was carried out atCollege of Agriculture, Shivamogga during summer 2016 to screen 107 rice genotypes including 4 checks (FR13A, Swarna Sub1, Hemavathi and Jyothi) for their survival ability under submergence using Augmented design. Among 107 genotypes, 49 genotypes with higher survival percentage were selectedand laid out using Randomized Complete Block Design with two replications under submergence during *kharif* 2016 for evaluating genetic variability, character association, path analysis and genetic divergence for thirteen traits.

The analysis of variance revealed a significant difference among the genotypes for all the characters under study. High PCV and GCV coupled with high heritability and high GAM was recorded in number of tillers per plant, number of productive tillers per plant, grain yield per plant, straw yield per plant and absolute growth rate. Correlation studies revealed highly positive significant association of grain yield per plant with number of tillers per plant, number of productive tillers per plant, number of spikelets per panicle, number of filled grains per panicle and straw yield per plant.The highest positive direct effect on grain yield was observed in straw yield per plant and harvest index. Using Mahalanobis D^2, 49 genotypes were grouped into eight clusters. The maximum inter cluster distance was observed betweencluster VII and cluster VIII. Among all the characters,absolute growth rate had maximum contribution towards genetic divergence. Hence from the present investigation three promising genotypes viz., IET 19171, IET 17393 andIET 18508 have been identified as high yielding submergence tolerant rice varieties.

August, 2017   (B. M. Dushyantha Kumar)

Major Advisor

21. Genetics of Yield and Yield Parameters in FCV (Flue Cured Virginia) Tobacco Hybrids (*NicotianaTabacum*L.)

MEGHA GANACHARI

ABSTRACT

The present investigation was conducted to assess the combining ability, gene action and heterosis in respect to leaf yield and its component charactersthrough 6 x 6 diallel mating design involving thirty hybrids (developed through full diallel) and six parents in FCV tobacco during *kharif*2016 at ZAHRS,CoA, Shivamogga.

The analysis of variance indicated significant amount of variability among genotypes for sixteen quantitative characters studied except for the characters like number of leaves per plant, reducing sugar and nicotine content.Heterosis was recorded for leaf yield and its component characters andthe studyon standard heterosis revealed that five hybrids *viz.,* 6 x 1, 3 x 1, 2 x 1, 4 x 1 and 6 x 2 exhibited significant positive heterosis for cured leaf yield over bestcommercial check Kanchan.

Combining ability analysis was carried out for leaf yield andits components in FCV tobacco. Both general combining ability (GCA) and specific combining ability (SCA) variances were highly significant for almost all the characters indicating the importance of both additive and non additive gene actions. Parents and F_1 hybrids differed significantly for GCA and SCA effects for all the characters respectively. The ratios of GCA:SCA variance revealed the predominance of non-additive gene action in the inheritance of all the traits and these traits can be improved for combining ability through heterosis breeding. Study on the combining ability revealed that the parents Kanchan, FCH-222 and Tobios-6 were found to be best general combiners for cured leaf yield than others. The highest significant positive SCA effect was observed in the cross 2 x 4 followed by 1 x 3, 6 x 1, 1 x 4 and 1 x 5 for cured leaf yield. These hybrids were found to be suitable for obtaining higher cured leaf yield in FCV tobacco.

July, 2017   (H. D. Mohan Kumar)
                                                                                                         Major Advisor

22. Assessment of variability and genetic divergence in cucumber (*Cucumissativus*L.)

MEGHA HOSAMANI
ABSTRACT

Thirty five diverse genotypes of cucumber collected from different indigenous sources were planted in Augmented design, during *kharif* of 2016 at ZAHRS, CoA, Shivamogga and were assessed to know the variability, correlation, path analysis and divergence for different yield related traits.

The analysis of variance indicated significant amount of variability among genotypes for nineteen quantitative characters studied.The high value of GCV and PCV was observed for characters like fruit weight, number of fruits per vine and yield per vine. Low GCV and PCV was observed for days to first female flowering, days to first male flower, internodal length, days to first fruit harvest and vine length. High heritability estimates coupled with high genetic gain were observed for fruit weight, no of fruits per vine and yield per vine.

Total fruit yield per vine had positive correlation with leaf length, leaf breadth, petiole length, no of female per node, number of male per node, vine length, number of branches per vine, node number at which male appears, fruit length, whereas positive significant correlation was observed for number of nodes per vine, fruit weight and number of fruits per vine. Phenotypic path co-efficient analysis for fruit yield per plant revealed that the characters like fruit weight and number of fruits per plant have high positive direct effect towards yield. The genotypes were grouped into two clusters and highest intracluster distance was found in cluster II (479.96). Intercrossing the genotypes from these two clusters generate wider variability and is expected to throw high yielding transgressive segregants in a population improvement programme.

July, 2017   (S. Gangaprasad)

Major Advisor

23. **Studies on genetic diversity for drought tolerance in local land races of rice (*Oryzasativa* L.) under aerobic condition**

NAVYA, G. T.

ABSTRACT

Rice is the principle food crop for more than half of the world's population. The frequent occurrences of abiotic stress are the key to decreased productivity of rice. Drought is identified as the major abiotic stress affecting the yield of rice.The present study was undertaken to evaluate 49 local land races of rice including checks in field and PVC pipes for screening drought tolerant genotypes, assessing genetic variability, correlation, path coefficients and genetic divergence under control and drought condition. ANOVA revealed highly significant difference for all the characters. Yield per plant was significantly and positively associated with productive tillers per plant, number of spikelets per panicle, number of filled grains per panicle, seed filling per cent and test weight. Physiological characters like chlorophyll content, relative water content, proline content, root length, root to shoot ratio and root volume showed significant positive correlation with yield under drought condition. Phenotypic path-coefficient analysis revealed that test weight in drought and number of spikelets per panicle under control showed highest direct effect on yield per plant and among physiological characters root length under drought and control condition exhibited highest direct effect on yield. Using Mahalanobis' D^2 statistics, genotypes were grouped into eightclusters, wide genetic variability was indicated by the intra and inter cluster distances. Maximum inter cluster distance was observed between cluster IV and cluster VIII under drought condition and between cluster VII and VIII under control condition. Based on yield and yield attributes results under both drought and control conditions the genotypes Sannavaalya, Manjakaime, JGL-1798, Gangadace, Madras sanna and Najarbadwere recommended for drought tolerance breeding programme as well as adoption under drought stress condition.

July, 2017   (B. M. Dushyantha Kumar)

                                                                                        Major Advisor

24. Heterosis and Combining Ability Studies for Yield and Yield Attributing Traits in Brinjal (*Solanum melongena* L.)

NIKHILA

ABSTRACT

The present investigation was conducted to assess the heterosis and combining ability in brinjal with respect to yield and yield attributing traits through line x tester mating design. Seven lines and three testers were crossed to develop twenty-one F_1 hybrids during *kharif* – 2016 and were evaluated during *rabi* 2016-17 at ZAHRS, CoA, Shivamogga.

The analysis of variance due to genotypes was highly significant for most of the characters except for plant spread. Heterosis was recorded for yield and yield attributing traits and the top five hybrids *viz.*, Bili chandu badane x Mullugai badane, Bili udda badane x Mullugai badane, 40 A badane x Mullugai badane, Desi jawari badane x Mullugai badane and Nati badane x Mullugai badane exhibited significant positive heterosis for yield per plant over standard check.

Combining ability analysis was carried out for fruit yield and yield attributing traits in brinjal. Both general a combining ability (GCA) and specific combining ability (SCA) variances were highly significant for almost all the characters indicating the importance of both additive and non-additive gene actions. SCA variances were higher than the GCA variances except for three characters, indicating non-additive gene action in most of the traits and these traits can be improved by heterosis breeding. These hybrids would be advantageous for production and quality improvement. The three characters like plant height, fruit length and fruit length to diameter ratio showed additive gene action which can be improved by reciprocal recurrent selection. The parents like Bili udda badane, Nati badane and Mullugai badane showed highly significant positive GCA effects, the crosses Thailand badane x Dodda mullina badane, Sakleshpur badane x Dodda mullina badane and Bili chandu badane x Mullugai badane showed the highly significant positive SCA effects for the yield per plant.

July, 2017   (T. H. Gowda)
                                                                                    Major Advisor

25. Variability studies in segregating populations of cowpea (*Vignaunguiculata* (L). Walp)

SHEELA, H. K.

ABSTRACT

The present investigation in cowpea (*Vignaunguiculata* (L). Walp.) was undertaken during 2015-2016 at ZAHRS, Shimogga tostudy the variability parameters, correlation, path analysis and to identify superior segregants in F_2 and F_3segregating populations of the crosses UAHS 47 X UAHS 34 for brown population and UAHS 58 X North bold for white population. F_2, F_3 and parental cultivars were evaluated for 12 quantitative characters and statistical parameters were estimated. The high GCV and PCV were observed for seed yield per plant, number of pods per plant, plant height, number of clusters per plant and test weight in F_2 and $F_3$of both the crosses.Heritability and genetic advance over mean were higher for plant height, number of primary branches, number of secondary branches, number of clusters per plant, number of pods per plant, pod length, number of seeds per pod, test weight and seed yield per plant in both generation of both the crosses.The correlation coefficient analysis revealed that number of clusters per plant, total number of pods per plant and test weight showing significant positive association with seed yield in F_2 and F_3 of both the crosses.In the path analysis the characters like number of pods per plant and test weight showed highest positive direct effect on seed yield.The diversity analysis between families in F_3 revealed that the selection of families from the clusters formed will helps us to retain the variability present in the families by reducing the families' number. Transgressive families were selected in F_3 for further generation. The selection for the seed yield along with number of clusters per plant, total number of pods per plant and test weight will be highly reliable for developing high yielding genotypes in further generations.

July, 2017

(T. H. Gowda)
Major Advisor

26. Variability and character association in F_3 generation of FCV (Flue Cured Virginia) tobacco (*Nicotiana tabacum* L.)

SHUBHA, K. N.

ABSTRACT

The present investigation was carried out at ZAHRS, UAHS, Shivamogga during 2016-2017 *Kharif* season to study the genetic variability, heritability, genetic advance, character association and path analysis in respect of cured leaf yield and its conributing traits in F_3 generation of FCV (Flue Cured Virginia) tobacco cross TB-70 x TB-102. The mean and variance in sixteen quantitative characters in F_3 generation of the cross TB-70 x TB-102 indicated wide variability among the families for all the traits *viz.,* leaf area per plant, internodal length, plant height, chlorophyll content, specific leaf weight, number of leaves, leaf length, leaf breadth, green leaf yield, cured leaf yield, top grade equivalent, reducing sugar content and nicotine content. GCV and PCV values were relatively higher for leaf area per plant. Heritability estimates were high for all the characters investigated except for nicotine content which exhibited moderate heritability. High heritability combined with high genetic advance as percent mean was observed for plant height, chlorophyll content, specific leaf weight, internodal length, number of leaves per plant, leaf breadth, leaf area per plant, green leaf yield, cured leaf yield, top grade equivalent and reducing sugar. The component characters *viz.,* green leaf yield, top grade equivalent, stem girth, number of leaves per plant, leaf length, leaf area per plant, plant height and leaf breadth exhibited significant positive correlation with each other and also with cured leaf yield. Path analysis in F_3 generation indicated maximum positive direct effect of number of leaves per plant, top grade equivalent, leaf breadth, leaf length and green leaf yield on cured leaf yield. In the present investigation superior promising individual families were identified in F_3 generation. Therefore, for improving cured leaf yield selection may be based on characters which have shown positive direct association with cured leaf yield.

July, 2017

(H. D. Mohan Kumar)
Major Advisor

27. Studies on genetic variability in segregating generation of green gram

VEERASENA REDDY

ABSTRACT

The present investigation in green gram(*Vignaradiata*(L). Wilczek.) was undertaken during 2015-2016 at ZAHRS, Shivamogga to study the variability parameters, correlation, path analysis and to identify superior segregants in F_2segregating populations of the crosses MLS x UAHS bold and MLS x BOLD-2. F_2, and parental cultivars were evaluated for 12 quantitative characters and statistical parameters were estimated. The high GCV and PCV were observed for seed yield per plant, number of pods per plant, plant height, and number of clusters per plant in F_2population of both the crosses.Heritability and genetic advance over mean were higher for plant height, number of primary branches, number of secondary branches, number of clusters per plant, number of pods per plant, pod length, number of seeds per podand seed yield per plant in both population of both the crosses. The correlation coefficient analysis revealed that number of clusters per plantand total number of pods per plant showing significant positive association with seed yield in F_2generation of both the crosses. In the path analysis the characters like number of pods per plant and pods per cluster showed highest positive direct effect on seed yield. Transgressive families were selected in F_2 for further generation. The selection for the seed yield along with number of clusters per plant and total number of pods per plant will be highly reliable for developing high yielding genotypes in further generations.

August, 2017

(S. Shivanna)
Major Advisor

28. Assessment of genotypes X environment interaction in advanced breeding lines of rice (*Oryzasativa*L.)

VITTAL TAPASI

ABSTRACT

Rice (*Oryza sativa* L.) isone of the staple food crops of the world. The present study was undertaken to evaluate twenty advanced breeding lines in a Randomized Complete Clock Design with two replications during *Kharif*2016 at six locations*viz,* AHRS, Kattalagere,College of Agriculture (CoA), Shivamogga, AHRS, Honnavile. ZAHRS, Mudigere. AHRS, Bavikere and AHRS, Ponnampetefor variability, diversity and stability for yield and its components. ANOVA revealed significant differences among all the advanced breeding lines for all the characters studied. High range of variation, PCV, GCV and high heritability coupled with high GAM was observed for days to fifty *per cent* flowering, days to maturity, plant height, and grain yield. Plant height, number of tillers, number of productive tillers,number of grains per panicle, test weight, harvest index and straw yield had significant positive association with grain yield at phenotypic level. Harvest index had the highest positive direct effect on grain yield, whereas highest positive indirect effect on grain yields by number of grains per panicle via number of spikelets per panicle. Using Mahalanobis' D^2 statistics, advanced breeding lines were grouped into five clusters, cluster I consists highest number of advanced breeding lines. Days to maturity and plant height had highest contribution towards the genetic diversity. The advanced breeding line JA-6-2 is identified as the stable variety for grain yield in all the six locations, whereas JT-2-16-1 (AHRS, Kattalagere), JT-2-22-5 (CoA shivamogga), JA-4-3 (AHRS,Honnavile), JT-2-15-1(ZAHRS, Mudigere), JB-1-20-2(AHRS, Bavikere) and JK-1-7-5 (AHRS,Ponnampete) are identified as stable lines for specific locations for grain yield.

June, 2017   (C. Malleshappa)
                                                                                    Major Advisor

29. Induced Mutagenesis in Groundnut (*Arachishypogaea* L.) cv. TMV-2 following EMS Treatment

AVINASH KUMAR

ABSTRACT

The present investigation was aimed to assess the extent of genetic variability, nature of association of yield and yield attributing traits in mutated population of cv.TMV-2 which was carried out at the ZAHRS, Shivamogga during *Kharif-*2017 and AHRS, Bhavikere, summer-2018. Mutagenic effectiveness and efficiency decreased with increase in dose of EMS. Dose 0.3 and 0.4 percent of EMS were found to be best for creating mutation in groundnut cv. TMV-2. Mean performance of the mutated plant progenies revealed a wide range of variability for the yield and yield related traits. The range was the highest for kernel per plant, plant dry weight and shelling percent. High PCV and GCV were observed for pod yield per plant and kernel yield per plant. Wide range of variability suggested greater phenotypic and genotypic variability among the plants and responsiveness of the attributes for making further improvement by selection. High heritability coupled with moderate to high genetic advance as percent of mean was observed for traits like pod yield per plant, test weight and harvest index which shows higher response for selection of high yielding plants. The highest positive and significant association was found between pod yield per plant, test weight and harvest index indicating that these characters are the primary yield determinants in groundnut. Thus selection for these traits might be rewarding. Superior mutants (line no. 37, 50, 97, 98, 99, 108, 112, 130, 163 and 239) which exhibited higher pod yield per plant (g), kernel yield per plant (g), test weight (g) and shelling percent than the parent groundnut cv. TMV-2, have to be advanced to next generation.

August, 2018   (H. D. Mohan Kumar)

                                                            Major Advisor

30. Gamma Rays Induced Genetic Variability in Groundnut (*Arachis hypogaea* L.) cv.TMV-2

BHEEMAREDDY

ABSTRACT

The present investigation was aimed to assess the extent of genetic variability, nature of association ofyield and yield attributing traits in mutated population of cv.TMV-2 which was carried out at the ZAHRS, Shivamogga during *Kharif*-2017 and AHRS, Bhavikere during summer-2018.The mutagenic effectiveness and efficiency decreased with increase in dose of gamma rays. 200 Gy and 250Gy doses of gamma ray found best for creating mutation in groundnut cv. TMV-2.The mean performance of the mutated plant progenies revealed a wide range of variability for all theyield and yield related traits. The range was the highest for kernel per plant, pod yield per plant and test weight. High PCV and GCV were observed for pod yield per plant and kernel yield per plant. Wide range of variability suggested greater phenotypic and genotypic variability among the plants and responsiveness of the attributes for making further improvement by selection.High heritability coupled with moderate to high genetic advance as percent of mean was observed for traits like, test weight, shelling per cent, plant height and pod yield per plant which shows higher response for selection of high yielding plants. The highest positive and significant association was found between pod yield per plant and kernel yield per plant, number of pods per plant and harvest index indicating that these characters are the primary yield determinants in groundnut. Thus selection for these traits might be rewarding. Superior mutants (line no. 47, 70, 72, 75, 76, 77, 80, 103, 160 and 256) recovered from mutation which exhibited higher pod yield per plant (g), kernel yield per plant (g), test weight (g) and shelling percent than the parent groundnut cv. TMV-2, and advanced to next generation.

August, 2018   (H. D. Mohan Kumar)
                                                                                                   Major Advisor

31. **Assessment of Genetic Variation Induced through Mutation in Okra [*Abelmoschus esculentus* (L.) Moench]**

BHUVANESHWARI

ABSTRACT

The present investigation was aimed to assess the extent of genetic variability, character association, path analysis and identification of mutant lines tolerant to sucking pests in M_2 population of cv, Arka Anamika which was carried out at the ZAHRS, Shivamogga during *Kharif*-2017. Highest variability was observed for fruit yield per plant followed by plant height, days to first flowering and seeds per fruit. High PCV and GCV were observed for fruit yield and number of fruits per plant. High heritability coupled with moderate to high genetic advance as percent of mean was observed for traits like, fruit yield per plant, number of fruits per plant and hundred seed weight suggested that the preponderance of additive genes. The highest positive and significant correlation coefficient of fruit yield per plant has been noted with number of fruits per plant per plant, plant height and fruit weight indicating that these characters are the primary yield determinant in okra. Path coefficient analysis revealed that number of fruits per plant had highest positive direct effect followed by fruit weight and plant height. Thus selection for these traits might be rewarding. Among the studied population 4 plants *viz.*, M-4, M-72, M-163 and M-342 showed resistant to both leaf hoppers and aphids. Superior mutants like M-258, M-66, M-4, M-71, M-2, M-253, M-36, M-423, M-41 and M-357 showing higher yield can be tested across location.

August, 2018   (Gangaprasad S)
                                                       Major Advisor

32. Assessment of Morphophysiological Traits related to Submergence Tolerance in Rice Genotypes for Rainfed Lowlands

CHANDANA, B. R.

ABSTRACT

The present investigation was carried out at Zonal Agricultural and Horticultural Research Station, Navile, Shivamogga.The experiment consisted of 177 rice genotypes including three checks FR13A, Hemavathi and Jyothi for screening them for submergence tolerance using augmented design during summer 2017.Among them, 43 genotypes including checks showing more than 50 per cent survival per cent were selected, evaluated for morphophysiological traits, genetic diversity, variability, character association and path analysis for thirteen traits using Randomized Complete Block Design during *Kharif* 2017. Analysis of variance showed significant differences among the genotypes for all the traits studied. The phenotypic correlation for physiological parameters with grain yield and harvest index showed that the survival per cent, chlorophyll and harvest index had significant positive correlation with grain yield per plant.Whereas, stem elongation per cent showed negative correlation with grain yield per plant. High GCV and PCV coupled with high heritability and GAM was recorded in productive tillers per plant, number of tillers per plant, spikelet fertility and grain yield per plant. Correlation studies showed that plant height, number of tillers per plant, number of productive tillers per plant, number of spikelets per panicle, spikelet fertility, straw yield, harvest index and 1000-grain weight showed significant positive correlation with grain yield per plant. The highest direct positive effect was exhibited by harvest index followed by straw yield. Mahalanobis D^2 statistics grouped the 43 genotypes into eight clusters. The maximum inter cluster distance was found between cluster I and VII and the lowest distance was found between cluster I and III. Seven SSR markers revealed the presence of high molecular diversity among the genotypes grouping them into XI clusters. The present study showed that the genotypes Doddaaluru, Kagga, Nareminda, Bilidaddi and Kempudadimaratiga are submergence tolerant genotypes and are suitable for both submergence and non-submergence conditions.

July, 2018   (Dushyantha Kumar, B.M.)
                                                                            Major Advisor

33. Genetic Variability and Molecular Diversity in Groundnut (Arachis hypogaea L.,) for Aspergillus Flavus Seed Colonization and Aflatoxin Contamination

HASANALI NADAF

ABSTRACT

In recent times, edible groundnuts have attracted major attention in the international market. Aflatoxin contamination and pesticide residues are the major obstacles in its export. Hence, development of cultivars with resistance to seed colonization by *Aspergillus flavus* and aflatoxin contamination is a major objective in groundnut breeding. In the present investigation, significant differences were noticed among 66 groundnut genotypes for *in vitro* seed colonization by *A. flavus* (IVSCAF), aflatoxin contamination, yield and its component traits (under both normal moisture and moisture stress condition). Yield traits *viz.*, number of primary branches per plant, pod yield (kg/ha) and kernel yield (kg/ha) have exhibited high heritability coupled with high genetic advance over mean indicating better scope for selection for these traits. The genotypes SB-T10, ICGV-15138 and ICGV-15124 have shown high level of resistance to *Aspergillus* seed colonization. Popular cultivars TMV-2 and GPBD-4 were susceptible to seed colonization. The present study revealed an increase in aflatoxin contamination under moisture stress as compared to normal moisture condition. Genotypes *viz.*, ICGV-15119, Dh-234, Dh-246, Dh-216, Dh-101, Dh-86, K-9, SB-T13, SB-T14, VB-T31, SB-T2 and J-11 have recorded no aflatoxin contamination under both normal moisture and moisture stress conditions indicating their tolerance to aflatoxin contamination. The molecular diversity analysis with 30 SSR primers revealed that, germplasm lineICGV 15143and cultivar Dh-101 were found to be most divergent genotypes. Single marker analysis has revealed that, marker S-21, S-80 and GM-1954 have significant association with tolerance to aflatoxin contamination. Four markers *viz.,* GM-1954, GM-1883, pPGPseq2F05 and S-03 were linked to IVSCAF. The marker GM-1954 was found to be associated with tolerance to both aflatoxin contamination and *in-vitro* seed colonization by *Aspergillus flavus*.

January, 2019

(Harish Babu B N)
Major Advisor

34. Assessment of Stability and Yield Performance of Advanced Breeding Lines of Rice (*Oryza sativa* **L.**)

MUTTURAJ MAHADEV DHAVALESHVAR

ABSTRACT

The present study was undertaken to evaluate twenty-seven advanced breeding lines in a Randomized Complete Block Design with two replications during *Kharif* 2017 at three locations *viz.,* ZAHRS, Shivamogga, AHRS, Kathalagere and AHRS, Ponnampet for variability, stability, correlation and path analysis for yield and yield attributing characters. ANOVA revealed significant differences for all the studied characters among the advanced breeding lines. Moderate GCV and PCV were recorded for traits *viz.,* plant height, number of spikelets per panicle, number of grains per panicle, test weight, straw yield and grain yield. High heritability coupled with high genetic advance as per cent of mean were recorded for plant height, L/B ratio, test weight and grain yield. Harvest index and straw yield had positive significant association with grain yield at phenotypic level. Among thirteen characters, eight characters had a positive and direct effect on grain yield at phenotypic level *viz.,* days to fifty per cent flowering, days to maturity, panicle length, number of productive tillers, number of grains per panicle, test weight, straw yield, and harvest index. In which harvest index had highest positive direct effect on grain yield. Advanced breeding lines KPR2IS 2-8-1 and MMBPT 1-11-4 were identified as the most promising advanced breeding line for grain yield as indicated by their higher mean performance across three locations. The advanced breeding lines MMKPR2 5-2-3 and KPR2IS 9-3-3 for ZAHRS, Shivamogga, JGK2 9-9-6-2-5, MMBPT 1-11-1 and KPR2IS 1-7-3 for AHRS, Kathalagere and MMKPR2 5-2-1 and JGK2 9-9-6-2-5 for AHRS, Ponnampet respectively, were identified as stable lines for specific locations for yield.

August, 2018   (C. Malleshappa)
                                                                                      Major Advisor

35. Assessment of Genetic Variability and Diversity in Finger Millet (*Eleusine coracana* (L.) Gaertn) Genotypes

PRASHANTHA, B. N.

ABSTRACT

The aim of present investigation was to assess the extent of genetic variability, divergence, nature of association and micronutrient content in sixty genotypes of finger millet which was carried out at the Zonal Agricultural and Horticultural Research Station, Shivamogga during *kharif* 2017. The analysis of variance revealed the existence of highly significant differences among the genotypes for all the traits studied. A wide range of variability and high heritability coupled with high genetic advance was recorded for most of the yield, yield contributing and quality traits. Grain yield plant^{-1} possessed significant positive correlation with days to 50 per cent flowering, days to maturity and earhead weight plant^{-1}. Path analysis revealed that, the characters like days to maturity, earhead weight plant^{-1} and straw yield plant^{-1} had direct positive effect on grain yield plant^{-1}. The maximum inter cluster distances for grain yield and quality traits were recorded between cluster IV and cluster VIII and cluster IV and cluster I respectively. Genotypes from these clusters can be selected for hybridization programme to get desirable recombinants to improve further grain yield with quality. Plant height and calcium content had maximum contribution towards genetic diversity, indicates the presence of wide diversity among the genotypes under study for the traits. Two genotypes, Malali (25.30 g/plant) and IC-473155 (25.20 g/plant) recorded significantly higher yield than varietal check, GPU-28   (21.35 g/plant). Genotype, IC-474959 was superior for calcium (398.62 mg/100g), magnesium (167.77 mg/100g) and copper content (0.95 mg/100g). The higher iron and zinc content was exhibited by the genotypes, IC-473388 (14.19, 5.45mg/100g), IC-473143 (13.85, 5.65mg/100g) and Jeenumundaga Ragi (7.05, 5.65 mg/100g). These identified potential genotypes with high calcium, magnesium, iron, copper and zinc content can be further utilized as donor parents to transfer these traits to genotypes which are high yielding and well adapted.

July, 2018   (T. H. Gowda)
                                                                         Major Advisor

36. **Assessment of Genetic Diversity for Yield and its Component Traits and Screening for Blast Reaction in Rice (*Oryza sativa* L.) Genotypes under Low Land Condition**

RANGASWAMY D. M.

ABSTRACT

Rice (*Oryza sativa* L.) is one of the most important staple food crop for half of the world's population and grown worldwide. India being primary centre of origin it possesses huge diversity of rice genotypes of both wild and cultivated. The present study was undertaken to evaluate 145 rice genotypes for variability and diversity for yield and its component traits and all the genotypes were screened to blast disease according to IRRI scale. ANOVA revealed significant difference among the genotypes studied for all the characters. High PCV, GCV coupled with high heritability and high GAM was observed for total number of tillers per plant, number of productive tillers per plant, number of filled grains per panicle, grain yield per plant, straw yield per plant and harvest index. Number of filled grains per panicle and harvest index exhibited significant association with grain yield. Harvest index followed by straw yield per plant had the highest positive direct effect on grain yield whereas highest positive indirect effect of grain yield with trait number of filled grains per panicle *via* harvest index were recorded. Using Mahalanobis' D^2 statistics, genotypes were grouped into thirteen clusters the cluster II consists of maximum number of genotypes (30). Based on cluster distance, highest intra cluster distance were recorded in the cluster VII and highest inter cluster distance between cluster XII and XIII. Cluster mean analysis reveals that cluster XII received the first rank. Among all the characters, number of filled grains per panicle followed by plant height possessed high contribution towards the genetic divergence. Rice genotypes screened for to blast disease showed that the genotypes IET-17320, IET-21463, IR8609-79-33 and advanced breeding line MMKPR$_2$ 5-2-3 resistance. Among them advanced breeding line MMKPR$_2$ 5-2-3 had recorded the highest grain yield per plant.

August, 2018   (Dushyntha Kumar B. M.)

Major Advisor

37. Characterization of Local Rice (*Oryza sativa* L.) Genotypes for Various Morphological, Yield and Yield Attributing Traits

SACHIN KUMAR, H. M.

ABSTRACT

The present investigation was carried out to characterize 55 rice genotypes at ZAHRS, Shivamogga, during summer and *Kharif* 2017 using Randomized complete block Design.Thirty three qualitative and eleven quantitative characters were evaluated as per the guidelines of PPV&FRA, 2001.Out of 33 qualitative characters studied five characters were monomorphic, ten were dimorphic and 18 were polymorphic. Out of 11 quantitative characters studied five were dimorphic and six were polymorphic.The analysis of variance revealed highly significant difference among genotypes for all the characters studied.The high PCV and GCV values coupled with high heritability and high genetic advance as per cent mean were noticed for traits *viz.,* number of grains per panicleandgrain yield per plant. Correlation analysis revealed that traits *viz.,*days to 50 per cent flowering, days to maturity, stem thickness, numbers of tillers per plant, number of productive tillers per plant, number of grains per panicle and spikelet fertility showed significant positive correlation with grain yield per plant.Path coefficient analysis revealed that days to 50 percent flowering, stem thickness,numbers of tillers per plant, number of productive tillers per plant, panicle length, number of grains per panicle, spikelet fertility and test weight showed direct positive effect on grain yield.MahalanobisD^2 analysis clustered the genotypes intoeight clusters, the maximum intercluster distance was found between cluster VI and cluster VII. Assessment of molecular diversity using twelve SSR markers across fifty five rice genotypes revealed that six markers were monomorphic and six were polymorphic and genotypes were grouped into eleven clusters. The investigation showed the presence of some unique characters*viz.,* anthocyanin coloration, awns, black and brown caryopsis in fewgenotypes and also genetic and molecular diversity among the genotypes which could be utilized in the crop improvement program.

August, 2018   (Dushyntha Kumar B. M.)

                                                                                          Major Advisor

38. Pattern of Variability in F2 Segregating Generation of Brinjal (*Solanum melongena* L.)

VINUTHA PATIL S

ABSTRACT

The present investigation in brinjal (*Solanummelongena*L.) was undertaken during *kharif*, 2017 at college of agriculture, Navile, UAHS, Shivamogga, to study variability parameters, character association, path analysis and identification of transgressive segregants in respect of fruit yield and its component traits in F_2 population of Billichandubadane ×Mullubadane and Biliuddabadane × Mullubadane cross. GCV and PCV valueswere relatively higher for number of primary branches, number of fruits per cluster, number of fruits per plant for Billichandubadane×Mullubadane and number of flower per plant, number of fruits per cluster, number of primary branches, number of fruits per plant and fruit yield per plant for Biliuddabadane ×Mullubadane. High heritability coupled with moderate genetic advance as per cent mean for days to first flowering for Billichandubadane × Mullubadane anddays to first floweringfor Biliuddabadane×Mullubadane indicating additive gene action in their genetic control.

Fruit yield per plant was exhibited positive significant correlation with plant height, days to first flowering, number of flowers per plant, number of fruits per plant, fruit length forBillichandubadane ×Mullubadane and days to first flowering, number of primary branches, plant height, number of fruits per plant, fruit length for Biliuddabadane × Mullubadane.

Path analysis in F_2 generation indicated the positive direct effect for number of fruits per plant,for Bilichandubadane×Mullubadane and fruit width for Biliuddabadane × Mullubadane. Superior desirable transgressive segregants (P-31, P-54, P-69, P-116 and P-155) were identified in the crossBillichandubadane ×Mullubadane and (P-17, P-29, P-33, P-94 AND P-69) forBiliuddabadane ×Mullubadane advancing to the next generation.

July, 2018

(Gangaprasad S)
Major Advisor

39. Assessment of Genetic Variability and Diversity in Horse Gram (*Macrotyloma uniflorum* L.) Genotypes

VISHWANATHA, S. D.

ABSTRACT

Horsegram is an important and exploited tropic and sub-tropic legume crop grown mostly in dry land agriculture. The study involving 39 genotypes of horse gram (*Macrotyloma uniflorum* L.) was conducted at the Agriculture and Horticulture Research Station, Bhavikereduring late *Kharif*season of 2017 to assess the nature and magnitude of genetic variability, character association and path analysis for grain yield and its component trait and diversity analysis. The results indicated significant differences among the 39 genotypes for all characters studied, indicating the presence of new variability among genotypes. High variability and heritability coupled with high genetic advance were observed for number of branches per plant, plant height, number of pods per plant and days to 50% flowering depict the presence of additive gene action and possible scope for the improvement of these characters. The correlation coefficient analysis revealed that grain yield showed significant positive correlation with number of pods per plant, plant height, number of seeds per pod, number of branches per plant, and days to 50% flowering. In path analysis characters like number of pods per plant, seeds per pod and plant height showed highest positive direct effect on seed yield. Mahalanobis D^2 statistics grouped all the 39 cultivars of horsegram into eleven clusters. The maximum inter cluster distance (305.20) was noticed between cluster II and cluster X. The maximum intra cluster distance ranged from 0 (clusters III, IV, VII, VIII, IX, X and XI) to 38.06 (cluster V), indicating that the genotypes in these clusters were relatively more diverse than the genotypes within other clusters. Days to 50% flowering contributed maximum (41.43%) to the genetic divergence.

October, 2018   (T. H. Gowda)

                                                                Major Advisor

40. Genetic Variability and Molecular Diversity in Groundnut (Arachis hypogaea L.,) for Aspergillus flavus Seed Colonization and Aflatoxin Contamination

(Hasanali Nadaf)

ABSTRACT

In recent times, edible groundnuts have attracted major attention in the international market. Aflatoxin contamination and pesticide residues are the major obstacles in its export. Hence, development of cultivars with resistance to seed colonization by Aspergillus flavus and aflatoxin contamination is a major objective in groundnut breeding. In the present investigation, significant differences were noticed among 66 groundnut genotypes for in vitro seed colonization by A. flavus (IVSCAF), aflatoxin contamination, yield and its component traits (under both normal moisture and moisture stress condition). Yield traits viz., number of primary branches per plant, pod yield (kg/ha) and kernel yield (kg/ha) have exhibited high heritability coupled with high genetic advance over mean indicating better scope for selection for these traits. The genotypes SB-T10, ICGV-15138 and ICGV-15124 have shown high level of resistance to Aspergillus seed colonization. Popular cultivars TMV-2 and GPBD-4 were susceptible to seed colonization. The present study revealed an increase in aflatoxin contamination under moisture stress as compared to normal moisture condition. Genotypes viz., ICGV-15119, Dh-234, Dh-246, Dh-216, Dh-101, Dh-86, K-9, SB-T13, SB-T14, VB-T31, SB-T2 and J-11 have recorded no aflatoxin contamination under both normal moisture and moisture stress conditions indicating their tolerance to aflatoxin contamination. The molecular diversity analysis with 30 SSR primers revealed that, germplasm lineICGV 15143and cultivar Dh-101 were found to be most divergent genotypes. Single marker analysis has revealed that, marker S-21, S-80 and GM-1954 have significant association with tolerance to aflatoxin contamination. Four markers viz., GM-1954, GM-1883, pPGPseq2F05 and S-03 were linked to IVSCAF. The marker GM-1954 was found to be associated with tolerance to both aflatoxin contamination and in-vitro seed colonization by Aspergillus flavus.

January, 2019   (Dr. Harish Babu B N)
                                                                                        Major Advisor

41. Genetic Analysis in Segregating Population of Okra [Abelmoschus esculentus (L.) Moench] for Yield and its Related Traits

(PRIYANKA, S. R.)

ABSTRACT

The present investigation was aimed to assess the extent of genetic variability, character association, path analysis and identification of transgressive segregsnts in F2 population of cross Phule Utkarshi × ArkaAnamika along with the parents as checks.This study was carried out at the ZAHRS Navile,Shivamogga during Kharif-2018.Theanalysis of variance revealed that existence of significant amount of variability for all the traits studied in the segregating population. Highphenotypic coefficient of variation(PCV) and genotypic coefficient of variation (GCV) were observed for number of branches per plant, number of fruits per plant, fruit weight, number of seeds per fruits, number of picking and yield per plant.High heritability coupled with high genetic advance as percent mean was observed for traits like plant height at maturity, number of fruits per plant, fruit weight, fruit width, fruit length, number of seeds per fruit, number of picking and yield per plant. The highest positive and significant correlation coefficient of yield per plant has been noted with plant height at maturity, number of branches per plant, number of internodes, number of fruits per plant, fruit weight, fruit width, fruit length, number of seeds per fruits and number of picking,indicating that these are the primary yield determinant characters in okra. Path coefficient analysis revealed that number of fruits per plant had highest positive direct effect followed by fruit weight. Thus selection for number of fruits per plant and fruit weight traits might be rewarding. Among the studied population,identified superior transgressive segregantsviz., P-137, P-144, P-147, P-28, P-129, P-68, P-145, P-67, P-115, P-233, P-243, P-27, P-132, P-186 and P-14, for higher yield can be tested across location.

August, 2019

(T. H.Gowda)
Major Advisor

42. Assessment of Genetic Variability in Segregating Population (F2) of Cherry Tomato (Solanum lycopersicum L. var. cerasiforme).

RAJESHWARI, TELI, A.

ABSTRACT

The present investigationwas carried out to assess the extent of genetic variability and identification of transgressive segregants in segregating (F2) population (250) of cross IIHR 2358 (Tomato) and Australian red (cherry tomato) for yield and quality traits. The experiment was undertaken at ZAHRSNavile, Shivamogga during Kharif-2018.Genetic variability analysis showed that existence of sufficient amount of variability formost of the traits. High estimates of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were observed for number of cluster per plant, number of flowers per plant, number of fruits per plant, primary branches per plant, pericarp thickness(mm) and lycopene content (mg/100g). The estimates of heritability and GAM were high for all studied traits except for days to first flowering, number of locules per fruit, TSS (Brix) and pulp content (%). Correlation analysis revealed fruit yield per plant had significant and positive association with number of clusters per plant, number of fruits per plant, plant height (cm), number of branches, average fruit weight (g) and fruit width (mm). Path coefficient analysis had showed positive direct effect of fruit yield on number of clusters per plant, plant height (cm), number of branches per plant, average fruit weight (g)and fruit width (mm).Among the 250 F2 plants P-165, P-128, P-168, P-59, P-17, P-03, P-64, P-48, P-18 and P-41identified superior transgressive segregantscan be evaluated for further advanced to stabilization and can be used as parents in hybridization programmefor yield and quality traits.

August, 2019   (Gangaprasad S.)
                                                                                         Major Advisor

43. Genetic and Morphophysiological Studies for Submergence Tolerance in Rice Landraces (Oryza sativa L.)

(RANJITHA G. V.)

ABSTRACT

The present investigation was carried out at Zonal Agricultural and Horticultural Research Station, Navile, Shivamogga. 100 rice landraces including four checks Viz.,FR13A, Hemavathi, Tunga and Jyothi constituted the experimental material and were laid out in augmented design to screen for submergence tolerance during summer 2018. 46 rice landraces showing more than 50 per cent survival and four checks were selected and further evaluated for morphophysiological traits, genetic diversity and variability for thirteenyield and yield related traits using Randomized Complete Block Design during Kharif 2018. Analysis of variance revealed significant differences among the landraces for all the traits. Physiological traits like survival per cent, chlorophyll content, absolute growth rate and harvest index had significant positive correlation with grain yield per plant.Whereas stem elongation showed negative correlation with grain yield per plant. High GCV and PCV coupled with high heritability and genetic advance as per cent mean was recorded in number of tillers per plant, number of productive tillers per plant, plant height, spikelet fertility, 1000 grain weight, harvest index and grain yield per plant. Correlation studies showed that panicle length, spikelet fertility, 1000 grain weight and harvest index had significant positive correlation with grain yield per plant. Mahalanobis D2statistics grouped the 46 landraces and four checks into eight clusters. The maximum inter cluster distance was found between cluster V and cluster VIII.Molecular diversity analysis using six SSR markers showed the presence of high molecular diversity among landraces grouping them into seven clusters. Landraces such as Halagabatta, Kangalli, Shasti, Guddapairnel andmuttinasannaare identified as submergence tolerantand can be further utilized in crop improvement programme.

August, 2019   (Dushyantha Kumar, B.M.)
                                                                                      Major Advisor

44. Assessment of Genetic Variability in F2 Tomato Population of cross, IIHR 2373 × Arka alok (Lycopersicon esculentum L.)

SANGAMESH

ABSTRACT

The present investigation in tomato (Solanum lycopersicon L.) was undertaken during Kharif, 2018 at Zonal Agricultural Horticultural Research Station, Navile, UAHS, Shivamogga, to study variability parameters, correlation, path analysis and identification of transgressive segregants in respect to fruit yield and its component traits in F2 population of the cross, IIHR-2373 (high shelf life) and Arka Alok (high yield). The distribution pattern indicated large number of genes with dominance based complementary interaction in the inheritance of plant height, number of branches, fruit length, fruit weight, shelf life and fruit yield per plant and duplicate type of interaction was noticed for pH content and days to first flowering. Variability analysis showed the presence of sufficient amount of variability among all the traits studied in the segregating population. Very little differences were observed between GCV and PCV for all the characters except days to first flowering and number of fruit per cluster indicating that most of the traits were less influenced by environmental factors for their phenotypic expression. High heritability coupled with high genetic advance as per cent mean was observed for all the traits except fruit diameter, days to first flowering and number of fruits per cluster indicating wide scope for improvement through selection most of these traits. The highest positive and significant correlation coefficient of fruit yield per plant was noted with plant height, fruit length, fruit diameter and average fruit weight. Path coefficient analysis revealed that average fruit weight had highest positive direct effect followed by plant height, indicating that these are the most important character contributing towards fruit yield. Superior transgressive genotypes (P-34, P-12, P-180, P-127, P-227, P-212, P-157, P-237, P-66 and P-47) that exhibited higher fruit yield per plant with extended shelf life were identified in the cross for advancing to the next generation.

August, 2019   (Gangaprasad S.)
                                                                        Major Advisor

45. Identification and Characterization of Rice Genotypes (Oryza sativa L.) for Salinity Tolerance

(Sravya, P. K.)

ABSTRACT

The present investigation was carried out in farmer's field at Thyavanige village of Davanagere district. Sixty rice genotypes including four checksviz.,Pokkali, CSR 27, CSR 36 and Jyothi were screened for salinity tolerance using randomized complete block design with two replications during Kharif 2018. Most of the plants of highly sensitive genotypes were died in visual scoring of genotypes for salt injury based on Standard Evaluation System at seedling stage. The remaining fifty four genotypes were studied for yield and yield attributing traits under saline condition. The analysis of variance revealed highly significant difference among genotypes for all the characters studied. High heritability and high genetic advance as per cent mean along with high to moderate GCV and PCV were noticed for days to fifty per cent flowering, number of filled grains per panicle, spikelets per panicle, spikelet fertility, plant height, grain yield per plant, number of tillers per plant, L/B ratio, test weight and productive tillers per plant. The correlation analysis revealed that, the characters viz., total number of tillers per plant, number of productive tillers per plant, number of filled grains per panicle, number of spikelets per panicle, spikelet fertility, test weight, chlorophyll content and L/B ratio had significant positive association with grain yield. The highest direct positive effect on yield was exhibited by number of filled grains per panicle followed by total number of tillers per plant. The Mahalanobis' D2 analysis grouped the genotypes into eight clusters. The maximum inter cluster distance was noticed between cluster III and cluster VIII. Seven SSR markers revealed the presence of high molecular diversity among the genotypes grouping them into seven clusters. The present study showed that the genotypes Marnavamidoddiga, Shivadappavalya, Tulasoimog, Gulvadisannakki, and Kavalakannu are salinity tolerant genotypes and could be further used in salinity tolerance introgression breeding program.

August, 2019

(C. Malleshappa)

Major Advisor

46. Assessment of Morphological Characteristics and Genetic Variability Studies in Landraces of Rice (Oryza sativa L.)

(SUJATA)

ABSTRACT

Present investigation was carried out to characterize 51 landraces of rice at Zonal Agricultural and Horticultural Research Station, Shivamogga, during the Kharif2018, Shivamogga using Randomized complete block Design. Forty one qualitative and thirteenquantitative characters were evaluated as per DUS guidelines given by PPV and FRA, 2001. Five characters such as the presence of leaf ligule, split shape of leaf ligule, absence of male sterility and presence of secondary branching characters were common in all the 51 landraces of rice. Remaining 36 characters were unique and distinct among the landraces of rice. Analysis of variance revealed a significant difference for all the characters. The high GCV, PCV and heritability with maximum genetic advance per cent mean was recorded for days to 50 per cent flowering, days to maturity, leaf length, stem thickness, plant height, total number of tillers per plant, number of productivetillers per plantand test weight.Correlation analysis revealed that traits viz.,total number of tillers per plant, number of productive tillers per plant, test weight, panicle length and panicle fertility showed significant positive correlation with grain yield per plant. Path analysis revealed that days to 50 per cent flowering, leaf width, the total number of tillers per plant, number of productive tillers per plant, panicle length and test weight showed a direct and positive effect on yield.Mahalanobis' D2clustered the landraces of rice into eight clusters, cluster IV and cluster V showed highest inter-cluster distance. The study will be useful for breeders, researchers and farmers to identify and choose the restoration and conservation of beneficial genes for crop improvement and also to seek protection under Protection of Plant Varieties and Farmer's Rights Act, 2001.

August, 2019   (Shridevi A. Jakkeral)

                                                                  Major Advisor

47. Assessment of Genetic Variability and Diversity in Advanced Breeding Lines of Rice (Oryza sativa L.)

(Supriya, R. V.)

ABSTRACT

The present investigation was carried out at Zonal Agricultural and Horticultural Research Station, Navile, Shivamogga during kharif 2018. Forty advanced breeding lines of F4 generation with four checks viz., KMLT-4, JGL-1798, KPR2 and JYOTHI constituted the experimental material and were laid out in Randomized Complete Block Design to study genetic variability, diversity, character association and path analysis for fourteen yield and yield attributing traits. The analysis of variance revealed significant differences among the advanced breeding lines for all the characters studied. High GCV and PCV coupled with high heritability and GAM was recorded for number of productive tillers per plant, number of spikelets per panicle, number of filled grains per panicle and straw yield per plant. Correlation studies revealed that days to 50 per cent flowering, number of tillers per plant, number of productive tillers per plant, number of spikelets per panicle, number of filled grains per panicle, spikelet fertility, test weight and harvest index had significant positive correlation with grain yield per plant. The highest direct positive effect on grain yield per plant was exhibited by straw yield per plant followed by harvest index. Mahalanobis' D2 statistics grouped the forty advanced breeding lines and four checks into seven clusters. The maximum inter cluster distance was recorded between clusters IV and VII.The maximum per cent contribution towards divergence was made by days to fifty per cent flowering and number of spikelets per panicle. The advanced breeding linesviz., KMLT-4 x KPR2 1-4-1-3, KMLT-4 x KPR2 2-15-1, KMLT-4 x KPR2 2-12-1, JGL 1798 x KPR2 1-8-6-1, JGL 1798 x KPR2 2-2-1-1, JGL 1798 x KPR2 2-2-3-2, KPR2 x JYOTHI 1-4-3-1 and KPR2 x JYOTHI 3-9-4-1 exhibited higher mean yield performance compare to the checks. Hence these lines should be advanced to next generation and evaluated for stability and adaptability.

August, 2019   (Dushyantha Kumar, B. M.)

Major Advisor