Abstracts of ICAR-IIHR Ph.D Thesis

Compiled and edited by
Dr. M. Sankaran
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Dr. Smaranika Mishra
Dr. Pritee Singh
Mr. Shankar Prasad
Mr. Rajesh Kannan

भा.कृ.अनु.प.–भारतीय बागवानी अनुसंधान संस्थान
हेसरघट्टा लेक पोस्ट, बेंगलूरु – ५६००८९

ICAR - Indian Institute of Horticultural Research
Hesaraghatta Lake Post, Bengaluru – 560089

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FOREWORD

The ICAR-IIHR has been mother to 2 National Institutes (ICAR-Central Institute for Subtropical Horticulture, Lucknow and ICAR-Central Citrus Research Institute, Nagpur), fostered 3 NRC's (ICAR-National Research Centre for Banana, Tiruchirappalli; ICAR-National Research Centre for Pomegranate, Solapur; ICAR-National Research Centre for Grapes, Pune) and one Directorate (ICAR-Directorate of Medicinal and Aromatic Plants Research, Anand) as on today. The main research program of the institute in the initial years was to improve the productivity of Horticultural crops but with the emergence of new challenges in horticulture, emphasis was later shifted to breeding hybrids/varieties for biotic and abiotic stresses, developing integrated water and nutrient management protocols, pests and disease management technologies, efficient post-harvest management practices and conducting frontier research in the areas like hi-tech horticulture, precision farming, information technology and biotechnological interventions.

This institute has 8 distinctive 'Divisions' (Fruit Crops, Vegetable Crops, Flower and Medicinal Crops, Post Harvest Technology and Agricultural Engineering, Basic Sciences, Crop Protection, Natural Resources and Social Sciences & Training). The Pesticide Residue Laboratory at IIHR has been accredited in accordance with the standard ISO/IEC 17025:2005 in the field of chemical testing by NABL (National Accreditation Board for Testing and Calibration Laboratories, Department of Science and Technology, India). State of art Food Safety Referral Laboratory for testing contaminants in food, especially in horticultural produce has been recently established at ICAR-IIHR. Nearly 65 high standard laboratories having state of art equipment like electron microscope, ultra centrifuge, HPLC, GLC, GC-MS, ICP-MS, Liquid Scintillation Counter, Atomic Absorption Spectrophotometer, Gamma Chamber etc, to conduct research. Infrastructural facilities like phenomics facility, growth chambers, mist chambers, cold storage facilities, gene bank, seed processing and nursery units, poly houses and net houses, 100 % drip irrigated fields for crop divisions, local area network with video conferencing facilities, etc have been developed to enhance the research output. The institute also houses an ultramodern library, conference hall, auditorium, training hostel, bank, hospital, essential quarters and other facilities.

The ICAR-IIHR has been serving as a "Higher Educational Institute" for Post Graduate Students across the Country since the inception. This institute has signed an MoU with 15 State Agricultural Universities and 26 Private Educational Universities and Institutes for high quality research, education and training.

I am happy to note that the institute has produced more than 145 PhD students till 2022 and currently 130 PhD students are on roll

I complement Dr. M. Sankaran, Dr. D. Kalaivanan, Dr. Smaranika Mishra, Dr. Pritee Singh and Mr. Rajesh Kannan for the systematic compilation of Ph.D thesis abstracts under 12 ARS discipline which will be useful for the researchers and students in the respective discipline and also will be useful for planning the future research works.

(BNS Murthy)
Director, ICAR-IIHR

PREFACE

ICAR- Indian Institute of Horticultural Research, Bengaluru is a premier research institute for horticultural crops. It was established in 1968 with an objective to increase the yields of horticultural crops by developing high yielding varieties in fruits, vegetables, ornamentals, medicinal & aromatic plants and mushroom and also to develop advanced production technologies to increase the productivity of horticultural crops. Later with emergence of new challenges in crop production and protection in resource poor condition, more emphasis was given on breeding varieties for biotic and abiotic stress tolerance, breeding F1 hybrids, developing integrated pest and disease management technologies, developing integrated soil, water and nutrient management protocols towards optimum utilization of resources, developing post-harvest management practices to reduce the post-harvest losses and further value additions, and frontier research areas like hi-tech horticulture, precision farming, information technology, biotechnological interventions to increase yields, protect crops from insect- pests, disease and viruses, and extension of shelf life of crop produces. Research work carried out during the last four decades with the above objectives has paid rich dividends in terms of release of more than 300 varieties and hybrids and 145 sustainable production, protection and post-harvest management technologies. Apart from that the institute is recognized as the post graduate research and training centre in horticulture by good number of universities as a part of PG Education and currently it is working as an Outreach campus for PhD students of Horticulture from Indian Agricultural Research Institute, New Delhi and have MoUs with more than 40 State Agricultural Universities and Private Universities to carryout quality research, education and training. More than 145 PhD students have completed their degree from IIHR till 2021 and currently 130 PhD students are on roll.

Looking into the significant research contributions from institute, an effort has been made to compile Ph.D students research work in the form of an e-Book on research abstracts of Ph.D which can serve as a ready reckoner for the students and researchers while designing their research programme.

Editors

CONTENTS

Fruit Crops

Title: Effect of variety, maturity and season on composition and quality of musts and wines (1982)

Chikkasubbanna, UAS, Bangalore, Guide: Dr.K.L.Chadha

The effect of variety and maturity on the composition of grapes and wines of Bangalore Blue, Thompson Seedless, Black Champa and Malvasia Bianca Di-wapolis was studied. Fruits from these four varieties were harvested at five different maturity levels and the wines were prepared. Both the musts and wines were analyzed for various organic and inorganic constituents. Distinct variation in organic and inorganic constituents was noticed due to variety, maturity and season. Among the nitrogenous compounds, total nitrogen, protein and proline showed an increasing trend with maturity. Ammonia content was found to decrease in Thompson Seedless and Black Champa whereas in Bangalore Blue and Malvasia Bianca Di-wapolis it increased with maturity. Tannin content increased in Thompson Seedless, Bangalore Blue and Malvasia Bianca Di-wapolis while in Black Champa it did not show much variation with maturity. Inorganic constituents such as phosphorus, calcium and magnesium increased with maturity in all the varieties. Potassium content increased in Thompson Seedless and Bangalore Blue while in Black Champa and Malvasia Bianca Di-wapolis, it remained unchanged. Iron content increased in Thompson Seedless but not in other varieties. Zinc and Manganese remained constant while copper showed variation between samplings. In wine samples total acidity, tartaric acid and malic acid decreased while pH increased with maturity. The wine prepared from third, fourth and fifth stage of maturity scored higher rankings than wines from earlier samples. The results suggested that a Brix/Acid ratio of about 30±5 is near optimum for making good quality dry wines from these varieties for this region.

Title: Effect of time and different doses of N and K on growth, yield and quality of Thompson Seedless grape (*Vitis vinifera L.*) (1983)

S.D.Shikhamany, UAS, Bangalore, Guide: Dr.K.L.Chadha

A field experiment was carried out with the object of improving the efficiency of nitrogenous and potassic fertilizers by split application in Thompson Seedless grape. Four annual doses, viz., 250, 500, 750 and 1000 kg each of N and K_2O/ha were tried in 12 split combinations. Application of potassium in April resulted in increased pruning weight in the following April. Higher weights of pruning were associated with reduced number of bunches/vine. Increasing levels of N and K_2O resulted in reduced length of the internode below the index leaf in December. Internodal length in December was negatively related to the cane and vine productivity and Brix-yield. Area of the index leaf in May and petiole length in June were positively correlated with mean bunch weight at harvest, though they did not vary significantly among the treatments. Petiole nutrient contents in June did not vary significantly among the treatments, while the interaction effects on the petiole nutrient contents in December were significant. Reciprocal antagonism between N and K was observed. Petiole NO_3-N and total N contents correlated positively with the mean bunch weight at harvest. Through the leaf chlorophyll 'b' content in December did not vary significantly among the treatments, it was positively related to the reducing sugars content of the berries. Growth and vigour of the vines under all treatment combinations were far in excess than that required for productivity and affected it adversely. A cane load of 50-60/vine was found to be optimum for vines spaced at 3m x 3m. An annual dose of 500 kg each of N and K_2O at a P_2O_5 dose of 500 kg/ha was found to be optimum. Split application of either N or K_2O during the growth season was not found to be favorable.

Title: Studies on growth and productivity of acid lime (*Citrus aurantifolia* Swing) cv. Kagzi as affected by moisture regimes (1985)

H.P. Singh, UAS, Bangalore, Guide: Dr.K.L.Chadha

Fruit yield and quality were significantly correlated with consumptive use of water and best fit of line was obtained with quadratic equation for yield and physical quality. The consumptive use of water at productive stage was estimated to be 875 mm year $^{-1}$. At young age, liner correlation existed between plant growth and consumptive use. Best water use efficiency was obtained at 20 KPa soil moisture potential. Stomatal intensity, cuticular thickness, specific leaf weight and transmission coefficient increased under moisture stress while stomatal size and absorption coefficient decreased. Flushing and leaf fall were cyclic and were affected by soil moisture potential. Mild moisture stress (pre-dawn leaf RWC of 90.97 to 93.00%) followed by alleviation increased the intensity of flushing and flowering. Changes in fruit weight and size exhibited sigmoid pattern and moisture stress at an early period of fruit development (I and II stage) was critical. Moisture stress caused increase in TSS, acidity, sugar and delayed the maturity. Irrigation at 10 KPa increased the yield significantly. Low soil moisture coupled with high evaporative demand caused the accumulation of NO3-N in leaf. Accumulation and partitioning of dry matter, protein, carbohydrates and nutrients were affected by soil moisture potential. Excessive soil moisture at active period of growth was more detrimental for growth than moisture stress as indicated by leaf area increment recovery in conductance. Seed germination percent and radicle growth were significantly reduced with increasing moisture stress monitored by polyethylene glycol.

Title: Studies on growth and development of Pomegranate (*Punica granatum* L.) fruit and seed with special reference to hard and soft seededness (1986)

B.Prasanna Kumar, UAS, Bangalore, Guide: Dr.A.G.Purohit

Studies were conducted in four pomegranates varieties on time of initiation and degree of lignifications of seed testa which causes hard seediness. The physicochemical changes during growth and development of fruits were also investigated. Fruit growth pattern in pomegranate followed a simple sigmoid curve almost approaching a liner relationship. Length and breadth of the fruit, fresh weight of rind and weight of seed increased continuously from fruit set to maturity. During most stages of fruit development, the seeds constituted roughly half of the fruit weight. Dry matter content in fruits increased continuously till 50 days of fruit growth and then gradually declined towards maturity, but it seeds, dry matter content increased continuously from fruit set to maturity. Specific gravity of fruits was higher in early stage of fruit development and then gradually declined. TSS increased gradually during fruit development and acid content decreased with maturation of fruits. Both reducing and total sugars continued to increased during the development of fruits. The nitrogen and phosphorus content of both fruits and seeds was maximum and highest immediately after fruit set and second highest nitrogen content was seen at maturity. The potassium content of fruit was highest at 10 and 120 days of fruit growth. The seeds contained very high potassium content both immediately after fruit set and also at maturity. The micronutrient contents of fruits were high initially, after fruit set, they declined in the intermediate stages and finally reached maximum levels at maturity. The seeds had maximum micronutrient immediately after fruit set. Histological studies revealed that after 40 days of seed growth lignification started and it was more pronounced in hard seeded varieties.

Title: Investigations on the effect of rootstocks in Anab-e-Shahi grape (*Vitis vinifera* L.) (1988)

B.M. Chandrasekhara Reddy, UAS, Bangalore, Guide : Dr.K.L.Chadha

An investigation was carried out on the effect of roostocks on Anab-e-Shahi grape employing the rootstocks St. George, Teleki 5-A, Dogridge, 1616, 1613 and Gulabi in comparison with own- rooted vines to identify the most suitable rootstock. Rootstocks Dogridge and 1616 were found to impart vigour to Anab-e-Shahi grape but adversely affected the yield and yield attributes. Rootstock Gulabi lowered most of the vigour attributes and resulted in the highest yield. St.George and 1613 similar vigour attributes as own-rooted vines, but influenced the yield favourably. Rootstocks Gulabi, 1613 and St. George increased the yields through increased fruitfulness of canes. Fruit quality parameters were not influenced by any of the root stocks. Higher levels of total and NC3- N were associated with lower yields in the rootstocks Dogridge and 1616 and it was reverse in Gulabi. St. George appeared to be an ideal rootstock for economizing N inputs. Higher petiole K contents during June were associated with higher yields. Lower Mg and higher Zn contents were in general associated with higher yields. Rootstocks Dogridge, 1616 and St. George had low levels of chloride content and may be suitable for areas with high chloride in irrigation water. Among the petiole nutrients, NO3-N, Mn, K and Zn contents in June and total N, Mg and CI in December were found to be useful in yield prediction. Leaf sampling in June may be useful to work out relationship between petiole nutrient contents and yields under double pruning and single cropping conditions. Rootstock Gulabi may be employed to increase productivity of Anab-e-Shahi grape. St. George and 1613 are useful on sodic soils and in locations where irrigation water has high chloride content.

Title: Root distribution and activity in grape cultivars as influenced by systems of training (1988)

G.S. Prakash, UAS, Bangalore, Guide: Dr.K.L.Chadha

Studies on the distribution pattern of root density and activity using radioactive ^{32}P were carried out in four grape cultivars namely, Thompson Seedless, Gulabi, Black Champa and Bangalore Blue as influenced by three systems of training viz., bower, kniffin and head systems. Of the four cultivars studies, root density was found to be the highest in cultivar Bangalore Blue followed by Thompson Seedless, Gulabi, Black Champa. All the cultivars had greater root density nearer the trunk at 50 cm radial distance and at a shallow depth of 0-15 cm in the soil. In all the cultivars the highest root density was observed in the vines trained on bower system. Bower trained vines showed a greater root spread as compared to those on kniffin and head systems. Root activity was the highest in cultivar Gulabi as indicated by greater absorption of ^{32}P followed by Thompson Seedless and Black Champa. The lowest activity was noticed in the cultivar Bangalore Blue. In all the cultivars Thompson Seedless and Bangalore Blue root activity was more nearer the trunk (40 cm radial distance) at a depth of 15 cm under all the training systems. On the other hand, in the cultivars Gulabi and Black Champa, the activity was more widespread even up to 120 cm radial distance and up to, 30 to 45 cm depths. Even though, the total root activity under different training systems did not differ significantly, the spatial distribution of root activity varied. In general, both root density and activity were found to decrease with increasing depths and radial distances in all the cultivars except in Black Champa. Mathematical functions worked out for fitting root activity as a function of depths and distance indicated that only in Bangalore Blue and Thompson Seedless the spatial distribution was system followed by kniffin and head systems.

Title: Genetical studies in Papaya (*Carica papaya* L.) (1990)

M.R.Dinesh, UAS, Bangalore, Guide : Dr.C.P.A.Iyer

A study was undertaken to assess the genetic potential in papaya so that the information thus obtained could form the basis for further breeding work in papaya. For this purpose an experiment was conducted during the years 1984 to 1986, at the fields of the Indian Institute of Horticultural Research, Hessarghatta. The diallel analysis indicated the importance of additive and non-additive gene action for the sixteen characters studied. The F1 hybrids exhibited heterosis over mid parental values (Heterosis), better parent (Heterobelfiosis) and the best parent or standard parent (standard heterosis). The parents Coorg Honey Dew and Pink Flesh Sweet were observed to be the best combiners for yield. The cv. Pink flesh Sweet was also found to be the best combiner for fruit length, fruit breadth, fruit weight, fruit volume, pulp thickness, TSS, fruit cavity index and reducing sugars. The cvs. Sunrise Solo and Waimanalo were also noticed to be good combiners for pulp thickness and TSS. Heritability (in narrow sense) values were observed to be higher for the characters plant spread, total sugars and carotene. In general genotypic correlation coefficients were higher than the phenotypic correlation coefficients between pairs of characters, indicating that strong intrinsic correlations are reduced at the phenotypic level due to environmental effects. Correlation studies indicated that yield was significantly associated in positive direction at the phenotypic level with number of fruits, fruit weight and reducing sugars, association in negative direction was significant with fruit cavity index, plant height and plant spread. The yield components number of fruits and fruit weight are significantly correlated with fruit cavity index in the positive direction. At the genotypic level, yield was correlated significantly in the desirable direction with number of fruits, fruit length, fruit breadth, fruit weight, fruit volume and pulp thickness. Association in negative direction was significant with plant height. The co- heritability estimate with regard to yield was positive in all the characters maximum estimate was obtained with fruit volume and minimum with pulp thickness.

Title: Phenotypic variability for qualitative and quantitative attributes of certain grape hybrids (1991)

S.Venkataram, UAS, Bangalore, Guide: Dr. Rajendra Singh

Hybrids of the crosses Anab-e-Shahi, Angur Kalan, Bangalore Blue, Black Champa, Convent Large Black, Thompson seedless and Queen of the Vineyard were evaluated with petiole nutrient contents and resistance to diseases. Hybrids derived from Anab-e- Shahi x Queen of the Vineyard (9/3), Angur Kalan x Anab-e-Shahi (5/4), and Angur Kalan x Black Champa crosses (26/8) were found to perform better. Dry matter content of the petioles appears to be a suitable index for higher yield. Higher chlorophyll ‘b’ content (light harvesting complex) was related to high yield in Bangalore blue. Use of Black Champa as seed parent and Queen of the Vineyard as pollen parent is good for imparting high vigour to the progeny. Duration for ripening depended on genetic constitution rather than on climatic factors. Glucose and fructose contents were high in Thompson seedless. Thompson seedless was very efficient in N uptake than Bangalore Blue. Hybrids 9/3 and 26/9 possessed higher P content which was related to high fertility. Ca and Mg contents had no relationship with yield whereas Fe, Zn and Mn showed some positive relationship. Seedless berries were obtained in hybrids derived from Black Champa and Thompson seedless. Hybrid 21/28 showed tolerance to downey mildew while Hybrid 30/14, tolerance to anthracnose and hybrid 21/28 to powdery mildew.

Title: Fertigation studies in Pomegranate (*Punica granatum* L.) (1997)

N. Devakumar, UAS, Bangalore, Guide : Dr.K.Srinivas

Field experiments were conducted at IIHR, Bangalore in order to study the response of pomegranate to irrigation systems, irrigation levels, and nitrogen and potassium fertilization. Drip system of irrigation gave higher fruit yield of 14.97 and 12.38 t/ha with N and K fertilization experiments, compared to basic system (12.38 and 9.38 t/ha). The drip system was superior to basin system with respect to fruit growth, yield attributes and quality. Irrespective of the irrigation systems scheduling irrigation at 0.8 CPE was found to be optimum by registering significantly higher fruit growth, yield and quality of fruits. Irrespective of the irrigation systems and levels, application at 500 kg/ha through drip systems was optimum to get higher fruit yield (19.57 t/ha) with good quality compared to lower level of nitrogen through drip or same level of soil application through basin irrigation (15.60 t/ha). Similarly, potassium fertigation at 300 kg/ha gave higher fruit yield of 16.55 t/ha compare to soil application of potassium at 300 kg/ha under basin irrigation (13.35 t/ ha). However, overall interaction between irrigation systems, irrigation levels, nitrogen and potassium levels were absent. Drip irrigation systems maintained constantly higher soil moisture compared to basin system. Drip irrigation at 0.6 and 0.8 CPE maintained soil moisture nearer to field capacity throughout the irrigation cycle, but not under basin system with same irrigation levels of irrigation were 300,600,900 and1200 mm, under drip and basin irrigation.

Title: Effect of diferential irrigation, soil moisture stress and mulch on growth, yield and water use in Banana (*Musa paradisiaca* L.) (2003)

K. Murali, UAS, Bangalore, Guide: Dr.K.Srinivas

Field experiments were conducted at Indian Institute of Horticultural Research, Hessarghatta, Bangalore during June 1994 to August 1996 to study the effect of differential irrigation, soil moisture stress and mulch on growth, yield and water use in Elakki banana (Musa paradisiaca L.).The results revealed that irrigation scheduled at an IW/CPE ratio of 1.0 during vegetative stage recorded significantly higher fruit yield (main cop: 28.75 t/ha, ratoon crop: 24.89 r/h) and it was lower with an IW/CPE ratio of 0.4 (main cop: 21:89 t/ha, ratoon crop: 18:81 t/ha). Similarly, irrigation scheduled at an IW/CPE ratio of 1.0 during reproductive stage recorded higher fruit yield (main crop: 27.13 t/ha ratoon crop: 23:22 t/ha) and it was lower with an IW/CPE ratio of 0.4 (main crop: 24:42 t/ha, ratoon crop:21.52 t/ha).Irrigation scheduled at an IW/CPE ratio of 0.8 (no stress throughout the crop growth) gave significantly higher fruit yield (man crop: 30.25 t/ha, ratoon crop: 24.41 t/ha) and it was lower with stress imposed during 201 to 240 days after planting (main crop: 23.91 t/ha, ratoon crop: 18.28 t/ha). Among the stress treatments, stress imposed during 321 to 360 Days After planting (DAP) gave higher banana fruit yield (main crop: 29.16 t/ha, ratoon crop: 23.53 t/ha) and it was lower with stress given during 201 to 240 days after planting (main crop: 23.91 t/ha, ratoon crop: 18.29 t/ha). Stress imposed during 321 to 360 DAP gave increased yield to the extent of 18.01 and 22.32 per cent with main and ratoon crops respectively as against stress imposed during 201 to 240 DAP. Irrigation scheduled at an IW/CPE ratio of 1.0 recorded higher fruit yield (main crop: 32.47 t/ha, ratoon crop: 26.56 t/ha) and it was lower with an IW/CPE ratio of 0.4 (main crop: 23.29 t/ha, ratoon crop: 19.35 t/ha). The fruit yield was higher with mulch treatment (main crop: 26.53 t/ha, ratoon crop: 24.82 t/ha) as compared to no mulch (main crop: 23.53 t/ha, ratoon crop: 22.16 t/ha).

Title: Genetic investigation of Pomegranate genotypes tolerant to drought using morphological, physiological and molecular markers (2005)

Nagarajappa Adivappar, UAS, Bangalore, Guide: Dr.S.H.Jalikop

Several pomegranate genotypes including commercial cultivars, exotic lines, ornamental types, F1, F2, BC and multiple hybrids were evaluated for morphological, physiological and biochemical parameters for drought tolerance like cell membrane stability (CMS), osmatic potential, water potential, relative water content (% RWC), root length, number of secondary roots, root fresh weight and root dry weight. ‘Nana’ and ‘Double Flower’ and their hybrids exhibited tolerance for moisture stress. Selected tolerant lines were used for DNA fingerprinting using RAPD’s. Identification of RAPD markers for root traits in F2 population for drought tolerance was developed. Data on drought related parameters have been collected for understanding the genetics of drought tolerance using six generation mean analysis.

Title: Studies on genetic variability in water use efficiency of Grape varieties, rootstocks and their stionic combinations (2005)

J.Satisha, UAS, Bangalore, Guide: Dr.G.S.Prakash

Four grape varieties namely Flame Seedless, Thompson Seedless, Sharad Seedless and Tas-a- Ganesh of six month old plants were subjected to three levels of moisture stress viz., control, 50% stress and 100% stress for 14 days. There was marginal reduction in photosynthesis and greater reduction in transpiration with increased water use efficiency (WUE) in all the varieties from control to 50% stress. None of the varieties could survive beyond 3-4 days at 100% stress. Among the varieties Flame Seedless had highest WUE followed by Thompson Seedless at 50% stress. A nine fold increase in abscises acid content was observed in Flame Seedless at 50% stress than at control while it was about 1-3 fold in other varieties. Reduction in cytokinin content was observed with increased moisture stress. Root to shoot length ratio (RSLR) and root to shoot dry matter ratio (RSDWR) was maximum in Flame Seedless and was least in Tas-a-ganesh at 50% moisture stress. Under similar set of experiments with five grape rootstocks namely Dogridge, 1613 C, Salt Creek, St. George and VC clone, Dogridge and salt Creek maintained higher water potential and osmotic potential (less negative values) under increased moisture stress indicating their better osmotic adjustment to maintain higher heater content. Higher WUE was observed in Dogridge and Salt Creek at 50% moisture stress as a result of marginal reduction in photosynthesis and greater reduction in transpiration rate. Higher ABA content accumulated in Dogridge with increased moisture stress resulted in reduced stomatal conductance thus minimizing transpiration rate. A three fold increase in RSLR was observed in Dogridge from non-stress to stress conditions while there was no much increases in other rootstocks. Reduced shoot length in Dogridge was attributed to less cytokinin content under soil moisture stress. Dogridge rootstock influenced the photosynthesis behaviour of Flame seedless and Sharad Seedless when they were budded on it. Sharad Seedless recorded maximum WUE when budded on Dogridge followed by Flame Seedless on Dogridge at 50% moisture stress. Flame seedless and Sharad Seedless budded on Dogridge recorded highest ABA accumulation at 50% moisture stress than when they are budded on Salt Creek and VC clone. Rootstocks strongly influenced the carbon isotope discrimination of scion varieties budded on them.

Title: Propagation of some grape rootstocks in enriched organic media and their subsequent graft success (2008)

Husameddin Al-Said, UAS, Bangalore, Guide: Dr.G.S.Prakash

Three experiments were carried out at Indian Institute of Horticultural Research (IIHR), Hessarghatta, Bangalore–89 during the year 2006-07 to study the effect of various substrates and microbial combinations on rooting and graft success of grapevine rootstocks. The experiments consisted of three grapevine rootstocks viz., Dogridge, St.George and 1613 and three substrates namely plant sap, humic acid, vermiwash and a control and seven microbial combinations (M1: Glomus mosseae + Trichoderma harzianum, M2: Glomus mosseae + Bacillus subtilis, M3: Glomus mosseae + Pseudomonas fluorescens, M4: Glomus mosseae + Trichoderma harzianum + Bacillus subtilis, M5: Glomus mosseae + Trichoderma harzianum + Bacillus subtilis + Pseudomonas fluorescens, M6: IBA and M7: control). Among the substrates used, humic acid significantly influenced almost all the root and shoot parameters in hardwood grapevine cuttings of the three rootstocks. Next best treatments were vermiwash and plant sap. Among various microbial combinations tried, treatment M5 was the most effective for almost all the root and shoot parameters studied as compared to control. Other microbial combinations (M1, M2, M3 and M4) gave similar results as IBA treatment. Among different grape rootstocks tested, the root development was significantly superior in 1613, while St. George rootstock showed the best shoot development. Early budbreak was recorded in the cuttings treated with plant sap which was on par with the cuttings treated with vermiwash. Among the different microbial combinations M2, M3 and M5 gave early budbreak as compared to control. The percentage of graft success and root colonization was significantly increased by humic acid, whereas other substrate treatments were not significant. The percent graft success was significantly increased by M4 and M5, while the percentage of root colonization was significantly increased by all the microbial combinations (M1, M2, M3, M4 and M5). The rootstock 1613 gave the highest percent graft success, while St. George showed the highest percentage of root colonization

Title: Studies on morphological and molecular characterization and conservation of mango germplasm (2010)

C.Vasugi, Annamalai University, Chidambaram, Guide: Dr.M.R.Dinesh

Studies on morphological and molecular characterization and conservation of mango germplasm were carried out in the Department of Horticulture, Faculty of Agriculture, Annamalai University, during December, 2005 to December, 2009. Four systematic experiments were carried out to characterize the variability; to assess the genetic diversity; to evaluate for fruit and pickling characters and to study the effect of cryopreserved pollen. Characterization of 43 accessions maintained in the field gene bank of Indian Institute of Horticultural Research based on IPGRI (Biodiversity International) mango descriptor reveled wide variability for leaf, fruit, flower, inflorescence, pulp and stone characters. Genetic divergence and cluster analysis based on both phenotypic and molecular markers were carried out. Accessions were grouped based on similarity/ dissimilarity index. Principal Component Analysis (PCA) indicated that fruit descriptors contributed more towards divergence. Cryopreserved pollen was found to be as good as fresh pollen in the inter-specific and inter-varietal crosses. Comparative evaluation of pickling accessions with the commercial and polyembryonic varieties revealed that Dantimamidi and Kovesara possessed good quality characters and was on par with the commercial varieties used in the study. Based on the evaluation of tender mango pickle quality, Chansi Appe, Dodderi Jeerige, Mani Bhatta Appe, Gorana Appe, isagoor Appe, Malange, Dantimamidi, Gurumurty Appe and Kashimidi were identified as good pickling accessions. Possible gene donors for specific traits like attractive skin colour, pulp colour, fruit weight, pulp per cent and TSS was also observed. The morphological characterization data generated in the present study was used to develop a Mango Information System to run on Windows Operating System for ready retrieval and visual comparison.

Title: Biochemical and molecular studies on peel colors of different colored mango cultivars (2016)

Karanjalker Gourish Ranganath, UHS, Bagalkot, Guide: K V Ravishankar

Mango (Mangifera indica L.) is the choicest fruit of the India that has huge demand in domestic as well as the international markets. The fruit peel color is the most important criteria for successful marketing and has also been considered as the first perception for the consumers. This fact is more emphasized in case of mangoes, w herein attractive red blush types are preferred by the consumers. The present investigation aimed at studying mango peel colors in some of the colored mango cultivars through morphological, biochemical and molecular aspects at ripening stages. Colored mango cultivars were characterized for morphological traits. The results revealed a considerable diversity amongst them. They were further analysed following biochemical and molecular techniques. Eight carotenoid compounds and 24 anthocyanins were identified by mass spectrometry analysis, which showed significant variation amongst 12 cultivars (belonging to green, yellow and red color categories) studied. J3- carotene and violaxanthin were the most abundant carotenoids in the peels of mango fruits. Yellow-orange colored mango cultivars had high carotenoid, the majority of which consisted of 13-carotene (35.18 to 98.06%). In addition, the presence of compounds belonging to anthocyanin groups viz. cyanidin, peonidin, petunidin, pelargonidin delphinidin and malvidin were recorded. Cyanidin-3- monoglucosides and peonidin-3-0- glucosides were the dominant compounds recorded in the mango peel. Amongst cultivars, red colored 'Tommy Atkins' and `Janardhan Pasand' were having higher content of anthocyanin. Gene expression studies by qRT-PCR suggested higher expression of carotenoid biosynthetic genes viz. lycopene-β-cyclase and violaxanthin-de-epoxidase in yellow colored cultivar ‘Arka Anmol' that increased with ripening. However, in red colored cultivar `Janardhan Pasand', higher expression of all anthocyanin biosynthetic genes and transcription factors MYB and Basic helix loop helix was observed, indicating their involvement in red color development. This study explained the accumulation pattern of carotenoids and anthocyanins and genes involved in differently colored mango cultivars.

Title: Studies on diversity of indigenous mango (*Mangifera indica* L.) genotypes (2018)

Veena, G. L., UHS, Bagalkot, Guide: M. R. Dinesh

Western Ghats region of Karnataka is one of the diversity centres of indigenous pickling mango variety Appemidi'. Keeping this in view, the present investigation entitled "Studies on diversity of indigenous mango genotypes" was conducted at ICAR-IIHR, Bengaluru,during 2013-2014 and 2016-18. An attempt was made to study the diversity ofindigenous mango genotypes with special reference to Appemidi from Chikmagalur district, by conducting a survey. Morphological characterization of 40 genotypes was described systematically as per the IPGRI mango descriptor, which consisted of leaf, inflorescence, fruit and other parameters. Among the characters studied, fruit diameter contributed most to the total diversity followed by fruit weight and inflorescence diameter. Among the pollen characters, colpi per cent showed the maximum contribution towards total divergence followed by equatorial diameter and colpi length. 14 SSR primers were also used to analyse the inter and intra cultivar diversity. The morphological, palynological and molecular diversity analysis showed grouping of genotypes into different clusters irrespective of their place of collection. Appemidi leaf volatiles were profiled and compared with their fruit sap aroma constituents using GCMS/MS. A total of 80+ volatiles were observed in all the genotypes belonging to mono and sesquiterpenoids groups. The highest significant positive correlation was observed between major monoterpenoids of leaf and fruit sap, particularly for β-Phellandrene, which proved that leaf volatiles were directly correlated with fruit sap in appemidi, which can be used as a pre-selection index. Water soluble and fat soluble vitamins, as well as important organic acids were profiled in fifteen genotypes at three different forms. Indigenous traditional knowledge associated was also documented. Conservation of important genotypes were carried out by grafting in addition pollen samples were cryopreserved.

Title: Response of different propagules and chemicals on inducing flowering and fruiting in Pomegranate (*Punica granatum* l.) cv. bhagwa" (2018)

S. Firoz Hussain, Dr. Y.S.R.Horticultural University, Guide: Dr. P. Sampath Kumar

The investigation was categorized into two experiments (Experiments I and II). Experiment I was conducted on three propagules (tissue culture, grafts and air layers) and comprised of ten treatment, replicated thrice and the statistical design adopted was Factorial RBD while Experiment II applied only on tissue culture plants and included eleven treatments, replicated thrice in randomized block design. The tissue culture plants registered highest number of hermaphrodite flowers (335.33), percentage of fruit set (70.36), yield (41.20kg plant^{-1}), total aril weight (112.31g) and TSS (20.44^{0}B) with paclobutrazol @ 0.375 g a.i.m^{-1} canopy diameter 60 days after bahar treatment.Lower GA$_3$ content was observed due to soil drenching of paclobutrazol @0.375 g a.i.m^{-1} canopy diameter 60 days after bahar treatment to tissue culture plants at both flowering (158.33ng g^{-1} FW) and fruit set (95.50 ng g^{-1} FW) stages. Higher IAA content was observed due to soil drenching of paclobutrazol plants at both flowering (928.00 ng g^{-1} FW) and fruit set (556.00 ng g^{-1} FW) stages. High total chlorophyll content was observed due to soil drenching of paclobutrazol @ 0.375 g a.i. m^{-1} canopy diameter 60days after bahar treatment to tissue culture plants at both flowering (3.03 mg g^{-1}) and fruit set (2.00mg g^{-1}) stages. Foliar application of Uracil @ 50ppm litre^{-1} plant $^{-1}$ implicated in enhancing in the number of hermaphrodite flowers (264.66).The plants when sprayed with cycocel @ 1500ppm plant^{-1} displayed lesser GA$_3$ content at flowering (163.33 ng g^{-1} FW) and fruit set (276.00 ng g^{-1} FW) stages. During flowering and fruit set stage, plants sprayed with cycocel @ 500ppm plant^{-1} displayed high IAA content (946.66 ng g^{-1} FW) and (633.00 ng g^{-1} FW). At flowering and fruit set stage,application of cycocel @ 1500 ppm plant^{-1} has enhanced the total chlorophyll content (2.27mg g^{-1}) and (2.35mg g^{-1}) in plants.

Title: Studies on salt tolerance in polyembryonic mango (*Mangifera indica* L.) rootstock seedlings (2018)

Nimbolkar Prashant Kisan, IARI, Guide: Dr. Reju M. Kurian

Mango (Mangifera indica L.) is considered as salt sensitive crop. The use of salt tolerant genotypes as rootstock to combat the adverse effect of salinity could be helpful for commercial mango production in salt affected areas. The present investigation was carried at the Division of Fruit crops, ICAR-Indian Institute of Horticultural Research, Hessarghatta Lake Post, Bengaluru 560 089, Karnataka during the years 2015-17, wherein we studied the germination percentage, morpho-physiological changes, biochemical alterations and nutrient consistency of four and half months old candidate polyembryonic mango genotypes namely EC-95862, Bappakkai, Vellaikolamban, Nekkare, Turpentine, Muvandan, Kurukkan, Kensington, Olour, Manipur, Chandrakaran, Deorakhio, Vattam, Mylepelian, Sabre and Kitchener subjected to salinity stress by NaCl+CaC12 (1:1 w/w) at 0 mM, 25 mM, 50 mM and 100 mM concentrations in in-igation water. For germination studies the `Arka Fermented Coco peat' was used as growing media and salinity levels of NaCl having concentration 0 and 50 mM were used. Among these genotypes, Mylepelian, Turpentine and Kurukkan showed early and maximum germination and it is confirmed that the mango seeds can germinate under 50 mM salinity stress with congenial environment and growing media. Our findings stated that the salinity caused reduction in seedling growth, biomass content and gas exchange characters and increases the antioxidant enzymes activity (CAT, PDX, SOD and PPO) and ABA level. Salinity accelerate the accumulation of Na^+ and Cl^- ions in both leaf and root tissues and slowed down the uptake of essential nutrients viz. K^+, Ca^{++},Mg^{++}, Fe^{++}, and Zn^{++}. Mylepelian, Kitchener, Vellaikolamban, Sabre, Manipur, EC -95862, Muvandan, Kensington, Kurukkan, Nekkare, Vattam, Bappakkai, Olour, Deorakhio and Turpentine were in increasing order of tolerance to salinity stress.

Title: Studies on metaxenic effect and interspecific hybridization in Annona species (2018)

Vinay, G. M., UHS, Bagalkot, Guide:Dr. T. Sakthivel

Annona belongs to the family Annonaceae, which comprises about 120 genera with 2000 species. Annonaceous fruits are characterized by a serious problem of fruit set and assisted pollination is commonly practiced for improving the set. Four species of annona;- Annona squamosa L, A. atemoya Hort, A. cherimola Mill and A. reticulata L. were used to study the metaxenic effect. Results showed that maximum fruit set was recorded when A squamosa L. (81.73 %), A. cherimola Mill (82.86 %) were crossed with the pollen of A. reticulata L. and A. atemoya Hort. (97.54 %) A. reticulata L. (69.66 %) were crossed with A. squamosa L. In another study, four hybrids were evaluated for fruit yield, quality and selffruitfulness. Results showed that Arka Sahan (54.85 kg/tree) performed well with assisted pollination, whereas the Hybrid 19/26 (48.64 kg/tree) and Hybrid 16/14 (48.99 kg/tree) were rated as very good followed by Hybrid 16/10 (21.66 kg/tree) rated as good under natural pollination. Chromosome number, floral biology and hybridity confirmation of hybrids and their parents were studied and the results showed that the somatic chromosomes were 7 (2n=14) in all interspecific hybrids including Arka Sahan and their respective parents. Pollen viability, pollen fertility, pollen germination were found relatively maximum in the parents than in their hybrids. The stigma receptivity was found maximum on the day of anthesis in the early morning. ISSR UBC- 826 primer clearly confirmed the hybridity of different annona hybrids.

Title: Physiological and Biochemical basis of different sources and methods of Potassium application on growth, yield, quality and disease incidence in Grapes cv Sharad Seedless (2018)

Y.Pusphavathi, YSR, Horticultural University, AP Guide: Dr.J.Satisha

The present investigation entitled "Physiological and biochemical basis of different sources and method of potassium application on growth, yield, quality and disease incidence in Grapes cv. Sharad Seedless" was carried out during two consecutive years from 2016-17 and 2017-18 at the experimental vineyard of the ICAR - Indian Institute of Horticultural Research (ICAR - IIHR) located at Hessarghatta, Bengaluru. The present experiment was laid out in Randomized Block Design (RBD) consisting of eight treatments replicated four times. Significant differences were observed among the treatments with respect to growth, yield, quality and downy mildew disease incidence. Irrespective of sources, 60% SOP through soil application resulted in maximum pruned biomass vine^{-1} (T7, 4.32 kg vine^{-1} at back pruning and T6, 1.42 kg vine^{-1}at forward pruning).During both back and forward pruning, T5 treatment recorded significantly least mean per cent of infected plants (34.91% and 32.47%), minimum per cent disease index (30.32 and 25.82) and lowest number of sporangia cm^{-2} (6.94 and 6.90) followed by T6 treatment.T5 treatment showed highest concentration of total phenols, phenylalanine ammonia-lyase, peroxidase and super oxide dismutase activity in healthy as well as downy mildew infected leaves and magnitude of change in their respective concentrations subsequent to downy mildew infection over healthy period, after both back and forward pruning followed by T2 and T6 treatments. Potassium per cent in petiole was significantly highest in T5 treatment followed by T2 treatment and least potassium percent was noted in T8 treatment. T5 and T2 treatments also recorded highest content of copper and zinc and lowest per cent of nitrogen, phosphorus, calcium, magnesium, iron, manganese and boron. T5 and T2 treatments showed highest content of phosphorus, manganese, copper and zinc and lowest content of organic carbon, nitrogen, calcium, magnesium and iron. Among the different source and application methods, 60% SOP through soil along with 40% nitrogen containing potassium sources (KNO_3 and 19:19:19) through fertigation were reasonably good for improved vegetative growth, flower bud differentiation and ultimately to increased yield in grapes. Application of only SOP more through soil (60%) and less (40%) through fertigation was favourable for least disease incidence by increased potassium content in petiole thus increasing the constitutive and post inflectional accumulated total phenols and phenolic acids with augmented phenylalanine ammonia-lyase, peroxidase and super oxide dismutase activity in leaves. Among the phenolic acids, o-Coumaric acid, p-Coumaric acid have characteristic role in disease resistance.

Title: Crop regulation and source-sink relation studies in Annona cultivars Arka Sahan and Balanagar (2019)

Subhash Chander, IARI, Guide: Dr. Reju M. Kurian

The investigation was carried out at ICAR-Indian Institute of Horticultural Research, Hessarghatta Lake Post, Bengaluru 560 089, Karnataka during 2016-2018to advance fruiting in Annona cultivars Arka Sahan, an inter-specific hybrid of Annona atemoya ×A. squamosa and Balanagar through pruning and defoliation, respectively. Early sprouting, flowering and fruit harvest were recorded in 75 percent pruned trees in both the years. Earliest fruits were harvested in 271 (3rd week of June), 268 (2nd week of June) days in 75 per cent trees pruned during first week of October. Pruning during October first week in first year (T1L1) and during December first week in second year at 25 per cent level recorded the maximum fruit yield (12 kg/tree, 20.6 kg/tree respectively). Fruits with maximum TSS content were harvested from trees pruned to 25 per cent level during October 3rd week (T2L1) (37°B) and T1L1 (33.9°B) in first and second year, respectively. Fruiting could be advanced by 8-9 weeks to June from the normal season, August- September with pruning treatment (T1L3 or T2L3) in Annona cv. Arka Sahan. The influence of chemical defoliants urea and ethrel and bud sprout promoter KNO3 was also studied in cv. Balanagar. Maximum defoliation (97%, 96.5%) was recorded with ethrel 4000 ppm spray during both the years. Early sprouting (26 days, 16.1days) and flower initiation (35 days, 23.03 days, respectively after treatment)were recorded in trees sprayed with urea 15 per cent during both the years. Bigger fruits weighing 329.5 g and 294.9 g respectively were harvested from trees sprayed with ethrel 4000 ppm in 2016-17 and ethrel 3000 ppm in 2017-18. Average fruit weight decreased while the number of seeds increased as crop load increased. Bigger fruits with maximum pulp content and less number of seeds could be harvested during July by maintaining optimum fruit load of 0.17 to 0.19 kg cm^{-2} TCSA of fresh fruit weight or 60 fruits per tree and pollinating basal flowers of vigrous shoots. A rapid decrease in pollen germination was observed from maximum at 6 am to no germination at 2 pm. Pollens lost viability within one month when stored at 4°C while retained germination for 2 months at -196ºC, but germination and pollen tube growth progressively declined drastically with storage time and revealed deformed and shriveled structure following cryopreservation.

Title: Wide hybridization and colchi-ploidy studies in guava (*Psidium guajava* L.) (2019)

Jagadeesha Mulagund, IARI, Guide: Dr. M.R. Dinesh

The present investigation entitled "Wide hybridization and colchiploidy studies in guava (Psidium guajava L.)" carried out at ICAR-Indian Institute of Horticultural Research, Hessaraghatta Lake Post, Bengaluru, and Karnataka during 2016-2018. The phenological results revealed that synchronization of flowering time (February-April and August-September), duration of flowering (32 to 68 days), anthesis (6.00 to 8.30 a.m) as well as anther dehiscence (7.00 to 10.30 am) was recorded in P. guajava cultivars and wild species P. guineense and P. chinensis and P. molle. The palynological results revealed that, pollen of the Psidium species was found to be ricolporate or tetracolporate with granulate/ scabrate or verrucate/scabrate exine ornamentation and colpal morphology was mainly brevicolpate or less often syncolpate. Hybridity confirmation of interspecific hybrids using SSR markers revealed that, 8 markers were found to be co-dominant and confirmed the hybridity of interspecific hybrid combinations. Leaf volatile profiling of Psidium species and cultivars revealed that the total compounds responsible for the aroma falls under seven major groups viz., monoterpenoids, sesquiterpenoids, alcohols, aldehydes and ketones, esters, oxocompounds and others. Higher concentration of colchicine significantly decreased the per cent seed germination and seedling survival among the three methods of application i.e., seed treatment (method-1), seedling meristem treatment (method-2), seed treatment followed by seedling meristem treatment (method-3). Plant height, stem girth and internodal length recorded maximum in higher concentration of colchicine treatment compared to non-treated control.Among the treatments, T8 (Seeds treated with 0.8 % colchicines followed by seedling apex treatment at 1.5 % colchicine) resulted in all the three forms of polyploids i.e., 2 mixaploids, 2 tetraploids and one hexaploid. Character association studies between ploidy level and confirmed polyploids revealed that ploidy level was highly significant and positively correlated with plant height (0.712), leaf length (0.685) and leaf width (0.570), stomatal length (0.605) and stomatal width (0.580), WUE (0.582), net photosynthesis rate (0.610) and internal leaf $CO2$ (0.613), total chlorophyll content (0.665) total phenols (0.590), total flavonoids (0.586) and total antioxidants (0.650) with a highly significant and negative correlation for stomatal density (-0.678).

Title: Genetic Diversity and Characterization Studies in Mango (2019)

Donald Mree Sangma, IARI, Guide: Dr. M.R. Dinesh

Knowledge about the extent of genetic diversity/relatedness in mango germplasm is vital for developing coherent strategies for future gains in productivity and quality. The present investigation was conducted at ICAR-Indian Institute of Horticultural Research (ICAR-IIHR), Bengaluru during 2015-18 by studying the morphological and biochemical characters to assess the extent of variability and the genetic diversity by using SSR markers. Wide variation was recorded among the 156 genotypes and these genotypes differed significantly for all the morphological and bio-chemical characters studied. Genetic variability studies revealed that the range of PCV was 14.85 to 76.73, while, the range of GCV was 12.73 to 75.83. The estimates for heritability ranged from 70.27 to 99.33 and genetic advance as per cent mean ranged from 22.48 to 154.40. The 156 mango cultivars were grouped into thirteen clusters in D2 analysis. The analysis of 12 SSR markers resulted in the detection of alleles, with an average of alleles/ SSRs, ranging from 23 alleles in Mi IIHR- 30 to 105 alleles/SSRs in MiKVR-965. The polymorphic information content (PIC) value was maximum (0.987) in MiKVR-965 and minimum (0.877) in Mi IIHR-18. Parentage analysis was also carried out in mango hybrids using eight SSR primers. LOD score was calculated for candidate parents, and out of 42 hybrids involving crosses between Amrapali, Vanraj and M. odorata, it was possible to assign parentage for 14 hybrids with strict confidence (95%) and 10 hybrids with relaxed confidence (80%).The chemical diversity of the leaves of 39 mango cultivars were determined independently with HS- SPME-GC-MS technique, the major proportion being contributed by the monoterpenoids and sesquiterpenoids composition. The seventy seven different volatile constituents detected were composed of various chemical classes, namely, hydrocarbons, alcohols, aldehydes and ketones, monoterpenoids and sesquiterpenoids.

Title: Somatic embryogenesis mediated micro propagation of polyembryonic mango with marker assisted confirmation of maternal or zygotic origin of embryos (2019)

Sajana. S, IARI, Guide: Guide: Dr. Reju M. Kurian

Studies were carried out for somatic embryogenesis mediated micro propagation of polyembryonic mango and marker assisted confirmation of maternal or zygotic origin of embryos during 2017-2019 in the Central Laboratory Facility, Division of Biotechnology and Division of Fruit crops, ICAR- Indian Institute of Horticultural Research, Bengaluru. Maximum callus proliferation (93.33 and (93.33) was observed in the medium supplemented with 5 mgL-1 2,4-D + 5 mgL-1 GA3 + 6 percent sucrose + Glutamine - 400 mg/L in cv. Vellaikolumban and cv. Olour respectively. Organic media supplements such as coconut water at 20 percent v/v and casein hydrolysate at 200 mgL-1 found to best combination with maximum conversion of embryos (87.55 and 84.67), intensity of embryogenesis (10.50 and 11.46) in cv. Vellaikolumban and cv. Olour respectively. Organic supplements like coconut water at 20 per cent v/v and casein hydrolysate at 200 mgL-1 resulted in maximum per cent of mature embryos (70.00 and 75.00) and minimum abnormalities (15.00 and 10.00) in cv. Vellaikolumban and cv. Olour respectively. Zeatin at 5 mgL-1 induced shoot and root formation in maximum percent embryos in cv. Vellaikolumban (53.33) and cv. Olour (60.00). SSR markers used in the study detected a total number of alleles per locus with the mean number of alleles ranging from 8 alleles in MiKVR-81 to 11 alleles /SSRs in MiIIHR- 21478. The polymorphic information content (PIC) value was maximum (0.895) in MiIIHR-21478 and minimum (0.830) in MiIIHR- 78. In both cv. Vellaikolumban and cv. Olour, the position of barcode for all nucellar embryos were observed to be similar to that of the maternal parentand embryos produced from zygotic embryo in vitro were observed to be different from the mother plant with all 16 primers which confirmed that the explant which was presumed as nucellus is proved to be similar to the mother plant and the explant which was presumed as ofzygotic origin is proved to be different from the mother plant. Dendrogram constructed using Neighbour joining method resulted in two main clusters with Vellakolumban and Olour samples in separate clusters. Each cluster was divided into two subclusters consisting embryos produced from nucellus tissue and mother plant in one sub cluster and embryos produced from zygotic embryo formed a separate cluster in both cultivars.

Title : Studies on imparting on imparting papaya ring spot virus (PRSV) resistance through wide hybridization and mutation breeding for improved morphological and fruit traits in papaya (*Carica papaya* L.) (2019)

Deepa U. Pujar, UHS Bagalkot, Guide: C. Vasugi

The present investigation was carried out in the Division of Fruit crops, ICAR-Indian Institute of Horticultural Research, Bengaluru during 2015-2018. The study revealed that Arka Prabhath with V. cauliflora was found to show good compatibility resulted in highest fruit set (97.92 %), fruit retention (98.96 %), recovery of more crossed fruits (30.00) and more mean number of bold seeds (63.99). In the intergeneric hybridization, out of 1802 flowers crossed under 18 different cross combinations, 6387 seeds were recovered, out of which only 198 seedlings emerged. From this population, only 95 inoculated and 44 un-inoculated seedlings survived under field condition were evaluated further for yield and horticultural traits. The only combination of Arka Prabhath X V. parviflora (un-inoculated) yielded fruits of desirable fruit quality and the tolerant plant (IGHS7) was advanced for next generation, while all other combinations developed PRSV symptoms after eight months of field planting and could not be advanced further. In the use of molecular markers for PRSV tolerance, the SCAR marker OPK4-1R showed amplification only for the male parents and produced dominant band at 348 bp, while the female parents and intergeneric progenies were not amplified indicating the susceptibility nature. Among the male parents, banding pattern was different for susceptible (V. parviflora) and resistant ones (V. caul flora and V cundinamarcensis). Further sequencing and BLAST analysis showed that the resistant male parents (2) showed 93 % identity to UlsnRNP of papaya and are involved in virus resistance. The hybridity test performed using RAPD and SSR markers showed that OPF-12 (400 bp), OPG-10 (350 bp) and P6K72CCF/R (300 bp), CP-07 (210 bp) showed clear bands to distinguish the intergeneric hybrid progenies. Mutation was induced to create variability for plant height, shelf life, PRSV tolerance and fruit quality traits. The selected mutants (M1-4-2; ultra dwarf, M1 1-8; true type hermaphrodite and MI 14-5; yellow pulp) were advanced for next generation.

Title: Studies on screening for resistance to papaya ring spotvirus in Papaya genotypes (*Carica papaya* L.) and Vasconcellea species (2019)

Linta Vincent, TNAU, Guide: Dr. K. Soorianathasundaram

The present studies to screen selected genotypes of Carica papaya and Vasconcellea species against Papaya Ring Spot Virus (PRSV), document the physiological and biochemical changes due to PRSV infection and to further characterize the differential gene expression of resistant and susceptible genotypes by transcriptome analysis. In Carica papaya genotypes TNAU papaya C08, IG1I1 and IGH2 which reached reproductive stage, significant reduction in yield and yield related parameters were registered. Based on scoring, Arka Surya, Arka Prabhath, Red Lady and Pusa Dwarf were classified as highly susceptible; 'TAU papaya CO8 and V. goudotiana as susceptible; IGH1 and 'ICH2 as moderately susceptible; Pusa Nanha and V, paryiflora as moderately resistant and V. cazdillora as resistant. PCA analysis between enzyme activity and genotypes revealed that major enzyme contributing to PRSV resistance was Phenylalanine Ammonia Lyase (PAL).Serine Threonine Kinase (corresponding to STK I gene), one of the protein responsible for signal transduction as Pattern Recognition Receptors (PRRs) and effector recognition of PRSV was detected in the resistant genotypes Vcauliflora, Kgodotiana and V.cundinamarencis and not in Carica papaya genotypes involved in the study indicating its potential role in resistance. In transcrptomics analysis, Salicylic acid, ethylene response genes and transporter genes, gibberellins and auxins related genes were found upregulated along with phenylalanine ammonia lyase genes in this resistant genotype. The genes involved in the precursor of phenylpropanoid pathway viz., fructose- 1 ,6- bisphosphate, phenylalanine ammonia lyase, shikimate kinase, 4- coumarate CoA lipase and Cinnamate.4-hydroxylase were also found to be upregulated providing resistance. The pathogenesis related proteins namely LRR-receptor-like proteins, F- box proteins, Serine threonine kinases, thaumatin and WRKY transcripts were significantly expressed in resistant genotype.

Title: Characterization studies in Annona species and varieties (2019)

Priyanka, H.L. UHS, Bagalkot, Guide: Dr. T. Sakthivel

The present investigation on Characterization studies in Annona species and varieties was carried out in the Division of Fruit Crops, ICAR-Indian Institute of Horticultural Research, Bengaluru during 2015-2018.The study consisted of four objectives. Among all Annona squamosa varieties and half sib progenies, the hybrid Arka Sahan was found to be the best with respect to almost all the characters like fruit weight (497.83g), less peel percent (13.16%), high pulp weight (385.36g)and TSS (31.44°B) suggesting a good choice for fruit breeders and consumers. The criteria for selection of superior genotype were the high pulp percentage with minimum number of seeds was recorded in A. muricata, hybrid Arka Sahan and Bullocks Heart. Highest pollen germination was found in the species A. squamosa (61.68%) , Mammoth (87.78%) and Island Gem (33.86%) can be used as pollen parent. The highest TSS: Acidity ratio was observed in the species A. cherimola which is an important character for consumer acceptance. The correlation coefficient analysis revealed that direct selection for quantitative traits i.e., fruit length, fruit width, peel weight, pulp weight, pulp percentage, number of seeds, acidity and ascorbic acid. Based on the D^2 values, the 44 genotypes were grouped into 7 clusters. Among the 12 characters studied, fruit weight (46.19%) contributed maximum towards total genetic divergence followed by peel weight (20.72%), weight of seeds (15.86%), pulp per cent, (9.51%) number of seeds, TSS : Acidity, fruit width , ascorbic acid, TSS and titrable acidity. The genotype 8/3, 8/4 and 8/7 can be extensively used for further breeding programme to develop new annona varieties. Molecular study revealed the existence of genetic diversity amongst different genotypes of Annona species. The ISSR markers proved to be suitable for characterizing Annona species differentiating them into independent cluster depicting that these are more divergent from each other and can be utilized for further annona improvement programme.

Title: Genetic Diversity Studies and Characterization in Pomegranate (2020)

Shaili Kumari, IARI, Guide: Dr. M.R. Dinesh

The present study was carried out in the experimental block no.2 under the Division of fruit crops, ICAR-IIHR, Bengaluru during 2015-2018. A total of 154 pomegranate genotypes along with their hybrid parents (Bhagwa, Double flower and Nana) have been used for morphological, biochemical and molecular characterization. The morphological characters such as plant growth parameter, fruit parameters and leaf parameters; biochemical parameters like total phenol, flavonoids, anthocyanin, antioxidant activity (FRAP, DPPH), sugar, TSS and acidity were studied. Molecular characterization has been done using 162 SSR markers for the genetic diversity analysis and population structures among pomegranate genotypes. Hybrid progenies had erect and semi spreading type growth habit whereas the mutant genotypes possess erect type growth habit and most of the wild accessions retaining erect growth habit. Based on puncture test, the seed hardiness ranged from 4.4 to 19.6 N/mm of which average was 10.56 N/mm. Fruit characters like fruit weight, fruit length, fruit breadth and aril (%) were positively correlated to each other. Whereas Fruit weight and seed hardiness was negatively correlated to each other. Total antioxidant potential (FRAP (mg/100g) and DPPH (mg/100g) with 186.93 and 193.11, respectively. The average TSS, acidity and total sugar for all genotypes was with 15.330B, 1.77 % and 11.77 mg/100g whereas the TSS and acidity was observed in wild genotypes. The result showed that the highest amount of total phenolic content and total flavonoid content had the maximum radical scavenging effect. Genetic diversity ranged from 0.87 to 0.98 with mean value of 0.92. The value of heterozygosity ranged between 0.851 (SSR32) to 0.006 (SSR54) with mean heterozygosity 0.199. The polymorphic information content (PIC) ranged from 0.866 (SSR8) to 0.0.975(SSR32) with means 0.949. The most diverse genotype on the molecular basis was accession number IC 3187581. Hybrid parents (Bhagwa x DF x Nana) grouped along with progeny showing relatedness and confirm its hybridity. Genetic distance was high in genotype 1/1(Mutant) and 318699(Wild), 14/20(Hybrid) and 11/10(Hybrid) which could be used for further breeding for soft seediness /colour/sweetness. The results of this investigation showed a great diversity among three different pomegranate genotypes (Hybrid, Mutant, Wild) that can be used for studies of pomegranate germplasm and future breeding programs.

Title: Evaluation of Putative Ploidy Progenies of Guava (*Psidium guajava* L.) (2021)

Kiran Kumar G N, IARI, Guide: Dr. M.R. Dinesh

Knowledge about the extent of genetic diversity/relatedness in guava is vital for developing coherent strategies for future gains in productivity and quality. The present investigation was conducted at ICAR-Indian Institute of Horticultural Research (ICAR- IIHR), Bengaluru during 2018-2020 by studying the morphological and biochemical characters to assess the extent of variability and the genetic diversity by using SSR markers. Wide variation was recorded among the 551 putative polyploid progenies and these progenies differed significantly for all morphological and biochemical characters studied. Genetic variability studies revealed that the range of PCV was 10.48 to 45.31, while, the range of GCV was 7.26 to 41.66. The estimates for heritability ranged from 19.30 to 98.60 and genetic advancement showed highest for fruit weight and number of seeds per fruit in all the progenies. Among putative polyploid progenies, Arka Mridula progenies developed by seed treatment were grouped highest number of clusters in cluster analysis. The 2C DNA content has significant positive correlation with leaf characters, stomatal size and TSS whereas, significant negative correlation with shoot internodal length and stomatal density. Diversity analysis identified 151 alleles with 6-16 alleles having an average polymorphic value 0.732 (mean of 9.44 alleles/ loci). The polymorphic information content (PIC) value was maximum (0.927) in MPg CIR097 and minimum (0.436) in MPg CIR334. Among all treatments, the seed treated progenies of Arka Kiran recorded highest variability parameter including highest number of alleles (5.563) and Shannon information index (1.283). Clustering and population structure of progenies distinctly separated Arka Kiran and Arka Mridula into two major groups. Principle coordinate analysis (PCoA) showed 37.79% of variation contributed by first three coordinates. Analysis of molecular variance (AMOVA) showed 16%, 75% and 9% variation among population, among individual, and within individual, respectively. This genetic variation in colchicine treated progenies can be used for improving fruit yield and quality of guava.

Title: Hybrid Papaya (*Carica papaya* cv. Surya and *Vasconcellea cauliflora* L.) (2021)

Kaluram, IARI, Guide: C.Vasugi

The present investigation on “Micropropagation and Field Evaluation of Intergeneric Hybrid Papaya (Carica papaya cv. Surya and Vasconcellea cauliflora L.)” was carried out during 2016-2020 at the Division of Basic sciences, ICAR-Indian Institute of Horticultural Research, Bengaluru. MS basal medium resulted in highest establishment with healthy cultures (80%) as compared to RO medium. The maximum mean shoot length (1.16 cm) was recorded in control (without hormone) on MS medium while the highest number of shoots (5.68, 6.81) per explant was recorded with 1 µM BAP+1 µM GA3+0.1 µM IAA on both MS and RO medium.In ex vitro rooting, plantlets dipped with 100 µM IBA recorded highest rooting per cent (50%) and number of roots (2.20) while, 1000 µM PG produced maximum rooting per cent (82.00) and number of roots (7.00) followed by 500µM PG. Six isolates of endophytic bacteria designated as IGH SR F9 02, 04, 05, 06, 07 and 08 (Staphylococcus haemolyticu,Rhizobium oryzihabitans, Kocuria rosea, Pseudomonas citronellolis, Arthrobacter globiformis and Microbacterium chocolatum) were successfully identified through 16S Rrna gene sequence homology analysis. All isolates exhibited rooting which ranged from 30.00 to 99.30 per cent except control. Highest rooting per cent (99.30) from ex vitro rooting was recorded from endophytes followed by phloroglucinol (82.00) and lowest from IBA (50.00). For acclimatization of rooted plantlets, sachet method was found effective (100 per cent). The SCAR markers employed for sex determination at seedling stage revealed that the markers T12 and W11 could successfully differentiate both female and hermaphrodite plants (99.90% accuracy) in both IGH and Arka Surya which had exhibited a band of 800bp in hermaphrodite only. In the evaluation of micro propagated plants in comparison with seed derived plants (intergeneric hybrid and Arka Surya) out of 192 plants evaluated for morphological, fruit parameters and PRSV tolerance it was observed that the micro propagated IGH.SD.3 and IGH.SD.4 showed field tolerance to PRSV coupled with desirable fruit quality. The micro propagated plants (IGH and Arka Surya) were comparatively dwarf with shorter internodal length, lower fruit bearing height coupled with early flowering compared to seedling progenies.

Title: Studies on morphological, biochemical and molecular characterization of Rambutan (*Nephelium lappaceum* Linn.) (2021)

G. Ranganna, Y.S.R H University, Guide: Dr. T. Sakthivel

The present investigation, “Studies on morphological, biochemical and molecular characterization of rambutan”, was carried out during 2018-2020 at ICAR - Central Horticultural Experiment Station (CHES), Chettalli and ICAR- IIHR, Bangalore, Karnataka. Genetic diversity was evaluated in eighty- nine accessions of rambutan by tree morphological, fruit biochemical and molecular markers. Twenty- five ISSR markers were employed to analyse the molecular diversity among the accessions. The analysis of variance for the thirty quantitative traits revealed significant differences for all the characters studied thus indicating wide variation among the rambutan accessions. Correlation coefficient and Path coefficient analysis revealed that the association of leaf width, leaf length, fruit width, fruit length, fruit weight, rind weight, seed weight, seed length, aril weight and pulp weight with yield/tree and among themselves was positive and highly significant and these traits were identified as fruit yield components and exerted high positive direct influence on yield per tree. In D2 analysis, the characters viz., leaf width, fruit weight, fruit length, fruit volume, rind weight, TSS, total sugars, non-reducing sugars, ascorbic acid, acidity, total phenols, flavonoids and antioxidants contributed more for the divergence. In PCA, the characters viz., yield per tree, total sugars, TSS, ascorbic acid, sugars, total phenols and antioxidants in PC1 contributing more towards variability. In present investigation polymorphic patterns of ISSR primers indicated that out of a total 195 loci, 110 loci were polymorphic (56.10%). Which could be exploited for DNA fingerprinting of these accessions by converting ISSR markers into SCAR and STS markers and this was highly useful for detecting mixes between accessions. Based on outcome of the present investigation, it can be concluded that molecular markers for fingerprinting as well as estimation of genetic diversity and genetic relatedness in rambutan accessions is effective, precise and more efficient than morphological markers.

Vegetable Science

Title: Studies on gene-action, combining ability and heterosis of some economically important characters in Tomato (*Lycopersicon esculantum*) with particular reference to processing (1982)

Tikoo, UAS, Bangalore, Guide : Dr.A.B.Pal

The possibility of breeding tomato genotypes with high soluble solids-an important trait for both fresh market and processing varieties-large fruit weight, heterosis, gene-action and combining ability of some physiological, biochemical and morphological components of yield and/or quality with particular reference to processing were studied. Although total soluble solids (TSS) and fruit weight were negatively correlated, simultaneous selection for both traits from F2 onwards in the crosses involving 249-2 (TSS 8.5%) and low solid parents (TSS 4%) helped in breaking the correlation. By F6 many genotypes with high solids of above 6% and fruit weight of above 60 g were obtained. Relatively lower coefficient of variation for TSS and fruit weight from F 2 onwards than yield and fruit number suggest these traits to be governed by fewer genes than reported earlier. The dialed analysis revealed additive and dominant genetic effects to be mainly governing most of the traits except fruit number and lycopene content. High general combining ability effects had a close correspondence with high mean expression for most of the traits. Five F1 hybrids with semi-determinate habit were heterobeltiotic for yield per plant, highest heterosis being of the order of 47% in the cross P 1 x P2. Crosses with the high solids parents 249-2(P8) were observed to be superior for nutritional quality. Heterosis was observed for ascorbic acid content, indicating dominant gene action for this trait. Specific leaf area (SLA) and specific leaf dry weight (SLDW) were positively correlated with each other as also fruit weight. Small leaf area was observed to be dominant over large leaf area. Genetic divergence between parents and heterosis were not associated. Specific combining ability was a more important factor in obtaining heterosis.

Title : Studies on improvement of Chillies for resistance to Anthracnose and Cercospora leaf spot diseases (1982)

Devinder Singh Cheema, UAS, Bangalore, Guide : Dr.D.P.Singh

Studies to locate sources of resistance to Anthracnose and Cercospora leaf spot diseases the inheritance of their resistance and to confirm the role of phenols in imparting resistance to these disease were carried out. Based on three years screening of 111 genotypes against Anthracnose disease and 123 genotypes against Cercospora leaf spot diseases, sources of resistance were located in 35 and 45 lines respectively. Inheritance of anthracnose resistance studied using five crosses involving three resistance and two susceptible parents. Five crosses involving two resistance and two susceptible parents were used for study of inheritance of resistance to Cercospora leaf spot. Two separate trials were laid out in kharif 1981 the six generations namely, P1, P2, F1, F2, B1 and B2 of the five crosses in each disease were planted in randomized block design with two replications each. The individual plants were visually scored for disease severity. Based on the number of spots per leaf, grading scales of 0-5 and 0-2 were used in anthracnose and Cercospora leaf spot diseases. The data in respect of Cercospora leaf spot indicated that inheritance of resistance governed by three complimentary genes. The quantitative analysis indicated that both the types of gene actions, i.e., additive (d) and dominance (h) were important. For resistance to Anthracnose, it is advocated to go for bi-parental crosses to exploit both types of gene actions involved. For Cercospora leaf spot resistance, it is advocated to resort to repeated backcrossing using the resistant parents. For simultaneous incorporation of resistance to both diseases, it is advocated to adopt recurrent selection. The role of total phenols could not be related with the resistance to both the diseases.

Title : Studies on important of qualitative and quantitative characters in Muskmelon (*Cucumis melo* L.) (1984)

K.R.M.Swamy, UAS, Bangalore, Guide : Dr.O.P.Dutta

Investigation were undertaken to study genetic variability, correlations, gene action, combining ability and heterosis for important economic characters in muskmelon (Cucumis melo L.). For this purpose 45 muskmelon genotypes were evaluated in addition to a 10x10 diallel cross analysis. Among the 20 characters studied, yield per plant showed maximum variability followed by average weight per fruit, main stem length, internodal length and ascorbic acid content. High estimates of genotype coefficients of variation were observed for fruit netting, sutures and shape index. The association of yield per plant was positive with number fruits, average weight per fruit, number of nodes on main stem, main stem length, internodal length, number of primary branches and fruit shape index. But the yield was negatively correlated with TSS, ascorbic acid and dry matter which in turn were found to be positively associated among them. Narrow-sense heritability was also low to moderate for these characters. Therefore, reciprocal recurrent selection and biparental mating could be successfully used. Parents 'Arka Rajhans', 'Hara Madhu' and 'Arka Jeet' were good general combiners for most of the characters. The cross 'Arka Jeet x UFG 515' exhibited the highest percent (111.4) of heterosis over better parent. For quality characters, the range of heterosis was low. The cross, 'Main stream x Arka Rajhans' exhibited significant heterosis over mid-parental value (39.6%) and non- significant heterosis over better parent (25.2%). Both the parents of this cross carry genes for resistance to powdery mildew and in addition 'Main stream' carries genes for field tolerance to downy mildew. Hence, there is scope for further evaluation to select desirable segregants. The dominance of orange fruit colour over yellow, white flesh over orange and green, green flesh over orange and white seed coat over yellow was observed.

Title: Studies on the nature and mechanisms of resistance to rust diseases in Peas (1985)

Abu Saleha, UAS, Bangalore, Guide: Dr.A.B.Pal

The nature of rust resistance and its interrelationship with other economic characters were studied. Parental F1 and F2 and two back cross generations of thirteen crosses were used for the study. Chi-square method for testing the segregation ratio, generations mean method to study gene action, contingency Chi-square for association of characters was adopted. Phenols and sugars were estimated to ascertain the biochemical basis of resistance. Resistance to rust was found to be governed by a single pair of dominant genes. Plant height, pods per plant, pod weight, 100 seed weight were the important economic characters which had positive association with resistance. No linkage was found between resistance and qualitative characters like flower colour, stipule base colour, seed colour and seed shape. Dominant gene action and epistasis was observed majority of characters. However, addictiveness was also found for flowering, 100 seed weight, pod length and pods per plant. High phenols and low sugar content appeared to be responsible for resistance.

Title: Response of Watermelon (*Citrullus lanatus* thumb. Musf.) to drip and furrow irrigation under different nitrogen and plant population levels. (1987)

K.Srinivas, UAS, Bangalore, Guide: Dr.M. Hegde

Two field experiments were conducted to study the effect of nitrogen, spacing and method of irrigation on watermelon in terms of growth, yield and water use. Growth parameters increased with increase in nitrogen levels up to 180 kg/ha. Fruit yield increased with nitrogen levels up to 120 kg N/ha (370 q/ha in 1984 and 345 q/ha in 1985) as compared to 60 kg N/ha (349 q/ha in 1984 and 308 q/ha in 1985). Reducing the row spacing from 300 cm to 200 cm increased the fruit yield from 336 q/ha to 389 q/ha in 1984 and from 303 q/ha to 336 q/ha in 1985. Fruit yield was higher under drip irrigation (418 q/ha in 1984 and 379 q/ha in 1985) as compared to furrow irrigation (307 q/ha in 1984 and 287 q/ha in 1985). Fruit yield was highest with irrigation at 1.00 IW/CPE ratio (338 q/ha in 1984 and 310 q/ha in 1985) and the lowest with irrigation at 0.25 IW/CPE ratio (327 q/ha in 1984 and 252 q/ha in 1985). Drip irrigation with one emitter per two plants recorded higher yields (367 q/ha in 1984 and 314 q/ha in 1985) than irrigation at5.0 cm depth (269 q/ha in 1984 and 227 q/ha in 1985) in furrows. Nitrogen level of 120 to 140 kg/ha was found to be optimum for obtaining high yields in watermelon. A plant population of 16,666 plants/ha (200 cm x 60 cm) was found to be ideal for yield maximization. Drip irrigation with daily application of water at the rate of 25% pan evaporation is suitable for realizing higher yields. Furrow irrigation at 0.50 or 0.75IW/CPE ratio with 2.5 cm depth of water can be adopted for watermelon for higher yields. Thus, nearly 50% saving in water was possible under drip irrigation, as compared to furrow irrigation.

Title: Studies on genetic resistance to Bacterial wilt (*Pseudomonas solanacearum* e.f. Smith) and root-knot nematode (*Meloidogyne incognita* Kofold and White, 1919;Chitwood, 1949) in tomato (*Lycopersicon esculentum* Mill.) (1987)

S.Nirmala Devi, UAS, Bangalore, Guide: Dr.S.K.Tikoo

Present study was undertaken to study the inheritance of combined resistance to bacterial wilt and root-knot nematode in tomato, to study the interaction of these soil borne pathogens on the resistant genes present in the host genotype and to identify a broad spectrum resistant source of wilt amongst known lines/varieties. The results showed that F1s of parents having dominant sources of resistance to wilt and root-knot nematode were resistant to both the diseases in the field. The combined resistance to both the diseases was inherited digenically in 'BWR-1' crosses. The interaction between the pathogens had modified the genetic ratio in the crosses. The sequential inoculation (N+B and B+N) of both pathogens, in the pots, showed that the digenic ratio was modified to 9:3:4 irrespective of the sequence. The interaction between the pathogens was more severe in 'BWR-1' hybrids as a result of simultaneous inoculation. On the other hand, 'CRA-66- Sel-A' hybrids could withstand the interaction because at the seeding stage partial dominance to wilt was operational in them. The significant correlation between ooze index and gall index proved that the nematodes predisposed the plants to bacterial wilt. The lines selected for resistance to bacterial wilt in Hessaraghatta showed differential response to isolates of P. solanacearum from Maharashtra, Kerala and Chethalli. The best F1 hybrids for fresh market were 'BWR-1' x 'Rossol', '83 BWR 12-2' x 'IHR-998', '83 BWR-120' x 'Patriot' and'MITA-668' x '83 BWR 120'.

Title: Genetics of resistance to yellow vein mosaic virus, yield and yield components in Okra (*Abelmoschus esculentus* L. Moench) (1988)

A.T. Sadashiva, UAS, Bangalore, Guide : Dr.O.P.Dutta

Screening of thirteen inbred lines of okra under field as well as under artificial controlled conditions indicated that all the inbred lines of okra were completely resistant to YVMV but the resistance was of symptomless carrier type. Segregation pattern for disease reaction in F2 generation of two crosses revealed seven (resistant): four (intermediate) and five susceptible. This segregation pattern can be explained assuming existence of two genes viz., YV1 and YV2 at two separate loci determining resistance. While their recessive alleles determine the susceptibility, this model entails that the resistance was imparted only when at least one of the genes was in homozygous dominant condition i.e., either YV1,YV1-or-YV2 YV2 genotype. While the intermediate expression was seen when both genes are in heterozygous condition (YV1, YV1-YV2 YV2). Combining ability studies indicated that both GCA and SCA effects were important for all the characters. However GCA variances were higher than SCA variances suggesting predominance of additive genetic variances for all characters.

Title: Studies on the genetics of yield and quality characters in bulb and seed crop of Onion (*Allium cepa* L.) (1988)

R.Veere Gowda, UAS, Bangalore, Guide : Dr.C.S.Pathak

The main objectives of the investigation were to study extent of heterosis, combining ability and nature of gene action in respect of twenty five characters in bulb crop and nine characters in seed crop of onion using the diallel technique. The variance due to hybrids was highly significant for height of the plant, earliness, split bulbs, dry weight of leaves, fresh and dry weight of the bulbs, ten bulb-weight, marketable and total bulb yield, double centres, firmness of the bulb, storage rot, sprouts and loss in the bulb crop where as in seed crop there were significant difference for days to flower initiation, height of umbel stalk, diameter of umbel, seed yield per plant and seed yield per hectare. The extent of heterosis estimated over mid, better and best parents revealed superiority of some outstanding F 1s over best parent; The variances due to GCA were greater than SCA for all characters in bulb in seed crop; except for the character seed yield per umbel where in SCA variance was greater. A comparison of gca effects revealed that none of the parents were good in respect of all the characters. However, parent 1 (IHR 52-80) was found to have best performance as it has significant gca effects for 12 characters followed by parent 6 (IHR- 68) for 10 characters, parent 2 (IHR-60-94), 4 (IHR-400), 5(IHR 121-26), 7(IHR 399), and 8 (IHR-6). Best parental combination i.e., parent 2 (IHR-60-94) and 8 (IHR-6) were found to be top combiners for most of the characters (14) followed by the combination, parent 1(IHR 52-80) and parent 11(IHR56-198) for 11 traits each. All these parents have additive genetic variance for these traits which could be utilized for improving these characters through selection. For the exploitation of heterosis; the specific combining ability is important. On the whole in most of the characters studies, all the three types of generation were observed. Under such situation, improvement in such characters may be expected through standard selection procedures which may first exploit additive genetic variance simultaneously the dominance variance should be concentrated. For this, reciprocal recurrent selection breeding procedures seem to be the best method to meet the requirements as it will utilize simultaneously all the 3 kinds of gene effects.

Title: Exploitation of residual heterosis in F2 for better performance and fruit rot (*Colletotrichum capsici* (syd.) Butler and Bisby) resistance in chillies (*Capsicum annum* L.) (1991)

H.B.Patil, UAS, Bangalore, Guide : Dr.N.Anand

Selection of parents to produce heterotic Fls and choice of Fls for advancing to obtain heterotic F2s besides adaptability of a parent, F1s and F2s populations for fruit yield and fruit rot resistance. While studying F2 population from a 8x8 diallel, it was observed that the parents IHR 328-9 and IHR 309-3-18 possessed high general combining ability in most environments. F2s of 384 x 328-9, 309-3-18 x 472-12-6-4 exhibited high degree of heterotics. In unfavorable environments additive gene effects and in favorable environments non-additive gene effects were important for yield and its components. The overall means of F1s and F2 s excelled the parental mean in all four environments tested, while means of F1s and F2s were identical in unfavorable environment. Maximum heterotic in F2 was exhibited by 328-9 x 473-11-3-1 in unfavorable and by 328-9 309-3- 18 in favorable environments. Heterotics in F2s was attributed to near complete additivity and accumulation of trangressive segregants. Co-efficient of variation for fruit traits was less than 20%. In the other set of diallels with 5 fruit rot resistant parents and two susceptible, it was found that F1s and F2s of all resistant x resistant were resistant indicating the alleles confirming resistance to be at the same loci. Resistance was shown to be governed by a single recessive gene with modifiers, in all such parents. The F 2 hybrids have the advantage of yield and adaptability besides resistance to fruit rot, and the cost of their seed production was comparable with open pollinated varieties.

Title: Genetics of resistance to bacterial soft rot (*Erwinia carotovara* John), root- knot nematode (*Meloidogyne incognita*), yield and yield contributing characters in carrot (*Daucus carota* L.). (1997)

T.V.Narayana Murthy, UAS, Bangalore, Guide : Dr.O.P.Dutta

Bacterial soft rot and root-knot nematodes cause great loss in yield and quality of the carrot root. The development of varieties resistant to bacterial soft rot and root-knot nematode is one of the ways to overcome these diseases. The present investigation was carried out i) to locate the source of resistance to bacterial soft rot and root-knot nematode ii) to locate the source of combined resistance to bacterial soft rot and root- knot nematodes and iii) to study the genetics of resistance to bacterial soft rot and root- knot nematode and yield contributing characters. Ten genotypes including 5 resistant and 5 susceptible lines each for soft rot and root-knot nematodes were selected by screening under natural epiphytotic and pot conditions. These lines were crossed in a diallel manner (excluding reciprocals). The data were collected for nine quantitative traits each for soft rot and root-knot nematodes. Ten lines exhibited resistance to soft rot viz., IHR 174-2, IHR-89, IHR 37-B-III, A+-PHG, IHR 64-89-HC-1, IHR 308 X PP-A, HYDC-4, IHR 309 and IHR 190 and ten genotypes for root-knot nematodes viz., HYDC-4, PKR, IHR 310, IHR 174-1, IHR 308, IHR 181, Danvers Half Long, Nantes, PYD-III AND Avenger and also combined resistance in two genotypes HYDC-4 and IHR 308. The heterosis over mid parental value indicated non-additive gene action for all the characters. Combining ability analysis revealed higher gca to sca variance for all the characters except for percent disease index suggesting predominance of additive genetic variance for these characters. Dominant gene action was more involved than additive gene action for all the characters except PDI and PGI for which additive gene action was found to be operating. The hybrids IHR174-2 x Desi Red, IHR 37-B-III x Sersa local, PPA x Sersa local, PP-A x IHR 21, IHR 64 x LL-2 and the crosses IHR 174-1 x IHR 301, IHR 301 x IHR 174-2, IHR 301 x IHR 300 and IHR301 x IHR 181-2 could be used in recurrent selection for sca and heterosis over mid parent to bring about desirable improvement in terms of high root weight, and resistance to bacterial soft rot and root-knot nematode, respectively.

Title: Genetical studies on leaf curl virus resistance in Tomato (*Lycopersicon esculentum* Mill.). (1998)

M.Jagadish, UAS, Bangalore, Guide : Dr.A.A.Deshpande

An investigation was carried out in tomato to study the genetics of TLCV resistance and yield attributes, establish strainal differences in TLCV if any identify/confirm tomato leaf curl virus resistance through graft transmission. The salient findings of the present investigation are given below: TLCV resistance is governed by two complementary genes in the resistance parent RP1 (4- 1/3) and it is controlled by recessive gene in the parent RP 2 (55-3/7). The artificial whitefly inoculation is advantageous once field screening as it advances the expression of TLCV symptoms by weeks. Major contribution of dominance x dominance epistasis was observed for the inheritance of number of fruits, average fruit weight and fruit yield per plant in all the three crosses studied (SP 1 x RP1, SP1 x RP2, SP2 x RP2). High magnitude of phenotypic coefficient of variation coupled with high genetic advance as percent of mean and low heritability (narrow sense) was observed for all the characters studied viz., number of fruits, average fruit weight and fruit yield per plant in all three crosses. Maximum frequency of transgressive segregants with TLCV resistance and fruit size (70 g and above) were observed in the crosses SP1 x RP1 compared to the other crosses viz., SP1 x RP2 and SP2 x RP2. Four different types of leaf curl symptoms could be differentiated based on symptom expression on a common genotype Arka Saurabh. They are termed as TLCV group A, TLCV group B, TLCV group C and TLCV group D. these were considered to be due to distinct TLCV strains. Five accession of L. Peruvianum (EC 251615, LA 1954, LA 2151, LA 2959 and PA 128659), two accessions of L. Chelense (LA 2729 and LA 1969) and three interspecific derivatives (4-1/3), RP2 (55-3/7) and 73-1/3) were found to be persistently resistant to TLCV.

Title: Identification of molecular marker linked to purple blotch disease resistance in Onion (*Allium cepa* L.) (2003)

C.T. Ganesh, UAS, Bangalore, Guide: Dr.R.Veere Gowda

Investigations entitled "Identification of molecular marker linked to purple blotch disease resistance in onion (Allium cepa L)" was conducted at the Division of vegetable crops, Indian Institute of Horticultural Research, Hessaraghatta, Bangalore and at the Plant Molecular Biology Laboratory, Division of Horticulture, University of Agricultural Sciences, Bangalore. The salient achievement of the investigation is summarized. RAPD markers were used in onion due to the advantages over other kinds of markers to study its association with resistance. Identification of molecular linked to disease resistance included selection of resistance and susceptible parents, primer screening to identify the polymorphism between the parents and analysis of the mapping population segregating for resistance to associate DNA marker linked to resistance. Screening of onion germplasm for purple blotch disease resistance under natural and artificial epiphytotic conditions resulted in identification of one resistant genotype PBR 287(PDI 4.85) and other two moderately resistant genotypes viz., Arka Kalyan 704 (12.12) and MS-65- 268 (14.91). These three resistant genotypes were utilized as source of resistance to purple blotch disease. Studies on growth, yield and quality parameters on these identified resistant genotypes revealed the similarities in plant growth and bulb qualities and they were also found superior over other genotypes. The three purple blotch resistant genotypes viz., PBR 287, Arka Kalyan 704 and MS 65-268 were fingerprinted using 20 selected arbitrary primers, which could effectively distinguish the resistant and susceptible genotypes. Further, genetic analysis of the four genotypes using RAPD markers revealed high polymorphism among the genotypes confirming the high heterozygous nature of the population due to its highly cross pollinated breeding behavior. Dendrogram analysis of three genotypes revealed the existence of high genetic similarity between MS-65-268 and PBR 287(40% dissimilarity). Further dendrogram also clustered Arka Kalyan 704 and Arka Niketan 709(65% dissimilarity) together but with comparatively lesser genetic similarity.Results revealed that the inheritance of resistance in PBR 287 was governed by single dominant gene and segregated according to classical Mendalian ratio 3:1 in F2 population derived out of cross between PBR 287 (resistant) and Arka Niketan 709 (highly susceptible). A RAPD marker OPC12 900 was found closely linked to purple blotch disease resistance as indicated by bulked segregant analysis and analysis of F2 individuals. This marker could be effectively employed for MAS of large population for purple blotch disease resistance even in the absence of the pathogen and at the early stage of the life cycle of onion crop.

Title: Genetics of yield and yield components in Muskmelon (*Cucumis melo* L.) (2005)

J.S.Aravinda Kumar, UAS, Bangalore, Guide : Dr.M.Prabhakar

An investigation was carried out to find out the combining ability, heterosis, heritability and genetic advance and gene effects of fifteen quantitative traits in muskmelon during 2003-2004. The study involved the evaluation of 49 hybrids along with their 14 parents to assess combining ability and estimation of heterosis over mid parent, better parent and commercial check. The combining ability studies indicated that the parents Punjab Sunheri, IIHR-615-5-2 and IIHR-616-2-3 could be utilized in breeding programme since they expressed highly significant and positive GCA effects for total fruit yield per vine. Evaluation of F1s hybrids indicated that the Kajri x IIHR-615-5-2, Pusa Madhuras x Durgapura Madhu, RM-43 x Durgapura Madhu and Kajri x Durgapura Madhu were found promising and these could be exploited for commercial purpose. Studies on heritability and genetic advance indicated the presence of non additive gene action for days to first male and female flower opening, days to first fruit harvest, vine length, number of branches per vine, TSS and total yield per vine, where heterosis can be exploited. Whereas other traits were under the control of additive gene action. Where simple selection can be done. To understand the nature and magnitude of gene effects six crosses were analyzed through generation mean analysis for 15 characters. The study indicated that traits such as days to first male and female flower opening, node at first female flower appeared, vine length, number of branches per vine, fruit length, TSS, number of fruits per vine and fruit yield were under the control of non additive gene effects. In order to exploit non additive gene effects development of hybrid is suggested involving the parents having high fruit quality traits. Among the hybrids Kajri x IIHR- 615-5-2 showed high per se performance with high heterotic effect which can be exploited for commercial purpose.

Title: Development of molecular markers linked to moisture stress tolerence in Onion (*Allium cepa* L.) (2006)

M. Sangeetha Kutty, UAS, Bangalore, Guide : Dr.R.Veere Gowda

Onion is an important vegetable crop in India, having great demand in the domestic and international market. However, onion productivity in tropical countries is strikingly low. Onion is predominantly grown as a rain fed crop hence exposed to moisture stress during different stages of crop growth, resulting in heavy yield losses. At present there is no onion varieties suited for cultivation under rain fed condition. Hence there is need for development of varieties suitable for rain fed conditions. Screening of large germplasm collections for moisture stress tolerance employing conventional techniques would be cumbersome and time consuming. Therefore, a more accurate and easy alternative is marker assisted selection..Twenty four onion genotypes were screened during kharif and rabi seasons under field and pot conditions to identify the moisture stress tolerant and susceptible genotypes. The genotypes AFLR, AK-649, S.Local, PBR-140 and hybrid H-1 maintained higher plant water status even under moisture stress. The genotype AK-649 and hybrid H-1 showed highest increase in leaf ABA in response to moisture stress. ABA accumulation has been depicted as an important trait of adaptation to drought, thus the genotype accumulating more ABA is expected to perform better under water deficit. A strong negative correlation between ABA and genotypes was suggestive of the role of ABA in regulation of stomata. The genotypes Sel-11 and AN-650 showed lowest leaf ABA under stress indicating their susceptibility to moisture stress.Significant differences were observed for CID among the onion genotypes. In all the genotypes the CID was reduced under stress. One hundred and thirty seven RAPD markers generated by 15 primers were used for estimating the genetic diversity among 24 onion genotypes. Dendrogram based on Squared Euclidian distance grouped the onion genotypes into two major clusters (northern and southern India). The maximum distance was between genotypes PBR-139 and AK-649 and the minimum between AFLR and PBR-140. PCA also differentiated genotypes of northern region from those of southern region. F 2 population of the cross AN-650 x AK-649 was phenotyped based on morphological and physiological parameters and phenotypically extreme plants were identified. BSA was carried out using DNA from ten tolerant and ten susceptible F2 plants. Three hundred RAPD and 22 SSR primers were used to screen the tolerant and susceptible bulks along with parents.Fifty one primer pairs specific to selected genes were designed and used to amplify complementary sequences from onion leaf cDNA. The amplified fragments were sequenced and characterized using BLAST programme of the NCBI. Significant homology was obtained for HSP, DREB, Aquaporin, Calcium Sensor homologue, Catalase, CDPK, Ubiquitin, Hexose transporter and SAPK. These genes have a crucial role to play in moisture stress tolerance.

Title: Studies on genetics of resistance to purple blotch disease, yield, yield components and quality traits in Onion (*Allium cepa* L.) (2007)

Shashi kanthevoor, UAS, Bangalore, Guide : Dr.R.Veere Gowda

The studies on genetics of resistance to purple blotch, yield, yield components and quality traits in onion was taken up during 2002-2004 at the Division of Vegetable Crops, Indian Institute of Horticultural Research, Hessaraghatta, Bangalore. The material for the heterosis study comprised of five lines (resistant to purple blotch) and six testers (susceptible to purple blotch) which were crossed to get 30 hybrids. The crosses PBR 139 x AN 184 and PBR 140 x AN 187 were found promising over standard check for higher total bulb yield along with purple blotch resistance. Inheritance of resistance to purple blotch disease in four crosses PBR 138 X AN 187, PBR 139 X AN 184, PBR 139 X AP 195 and PBR 140 X AN 184 indicated the presence of both additive and non-additive gene effects. However, dominance and dominance x dominance gene actions were more predominant than other gene actions with duplicate type of epitasis. So it is suggested to go for heterosis breeding to exploit dominant gene action. Joint scaling test suggested the presence epitasis in all the yield and quality traits except days to maturity (dominance), neck thickness (additive), unmarketable bulb yield (additive), and per cent loss due to sprouting (additive). Hence, it is suggested to follow simple selection for the characters neck thickness, unmarketable bulb yield, and per cent loss due to sprouting and heterosis breeding for the character days to maturity. The other characters which were governed by all the gene effects and their interactions, it is suggested to follow reciprocal recurrent selection to improve those traits.The heritability and genetic advance as per cent over mean ranged from -10.0 (total soluble solids) to 130.55 (per cent dry matter and bulb) and 0.49 (ten bulb weight) to 432.64 (neck thickness of bulb), respectively. Most of the traits under study showed high heritability and genetic advance. So, improvement of these traits would be easy in reciprocal recurrent selection method

Title: Genetic studies of downy mildew resistance in Indian slicing Cucumber (*Cucumis sativus* L.) (2018)

Bommesh, J. C., IARI, Guide: Dr.M. Pitchaimuthu

Cucumber (Cucumis sativus L.) is one of the most important Cucurbitaceous vegetable crop grown extensively in tropical and sub-tropical parts of the world. However, cucumber production is limited by the most devastating disease downy mildew. The present work objective is to identify the resistance source for downy mildew disease in cucumber and to study the inheritance of downy mildew resistance along with yield traits. The experiments were conducted at the experimental farm of Division of Vegetable Crops, ICAR-IIHR, Bengaluru, Karnataka, during 2015-2018.Based on the screening of genotypes under field conditions, sporulation of pathogen, progress of disease, detached leaf assay and non-linear statistical analysis it was observed that none of genotypes were immune to downy mildew but genotypes IIHR -438 and African horned cucumber were resistant to downy mildew disease. Ten genotypes recorded susceptibility PDI and rest of the genotypes recorded highly susceptibility with PDI of > 60. The six generation populations of two cross combinations were planted in randomized block design with three replications. Result indicates that resistance in both crosses was controlled by two pairs of dominant and recessive interacting genes (inhibitory recessive epistasis). In generation mean analysis the epistatic interaction was greater importance than main effects in Swarna Agethi x IIHR-438 cross whereas, dominance x dominance epistasis effect was higher and duplicate epistasis was prevailing in IIHR- 431x IIHR-433 cross. The estimates of gene effects of yield traits through analysis of six generations revealed that the magnitude and direction of the gene effects varied in crosses. In Swarna Agethi x IIHR-433 cross showed preponderance of both additive and dominance effects for number of fruits per plant and epistatic interactions were observed for yield per plant. However, scaling test was non-significant for fruit length, diameter and weight. Epistatic interactions were observed for node to first flower, number of fruits per plant, fruit diameter.A total of 143 SSR primers were employed to identify polymorphic primers using 225 F2 populations of Swarna Agethi x IIHR-438 through BSA, SSR 3-5 and SSR 4-13 are co- segregated with disease reaction in BSA. The ‘dm’ genes were tagged with SSR 3-5 and SSR 4- 13 markers loci with distance of 16.6 cM in linkage group 3 and 18.1 cM in linkage group 4, respectively. The backcross breeding along with marker-assisted selection (MAS) can be employed for early selection of downy mildew resistance gene in cucumber and its introgression to develop a resistant variety or hybrid

Title: Genetics and mapping of resistance to watermelon bud necrosis orthotospovirus (WBNV) in Watermelon [*Citrullus lanatus* (Thunb.) Matsum & Nakai] (2018)

Nagesh, G. C., IARI, Guide: Dr. E. Sreenivasa Rao

An experiment was conducted to study the genetics and mapping of resistance to watermelon bud necrosis ortho to spovirus (WBNV) in watermelon. The experimental materials comprised of two resistant (BIL-53 and IIHR-19) and two susceptible (IIHR-140- 152 and IIHR-140) parents. Each of the resistant parents was crossed with the susceptible parent to develop six generations (P1, P2, F1, F2, BC1 & BC2) to study genetics. The results of segregation in F2 and back cross progenies suggested that resistance is governed by a major dominant gene along with other background minor genes in both the crosses exhibiting a quantitative inheritance. Generation mean analysis revealed that both additive and non- additive gene actions are involved in WBNV resistance in these crosses.BIL-53 was found to possess higher degree of resistance with simple inheritance and hence may be of interest to breeders. Simple selection can be effective for improving the trait in the cross BIL-53 × IIHR-140-152 as additive gene action is prevalent. Since both additive and dominance × dominance components are prevailing in the cross, IIHR- 19 × IIHR-140, recurrent selection/heterosis breeding can be adopted for improving the trait. The map constructed with 112 F2 populations derived from BIL-53 × IIHR-140-152 with 140 markers (99 SSR's, 39 Indels and 2 Sv's) consisted of 11 linkage groups spanning a total length of 1982.90 cM with an average interval between markers of 14.16 cM. The $\chi 2$ analysis in F2 and backcrosses showed that WBNV resistance is governed by major dominant gene along with other background minor genes. However, the frequency graphs of AUDPC for WBNV in F2:3 population showed that there was a continuous distribution, confirmed that trait is quantitative in nature. The QTL analysis for WBNV resistance related traits in F2:3 population revealed15 major QTL's with a maximum PVE up to 17.4%. Out of several QTL's detected Chr 2, Chr 4, Chr 7 and Chr 8 were considered as hot spots for QTL's. The results obtained in the present study may provide a guide to fine map hotspot regions for resistance to WBNV.

Title: Marker assisted breeding to incorporate combined resistance to late blight and Tomato leaf curl virus disease in tomato (*Solanum lycopersicum* L.) (2019)

Ashish Kaushal, IARI, Guide: Dr. A.T. Sadashiva

Occurrence of tomato leaf curl virus (ToLCV) and Phytophthora infestans (Mont.) DeBary causing Late blight (LB) in tomato (Solanum lycopersicum L.) is distributed globally. These two pathogens are known to cause substantial damage and yield reduction. Identification of resistant sources and breeding for resistance to ToLCV and late blight is an important goal for tomato improvement programme. The present study was undertaken to identify resistance sources to LB and ToLCV and to incorporate late blight and tomato leaf curl virus resistance genes through marker assisted selection complemented with phenotyping. On ToLCV screening, 4 lines IIHR 2895, IIHR 2896, IIHR 2899 and Kashi Aman carried Ty-3 alone in homozygous condition and 4 lines IIHR2900, IIHR2901, IIHR2902 and IIHR2903 carried Ty-2 and Ty-3 in homozygous condition were exhibited highly resistance reaction against ToLCBaV. Accumulation of viral genomic units and symptom severity were significantly low in tomato lines carrying Ty-3 and Ty-2+Ty-3 compared to those carrying Ty-2 alone. Nine tomato genotypes exhibited highly resistance reaction against late blight. Seven stable pyramided tomato lines were developed differing in fruit characteristics and other horticultural traits. The response of these lines to ToLCV was assessed using whitefly mediated virus inoculation and late blight by whole plant assay and detached leaflet assay. The putative gene combination of Ty-2, Ty-3, Ph-2 and Ph-3 genes in pyramided lines exhibited a high level of resistance to both diseases with acceptable yield and other horticultural traits. The late blight resistance test also showed that Ph-3 is critical for achieving resistance to P. infestans isolate (A2 _13 clonal blue lineage) prevailing in India. Twenty-seven hybrids were developed using 3 pyramided lines and 9 testers and almost all the hybrids exhibited superior standard parent heterosis for yield per plant. In our study, marker assisted selection facilitated generation of seven highly resistant pyramided lines and 27 tomato hybrids resistant to tomato leaf curl virus and late blight which could be, used for area where high disease incidence of ToLCV (summer in south India and autumn in north Indian) and late blight occurs (cold and humid weather Dec. to Feb. in north India). However, integrated disease management practices can also complement the resistance in the pyramided lines with enhanced durability.

Title: Trait dissection and genetic analysis for heat tolerance in Garden Pea (*Pisum sativum* var. hortense) (2019)

Deven Verma, IARI, Guide: Dr. T. S. Aghora

The present investigation was undertaken on “Trait dissection and genetic analysis for high temperature tolerance in garden pea (Pisum sativum var. hortense)” at ICAR- Indian Institute of Horticultural Research, Hessarghatta Lake Post, Bengaluru during 2016-2018. The objectives of the research were to screen the garden pea germplasm lines for high temperature tolerance, to identify traits associated with high temperature tolerance in garden pea and to study inheritance of traits conferring tolerance to high temperature. Garden pea is a highly nutritious leguminous cool season vegetable crop, grown all over the world for its fresh as well as dried seeds. The anthropogenic activities around the world has increased the atmospheric CO2, thus, increasing average global temperature. This threatens the area as well as duration for growing of the garden pea. Garden pea germplasm available with ICAR-IIHR was screened for high temperature tolerance at lethal temperature (43°C for 3 hours) followed by induction temperature (30-38°C for 3 hours) using the Temperature Induction Response (TIR) technique. Ten garden pea germplasm lines were found to be tolerant to heat stress at seedling stage by using normal z- distribution for classification of genotypes into tolerant, moderately tolerant and susceptible. The genotypes IIHR 544 and Arka Uttam were found to be tolerant to heat stress at seedling stage. The garden pea lines were sown in field crops summer season of year 2016 (35.3°C/22.4°C) and 2017 (31.9°C/ 20.8°C) in Bengaluru, Vegetable Farms, for the identification of traits associated with high temperature tolerance in selected garden pea lines. The results depicted that the traits associated with heat tolerance are pollen viability, per cent pollen germination, pollen tube growth, per cent electrolyte leakage, membrane stability index, pod yield, pod filling percentage and shelling percentage. For all the studied traits heat tolerant lines showed better results as compared to susceptible garden pea lines.The results obtained from the genetic analysis of the inheritance of traits associated with high temperature tolerance showed the prevalence of epistatic interaction governing almost all the characters. Also the type of epistasis prevalent in the cross combinations was duplicate type. Thus, to improve garden pea lines for concerned traits, selection for transgressive segregants from F2 onwards should be taken up to develop heat tolerant, high yielding line in garden pea.

Title: Genetic and molecular analyses for chilli leaf curl virus resistance in Chilli (*Capsicum annuum* L.) (2019)

Rajeev Kumar Yadav, IARI, Guide: Dr. K. Madhavi Reddy

Identification of resistance sources and breeding for resistance to ChLCV and its vector whitefly is an important goal for chilli improvement programme. The present study was undertaken to characterize the virus and vector; identify resistance sources to the virus, ChLCV & the vector, B. tabaci; the effect of ChLCV on the plant host & vector; to understand the genetics of inheritance for ChLCV resistance; and identification of molecular markers linked to ChLCV resistance in chilli. To recognize the begomovirus related withchilli leaf curl disease, chilli leaf samples showing acute leaf curl symptom were collected from Raichur, Karnataka state of India. Genome of DNA-A comprised of 2759 nucleotides and beta satellite comprised of 1380 nucleotides. Sequence comparisons of DNA-A reveal highest sequence identities of 99.5 per cent with Chilli leaf curl virus-Ahmedabad (Gen acc.JN663846) and beta satellite showed 98 per cent identity with Tomato leaf curl beta satellite. The sequence analysis of mtCOI gene of whitefly showed more than 98% nucleotide similarity with Asia-II-5 group of whitefly cryptic species. Out of 239 genotypes evaluated, one genotype (IHR4591) showed immune reaction and three genotypes, viz. IHR4517, IHR4615 and IHR4630 showed highly resistance reaction.These selected genotypes were further subjected to no-choice screening and selected two chilli genotypes viz., IHR 4300 and IHR 4338 as tolerant to whitefly incidence. The morphological study showed that the total trichome and non-glandular trichome density is positively correlated with whitefly population and nymphal density, whereas glandular trichomes density is negatively correlated. The study on ChLCV induced changes in the host-vector association showed that the non- viruliferous whiteflies attracted more towards the virus infected plants, while viruliferous whiteflies attracted towards healthy plants.Transcriptomics study of viruliferous and non- viruliferous whiteflies showed that the total 1188 unigenes were differentially expressed and out of which 662 unigenes are over expressed and 526 were under expressed. The populations derived from two highly resistant genotypes viz., IHR4517 and IHR4615 and a common highly susceptible parent, IHR3476 were used for inheritance studies. The chi-square test best fitted to 3:1 and 1:1 ratio, respectively in F2 and test cross populations indicating single dominant gene control of resistance against ChLCV in the both the resistant lines. To identify molecular markers linked to resistance, two approaches viz., validation of Ty genes linked markers of tomato and use of resistant gene analogues (RGA) were taken up. Out of six Ty markers validated in contrast genotypes of chilli, two markers viz., Ty2 and Ty4 were amplified. Similarly 102 RGA primers were tested, out of which two viz., PloopF1/ GLPLR1 and PloopF2/ GLPLR2 primers showed amplification. However, no polymorphism was observed between resistant and susceptible chilli genotypes.

Title: Genetic analysis and identification of molecular markers linked to powdery mildew resistance in bitter gourd (*Momordica charantia* L.) (2019)

Prasanth K., IARI, Guide: Dr. B. Varalakshmi

Bitter gourd (Momordica charantia L.) is one of the widely grown cucurbitaceous vegetable crops in India. However, the production is limited by various diseases of which powdery mildew is a major fungal disease in most of the production areas. An experiment was designed to identify resistant source for powdery mildew, to study the inheritance pattern of resistance and to identify a molecular marker linked to powdery mildew resistance gene. The experiments were carried out in the Vegetable Research Block VIII, Division of Vegetable Crops, ICA.R- Indian Institute of Horticultural Research, Hessaraghatta, Bengaluru, Karnataka, during 2015 to 2018. Thirty one genotypes were screened under natural field conditions and artificial epiphytotic conditions to identify stable resistant source for powdery mildew. Two genotypes viz,, MIR-80-1-2 and 1114R-80-1-3 were immune to the disease, whereas, II1-1R- 144-1 was highly resistant reaction to powdery mildew with PD1 of 1.81 and4.28 under natural and artificial screening, respectively. MIR- 40-1 and 11HR-49- 34-5 were moderately susceptible with a PDI of 31.1 and 34.6 respectively. The six generation analysis (Pi, P2, F. F2, B1 and B2) of two cross combinations (Arka Harit x IIHR.-144-1 and 1114R Set-5-8 x IIHR-144-1) indicated that resistance in both crosses were controlled by interaction of two pairs of dominant and recessive genes (dominant inhibitory epistasis, 13:3). Quantitative analysis of resistance to powdery mildew in bitter gourd confirmed the insufficiency of simple additive - dominance model. The epistatic interaction was of greater magnitude than main gene effects in both the crosses and dominance x dominance (1) effects were higher magnitude and of duplicate nature. The estimates of gene effects of fruit colour and pattern of ridge indicated that green fruit colour and discontinuous ridges in bitter gourd was governed by single dominant gene.A total of 300 SSR markers were employed to identify polymorphic primers using 193 F2 populations of Arka Harit x 11IIR-144-1 to identify linked marker for powdery mildew resistance through BS A. The primer McSSR 57 produced a polymorphic DNA fragment that co-segregated with disease reaction. PCR amplification of all the 193 plants of F2 population using McSSR 57 gave a recombinant frequency of 18.13 % which indicates that the marker is linked to the gene for resistance at 18.13 cM distance. Marker assisted selection (MAS) can be employed for early generation selection of powdery mildew resistance gene in bitter gourd and its introgression to develop a resistant variety or hybrid in the desired genetic background.

Title: Inheritance studies and identification of molecular markers linked to bacterial wilt resistance in Brinjal (*Solanum melongena* L.) (2019)

P. Pandiyaraj, IARI, Guide: Dr. T.H. Singh

An experiment was conducted to identify the stable source of resistance, study the genetics of resistance and identify the molecular markers linked to bacterial wilt resistance in brinjal. Total seven genotypes were used to identify the high yielding genotype with bacterial wilt resistance in brinjal. Among all, Surya was recorded as best performing germplasm with respect to fruit yield per plant, number of fruits per plant, days to first flowering, number of primary branches per plant and bacterial wilt disease resistance. The other genotype CARI–1 was observed as immune to bacterial wilt disease with better yield performance. Thirty hybrids were developed based on resistance × resistance and resistance × susceptible fashion. Among all hybrid combinations, hybrid Surya × Rampur Local was observed as best performing hybrid with respect to yield traits and bacterial wilt resistance. The genetics of resistance to bacterial wilt was studied in two segregating populations derived from a cross between CARI–1 × Rampur Local (green background) and Surya × IIHR–586 (purple background) eggplant lines. The six generations, namely P1, P2, F1, F2, BC1 and BC2 of two crosses were evaluated in bacterial wilt sick plot followed by artificial inoculation. The results revealed that single dominant gene control bacterial wilt disease resistance in eggplant in both the populations. The molecular marker linked to bacterial wilt resistance loci two segregating F2 populations were developed by crossing CARI–1 × Rampur Local and IIHR-7 × Arka Kusumakar (IIHR–108) parental combination. Bulked segregant analysis (BSA) was performed in two segregating F2 populations with bacterial wilt resistance. A total of 390 single sequence repeat markers were used in the survey of parental polymorphism, and 42 SSRs were found to be polymorphic. The SSR markers, emb01D10, emh11I06, em h02E08, and SSR–46 co–segregate with resistant and susceptible genotypes of the two F2 populations and linked to bacterial wilt resistance loci. These four SSR markers followed mendelian genetics for subsequent generations. In addition, they are useful in marker-assisted selection and eggplant breeding effectively.

Title: Incorporation of Phytophthora root rot resistance genes into cytoplasmicand genic male sterile (CGMS) line through marker assisted selection in Chilli (*Capsicum annuum* L.) (2020)

Manish Kumar, IARI, Guide: Dr. Dr. K. Madhavi Reddy

Among soil borne fungal diseases, Phytophthora root rot caused by Phytophthora capsici posing serious threats to chilli cultivation in regions with high humidity and summer rainfall. Identification of resistance sources and breeding for resistance to root rot is an important goal for chilli improvement programme. The present study was undertaken to identify the stable resistant source against an Indian/ local isolate; genetic analysis to understand the inheritance of resistance of P. capsici; validation/ identification of the DNA markers linked to root rot resistance gene loci and easy and effective incorporation of such resistance into CGMS line (both A and B lines) through marker-assisted selection (MAS) in chilli. The experiments were conducted at the ICAR- Indian Institute of Horticultural Research, Bengaluru, Karnataka, during 2015 to 2018. Among the diverse chilli genotypes evaluated for Phytophthora root rot resistance under artificial epiphytotic conditions, the genotype IHR 3575 [an accession of Criollo de Morelos 334 (CM334)] was found highly resistant against the virulent local isolate PC-IIHR1 (Gene bank accession number: MK256294). To determine the inheritance pattern for Phytophthora root rot resistance, chi-square analyses was performed using segregating populations derived from the highly resistant parent IHR 3575 and IHR 3476, a highly susceptible genotype. QTL analysis for root rot resistance loci was done through bulked segregant analysis (BSA) method using F2 and F2:3 populations derived from contrast parents viz., IHR 3575 and IHR 3476. Three molecular markers (CAMS 405/ Hpms 1-62/ Hpmshs MADS), SSR 9 and CAMS 839 linked to root rot resistance loci that are available in public domain showed 83 per cent of phenotypic variation expected (PVE) against the local isolate. Of these forty-two markers utilized in BSA, only two viz., HpmsE034 and HpmsE062 were able to distinguish the contrast parents as well as corresponding DNA bulks and F2 individuals in accordance with phenotypic data. The sequence analysis of identified polymorphic product of HpmsE034 showed 93.36 per cent homology with known sock protein SRC2 resistance loci in pepper. The backcross (BC1F2) populations derived from the hybridization of male sterile (MS3A) and maintainer (MS3B) lines of chilli, and root rot resistant parent IHR 3575 were used to incorporate Phytophthora root rot resistance into CGMS background.Molecular analyses of

BC1F2 populations using mitochondrial gene specific markers (atp6-2 and orf456) for cytoplasmic male sterility and nuclear gene specific marker (CRF-SCAR) for nuclear male sterility revealed that five lines in each male sterile and maintainer backgrounds were selected with resistance to Phytophthora root rot through MAS. The developed advanced breeding lines are of great significance and can be employed in economical F1 hybrid seed production programme in chili.

Title: Genetic analysis and validation of molecular markers linked to Tomato Leaf Curl New Delhi Virus (ToLCNDV) resistance in Ridge Gourd [*Luffa acutangula* (L.) Roxb.] (2020)

Manpreet Kour, IARI, Guide: Dr. Dr B. Varalakshmi

Ridge gourd is one of the important cucurbit crops grown extensively in tropical and sub- tropical region of the India and abroad. Among viral diseases, recently reported yellow mosaic disease caused by Tomato leaf curl New Delhi virus (ToLCNDV) is very severe and causing 100 per cent yield loss under epiphytotic conditions. Therefore, identification of resistant sources and breeding for resistance to ToLCNDV is an important goal of ridge gourd improvement programme. The present study was undertaken to identify stable resistant sources against ToLCNDV; genetic analysis to understand the inheritance of ToLCNDV and validation/identification of molecular markers linked to ToLCNDV resistance loci in ridge gourd. The experiments were conducted at the ICAR-Indian Institute of Horticultural Research, Bengaluru, Karnataka, during 2017 to 2020. In the first experiment, fivty-two Luffagenotypes were screened against ToLCNDV resistance under natural conditions. Fifteen genotypes were moderately resistant (VI=26-50%) and 19 genotypes were moderatelyto highly susceptible (VI≥50%). Further, selected promising genotypes which showed resistance to ToLCNDV under natural conditions were selected for further confirmation through challenge virus inoculation (whitefly and mechanical sap inoculation) under insect proof greenhouse along with susceptible checks. Upon challenge virus inoculation, one germplasm line, 'IIHR 137' was symptomless and other two lines viz. 'IIHR 138' and 'IIHR- Sel-1' had some plants with mild symptoms after virus inoculation. Percent VI ranged from 0.0 to 80.96 wherein, the highest per cent VI was recorded in the genotype 'Arka Prasan' (80.96%), while it was the least in 'IIHR 137' (0.00).The results of segregating populations viz., F2 and backcross progenies suggested that a major recessive gene along with a few minor genes were involved in conferring resistance to ToLCNDV in both the cross combinations. Identification or validation of fifty-two molecular markers linked to ToLCNDV resistance was conducted inF2 population of 'Arka Prasan ×IIHR-Sel-1'. All the molecular markers were amplified in parents and out of fifty-two markers, one marker was polymorphic which clearly distinguished the contrasting parents. The primers LaRGAP 63 produced a polymorphic DNAfragment (455 bp) that co-segregated with ToLCNDV disease reaction in F2 population. Considering the possibility of cross compatibility between ridge gourd and sponge gourd, ToLCNDV resistance trait can be easily transferred to ridge gourd through hybridization and selection. Since resistance gene is monogenic recessive nature, therefore backcross breeding followed by selfing has to be performed to transfer ToLCNDV resistance gene. Also, marker assisted selection (MAS) can be employed for early generation selection of ToLCNDV resistance gene in ridge gourd and its introgression to develop a resistant variety or hybrid in the desired background.

Title: Genetic analysis of male sterility mediated three-way crosses for yield, quality and resistant to purple blotch disease in Onion (*Allium cepa* L.) (2021)

Ajay Kumar Pandav, IARI, Guide: Dr. B.Varalakshmi

The present study entitled "Genetic analysis of male sterility mediated three-way crosses for yield, quality and resistant to purple blotch disease in onion (Allium cepa L.)" was undertaken at Division of Vegetable Crops, ICAR-Indian Institute of Horticultural Research, Hesaraghatta, Lake Post, Bengaluru- 560 089, Karnataka (India) during the years 2016-2019. The research work was followed with the objectives namely to estimate the extent of heterosis for yield, quality and resistance to purple blotch disease in three-way cross hybrids, to confirm the hybrid purity by using molecular markers, to study the combining ability (GCA and SCA) for different traits and to study the gene action for various quantitative and qualitative traits. Thirty hybrids were developed through three- way cross pattern by using three female parents viz., Arka Kirthiman (F1), Arka Lalima (F1) and Super Flare (F1) and ten commercial male parents namely Arka, Bindu, Arka Pitamber, ArkaPragati, Arka Niketan, Arka Kalyan, Prema178, Bheema Red, Bheema Raj, Bheema Super and N-2-4-1.Forty-four genotypes including check were evaluated for different quantitative and qualitative attributes. The three-way hybrids namely Arka Kirthiman (F1) x Arka Kalyan (7.89), Arka Lalima (F1) x Arka Kalyan (8.75) and Arka Lalima (F1) x Arka Pitambar (9.78) were found to be resistance under both natural epiphytotic condition as wellas artificially inoculated under controlled polyhouse condition against purple blotch disease. Evaluation of all the genotypes for storage losses, the hybrids Arka Kirthiman x Arka Niketan, Arka Kirthiman x Arka Kalyan, Arka Lalima x Arka Niketan and Arka Lalima x Arka Kalyan were observed for less storage losses and suitable for higher shelf-life of bulbs. These hybrids also performed better for qualitative characters. In these developed hybrids, itwas found that the combination of light green with semi glossy foliage's having no harmful effect on the plant growth and observed negligible or very low- level infestation of thrips. Three-way cross hybrid purity was confirmed by using molecular markers from which, onion genomic DNA, screened with SSRs/MK primers, which were specific to S cytoplasm, and male fertile and sterile line screened with ORF primers (designed by using mitochondrial DNA sequence of onion). SSR primers have the capability to differentiate the hybrids even among closed groups.The studies of extent of heterosis and combining ability for different traits were done by using three lines, 10 testers and 30 cross combinations. A significant heterosis overstandard check Satara Garva was attained for almost characters, which possesses commercially more importance. Line 2 (Arka Lalima) and tester T4 (Arka Kalyan) has been found best as general combiner for yield and most of the yield attributing parameters. Three- way crosses namely Arka Lalima (F1) x Arka Kalyan, Arka Lalima (F1) x Arka Niketan, Arka Kirthiman (F1) x Arka Kalyan and Arka Kirthiman (F1) x Niketan were showed overall best performance for yield, storage and resistance to abiotic and biotic stress in terms of SCA effect. These cross combinations were also concluded as superlative to exploit heterosis over standard check.

Title: Breeding for Combined Resistance To Leaf Curl And bud Necrosis Diseases in Tomato (*Solanum lycopersicum* L.) (2021)

Amarjeet Kumar Rai, IARI, Guide: Dr. A.T. Sadashiva

The present study was undertaken to initiate the breeding process, to combine the resistance against leaf curl and bud necrosis diseases of tomato. In this study, 47 and 40 genotypes of tomato were screened for leaf curl disease (LCD) and bud necrosis disease (BND) respectively, at two locations (ICAR-IIHR, Bengaluru and ICAR-IARI, New Delhi) under open field as well as controlled conditions. Only three genotypesi.e., IIHR-2901, IIHR-2905 and IIHR- 2913 was found to have stable resistance to both species,[Tomato leaf curl Bangalore virus (ToLCBaV) and Tomato leaf curl New Delhi virus (ToLCNDV)] of LCD, while the line IIHR- 2988 (S. chilense) was found immune against the ToLCBaV. Similarly, for BND three genotypes viz., IIHR-2988, IIHR-1940 and IIHR-2901 and another three genotypes (IIHR-2809, IIHR-2953 and IIHR-2101) were found resistance and moderately resistance respectively. Later, marker validation of tomato genotypes for LCD, revealed that the gene Ty-3 alone or in combination with Ty-2 and ty-5is sufficient to provide resistance against both species of tomato leaf curl virus (ToLCV), while the gene combination of Ty-2 + ty-5, was only effective against ToLCBaV. Resistant genotypes (IIHR-2901 and IIHR-2953)were crossed with the PKM-1 (Susceptible) to develop two different populations (F1, F2, BC1P1, BC1P2), tostudy the genetics of BND. It was found that the resistance to BND in IIHR-2901 was governed by one or two recessive genes with additive × dominance gene action, while in IIHR-2953, it was governed by one or two dominant gene with additive× additive and additive × dominance gene action. Then, the attempt was made to identify the genomic regions having QTLs (quantitative trait loci) resistance to bud necrosis disease in the cross (PKM-1 × IIHR-2901). This led to the identification of seven QTLs (gbnv1.1, gbnv1.2,gbnv2.1, gbnv2.2, gbnv2.3, gbnv9.1 and gbnv9.2) coding four candidate genes (Auxin induced SAUR-like protein, Peptidyl-prolyl cis-trans isomerase, Receptor like protein kinase and NBS-LRR disease resistance protein) across three chromosomes i.e., chromosome number 1, 2 and 9. Finally, through conventional and molecular approach, four F2 individuals (PKM-1 × IIHR-2901) having combined resistance to LCD and BND was identified. This research will pave the way for future breedingprograms related to leaf curl and bud necrosis diseases of tomato.

Title: Mapping of Fusarium wilt resistance in Watermelon (*Citrullus lanatus* (Thunb.) Matsumand Nakai) germplasm and assessing their potential as rootstocks (2021)

Saheb Pal, IARI, Guide: Dr. Dr. E. Sreenivasa Rao

The present investigation was carried out to designate two selected virulent Indian Fusarium oxysporum f. sp. niveum (Fon) isolates collected from different regions of the country into races, identify stable source resistance against these races, to study the mode of inheritance of resistance, mapping of the resistance employing candidate QTL and QTL-sequencing approach and to study the influence of the resistant accessions on yield andquality of grafted watermelon at ICAR-Indian Institute of Horticultural Research,Hesaraghatta Bengaluru during 2016-2020. In this study, we have designated two virulent Indian isolates into races 1 and 2 of Fon by studying their ability to infect a specificset of host differentials inoculated with both pipette and root-dip inoculation methods. Based on the reaction of the segregating generations, the resistance in these accessions (IC0523047, EC794455 and EC759804) was found to be governed by two major complementary dominant genes with the involvement of modifying genetic factors. The F2 and backcross progenies of the other two accessions (IIHR-9 and EC794421) did not follow any of the Mendelian/epistatic ratios tested. Generation mean analysis revealed presence of epistasis inBIL-53×EC794455 and BIL-53×EC759804 while in the other three crosses, simple additive interaction was observed. Allelism test revealed the absence of any allelic relationship between IIHR-9 and IC0523047 for resistance. The genetic diversityand population structure of a germplasm panel comprising ofCitrullus sp. Accessions were studied and a core collection of Indian Citrullus sp. accessions was formulated. Among them, four markers were significantly associated with the resistance and the marker InDel-4 explained maximum phenotypic variations, thus can successfully be utilized for marker- assisted introgression of Fon race 1 into elite commercial backgrounds. Two statistically significant genomic regions were identified each on chromosome 1 (spanned to 5.5 MB) and chromosome 7 (spanned to 2.5 MB) governing resistance to Fon race 2 in EC794421. The markers viz., BVWS 02309 and BVWS01116 within QTL on chromosome 1 and BVWS00358 within QTL on chromosome 7 were found to be significantly associated with resistance. The grafts on Citrullus sp. rootstocks could maintain the oblong fruit shape of the scion compared to those onto Cucurbita hybrid and Lagenaria sp. rootstocks which yielded flat-globe to spherical shaped fruits. A wide variation of TSS and carotenoid content was observed upon grafting while the pulp pH remained largely unaffected. An increase of average fruit weight by 50.69%, 55.37% and 82.37% and yield per plant by 112.15%, 89.54% and 107.06% was observed in grafts onto RS-10, RS-11 and RS-18 respectively.

Title: Breeding for combined resistance to bacterial wilt and root knot nematodes in Tomato (*Solanum lycopersicum* L.) (2021)

Vinod Jatav, IARI, Guide: Dr. A.T. Sadashiva

The present investigation was carried out at ICAR-Indian Institute of Horticultural Research, Hessarghatta Lake Post, Bengaluru 560089, Karnataka during 2016-2019 to develop the advanced breeding lines for combined resistance to bacterial wilt and root knot nematodes through Marker assisted selection (MAS) in tomato (Solanum lycopersicum L.). For development of advance breeding lines having combined resistance to bacterial wilt and root knot nematodes, based on phenotypic and molecular screening six lines viz., IIHR-2296, IIHR-2042, IIHR-2834, IIHR-2867, IIHR-2835 and IIHR-2920, which were found resistant to BW selected as female parents and other six lines (IIHR- 2614, IIHR-2786, IIHR-2785, IIHR-2963, IIHR-2964 and IIHR-2965), which were found resistant to RKNs chosen as male parents. Nine novel advance breeding lines (six F6 and three BC3F3) lines were developed and evaluated at both phenotypic and genotypic level.Effects of root exudates from different resistant and susceptible lines against RKN were examined for relative suppression rate egg hatching (%), J2 mortality and chemotaxis movement of J2. In addition to that component analysis (HS-SPME) analysis using capillary GC–MS/MS of root exudates of resistant and susceptible lines was also performed in order to identify the underlying compound(s) responsible for resistance against root knot nematodes and bacterial wilt respectively. Among all the identified compounds, dibutyl phthalate was found directly linked to resistant reaction against the root knot nematodes, as its relative amount increased greatly post inoculation in all resistant lines along with novel developed resistant line, while the decrease was observed in root exudates from both the susceptible lines, after post inoculation of RKN. Whereas, elixene, 2-methyl-1-dodecanol, p- menthone and ethyl 4-ethoxybenzoate were found linked to resistant reaction against bacterial wilt disease, as their relative amount increased greatly post inoculation in all resistant lines along with novel developed resistant line, while the decrease was observed in root exudates from susceptible lines, after post inoculation of Ralstonia solanacearum. Novel advance breeding lines, which were developed in this study, may be used in future breeding programmes related to root knot nematode and bacterial wilt diseases and would facilitate pyramiding of resistance genes for multiple diseases in tomato.

Title: Incorporation of yellow mosaic disease resistance in pole type French bean (*Phaseolus vulcaris)* (2021)

Arindam Das, IARI, Guide: Dr. Aghora T S

Horse gram yellow mosaic disease (HgYMD) is an important limiting factor of legume production in India, which may cause up to 100%economic loss. The Present systemic breeding work was to identify the resistant source for HgYMD, molecular marker linked to HgYMD and the biochemical basis of resistance. Seventy-one genotypes of French bean have been screened under natural and artificial epiphytotic conditions during summer of 2018 at ICAR-IIHR, Bengaluru, India. The two resistant genotypes, selected through natural screening, were screened artificially using virulent whiteflies for confirmation of resistance. Average PDI of Arka Arjun and Jade-5058 were 13.33 and 12.22 under artificial screening, respectively, which were much lesser than the susceptible checks Arka Komal (PDI 92.22) and Arka Anoop (PDI 90.00) Both the resistant genotypes, Jade-5058 and Arka Arjun showed less AUDPC values of 350.54 and 359.16 compared to the other genotypes. The maximum disease progress was observed in Arka Suvidha (1363.34) and susceptible check value was 998.89 (Arka Komal) and 776.67 (Arka Anoop).A total of 119 different markers (SSR, RAPD, ISSR, SCAR and RGA) were used for validation of molecular marker linked HgYMD resistance, Fourteen markers screened exhibited polymorphism between the parents viz. Arka Arjun (Resistant), Jade-5058 (Resistant) and Allama (Susceptible). Bulk segregant analysis (BSA) was done in two segregating F2 populations viz. Arka Arjun × Allama and Jade-5058 × Allama against YMD resistance and it revealed that the YMD resistance in french bean is governed by a single recessive gene. The SSR marker Pvcomp 14 only co–segregated with resistant and susceptible individuals of the F2 populations of Arka Arjun × Allama and is linked to YMV disease resistance loci. phenolic Acids, gallic acid, p-coumaric acid and sinapic acids were present in higher quantities in the resistant genotypes. Benzoic and o-coumaric acids were higher in susceptible genotypes.

Title: Joint multiple family linkage analysis for resistance to watermelon bud necrosis virus and fruit quality traits in Watermelon (2022)

Siddharood Maragal, IARI, Guide: Dr. Dr. E. Sreenivasa Rao

Watermelon bud necrosis disease caused by watermelon bud necrosis orthotospovirus (WBNV) is one such tospovirus that has emerged asa devastating disease of watermelon in India. Genetic analysis in two pre bred lines viz., BIL-53 and BIL-99 derived from citron suggested that the genetics of most of fruit quality traits are governed by one or two genes suggesting simple inheritance. QTL analysis for seed traits revealed two QTLs viz., q_100SW_2.1 and q_100SW_6.1 for 100seed weight; three QTLs viz., q_SCC_3.1, q_SCC_5.1 and q_SCC_5.2 for seed coat color. Results validated the previously reported QTLs viz., ss2.1 and qSS6 for seed weight/size and qsc- c3-1 for seed coat color of watermelon. Results revealed fifteen major QTLs on Chr. 2, 4, 5, 6, 7 and 10 for flesh color at different regions. Candidate gene analysis predicted Cla020214 and Cla020121 on Chr.2; Cla005011 on Chr. 4; Cla018767, Cla018768, Cla018769, Cla018770, Cla018771 on Chr. 6; Cla017416 and Cla017593 on Chr. 10 as a probable candidates genes governing flesh color at different regions. For WBNV resistance, efforts have been made to integrate WBNV resistance QTLs from wide range of populations and screening experiments for a comprehensive analysis through QTL-meta-analysis and joint inclusive composite interval mapping (JICIM). Comprehensive analyses for QTLs suggested MQTL_WBNV_2.1 on Chr. 2, MQTL_WBNV_3.2 on Chr. 3 and MQTL_WBNV_7.2 on Chr. 7 as potential candidate QTL regions for WBNV resistance. The genes identified in these QTLs viz., Cla020173 encoding PR-1, Cla001733 encoding pathogenesis- related transcriptional factor and ethylene-responsive transcription (ERF), Cla001590 and Cla001591 genes encoding acid phosphatase, Cla019476 encoding TIR-NBS and Cla011771 belonging to TIR-NBS-LRR gene family may be investigated as putative candidates for WBNV resistance in watermelon. Overall results suggest that the breeders can use citron species as a source of resistance in breeding programs without apprehension of linkage drag on fruit quality traits.

Floriculture & Landscaping

Title: Seed germination and tissue culture studies in orchids (1982)

Ramachandran Nair, UAS, Bangalore, Guide: Dr.Foja Singh

Investigations were carried out to standardize in vitro culture techniques and find out the effect of different culture media, growth substances, and other additive on seed germination and tissue culture of orchids. Studies on cytological and histochemical changes associated with orchid seed development were also made. Comparison of five different media (Knudson, C., Murashige-Skoog, Vacin and Went, Burgeff N 3F and modified Vacin and Went) for germination and growth of seeds of six different orchid species showed that Vacin and Went medium was superior in respect of germination, growth and development of Bletilla hyacinthine, Phaius wallichii and Epidendrum radicans, while Murashige-Skoo medium was found superior for Spathoglottis plicata and Vanda coerulea. Burgeff N3F medium was found suitable for different Dendrobium species. Histochemical studies revealed that the seeds of Bletilla hyacinthine contained considerable amount of lipids and proteins but no starch. The developing protocorm exhibited a decreasing gradience in the size of its cells and its nuclei. Ribonucleic acid and proteins showed an increasing gradiance in the protocorm like body from its base to apex. The peripheral cells of the callus of Dendrobium pierardii contained rich cytoplasmic RNA and proteins and a few starch grains. Cytological evaluation of the cultured tissue revealed the presence of chromosomal variations in different cells. This may be due to the stress caused by the unnatural environment by cell fusion.

Title: Genetical investigations in china aster (*Callistephus chinesis*) (1984)

S.P.S.Raghava, UAS, Bangalore, Guide : Dr.S.S.Negi

Studies were carried out to evaluate 12 parents on the basis of combining ability and to analyse genetic basis of inheritance of 14 quantitative characters in 12x12 diallel set of crosses in two conditions, namely, field and pot culture. Inheritance of important quantitative characters like flower colour, flower doubleness, flower type and plant type was also studied. Diallel analysis revealed involvement of both additive and non-additive gene actions in the inheritance of 14 quantitative characters under both conditions. However, additive gene action played predominant role in the inheritance of number of ray florets per flower head and flower size, while the remaining 12 characters, viz., plant height, number of main branches per plant, number of laterals per plant, plant spread, stem girth, area per leaf, days to flower, number of flowers per plant, stalk length, flower weight, duration of flowering and cut flower life were found to be governed mainly by non-additive gene action under both conditions. Dominance and epistasis of complementary type played significant role in the inheritance of all characters which were reflected in terms of better parent heterosis for almost all characters under both conditions. As regards inheritance of quantitative characters, violet colour was found to be dominant all colours, deep pink over pink and pure white and pink over light pink and pure white. Deep pink was incompletely dominant over light pink. Four independent genes, A, B R and P were found to govern different flower colours. Gene B had ane dominant allele B. Doubleness (DD) was observed to be monogenically dominant over singleness (dd). Pompon type of flower was dominant over Chrysanthemum and Fluffy types. Chrysanthemum type was dominant over Fluffy type. Three independent genes Tu, D and C governed these three flower types. Dropping plant type (Dp Dp) was found to be incompletely dominant over erect plant type.

Title: Studies in vitro seed germination and morphogenesis in orchids (1986)

Sangama, UAS, Bangalore, Guide : Dr. Foja Singh

Most of the orchid species are cross pollinated viability and storage of pollen seeds and protocorms for getting desired hybrids were investigated. The pollen viability of Spethoglottis plicate Epidenrumradicans and Dendrobium "Jaquelyn Thomas" was reduced when stored with a dehydrant (silicagel). Storage at low temperature (4 °C) enhanced pollen viability compared to that at room temperature in all the three species. Seed viability of these three species was enhanced when stored with dehydrant. Protocorn regeneration of Dendrobium "Jaquelyn Thomas" was better when stored with glycerol 10% as a cryoprotectant. Among three media used, S.plicata seeds germinated successfully in Pundson's medium in a short time. Seed germination of E. radicans and Dendrobium "Jaquelyn Thomas" was better in MS medium. Seed germination of all three species was faster with NAA, GA and BA at 0.1 mg l-1 and 1 mg l-1 as compared to control. Among the three growth regulators, GA at 1 mg l -1 was best as the time required for germination was half that required with control. The percent seed germination in all three species was higher with NAA, GA and BA at 0.1 mg l -1 as compared to other treatments. Growth of the seeding was enhanced with growth regulators either alone or in combination than control in all the three species. Less time was required for complete growth of the seedling with IBA+GA+BA each at 5 mg l-1 compared to other treatments. Histochemical and ultra structural studies revealed the utilization of metabolites for organal development. Lipids, proteins and carbohydrates were utilized in the order mentioned during seed germination.

Title: Development of micropropagation systems and new in vitro strategies for some import ornamental plants (1993)

M.B.Ravindra, UAS, Bangalore, Guide : Dr.Foja Singh

The present Investigations were conducted at the IIHR, Hessarghatta, Bangalore to develop in vitro systems for some important ornamental plants. In Saintpaulia ionantha, leaf discs were found to be a superior source of explants than petiole section with respect to morphogenic responds. However, the axenic leaf explants responded at a faster rate during recurrent cultures. MS medium supplemented with NAA and BA at 0.5 mg l -1 was found to be optimum for callusing and differentiation of explants during initiation of cultures. Combination of IBA and BA at 1 mg l -1 resulted in maximum number of plantlets during both axenic cultures and subsequent subcultures. Higher intensity of rooting and better growth of plantlet was observed on MS medium without growth regulators. A potting mixture of soilrite + sand + compost (2:1:1 V/V) and hardening of plantlets using polythene covers for 3 weeks was found to be optimum for better establishment of plantlets. Begonia 'Lucerna' Petiole segments cultured on MS medium supplemented with NAA 1 mg 1-1 + BA 2 mg l-1 resulted in higher intensity of callusing and differentiation. Cymbidium aloifolium protocorms cultured on liquid Vacin and Went medium supplemented with 0.4 mg l -1 BA resulted in maximum proliferation of PLB's and multiple shoots. Similarly, the nodal segments also induced maximum number of shoots on the same medium. Anthurium scherzerianum leaf sections initiated callus from the veins when cultured on Vacin and Went medium supplemented with 2, 4-D and BA at 1 mg l-1. The protocorms of Cymbidium aloifolium; callus, petiole sections and shoot buds of Saintpaulia ionantha were encapsulated using 2.5% sodium alginate and it was found that these encapsulated plant material could be stored at 4°C temperature. This suggested the suitability of encapsulated material for efficient delivery system, storage and effective transport under limited refrigerated condition. Anothers of Saintpaulia ionantha culture Saintpaulia ionantha on MS + IBA 1mgI-1 + BA 1 mg-1 resulted in higher callusing and differentiation of haploid plantlets. Leaf mesophyll protoplasts of Dendrobium 'Jaquelyn Thomas' were isolated using 5 ml enzyme solution having 0.75% cellulose and 0.4% onozuka R-10 macerozyme and an incubation period of 16 hours.

Title: Encapsulation & regeneration of protocorms in orchid (*Spathoglottis plicate*) (1995)

B.V.Champa, UAS, Bangalore, Guide : Dr.Foja Singh

Encapsulation is a technique, where in cultured matter like a tissue piece, or an organ, or a cell is coated with synthetic polymer which later degrades and allows the plant to establish. An investigation on Encapsulation & regeneration of protocorms from encapsulated breads das carried out in the orchid laboratory, IIHR, Hessarghatta, Bangalore during 1993-95. Orchid Seeds from matured pods of spathoglottis plicate were sown on modified vaccine & went medium, Murashige & Skoog medium & Nitsch medium by green pod culture technique to standardize the media for protocorm production. It was found that modified vaccine & went medium; Murashige & Skoog medium gave satisfactory results & resulted in healthy protocorms. The protocorms were encapsulated using different hydrogels viz., sodium alginate, alsinic acid, agar & gelrite. Among these, sodium alginate was found to be best hydrogel for encapsulation. The encapsulated beads were stored in sterile pertriplates, wrapped with parafilm & kept under storage temperatures for long term storage temperature. Beads storage at this temperature, were viable even after 12th week of storage & gave good regeneration when cultured on artificial medium. The regenerated plants, when transplanted to community pots established well with 70-80% field establishment. This technique offers a unique way for efficient delivery system, storage & efficient transport of plant material from one to another place under limited refrigeration conditions.

Title: Mutation breeding in rose and pigmentation studies in rose and hibiscus

K.S.Shobha, UAS, Bangalore, Guide: Dr.R.N.Bhat

An investigation was carried out at IIHR, Bangalore to study the effect of gamma rays on 3 rose cultivars along with qualitative and quantitative estimation of flower pigments of rose and hibiscus cultivars. Bud woods of rose cvs. Paradise, Raja Surendra Singh of Nalagarh and Sindoor were irradiated at 3,4,5 and 6 kR gamma rays and budded on the rootstocks. Increased dosage of gamma rays reduced sprouting and survival of vegetative buds. Four induced mutants were reduced in cv. Paradise. However, the Raja Surendra Singh of Nalagarh was found to be less sensitive to higher doses of irradiation. The detailed morphological studies were carried out in the induced mutants. The morphological studies were also carried out in 6 spontaneous rose mutants developed at the institute along with their respective parents. Analysis of pigments in rose genotypes indicated that somatic flower colour is due to both qualitative and quantitative changes in pigments resulted by induced and spontaneous mutation. Paper chromatographic studies revealed that among the induced mutants, increased gamma irradiation reduced the anthocyanin contents where as the spontaneous rose mutants had higher concentration of anthocyanin than their parents exhibiting somatic flower colour change. The study of pigments was also extended to 15 hibiscus cultivars developed at the institute to understand the biochemical basis of their flower colour variation. More of anthocyanin with high concentration was observed in red and orange/orange yellow groups having darker shades as compared to yellow/yellow orange group of cultivars having lighter petal shades. Thus both in rose and hibiscus, the major pigment estimated was anthocyanin and tentatively as cyanin.

Title: Induction of mutation in carnation (*Dianthus caryophyllus* L.) through gamma rays and ethyl methane sulphonate. (1998)

K.Hemalatha, UAS, Bangalore, Guide : Dr.R.N.Bhat

Induction of mutation was attempted on two carnation genotypes viz., 'Sterlite Dop' and 'H-13' using gamma rays as physical mutagen and on one genotype 'Sterlite Dop' using EMS as chemical mutagen at different concentrations. The effect of mutagen treatments on various morphological and floral characters, histological and histochemical changes during rhizogenesis and organogenesis and pigment composition were studied. Increased dosage decreased sprouting and survival of cuttings. Induction of mutation reduced all the morphological characters at higher dosage of gamma rays. Some interesting leaf variegations like leaves with white and creamy yellow streaks were observed in cuttings treated at 1.5 and 2 kR gamma rays. Interesting changes were observed with respect to the floral characters. At 2 kR gamma rays, petal variegation was observed in genotype 'H- 13'. Two flower colour mutants were observed in cutting treated at 1.5 kR gamma rays in genotype 'Sterlite Dop' and 1 and 2 kR gamma rays in genotype 'H-13'. A miniature mutant with reduction in flower size was also observed in genotype 'Sterlite Dop' treated at 2 kR gamma rays. Induction of mutation through EMS showed very little response. However, few plants treated with 3% EMS showed creamy yellow streaks on the leaves of cv. Sterlite dop. Correlation studies revealed that environmental and genetic factors influenced to a great extent. Meager deviation in genotype and phenotopic co-efficient indicated the reliability of variation. Histological and histochemical studies of the shoot apex revealed the stepwise development of cellular damages like suppression in the growth of dome shaped apex, vacuolation of cells, damage of the apical initial layer, total damage of a small percentage of cells and formation of dichotomy with the extent of damage increasing in the dosage of gamma rays. Exposure of cutting to different doses of gamma rays resulted in correlative inhibition of root emergence. Considerable variation was observed in the anthocyanin, chlorophyll and carotenoid content among the seven carnation genotypes studied. Quantitative and qualitative studies using paper chromatographic and thin layer chromatographic methods were undertaken. By comparing athocyanin bands with that of authentic standards, the pigments present in carnation were tentatively identified as cyanin and pelargonidin.

Title: Micropropagation of Gerbera (1996)

S.M.Deepaja, UAS, Bangalore, Guide: Dr.C.Aswath

Gerbera is one of the popular flower crops in the world and is gaining importance in our country. Hardy upright flowers, leafless long stalks, numerous colours with long vase life have popularised gerbera. Availability of cheaper plant material is one of the major limitations in popularising this crop. The present investigations were carried out with varieties GJ-l, GJ-2 and OJ-3 to study shoot proliferation callusing and regeneration of leaf explant and rooting of in vitro developed shoots Half strength media of both MS and modified MS induced early shoot initiation and side shoot initiation but shoot number, shoot length and shoot weight was better in full strength media. The best treatment to produce higher shoot number with better growth was MS medium supplemented with 0.2 mg l-1 1AA and 1 mg 1-1 BAP in OJ-l and OJ-3. For GJ-2, MS medium supplemented with 0.1 mg 1-1 IAA and 2 mg l-1 BAP was best. It was noticed that the MS media supplemented with BAP induced higher multiplication rate with small plants and modified MS media supplemented with kinetin induced lower multiplication rate with good plant stature. Therefore, a protocol to obtain higher multiplication for a period of six weeks and transferring to kinetin supplemented modified MS media (5 mg 1-1 kinetin for GJ-I and GJ-2, I mg l-1 kinetin for GJ-3) for a period of four weeks before rooting is suggested. Callus initiation was earlier in media supplemented with 2,4-D and BAP when compared to media supplemented with IAA and BAP in all the three varieties. (Maximum amount of callus was produced by 0.5 mg l -1 2,4-D with 4 mg 1-1 BAP, 1.0 mg 1-1 2,4-D with 3 mg l-1 BAP and 0.75 mg 1- l lAA with 2 mg l-1 BAP. Two distinct type of calli were produced by leaf explant. Creamy callus which was frothy in GJ-l and GJ-2 and friable in GJ-3 was produced by 2,4-D with BAP. Green/ greenish white granular callus was produced by IAA and BAP. A higher cytokinin to auxin ratio in the media (IAA at 0.25,0.5 or 0.75 with BAP at 3 mg 1 -1favoured regeneration from petiole tips of young leaves. The response was better with IBA than with NAA. Both IBA and NAA induced swelling of roots in GJ-2 and NAA induced callus production in GJ-3. GJ-2 was the only variety to show good response for ex vitro rooting. Best treatment for ex vitro rooting was IDA at 1000 ppm. When varietal responses to treatments were observed, NAA at 500 ppm was best for ex vitro rooting in GJ-2 and IDA at 1000 ppm for GJ-1.

Title: Improvement in China aster [*Callistephus chinensis* (L.) Nees.] through hybridization and mutation (2018)

Pratiksha Kumari, IARI, Guide: Dr. Dr. Rajeev Kumar

The present investigation was undertaken on “Improvement in China aster [Callistephus chinensis (L.) Nees.] through hybridization and mutation” at 1CAR- Indian Institute of Horticultural Research, Hessarghatta Lake Post, Bengaluru during 2015-17. Hybridization was carried out in Line x Tester fashion with five lines viz., Arka Kamini, Arka Poornima, Arka Aadya, Arka Archana and Arka Violet Cushion and three tester lines viz., Arka Shashank, Local Violet and Local Pink. Results revealed that the number of days taken for seed maturity ranged from 31.33 (Arka Archana x Local Pink) to 39.83 (Arka Poornima x Arka Shashank). Average 100 seeds weight was ranged from 0.21 g (Arka Kamini, Arka Aadya and Local Violet) to 0.32 g (Arka Shashank).Among 15 F1 hybrids with their parents evaluated for flower quality and yield traits,Arka Aadya x Local Violet was found best with highest number of leaves/plant (312.47), number of branches/plant (23.19), number of flowers per plant (93.66), highest weight of flowers/ plant (293.87 g) and flower yield per hectare (24.68 tonne). Both spreading and semi-erect plant type were found to be dominant over erect type. Pompon flower form was completely dominant over powder puff .The violet colour was dominant over pink and white.Line 3 (Arka Aadya) and Tester 2 (Local Violet) were the best general combiner exhibiting significant general combining ability for number of leaves per plant, number of branches per plant, flower head diameter, number of ray floret per flower head, weight of flowers per plant and flower yield. The crosses Arka Aadya x Local Violet, Arka Archana x Local Pink and Arka Poornima x Arka Shashank were the overall best performing cross combinations in terms of sea effects as well as heterosis over commercial check for most of the vegetative and quality traits and are recommended for exploitation of heterosis.LD50 of six genotypes viz., Arka Aadya, Atka Archana, Arka Kamini, Arka Poornima, Arka Shashank and Arka Violet Cushion ranged from 65.99 Gy to 122.37 Gy gamma irradiation. Significant difference was observed in seedling survival, plant height, leaf size, days to first flowering and flower head diameter. Irradiation resulted in 17 putative mutants viz., in Arka Aadya (8 No.), Arka Kamini (6 No), Arka Violet Cushion (2 No.) and Arka Poornima (1 No.) with different plant type, novel flower colour and forms

Title: Induction of embryogeny and plant regeneration through induced androgenesis/gynogenesis in Marigold (*Tagetes spp*. L.) (2018)

Thaneshwari, IARI, Guide: Dr. Aswath C.

The present investigation “Induction of embryogeny and plant regeneration through induced androgenesis/gynogenesis in marigold (Tagetes spp. L.)” was carried out in the Division of Floriculture and Medicinal Crops, ICAR-IIHR, Bengaluru. Marigold, an important ornamental plant is also recognised as a potential source of carotenoids used as nutritional supplements and poultry feed. Improvement of this valuable species is hampered by its heterozygosity. Production of doubled haploid is one of the most efficient and time-saving innovative technology in varietal improvement. The present study was undertaken to investigate the potential of anther or microspores culture of marigold cv. ‘Pusa Narangi Gainda’ and unfertilized ovary or pseudo- fertilized ovule culture of marigold cv. ‘Arka Agni’ for the production of haploid plants.In case of anther culture, anthers containing microspores at uninucleate stage (pre-treated at 4°C for 72 hrs) cultured on MS media supplemented with 3% sucrose + 4.44 µM 6-benzylaminopurine (BAP) + 1.07 µM α – naphthalene acetic acid (NAA) + 0.8 % agar and incubated in dark for 3 weeks at 25°C resulted in highest callus induction (97.00 %). While isolated uni-unicleate microspores (pre-treated at 4°C for 72 hrs) cultured on MS media supplemented with 14% sucrose + 4.44 µM BAP + 1.07µM NAA and incubated in dark for 4 weeks at 25°C resulted in highest number of calli induction per Petri plate (17.60). ‘Arka Agni’ flowers was pollinated with 200 Gy gamma irradiated pollens. It was found that ovules cultured from pre-treated (at 4 °C for 24 hrs) flower capitula on MS media supplemented with 4% sucrose + 4.44 µM BAP + 2.68 µM NAA and incubated in dark for 4 weeks at 25°C showed highest per cent callus induction (62.00 %) as well as highest embryo germination (8.07 %).Besides, shoot differentiation was highest (96.33, 23.66, 25.33 %) from anther, unfertilized ovary and pseudo- fertilized ovule calli, respectively when calli were sub cultured on MS media supplemented with 3% sucrose + 4.44 µM BAP + 1.07 µM NAA and placed under 16 hr photoperiod at 25°C. Nonetheless, shoots derived from the above protocols rooted readily on hormone free MS media. Subsequently, among the fifty plants selected randomly, cytological analysis identified; 3 haploid, 3 triploid,1 mixoploid and 43 diploid from anther derived plantlets,3 triploid, 3 mixoploid and 44 diploid from unfertilized ovary plantlets and 2 haploid, 2 triploid,1 mixoploid and 45 diploid from pseudo- fertilized ovule plantlets. Henceforth, the present study builds useful foundation for further research towards the development of homozygous Tagetes erecta or other Tagetes species

Title : Morpho-biochemical and molecular characterization of China Aster [*Callistephus chinensis* (L.)Nees] (2018)

Veluru Bhargav, IARI, Guide: Dr. Rajeev Kumar

An investigation was carried out on "Morpho-biochemical and molecular characterization of China aster [Callistephus chinensis (L.) Nees]" at Division of Floriculture & Medicinal Crops, ICAR-IIHR, Bengaluru, Karnataka during the years 2015-16 and 2016-17. The objectives of the investigation was to characterize the China aster genotypes based on DUS test guidelines, anthocyanin and flavonoids profiling in different coloured groups, molecular genotyping and to assess the impact of diversity in heterosis. A total of 42 China aster genotypes were characterized for 21 traits by adopting DUS test guidelines developed by PPV & FRA, New Delhi. Out of 15 visually assessed DUS characters, 2 were monomorphic, 4 dimorphic and 9 polymorphic, and 6 measurable traits showed polymorphism. Six traits were identified for grouping of genotypes viz., plant height, plant type, flower head diameter, shape and colour of inner side of ray floret in outer row and type of flower head. Forty-two genotypes were evaluated for vegetative growth, flowering, yield and postharvest life during 2015-16 and 2016-17, revealed that the genotypes IIHRCC39 and IIHRI69-2 found promising for long stalk length (49.10 cm and 47.50 cm, respectively), whereas, IIHRG13 and IIHRJ3 for vase life (9.50 and 9.35 days, respectively) and these can be used for cut flower. The genotypes IIHRCC42 and Arka Poornima recorded highestweight of flowers per plant (235.21g and 231.62g, respectively), were found promising for loose flower yield.Among 15 different coloured genotypes ranged from red to dark purple, highest total anthocyanins and flavonoids were recorded in Arka Violet Cushion (469.36 mg/100g) and Matsumoto Yellow (243.01 mg/100g), respectively. The LCMS/ MS analysis for four anthocyanins, revealed maximum cyanidin (2,582.64 μg/100g) and delphinidin (5,223.54 μg/100g) in Arka Violet Cushion and pelargonidin (236.44 μg/100g) in Matsumoto Red. The LC-MS/MS analysis for 12 flavonoids, revealed that apigenin was present in maximumquantity irrespective of the genotypes. The highest apigenin (26.61 × 103 μg/100 g) was recorded in Matsumoto Pink, catechin (28.43 μg/100 g) in Matsumoto Yellow and naringenin (459.34 μg/100 g) in IIHRE10. All the 26 SSR loci showed polymorphism in genotypes. The dendrogram was generated, grouped the genotypes into five major groups, by using pooled binary data from 133 alleles of 42 genotypes.The crosses L2 x T3 (Matsumoto Red x IIHRJ3- 2), L5 x T1 (Matsumoto Scarlet x Phule Ganesh Violet), L5 x T4 (Matsumoto Scarlet x IIHRG13), L6 x T1 (Matsumoto x Phule Ganesh Violet) and L6 x T5 (Matsumoto x Local White) exhibited overall best performance for economic traits such as plant height, plant spread, flower stalk length, flower head diameter, 100 flower weight and vase life as SCA were also the best cross combinations for exploitation of heterosis over commercial check cv. Arka Kamini.

Title : Standardization of in vitro bulbing techniques for Lilium (*Lilium longiflorum* L.) mass multiplication (2019)

Narendra Singh Bhandari, IARI, Guide: Dr. C. Aswath

The present investigation entitled "Standardization of in vitro bulbing techniques for Lilium (Lilium longiflorum T.) mass multiplication" was carried out in ICAR-IIHR, Bengaluru, Karnataka, 560089. The present study revealed that inner bulb scales were more effective than outer bulb scales and leaves for bulblets induction. Full strength MS media with 3% sucrose was more effective than ½ MS media. Inner bulb scales inoculated in MS media supplemented with Picloram (0.50 mg L-1) + NAA (0.20 mg L-1) and incubated for 8 weeks at 25°C resulted in highest per cent callus induction (90.84%). Maximum per cent rooting (99.33 %), more number of roots (11.40) and highest root length (3.70 cm) was observed in MS media supplemented with ½ MS + IBA (1.0 mg L-1). The stage I bulbet (non dormant) of different sizes (2.00, 3.00 and 4.00 g) were further transferred to bioreactor and tested with different per cent of sucrose (3, 6, and 9) with MS liquid media +BAP+NAA (1.00+0.20 mg L-1) to develop stage II (10-20 g) bulbs. A sharp increase (181.50% to 494.00%) was noticed for bulb growth and development with increasing the concentration of sucrose from 3% to 9% in MS media. While hardening was more success full in the glass jars covered with polypropylene caps. The in vitro developed bulbs (stage II) were further forced in growing substrate to develop commercial grade bulbs. Maximum bulb weight (42.60 g), bulb diameter (6.53 cm), bulb circumferences (13.66 cm), recorded when stage II bulbs (20 g) were grown in media containing coco peat + soil (3:1). Percent increase in bulb weight was increased from 92.84% to108.15% as proportion of cocopeat was increased. The commercial grade bulbs (stage III) were screened at field level to check their fitness for various growth and flowering attributes. Maximum plant height (115.20 cm), highest number of leaves (74.00), maximum stem thickness (18.20 mm), maximum number of flower buds (5.0), longest flower bud (98.0 mm) and maximum diameter of flower buds (37.50) was observed with bulbs having maximum circumferences (13.00-14.00 cm) and more weight (40.00 g). Molecular study through ISSR markers revealed that plantlets regenerated through bulb scale did not show somaclonal variation and were true-to-type plants. Further, it can be concluded that inner bulb scale is the best explants source for largescale multiplication of plantlets in Lilium hybrid "Pavia". Bioreactor culture, which includes callus induction and bulblet formation (stage I) in MS solid medium and bulbing in bioreactors, is more efficient method for the mass production of high- quality Lilium bulblets.

Title: Breeding Chrysanthemum (*Dendranthema x grandiflora tzvelev)* for quality and resistance to white rust (*Puccinia horiana Henn.*) (2019)

Neelam Thakur, IARI, Guide: Dr. Sujatha A. Nair

The present investigation was undertaken on "Breeding chrysanthemum (Dendranthemax grandiflora Tzvelev) for quality and resistance to white rust (Pucciniahoriana Henn.)" at ICAR- Indian Institute of Horticultural Research, Hesaraghatta, Bengaluru during 2015-17. The objectives of the investigation were to screen chrysanthemum genotypes for resistance to white rust, to evaluate chrysanthemum genotypes for desirable horticultural traits, to develop induced mutants from selected genotypes for quality traits and white rust resistance, to analyze selected chrysanthemum genotypes for phenolics and flavonoid profilesand its correlation to white rust resistance. Twenty-seven genotypes wereidentified as resistant; five genotypes viz. Flirt, CO.1, Fitonia, Rekha and Arka Ravikiran as moderately resistant; eight chrysanthemum genotypes viz. Pusa Aditya, Marigold, Vijay Kiran, Ratlam Selection, Anmol, Shyamal, Vasanthika and Sunil as highly susceptible, nine genotypes viz. Rajat, Coffee, Arka Yellow Star, Kargil, Roopanjali, Winter Queen, Sharadmala, Sadbhavanaand Arka Chandrika as susceptible.The evaluation study of forty-nine chrysanthemum genotypes for desirable horticultural traits showed considerable morphological variation for all vegetative and flowering traits. These traits could be considered for selecting genotypes for cut flower, loose flower, pot-culture and garden display. Trait specific selection of parents for further improvement in chrysanthemum can also be undertaken. Ten chrysanthemum genotypes were gamma irradiated with 0, 10, 20, 30, 40 and 50 Gy and the LD50 ranged from 15.72 Gy (Marigold) to 30.10 Gy (Arka Chandrika). Significant difference was observed in plant survival, vegetative and floral traits among chrysanthemum genotypes with respect to gamma doses. Irradiation of rooted cuttings with gamma rays (10, 20 and 30 Gy) of different chrysanthemum genotypes resulted in putative mutants from Arka Chandrika, Arka Kirti, Arka Pankaj, Pusa Aditya, Arka Red Gold and Arka Yellow Gold which differed with respect to flower colour and flower shape. The putative mutant of Arka Yellow Gold at 10 Gy has been carried forward to VM3 generation and was found to be resistant to white rust. Total phenols and total flavonoids were positively correlated with white rust resistance in chrysanthemum genotypes. The genotypes resistant to white rust disease had higher levels of salicylic acid and t-cinnamic acids among the phenolic acids and apigenin, catechin, epigallocatechin, luteolin and rutin among the flavonoid compounds as compared to susceptible genotypes.

Title : Molecular studies on interaction of Gladiolus (*Gladiolus hybridus* Hort.) and *Fusarium oxysporum* f. sp. Gladioli (2019)

Raimani hembrom, IARI, Guide: Dr. T. Manjunatha Rao

The study titled “Molecular studies on interaction of gladiolus (Gladiolus hybridus Hort.) and Fusarium oxysporum f. sp. gladioli” was carried out in the Division of Floriculture and Medicinal Crops, ICAR-Indian Institute of Horticultural Research, Bengaluru during 2016-18. The objective of the study was to identify and analyze resistance gene analogs (RGAs) in gladiolus genotypes in response to Fusarium wilt disease.In this study, nine gladiolus genotypes were screened for resistance against Fusarium oxysporum f. sp. gladioli. Plant were inoculated with two geographically different isolates of F. oxysporum f. sp. gladioli i.e. FGS-SOL isolate and FOG-IIHR1 isolate. In the screening test, genotype „Psittacinus hybrid‟ was found to be resistant to Fusarium wilt disease with no disease incidence. Maximum average disease incidence percentage (66.67%) was recorded in the genotype „Pink Friendship‟ which was found to be susceptible to Fusarium wilt disease. FOG-IIHR1 isolate (24.07%) was found to be more virulent than FGS-SOL isolate (12.04%) based on maximum average disease incidence in all the tested gladiolus genotypes. Cluster analysis of the gladiolus genotypes inoculated with FGS-SOL isolate and FOG- IIHR1 isolate showed grouping of gladiolus genotypes into three clusters. Average inter-cluster distance in gladiolus genotypes inoculated with FOG-IIHR1 isolate was found to be maximum (5.63) between cluster II („Arka Gold‟) and cluster III (“Psittacinus hybrid” and “Gladiolus callianthus”) which revealed highest genetic diversity between these clusters. Twenty seven degenerate primers were designed for isolation of RGAs from genotype „Psittacinus hybrid‟. PCR with degenerate primers identified three RGAs viz. GhRGA5, GhRGA14 X1 and GhRGA14 X2. Sequence analysis showed that GhRGA5 belongs to NBS- LRR type of RGA proteins whereas GhRGA14 X1 and GhRGA14 X2 belong to RLK type of RGA proteins. Expression of GhRGA5 and GhRGA14 X1 was studied in the inoculated and uninoculated plants of “Psittacinus hybrid” and “Pink Friendship” genotypes at different time intervals (3, 6, 12, 24 and 48 hpi). Both the RGAs were observed to be highly expressed in inoculated “Psittacinus hybrid” i.e. GhRGA5 (11.44 folds) and GhRGA14 X1 (11.95 folds) as compared to its uninoculated samples. This study will be helpful in identifying resistance sources which can be used in breeding programs for development of resistant varieties. Identified RGAs can be used as molecular markers in marker assisted selection for disease resistance breeding.

Title: Evaluation of gladiolus genotypes for production of disease free planting material through aeroponic system (2019)

Hemlata, IARI, Guide: Dr. T. Manjunatha Rao

The study entitled "Evaluation of gladiolus genotypes for production of disease free planting material through aeroponic system" was carried out at ICAR- Indian Institute of Horticultural Research, Bengaluru- 560 089 during 2015- 2018. The main objective was to develop aeroponic system for production of disease free planting material of gladiolus (Gladiolus spp.). This is first ever attempt to produce gladiolus in aeroponic system. The aeroponic prototype was designed with 180 X 90 X 90 cm dimension. Integrated management practice with carbendazim (0.2%), hot water (54 2 for 25 minutes) and carbendazim tolerant Trichoderma harzianum GJ 16B (10 g sporulated isolate/L for 3 minutes) were found effective for corm rot management in both field and storage conditions. Cormel planting in summer season resulted in maximum average corm diameter, average corm weight, average cormel diameter and average cormel weight, compared to rainy or winter season. The corms from five genotypes were planted in pots and placed inside and outside polyhouse. From the pot experiment, it was inferred that low light intensity (10 DLI) with mean monthly temperature (ranged from 29.41 to 36.40) was not suitable for gladiolus growth and development, whereas, 14 DLI light with mean monthly temperature (26.43 to 30.56) produced spikes with increased corm diameter and corm weight.The corms of five genotypes were planted in aeroponic system. Among the genotypes, G. callianthus was found best performing with good vegetative growth, flowering and maximum average number of corm and cormel production. Genotypic variations in root phenotype were also observed in aeroponic system and scored using 1-5 scale. G. callianthus root health, growth and number at 40th, 60th and 80th day outranked rest of the genotypes. It produced maximum number of fine roots and minimum root length compared to the other four varieties.During storage, no disease symptoms were observed in aeroponically produced corms.Aeroponically produced corms with 2-3 cm diameter were planted in pots after the dormancy period was over. Vegetative, flowering and corm parameters were recorded and compared with plants raised from pot harvested corms (2-3 cm diameter). No significant difference between them was observed in vegetative and flowering parameters.Further, research is required to optimize nutrient solution composition, pH, electrical conductivity and temperature, for maximising corm and cormel productivity in aeroponic system. This study calls for utilization of aeroponic technology for production of disease free planting material for increased crop productivity in gladiolus.

Title: Studies on crossability and white rust resistance in Chrysanthemum (*Dendranthema x grandiflora Tzvelv*) (2021)

Sunil Kumar, IARI, Guide: Dr. Rajiv Kumar

The present investigation on “Studies on crossability and white rust resistance in chrysanthemum (Dendranthema x grandiflora Tzvelv)” was carried out in the research block of the division of Floriculture and Medicinal Crops, ICAR-Indian Institute of Horticultural Research, Bengaluru, during 2016-17 and 2017-18. The objectives of the investigation were floral biology studies of selected Chrysanthemum genotypes/lines, identification of compatible chrysanthemum genotypes and screeningof half-sib progenies for quality as well as resistance to white rust. The floral biology result revealed that day to first flower opening was recorded earliest in Local White (65 days) and Sweta Singar (65.50 days), peak time of anthesis from 9.30 h to 10.30 h. and line IIHR6-32 (4.11 days) recorded maximum days to anther dehiscence. The maximum pollen viability was recorded in Red Stone (95.02%) followed by IIHR6-26 (88.20%), IIHR9-3 (87.44%) and Sweta Singar (85.59%). The maximum pollen size was recorded in line IIHR9-3 (38.20 µm), while, PEG4000 at 20% recorded maximum pollen germination in 43.57% (IIHR9-3) followed by 19.43% (Kalpana) and 19.34% (IIHR6-29. The seeds collected from only one successful cross IIHR6-41 x MP recorded 25.68% (15% sucrose) to 40.74% (10 % sucrose) seed setting and IIHR6-41 x MP recorded 26.74% (15% sucrose) to 54.12% (control) seed germination. Among PEG4000 concentrations, the seed setting was ranged from 1.57% (Ajay x MP) to 31.35 % (IIHR6-41 x MP). The seed germination in one successful cross IIHR6-41 x MP recorded 54.48% germination. Among sucrose and PEG4000 concentrations, seed setting was observed in five crosses i.e. Ajay x MP, Arka Chandrika x MP, Arka Kirti x MP, Lal Pari x MP and IIHR6-41 x MP. Seed setting was recorded ranged from 1.69 (Ajay x MP) to 39.32 (IIHR6-41 x MP). Seed germination was recorded in four crosses i.e. Arka Chandrika x MP, Arka Kirti x MP, Lal Pari x MP and IIHR6-41 x MP, found significant seed germination ranged from 3.27% (Arka Chandrika x MP) to 49.02% (IIHR6-41 x MP). Seed setting was observed in five crosses i.e. Ajay x MP, Arka Chandrika x MP, Arka Kirti x MP, Lal Pari x MP and IIHR6-41 x MP. The Seed setting was observed in five crosses i.e. Ajay x MP, Arka Chandrika x MP, Arka Kirti x MP, Lal Pari x MP and IIHR6-41 x MP.Among crosses and sucrose + PEG concentrations, 10% sucrose + 15% PEG with crosses Arka Chandrika x MP and IIHR6-41 x MP recorded seed set ranged from 3.44% to 52.65%, respectively.Parents and half-sib progenies evaluation has been done for white rust. The11 genotypes/lines viz., Sweta Singar, Punjab Gold, Garden Beauty, Red Stone, Punjab Anuradha, IIHR6-32, IIHR9-3, IIHR6-41, Lal Pari, White Dolly and White Andaman were found to be resistant. Out of these, 11 genotypes/lines were found to be resistant. Out of total 54 half-sib progenies screened, 18 half-sib progenies nil disease index. These seven half-sib progenies also have superior horticultural traits such as flower colour, dwarf and compact growth habit, colour, dwarf and compact growth habit.

Title: A study on disease resistance mechanism against black spot (*Diplocarpon rosae*) and powdery mildew (*Podosphaera pannosa*) in Rose (*Rosa spp.*) (2021)

Saidulu Yeluguri, UHS, Bagalkot, Guide: Dr. Tejswini Prakash

The present investigation on rose was carried out in the Division of Flower and Medicinal crops, at ICAR-IIHR, Bengaluru to screen the available germplasm for disease resistance source and to study the role of various defense related biochemical compounds and physiological characteristics in resistance against black spot and powdery mildew. Based on the results of 57 genotypes screened in field for natural incidence of black spot over two seasons i.e., 2015 and 2016, Knock Out variety was found to be immune (0 PDI). The varieties Carefree Beauty and Crifty Duty were found highly resistant (1-5 PDI), IIHRR 3-7-12 and Arka Nishkant were categorized as resistant (6-10 PDI) while IIHRR 4-15-12 was found to be moderately susceptible (16-20 PDI). The progression of black spot disease was found slow in resistant varieties compared to susceptible ones. Further, selected eight genotypes that showed varied levels of resistance against black spot infection in field were studied in detached leaf assay with artificial inoculation of D. rosae to confirm their disease reactions. The variety Knock Out which was found to be immune for black spot in field has developed hypersensitive reaction upon artificial inoculation and was categorized as highly resistant (0.1-5 PDI). The variety Arka Nishkant was found to moderately resistant (10.1-15 PDI) under artificial inoculation against its reaction being resistant in field. It was found that compared to susceptible genotypes, the activity of defense related enzymes viz., catalase, peroxidase, polyphenol oxidase, superoxide dismutase and phenylalanine ammonia lyase and other defense related secondary compounds viz., phenols and flavonoids was high and quick during the progression of disease in resistant genotypes, contributing for resistance. The results of 55 genotypes screened under polyhouse over two seasons i.e., 2015-16 and 2016-17, for powdery mildew resistance revealed that no variety was either tolerant or moderately tolerant. Further, healthy leaves of eight selected genotypes exhibiting different levels of resistance against black spot and powdery mildew when investigated for different physiological characteristics viz., number of stomata and size of stomata, leaf thickness, epicuticular wax content and gas exchange parameters, the exact role ofthese studied characteristics in disease resistance could not be established.

Title: A study on shortening hybridization cycle in Rose: mechanism and regulation (2018)

Shivakumar, UHS, Bagalkot, Guide: Dr. Tejswini Prakash

The present study was carried out at ICAR-IIHR, to study the effect of pre-crossing treatment on hybridization, pre-sowing treatment on seed germination and to understand the level of endogenous hormone during different physiological stages of hip development. The experiment on pre- crossing treatment was conducted with nine pre- crossing treatments using different combinations of gibberellic acid (0,100, 200 ppm) and boric acid (0, 250, 500 ppm). Hybridization during August-December months with the application of either GA3 at 100 ppm or boric acid at 500 ppm prior to crossing enhanced the number of seeds per hip and could minimize the days to seed set. Levels of endogenous hormones was estimated during different physiological stages of hip development to understand the role of hormones in regulating the seed germination process in rose. GA3 content was found to be maximum and ABA was minimum during 28-35 days after pollination. Effect of various seed treatments was evaluated on seed germination in five rose genotypes. Seed germination percentage varied with the genotypes, treatments and incubation temperature. Among the different incubation temperature, maximum seed germination (19.11%) was observed at 15°C and minimum (2.66%) at 10°C. Among different treatments, maximum seed germination of 41.33 percent was observed in IIHRR 3-7-12 with the pre-sowing treatment of mechanical seed scarification by stirring in mixer-grinder. Based upon estimation of endogenous hormone concentration, two stages of seed development were identified one at 28-35 and another at 63 days after pollination, when GA3 as well as IAA were observed to be high and ABA was low. Our study suggested the possibilities of improving the seed germination by harvesting the seeds at these selected stages.

Title: Genetic and biochemical analysis of yield and quality parameters in Marigold (2018)

Santhosh, N., UHS, Bagalkot, Guide: Dr. Tejswini Prakash

The present research was under taken at the ICAR-IIHR, Hessarghatta, Bengaluru. Among eight pure lines inclusive of yellow African. orange African and French marigold tested, orange African marigold was found to be superior for all the biochemical components (lutein, zea-xanthin and total carotenoid content). Biochemical components were positively associated among themselves and had positive significant association with flower size and flower weight per plant. Phenotypic co - efficient of variation (PCV) and genotypic co-efficient of variation (GCV) were maximum for biochemical components. The SCA variance was higher than the GCA variance for flower weight per plant, flower size and biochemical components indicating the presence of non-additive or dominance gene action. Higher GCA variance over SCA variance was observed in case of flower number per plant, dumber of harvests, fresh and dry petal meal per flower indicating additive gene action prevailing for these characters. Selection approach can be followed during development of pure lines, a prerequisite for line development in heterosis breeding. Combining ability tested in petaloid and apetaloid sterile lines indicated the superiority of petaloid sterile lines for development of hybrids. Petaloid male sterile lines IIHRMO 9-8 and IIHRMO 9-7 were found to be good general combiners for flower weight and biochemical components respectively. On the contrary, apetaloid male steril e lines were easy to hybridise and quality of seeds were better than that obtained from petaloid male sterile lines. The study suggested possibility of hybrid development using the male sterile lines for both flower and biochemical components. For efficient and economical hybrid seed production, genes of apetaloid and petaloid male sterile lines needs to be combined.

Plantation, Spice, Medicinal & Aromatic Crops

Title: Pachytene analysis, interspecific hybridization and response to chromosomal doubling in two steroids-bearing Solanum species-*Solanum viraum* Dunal (1983)

D.L.Maheswar, UAS, Bangalore, Guide :Dr.R.Krishnan

In steroids-bearing Solanum viraum Dunal (Syn. Khasianum var. Chatterjeeanum) upgradation of solsodine content in berries and incorporation of resistance to wilt are major breeding objectives. Towards the former goal, autotetraploidy holds promise. Steroids-bearing Solanum mammosum Linn. could be a donor for genes conferring wilt resistance. The thesis provides cytogenetic basis for the above objectives through- cytomorphological study of induced autotetraploids in S. viarum and study of interrelationship of S. viarum and S. mammosum based on crossability, comparative pachytene karyology and homology (in interspecific hybrid), response to chromosomal doubling and distribution of leaf flavonoids. All the 12 differentiated pachytene chromosomes of haploid complement of S. viarum (n=12) were identified and characterized. They differ from the undifferentiated pachytene bivalents of S. mammosum (n=11) which have uniformly stained chromosomes along their entire length. Induced autotetraploids of S. viarum contain higher content of solasodine in berries (2.16%) than diploids (1.83%) with nearly normal meiosis. Diploids of S. mammosum and S. viarum were crossed successfully unidirectionally with former as pistillate parent. Reciprocal cross and crosses with reciprocal species grafts and induced autotetraploids (within and across ploidy) failed. Differential response to autotetraploidy between S. viarum and S. mammosum was evident in morphological and yield attributes as well as in meiotic behavior S. mammosum autotetraploids showed poor fruit set and high meiotic abnormalities. The results support potential value of autotetraploidy in S. viarum and provide comprehensive informations on species inter-relationships and underlying barriers to gene transfer in the two species.

Title: Evaluation of diploids and induced autotetraploids of *Solanum viarum* Dunal for effects of growth regulators, single plant progeny yields and chromosome number dunal (1984)

P.R.Ramanjini Gowda, UAS, Bangalore, Guide : Dr.R.Krishnan

A programme on the evaluation of induced autotetraploid varieties in Solanum viarum Dunal for three aspects, namely: (i) Effects of Growth Regulators, (ii) Evaluation of Single Plant Progenies, and (iii) Cytomorphic study of C3 generation plants. Effects of GA3 (250, 500 and 1000 ppm), CCC (400, 800 and 1600 ppm) and kinetin (25, 50 and 100 ppm) applied at 45 and 75 days on field planted diploids and autotetraploid were studied. Dry berry yield per plant in diploid and tetraploid was reduced in all treatments. Solasodine content was increased in diploid in 250 ppm GA3 and in tetraploid in 250 and 1000 ppm GA3, 16C0 ppm CCC and 50 ppm Kinetin treatments. Single plant Progenies of 17 diploids and 18 C2 generation autotetraploid were evaluated Six autotetraploid lines were on par with the high (dry) berry yielding diploids. Autotetraploids excelled in berries per node, berry wall weight and 100 seed weight. They were inferior to diploids in dry weight perberry, seed number and weight per berry. Autotetraploids produced adequate seeds (12,571 to 1,16,127 per plant) to permit their propagation on a commercial scale. Significant positive association between number of berry bearing nodes per plant and number of berries per node was unique to autotetraploids that permit simultaneous improvement in these components of total berry yield. The presence of aneuploids with 2n=46, 47, 49 and 50 was detected for the first time, which offer direct proof for transmission of gametes with 23 and 25 chromosomes. Chromosomes association in euploids and aneuploids consisted predominantly of quadrivalents (four to nine) and bivalents (4 to 14), besides trivalents (0 to 2) and univalent (0 to 4). Presence of hexavalent and pentavalents in euploids (2n=48) and aneuploids provide direct proof for participation of gametes with unbalanced chromosomal constitution. Among 15 different types of chromosomal distribution to gametes, n=24 was predominant (57.37%), favouring promotion of euploids (2n=48) in progenies. Seed number per berry was identified as criterion for distinguishing tetraploids from aneuploids in the field.

Title: Intervarietal hybridization and induction in autotetraploids in steroid-bearing Solanum species (1984).

D.Nandakumar, UAS, Bangalore, Guide : Dr.R.Krishnan

Solanum viarum Dunal (syn. S. khasianum Clarke var. Chatterjeeanum) is commercially exploited in India for preparation of steroid drugs. Solanum incanum Linn, an indigenous species, has similar potential. The thesis presents results of investigation on intervarietal hybridization in both these species and induction of autotetraploids in S. viarum. Intervarietal hybridization in S. viarum is reported for the first time and involved three morphologically different types. Using generation mean analysis, the mode of gene action was studied for solasodine yield, solasodine content, berry yield and its components and leaf spininess. Significant differences were observed for number of berries per node, fresh and dry berry weight, dry matter in berries and number of spenes per leaf. In view of the predominance of epistatic gene action for all these characters and the presence of additive and/or dominant gene action in them, reciprocal recurrent selection is suggested for improvement of this crop. Linear association of characters was also studied. An useful new recombinant combining high berry yield and solasodine content with fewer spines was isolated. Autotetraploids were induced in the three parents, their hybrids and backcrosses using colchicine. The production of less spiny autotetraploids is reported for the first time. Delayed flowering of autotetraploids could be partly traceable to delayed branching and protracted vegetative phase. A comparative study of diploid progenitors and their autotetraploids showed that differences in specific leaf weight, pollen fertility. Pollen size and hundred seed weight constituted diagnostic characters for identification of autotetraploids. Character interrelations were not altered by chromosomal doubling. In S.incanam intervarietal hybridization generated marked variability. Mode of inheritance of contrasting characters of parents such as stem, spine, flower and fruit colours was elucidated based on the study of parents, F1,F2 and backcross generations. Solasodine content in S.incanum unlike S. viarum increased with berry maturity.

Title: Growth analysis and nitrogen uptake studies on autotetraploids and diploids of *Solanum viarum* Dunal (1984)

G.Sreekantan Nair, UAS, Bangalore, Guide : Dr.R.Krishnan

Induced autotetraploids of Solanum.viarum (syn. S. khasianum Clarke var Chatterjeeanum) excel diploids in solasodine content in berries and constitute the only successful means of enhancement of solasodine content. In the present study the prospects of autotetraploids as commercial varieties was evaluated in two experiments. A total of 51 characters which included solasodine content, berry yield, its components, morphological characters and growth parameters were studied. In the first experiment three autotetraploids (differing in spine characters), their diploid progenitors and four promising varieties were compared. The three autotetraploids proved superior to diploids in solasodine content and were on par in berry (dry and fresh) and solasodine yields as well as most of the morphological and growth characters. Yield architecture differed in the two ploidy groups. Higher expression in number of fruits per node, berry wall weight, 100 seed weight and seed volume characterized tetraploids. Superiority in berry dry weight, dry matter, seed weight and seed number marked diploids. These characters, besides slow initial growth in tetraploidaid in distinguishing diploids and autotetraploids. In the second experiment, response of less spiny diploid and its autotetraploids to added nitrogen (@0, 30, 60 and 120 kg/ha) was assessed. Diploid and autotetraploid responded similarly and favourably in most of the characters including berry yield with increasing doses of nitrogen solasodine content also recorded increase with higher nitrogen doses in autotetraploids but decreased in diploid. Consequent to simultaneous increase in berry yield and solasodine content, autotetraploid recorded six fold increases in solasodine yield at 120 kg N as compared to control. The experiments demonstrated the superiority of autotetraploids over diploids in solasodine content and response to added nitrogen besides parity in berry yields.

Title: Progeny performance and microsporogenesis in eutetraploids and aneuploids of *Solanum viarum* Dunal (1987)

K.Lila Mathew, UAS, Bangalore, Guide :Dr.R.Krishnan

Evaluation of progenies of C3 generation eutetraploids and aneuploids for solasodine content, berry yield and other characters, and comparative study of male gametophytic development of diploids, induced eutetraploids and aneuploids was carried out in Solanum viarum syn. S. Khasianum var. Chatterjeeanum). Progenies of ten eutetraploids and 13 aneuploids were evaluated for their performance as parents and to estimate frequency of aneuploids in populations. Despite a wide range, solasodine content in eutetraploid and aneuploid lines was on par. Similarly for dry berry yield (economic character) and vegetative/reproductive characters, aneuploidy and eutetraploid were on par. Despite differences in chromosome number, eutetraploids and aneuploids appear to perform similarly as parents. Liner association among 22 characters was worked out. Solasodine content was not correlated with any character. Thirteen characters, associated with dry berry yield accounted for 99.5% of variation. The study of histological changes associated with microsporogenesis and male gametophotype development revealed an overall similarity among diploids, eu-and aneuploids. Differences were observed for cell size. RNA and starch accumulation. Excessive accumulation of starch in wall layers of eu- and aneuploidy anthers is also indicative that non-utilization, than non-availability of nutrients underlies the sterility of eutetraploids and aneuploids.

Title: Evaluation of plant densities and single plant progeny of less spiny diploid and advanced generation induced autotetraploids of *Solanum viarum*. Dunal (1988)

G.Sreekantan Nair, UAS, Bangalore, Guide : Dr.R.Krishnan

In Solanum viarum (syn.S. khasianum var. chatterjeeanum) a spiny species in which berries are supplementary industrial source of steroids in India, previous studies on development of less spiny diploid and induced autotetraploids paved the way for realization of higher berry and solasodine yields adopting higher plant densities and scope for selection among diploid and autotetraploid progenies. In the present study, evaluation of (i) diploid and autotetraploids under a wide range of plant densities and (ii) single plant progenies of diploid and C6 generation autotetraploid for berry yield, its components, morphological characters and/ or solasodine content was undertaken. Evaluation of diploid and autotetraploids for plant densities was carried out in two experiments. In the first experiment where nine spacing combinations of 60,90 and 120 cm row/plant spacings with population ranging from 6900 to 27,300 plant per hectare were evaluated, favourable effects of higher plant densities on berry and solasodine yields were observed. Rectangular spacing gave higher berry yields than square spacing. Solasodine content in berries was not affected by plant density differences. Rectangular spacing of 60 x 120 cm with wider spacing in East-West direction is suggested as optimal for realization of higher berry and solasodine yields without hindering cultural and harvesting operations. This spacing accommodates 14,000 plants per hectare as against 7000 plants in commercially adopted 90 x 150 cm spacing.In the second experiment on plant density evaluation, three plant densities of 17789,27778 and 49382/ ha arising from square spacings of 75,60 and 45 cm, respectively, were compared. Berry and solasodine yields in both ploidy types increased with closer spacing but solasodine content was not affected. High density planting appears to be suitable for seed crop. The second experiment also brought out the spacing for practicing selection in diploid and C6 generation autotetraploid for berry yield components. Seed fertility was not improved with advancing generation. In addition to confirmation of several morphological, physiological and berry yield characters for distinguishing diploid from autotetraploid, leaf transpiration and leaf temperature were the new characters identified. Character interrelationships were affected by plant density and diploid differed from autotetraploid.

Title: Studies on hybridization, chromosomal boubling, grafting and leaf anatomy in *Coleus forkohlii* Brig. (1993)

K.M.Naniah, UAS, Bangalore, Guide : Dr.R.Krishnan

In Coleus forkohlii Brig., an important medicinal plant both in Ayurvedic and modern medicines, four experiments were conducted at IIHR, Bangalore. In the first experiment, varietal crosses involving all three possible combinations among crossability, reciprocity and heterotic effects. Fifteen inter varietal hybrids were evaluated both as seedlings and after vegetative propagation. Hybrids of tuberous accessions exhibited positive heterobeltiosis for morphological and yield characters. In crosses involving tuberous x non-tuberous and non- tuberous x non- tuberous accessions, both positive and negative heterobeltiosis was observed for these characters. Hybrids AB and DA which combine higher harvest index and tuber yield hold promise for commercial utilization. In the second experiment autotetraploids were induced in three tuberous and three non- tuberous accessions using aqueous colchicine solution. Visual differences in leaf size and thickness increase in size of pollen grains and pollen sterility aided in identification of tetraploids. Autotetraploids and their diploid progenitors were evaluated both in pot and field. Field grown plants ere vigorous. Ploidy differences in the expression of tuber characters were similar in pot and field grown plants. In diploid and induced autotetraploid of accessionK' graded does of potassium failed to evoke response in dry matter production and other characters probably due to the high levels of native potash in soils. In the third experiment, graft compatibility of six tuberous and four non- tuberous accessions was assessed through reciprocal grafts in a total of 45 graft combinations. Graft take differed in different accessions. Stock-scion interaction was observed in the expression of various characters including tuberization. The profusely flowering non- tuberous accession 'E' hold promise as stock in studies on induction of flowering in non0flowering agronomically superior tuberous types. In the fourth experiment and comparative of leaf anatomy in accessions, tetraploids and hybrids, differences in relative abundance and distribution of starch grains in the mesophyll tissues were observed. Genetic control in the expression of these characters is reduced

Title: Intervarietal hybridization and autotetraploidy in *Coleus forskohlii* Briq. (1993)

Prakash, UAS, Bangalore, Guide :Dr.R.Krishnan

In Coleus forskohlii Briq., an important plant, four experiments were conducted at IIHR, Bangalore. In the first experiment, through controlled pollination, two hybrids viz., DXC and DXI; a double cross involving AXD and As XC hybrids and a bacvk cross to male parent of the cross AsXB were produced and evaluated. In the second experiment, in order to broden the genetic base for autotetraploidy breeding, autotetraploids were induced in an accession G, and three hybrids, HXB, HXC and AXG using aqueous colchicine solution. Autotetraploids were identified based on pollen size and fertility. Autotetraploids were inferior to their diploid progenitors in the expression of several morphological, growth and yield characters. In the third experiment, an interploidy cross was produced by crossing autotetraploid of A with diploid A. the only plant obtained was morphologically distinct from either parent. In the forth experiment, a comparative evaluation of 19 diploid and 22 induced autotetraploids of accession/intervarietal hybrids with standard check K as control was carried out both under pot and field conditions. Genotypic differences among the entries are obtained. Hybrids DxA under pot; AXB and CXA under field conditions exhibited standard heterosis for tuber yield to the extent of 25.5, 79.19 and 64.18%. these hybrids can be promoted as cultivars as the crop is vegetatively propagated. In pot experiment, AsXD, CXA, DXA, AxB4n, AsXD4n, and DXE4n and in field experiment, CXA, DXA, DXA4n, and KXA4n exhibited high standard heterosis values for harvest index over standard control. Genetic analysis of various characters showed a high heritability for most of the characters. Path co-efficient analysis brought out the positive or negative direct and indirect effects of five characters on dry weight of tubers/roots. The number of tubers/roots had very high direct and positive effect on yield without appreciable antagonistic indirect effects through the characters.

Title: Studies on fertility, storage and microsporogenesis in diploids and induced autotetraploids of *Catharathus roseus* L. (G) Don (1993)

N.Swami Rao, UAS, Bangalore, Guide : Dr.R.Krishnan

In Cathranthus roseus L (G) don, two experiments were conducted at IIHR (i) Pollen productivity, storage and fungicidal sensitivity. The ten single plant selections differed for or more morphological character such as root yield, fruit and seed characters. Average female fertility ranged from 74.7 to 98.5% and pollen productivity anther from 18133 to 330453. Protocol was worked out for in vitro pollen germination. 20% sucrose gave 100% germination. Pollen tube length variations had no relation with seed germination. Pollen stored in liquid nitrogen for 240 days gave very poor in vitro germination and that too in only seven selections. Stored pollen size was smaller than fresh pollen, but pollen size was not related in vitro germinability of stored pollen. Among the six fungicides, Dithane Z-78 at lower concentrations did not affect pollen germination, but Sulfex and Captan inhibited germination. Bavistin at lower concentration improved germination. A close relationship was observed between pollen tube growth the pollen germination. Autotetraploids (4n) induced by treating seeds with 0.2% colchicine for 12 hours were identified bases on larger pollen size and reduced fertility. Root dry weight of 4n was higher than diploids (2n). Pollen productivity in 4n was lower than 2n. Stainability and in vitro germinability of 4n pollen was not related. In vitro pollen germination was lower in4n. Pollen tube growth in 2n excelled 4n. In 4n ovules/ovary, seeds/follicle and follicles/branch were lower than 2n. (ii) Microsporogenesis and male gametophyte development in diploid and induced autotetraploids. The histological and histichemical changes during microsporogenesis in 2n and 4n were similar. But differences were observed in the size of various tissues. Pollen size and individual cell size were larger in 4n than in 2n. Reduction in the number of dyads and tetrads, PCM's and pollen grains was observed in 4n as compared to 2n. Polysaccharide content was similar in diploid and autotetraploids during microsporogenesis.

Title: Evaluation of less spiny diploid and autotetraploids varieties of *Solanum viarum* Dunal and genetics of spine character (1993)

M.Lakshmi Narayana Reddy, UAS, Bangalore, Guide : Dr.R.Krishnan

Five experiments were conducted using less spiny diploid (Arka Sanjeevini) and/or induced autotetraploid (Arka Mahima) varieties. Yield performance of Arka Sanjeevini was evaluated using five selected plant spacing viz., 30x30, 15x60, 30x120 and 60x120 cm with 90x150 cm control at three locations i.e., V.N. Pura, Solur and IIHR farms. The soil type in the three farms were sandy loan, sandy clay loam and sandy clay. Based on mean dry berry yield the three locations can be classified in descending order as IIHR>Solur> V.N.Pura. yield stability analysis using Finlay and Wilkinson method (1963) suggest suitability of 30x30 cm for sandy clay soils with high input facility. For adverse environments spacing of 30x120 cm is suitable. For locations, where data on soil type and other conditions are not available, 30x60 and 15x60 cm spacings are suitable. Diploids (Arka Sanjeevini) and autotetraploid (Arka Mahima) varieties were evaluated under 16 different planting density and/or arrangements resulting from combinations of 15,30,60 and 90 cm row and plant spacings. Planting densities ranged from 12,300 to 4,44,000 plants per hectare, Dry berry yield in diploid ranged from 2,589 to 6,716 kg per hectare. While in tetraploid from 1032 to 2,953 kg. berry yield under square planting increased with increasing planning densities. In diploid in the six rectangular spacings, berry yield plotted against increasing planning densities was bimodal in wider East-West spacings, unimodel when North-South spacings were wider. In autotetraploid reverse pattern was detected. Berry yield differences among planting arrangements were evident on comparisons across spacing treatments. Redundancy in planting densities on yield was observed in both the ploid types. On this basis, 15x90 cm spacing proved promising over 30 x 30 and 15-60 cm spacing for achieving higher yields. Yield performance of Arka Sanjeevini and Arka Mahima across season was assessed. Highest dry berry yield was recorded in November planting of diploid and June planting of autotetraploid. Yield disparity between the two ploidy types was narrower in June planting. Diploid was more stable than autotetraploid for berry yield across seasons. Yield variations in autotetraploid across planting dates are traced to variations in berry number and dry matter percentage in berries. Autotetraploid also showed wider variations in seed weight and seed number per berry than diploid.

Title: Studies on germplasm evaluation, induced autotetraploidy and hybridization in *Coleus forskohlii* (willd) Briq. (Syn.C. *Barbatus* benth.) (1993)

Laxminarayan Hegde, UAS, Bangalore, Guide : Dr.R.Krishnan

Roots of Coleus forskohlii (lamiaceae) yields forskolin used in the treatment of glaucoma, congestive cardiomyopathy and certain cancers. Experiments were conducted at the central farm of IIHR, Bangalore, on (i) the evaluation of varietal collections (ii) induction and evaluation of autotetraploids with a broad genetic base, and (iii) Production and evaluation of intervarietal hybrids using diverse genotypes. Thirteen collections were evaluated in three trials for 30 morphological, growth and yield characters. Wide genetic variability was observed for all characters. Metroglyph analysis enabled classification of tuberous and non-tuberous accessions based on number of leaves and branches. Promising accessions identified were: 'K' for tuber yield. 'D' for harvest index and photosynthetic efficiency (by virtue of lower LAD-TDM ratio): 'G' and l for high total dry matter per plant. Varietal differences in crop duration among tuberous collections were observed. The observed high positive correlation between root volume and fresh weight of roots vs dry weight of roots (economic yield), could be exploited for screening accessions for high dry tuber yield. Genetic analysis indicated additive genic control of harvest index, fresh weight of roots and total dry matter by virtue of their high heritability and genetic advance (% of mean) values. For induction of autotetraploids, seed and shoot apex treatment methods using aqueous colchicine (0.1 or 0.25%) were standardized in three tuberous and three non-tuberous accessions. These accessions differed in the expression of characters on chromosomal doubling. The autotetraploids 'K' has potential use as cultivar, while other autotetraploids can be used as parents for production of triploids. Intervarietal hybridization using tuberous and non-tuberous accessions revealed lack of crossability barriers. Heterobeltiosis for economic character viz., tuber yield was observed in two of the hybrids involving tuberous accessions, viz., As x B and As x D. None of the hybrids involving crosses between tuberous and non-tuberous accessions were promising for tuber yield. Hybrids of As x G and As x I were on par in dry matter production with the male parents, which are the highest dry matter producing accessions.

Title: Effect of planting density, mepiquat chloride, mode of pollination and or selection methods in diploid and colchiploid of *Solanum viarum* Dunal. (1998)

K.N.Srinivasappa, UAS, Bangalore, Guide : Dr.R.Krishnan

In steroid-bearing Solanum viarum Dunal. Using diploid (Arka Sanjeevini) and C11 generation induced autotetraploid (Arka Mahima), four experiments were conducted. In the first experiment on the effect of three planting densities, the highest dry berry yield of 9.95 tonnes/ha was obtained for diploid under the highest planting density obtained from adoption of 30 x 30 cm spacing. Among the berry yield components, number of berries per plant increased with decreasing planting densities but dry weight per berry was not affected. Diploid and autotetraploid responded differently to the different spacings adopted in the expression of several morphological and yield characters. In the second experiment, the effect of nine treatment combinations of Mepiquat chloride on the growth and yield characters of diploid and autotetraploid was evaluated. Interploid differences in character response to MC application was evident in several growth and yield characters. No beneficial effect of MC treatments was recorded in both ploid types. In the third experiment on female fertility, mode of pollination was found to affect seed number per berry and seed germinability. Higher seed set and germination were obtained in berries from open pollinated flowers followed by berries from flowers selfed with and without emasculaton. Inter-plant crosses involving one or two artificial pollinations recorded least number of seeds per berry. In the fourth experiment, evaluation of source population of autotetraploid revealed wide variation for morphological, growth and yield characters. Progeny testing using both single plant and bulk seeds showed that, as a selection method single plant selection (SPS) was more effective than bulking for improving higher fresh berry yield per plant and seed yield per plant. Contributing characters for higher fresh berry yield in SPS were number of berry-bearing nodes/plant and number of berries/ plant.

Title: Studies on genetic diversity and biochemical basis of bruchid resistance in Rice Bean (*Vigna umbellata*) genotypes (2011)

B.V.Pavithravani, UAS, Bangalore, Guide: Dr.K.Bhanuprakash

Rice bean, an underutilized pulse crop gaining more popularity in recent times due to its high nutritional value, is no exception to bruchid attack. Hence, an investigation was taken up in this direction in order to identify genotype(s) resistant to bruchid infestation in rice bean crop. One hundred rice bean genotypes were screened for resistance to bruchid based on bruchid assay. Results showed LRB238 (5% infestation) and JP1000304 (10% infestation) as bruchid resistant and LRB26 (75%) as susceptible genotypes. Cluster I (44 genotypes) represented bruchid susceptible genotypes having higher mean values for damaged seeds, holes per seed, seed resource utilization, growth index, dead seeds, loss in seed weight, germination and seedling vigour indices. On the contrary, lower values were observed in cluster III (27 genotypes) showing bruchid tolerant genotypes. Cluster II consisted of 29 moderately bruchid susceptible genotypes. LRB26 was found superior in Cluster I and LRB238 and JP100304 in cluster III. Besides these studies, multivariate analysis revealed three PCs with an Eigen value >1 explained over 72.43 per cent of the total variation and also indicated number of dead seeds, decline in germination and SVI-I and II values as important components contributing to genetic divergence. Out of 44 AFLP primer combinations used for genetic analysis, 41 were found to be polymorphic and generated 482 polymorphic amplified products. The primer combinations, E-CGA/M-GGA and E-CTA/M-TCG which recorded highest polymorphic information content (0.60 and 0.51, respectively), effective multiplex ratio (34.38 and 26.88, respectively), marker index (11.45 and 8.48, respectively), resolving power (21.00 and 15.20) and average genetic diversity (0.33 both) can be efficiently employed in diversity analysis for bruchid resistance in ricebean genotypes. With regard to α amylase inhibition activity which plays a protective role against bruchid infestation, genotype JP100304 showed highest inhibitory activity (33.40%) compared to susceptible genotype LRB26 (3.61%). All these biochemical constituents impairing tolerance to bruchid infestation were 60 to 80 per cent higher in resistant genotypes compared to susceptible genotypes.. Peroxidise isozyme profile clearly showed presence of a prominent and high intensity band (Rm value 0.654) only in tolerant genotypes LRB238 and JP100304 but not in susceptible genotype LRB26. Thus, the present study revealed vital information with respect to diversity for bruchid resistance based on physiological, biochemical and molecular markers. The same information can successfully be utilised in the conventional and molecular breeding programmes to evolve bruchid resistant cultivars in rice bean.

Title: Studies on physiological, biochemical and molecular aspects of seed invigouration in cucumber (*Cucumis sativus* L.) (2012)

K.J.Sowmya, UAS, Bangalore, Guide: Dr.K.Bhanuprakash

Cucumber is a popular Cucurbitaceous vegetable and the ever growing demand of this vegetable throughout the year exerts challenge for continuous production even during off seasons. The present study was conducted to standardize the seed invigouration protocol, to know the physiological, biochemical and molecular changes due to seed invigouration, to test the performance of invigourted seeds under aboitic stress conditions and to test the storage potentiality of invigourated cucumber seeds. The crop specific efficacy of all the popular methods of priming viz., hydropriming, osmopriming, chemo priming and biopriming, were standardized based on the performance of seed quality attributes. Results revealed that the best priming temperature was 25±1 oC, the optimum duration of soaking was 48h, best osmotica was PEG 6000 @-1.5 Mpa, the best chemicals were KNO3 @1% or Ethrel 1000 ppm .All the physiological attributes such as first count germination, final count germination, Bartlett's Rate Index (BRI), Coefficient of velocity (CV) of germination, germination energy (GE), Mean seedling length, Mean seedling dry weight, Seedling vigour index -I and Seedling vigour index - II were significantly higher (91.67%,92.33%, 0.544, 73.54%, 85.50% , 31.68 cm, 11.69 mg, 2929 and 1081, respectively) in KNO3 primed seeds. KNO3 primed seed recorded significantly higher Total dehydrogenase activity, total soluble protein, amylase activity, catalyse (CAT) activity, peroxidise activity (POX) and lower Electrical conductivity and total soluble sugars in the seed leach ate. The total soluble seed protein profile of native PAGE and SDS PAGE had revealed . Priming induced proteins were expressed in all the priming treatments which can be employed as a markers for optimum priming. Esterase and peroxidise isozymes expression also varied in primed and unprimed seeds. Primed seeds expressed specific is forms of isozymes compared to unprimed. Among priming treatments, higher (88.63%) FEM, BRI (0.479), PSP (86.13) and PDW (2.06 g) was indicated in seeds primed with KNO3 @ 1% and it was lower (67.50%, 0.391, 53.13% and 1.77 g) in unprimed seeds (control).In order to test the longevity of primed seeds during storage, primed seeds were sealed in various packaging material and stored at ambient and refrigerated conditions. Among storage treatments, seeds stored under refrigerated condition showed slightly higher germination and field emergence (82.25% and 80.58%) compared to ambient condition (81.67% and 79.50%), respectively. Results indicated primed seeds can be stored for a short period of 80 days under ambient conditions of Bangalore without significant reduction in seed quality attributes. However, refrigerated storage is advised for long term storage of primed cucumber seeds.

Post Harvest Technology

Title: Mineral composition and anatomical changes in Alphonso mango during storage with reference to internal breakdown (1992)

K.Haribabu, UAS, Bangalore, Guide : Dr.Shantha Krishnamurthy

The investigations were made on (i) Physico-chemical changes, mineral composition, histological and histochemical changes, during growth, development, storage and ripening and (ii) the effect of pre-harvest spray and post harvest spray and post harvest infiltration with calcium chloride on the above mentioned changes and also on the occurrence of internal breakdown (spongy tissue) in Alphonso mango. Fruit length, diameter, weight of fruit, pulp and peel increased gradually up to 45 days, followed by a sudden increase to maximum of 90days and pre harvest spray of calcium at 5000 and 10000 ppm significantly enhanced this increase. The effect of post harvest calcium infiltration was more prounced in delaying ripening, reducing the weight loss and firmness, increase of peel colour, pulp colour (carotenoids), sugars and decrease of acidity during storage as compared to pre harvest sprays. Analysis of calcium (Ca), Potassium (K), Sodium (Na) and Phosphorus (P) during growth and development, in general indicated reduction in the concentrations from 15 days to 90days after fruit set both in the peel in the pulp. The distribution of minerals in 6 different pulp tissues during ripening indicated that Ca content was maximum in the basal pulp portion as compared to middle and apical parts. The distribution of minerals in 6 different pulp tissues during ripening indicated that Ca content was maximum in the basal pulp portion as compared to middle and apical parts. Further, the pulp towards the peel showed more Ca than in the pulp towards endocarp. In case of K & P, it was more in the pulp nearer to endocarp and no change was seen from base to apical portion of the pulp. Spongy tissue affected pulp showed low Ca (19.25 mg), high K (726 mg), P (135.6 mg) & Na (45 mg) as compared to 41.8 mg Ca, 501 mg K, 85 mg P & 37 mg Na in the healthy tissue. Both the pre & post harvest Ca treatments had no effect on spongy tissue development. Histochemical studies indicated the appearance of starch granules after 60 days of fruit set in all the tissues of the fruit & maximum accumulation was found after 90 days of fruit set. In pre harvest sprays of Ca, the cell of the fruit were bigger in size with more starch grains & degradation of these grains was delayed during ripening. Ripening process was initiated in monocarp region. Development of spongy tissue was found in pulp near endocarp. The cells in this were small, globular & thick walled with numerous starch grains.

Title: Studies on low temperature storage of guava (*Psidium guajava* L.) (1996)

G.Ramesh, UAS, Bangalore, Guide : Dr.Shantha Krishnamurthy

A detailed investigation was made on the effect low temperature storage on shelf life and quality of 3 cvs. of guava viz., Allahabad Safeda, Luckow-49 and Arka Mridul a selection released from IIHR. Fruits were harvested at physiologically mature stage. Uniform size fruits with green colour were packed in 100 g polybags and stored at 24 ºC with 45% RH (RT). Studies on changes in physic-chemical composition rate of respiration and ethylene release were made periodically both at RT and LT storage. The total weight loss range from 3-4% at RT storage as compared to less than 2% at LT storage. Firmness of the fruit at harvest in the 3 cultivars ranged from 21.6 to 26.5 kg/cm2 and it decreased to 3.5kg/cm2 at the end of storage. Rate of respiration increased from 49-180 mg CO 2 in Allahabad Safeda and 148-254 mg CO2/kg/hr in Lucknow-49 after 9 days of storage and in Arka Mridul it enhanced from 90-275/mg/kg/hr after 7 days. Acidity decreased slightly in all the cultivars i.e., the range was from 0.4-0.68 to 0.25-0.56. a slight increase in Vit.C was observed during storage in all the cultivars. Lucknow -49 had the maximum Vit.C content of 260 mg/100 g as compared to 180 mg in the other 2 cultivars. A total soluble solid was in the range of 10.8-14.6 and there were minimum changes during storage both at LT & RT. Lucknow-49 and Arka Mridul. Yellowing of the fruit at RT was faster (4 th day) in Lucknow-49 and Arka Mridul as compared to Allahabad Safeda (7th day). At LT storage Allahabad Safeda remained firm and green for 18 days and it could be kept for a period of 22 days. Allahabad Safeda and Lucknow-49 could be kept for 15 days.

Title: Storage studies on sapota (*Manilkara achras*) cv. Cricket ball (1996)

H.Nagaraja, UAS, Bangalore, Guide: Dr.Shantha Krishnamurthy

An investigation was made to study the optimum low temperature for extending the shelf life of sapota cv. Cricket Ball. The fruits were stored at 29+1, 25+1, 20+1 and 15+1 ºC and the effect of temperature on ripening. Shelf life and physic-chemical changes were studied. Fruits at optimum mature stage and of medium size were manually harvested and used in the study. The fruits were packed in ventilated polybags and stored at the above temperatures and RH ranged from 40-75%. Periodical observations on changes in weight loss, respiration, firmness, total soluble solids, acidity, Vit.C, reducing and non-reducing sugars, rate of ripening and sensory evaluation of the ripe fruit were made at each storage temperature. The weight loss was 7.5% in 13 days at 29 ºC storage and it decreased to 2- 3% after 14-23 days at other temperatures. The firmness at harvest was more than 12 kg/cm and it decreased to 2.22 kg/cm2 at the end of storage. A slight decreased in TSS from 23.6 to 20.0 was observed. Negligible changes were seen in acidity (0.13%), Vit.C (5 mg/100 g) reducing sugars (8.2-8.8%) and total sugar (13.1-13.5%). Rate of respiration showed an increase from 58 mg to 105 mg CO2/kg/hr at the peak stage after 7 to 8 days of storage followed by a decline to 40 mg CO2/kg/ht at the full ripe stage. The shelf life of the fruit was 13 days at 29 and 25 ºC weight 95% of ripe fruits whereas at 20 and 15 ºC it was 17and 23 days respectively.

Title: Effect of shrink film wrapping on storage behavior of Banana (*Musa paradisiaca* L.) cv. Robusta (1996)

M.K.Honnabyraiah, UAS, Bangalore, Guide : Dr.Shantha Krishnamurthy

Investigations on the effect of shrink film wrapping in Robusta banana stored at room temperature (RT 25+ 1 ºC with 45% RH) and low temperatures (LT 15 ºC with 65% Rh) on shelf life and quality was studied. Banana hands with 6-8 fingers, of optimum maturity were wripped in shrink films BDF-2001 (100 guage) and D-955 (100 guage) and stored at RT and LT. periodical observations were recorded on weight loss, respiration rate, firmness, other chemical changes, shelf life and organoleptic quality of the stored fruit. The weight loss at RT was 11% in unwrapped fruits as compared to 2.5% in film wrapped fruits and this was reduced to 1-4% at LT storage. Fruit firmness decreased from 12.5 kg to 2.5 kg/cm during 14 days of storage at RT but LT this decrease was seen after 35 days of storage. Ripe fruits in film wrapping retained more firmness (3.5-4.5 kg/cm) both at RT and LT. Starch content was more in the film wrapped fruits (2.1-4.3%) at LT storage and less (1.8-2.1%) at RT storage. The increase in reducing sugar content was from 0.6 to 9.7 to 11.0% and total sugar content was in the rage of 13.0-17.5%. The rate of respiration increased from 14 mg to 145 mg CO2/kg/hr followed by a decline in the unwrapped fruits and the rate was reduced significantly in film wrapped fruit. The shelf life of unwrapped fruits was 14 and 30 days at RT and LT storage respectively. This was enhanced to 21 to 23 days by rapping with BDF and D 955 films at RT and 30 to 37 days at LT.

Title: Studies on growth, development and storage of Pomegranate (*Punica granatum* L.) cv. Ganesh (1997)

S.Nanda, UAS, Bangalore, Guide : Dr.Shantha Krishnamurthy

The investigations on (i) Pattern of growth and development to determine harvest maturity of Pomegranate fruit cv. Ganesh grown in two agro-climatic conditions viz., Bangalore & Bijapur (ii) determination of optimum glow temperature for storage for maximum shelf life(iii) the quality of the fruits stored at 8,15 and 25 ºC and (iv) the histological changes in the fruits during growth, development and storage were made. The salient findings were the fresh weight, length, breadth and volume of the fruit increased with growth of the fruit. The specific gravity of the fruit increased up to midgrowing period followed by a decline towards maturity. The rind weight increased with decrease in rind thickness. The maximum juice content of 122-165ml per fruit was observed at the harvesting period. There was a significant respiratory peak (113 mg CO2/kg/hr) a few days after fruit set followed by a decline at harvesting stage (47 mg/kg/hr). There was a decrease in acidity and increase in ascorbic acid, total soluble solid and sugars. The fruits reached harvest maturity after 105-110 days of fruit set having a specific gravity less than 1.0 bright greenish yellow to full yellow coloured rind with a shining waxy surface, opening of the calyx and deep red colour soft juicy arils. Histological changes during growth showed increased thickness of epidermis and cuticle. Size of the cells below the epidermis increased and starch grains started accumulating after 60 days of fruit set. During storage, lateral compression of cells in the rind of unwrapped fruits was observed resulting in desiccation of the fruit. There were significant differences in all the parameters studied during growth storage between the cv. Ganesh grown in two different agro- climatic conditions.

Title: Studies on growth, development and storage of post harvest handling of Custard Apple (*Annona squamosa* L.) (1997)

Vishnu Prasanna, UAS, Bangalore, Guide : Dr.Shantha Krishnamurthy

Investigations on physico-chemical and histochemical changes during growth, development, ripening and storage were made in custard apple fruit cv. Balanagar to determine maturity indices for harvest and to extend the shelf life without affecting the quality. (i) Development of yellow colour between aeroles, age of the fruit (100-110, days after flowering), specific gravity of about 1.00, firmness of 3.00-3.50 kg/cm, moisture content of 67-695,dry matter content of 31.0-33.0%, sugars of 3.5-54.0%, starch of 12- 14% could be used as reliable maturity indices for the harvest of the custard apple fruits. Studies on the storage of harvest maturity on post harvest behaviors indicated that fruits harvested after 90, 100 and 110 days after flowering required 7,5 and 4 days for ripening. Only 50-60% of the fruits were ripe with less taste when harvested after 90 days. Highest soluble solids (27.8), and total sugars (14.0%) with 0.28% acidity were recorded in fruits harvested after 110 days of flowering. Among the storage treatment, precooling of the fruit was advantageous in retention of texture during low temperatures storage. Shelf life of the fruit was extended 2-3 folds when they were stored at 10 and 15 ºC. Histochemical changes during growth indicated increased starch granules after 60 days of growth till maturity. Degradation of starch granules were observed during ripening. In fruits held at 4ºC due to chilling injury, this was not observed.

Title: Development of beverages from Sweet Orange (*Citrus sinensis* Osbeck) using sugar and sugar substitutes (2010)

C.N.Byanna, UAS, Bangalore, Guide : Dr.I.N.Doreyappa Gowda

Investigation on “Development of beverages from sweet orange (Citrus sinensis Osbeck) using sugar and sugar substitutes” was carried out at processing laboratory of Division of Post Harvest Technology, Indian Institute of Horticultural Research, Bengaluru during2008-09 and 2009-10. Sweet orange beverages viz., RTS beverage, nectar, squash, and blended beverages with kokum and pomegranate were prepared with different recipes. The products were subjected to chemical analysis and organoleptic evaluation at initial, 90th and 180th day of storage at ambient conditions RTS with 18 percent juice, 15 o Brix and 0.3 per cent acidity, Nectar with 24% juice, 15 oBrix, 0.3 per cent acidity, Squash with 35 per cent juice, 40 oBrix, 1.0 per cent acidity, sweet orange : kokum (88:12), 15 per cent juice, 15 oBrix, 0.3 per cent acidity, sweet orange: pomegranate (50:50), 15 per cent, 15 oBrix, 0.3 per cent acidity were found to be superior recipes organoleptically. These superior recipes were used to prepare the products with sugar substitutes based on the sugar equivalents. Sugar substitutes were used in place of sugar for preparation of products. These products were subjected to chemical analysis and organoleptic evaluation over a period of 180 days starting from initial stage and subsequently at 3months interval. RTS with fructose followed by RTS with 50 per cent sucrose + 50 per cent fructose and RTS with 50 per cent sucrose +50 per cent sucralose, Nectar with fructose followed by nectar with 50 per cent sucrose + 50 per cent sucralose,nectar with sucralose and nectar with 50 per cent sucrose +50 per cent fructose ; Squash with sucralose, squash with 50 per cent sucrose + 50 per cent sucralose, squash with 50 per cent sucrose + 50 per cent fructose and squash with fructose ; Sweet orange : kokum (88: 12) with 50 per cent sucrose + 50 per cent fructose followed by 50 per cent sucrose + 50 per cent sucralose and fructose ; Sweet orange : pomegranate (50:50) with 50 per cent sucrose + 50 per cent fructose and 50 per cent sucrose+ 50 per cent sucralose were rated as superior recipes based on over all acceptability scores in sensory evaluation. In general, TSS, reducing sugars, titrable acidity and non-enzymatic browning increased, while pH, total sugars, non- reducing sugars, ascorbic acid and antioxidant activity decreased during storage in all type of beverages.

Title: Studies on processing and preservation of minimally processed Onion (*Allium cepa* L.) (2015)

S.Bhuvanewari, Gandhigram Rural Institute, Tamilnadu, Guide: Dr.C.K. Narayana

Onion is one of the most important vegetables, valued for its pungency. It also acts as a spice, as much as it can provide an aromatic undertone to various dishes, without being a major ingredient. The study has been conducted to identify suitable cultivar, effect of cut, dip treatment, packaging and storage condition for minimal processing of onion. In addition, a portable Onion dicing tool was developed to overcome the drudgery and improve the efficiency of cutting. Onion cultivars Atka. Sona, Arka Vishwas, Arka Swadista and Arka. Kalyan released from Indian Institute of Horticultural Research (IIHR), Bengaluru, India were selected based on the desirable characteristics for minimal processing. Onion cv. Arka Sona dipped in calcium lactate (2%) was found to have best shelf life of 14 followed by cv. Arka Swadista and cv. Arka Vishwas each had a shelf life of 13 days and with a least shelf life of 9 days in cv. Arka Kalyan. The cv. Arka Sona dipped in calcium lactate (2%) had been selected for further packaging and storage studies. The onion samples were packaged in PP bag of 25µm, 50 µm and 75µm thickness and stored at 8±1ºC, 85% RH; 10±1ºC, 83% RH; and 12±1ºC, 81% RH. The samples packaged in 50 µm thick PP bag and stored at 8±1ºC, 85% RH recorded a maximum shelf life of 14 days and found to be the best. It also had less weight loss (2.51%), more firmness (1.50 kg/cm2), better pungency (pyruvic acid content 7.61 µmol/g) and lower respiration rate (1.2 ml CO2/kg-h) at the end of the storage period. The samples were found microbially safe as total CFU was found nil in 102 dilution at the end of the storage period of 14 days when compared with control. In addition, samples retained flavour (propyl disulphide 0.342%) and had an acceptable sensory score of colour (3.85), texture (3.82), pungency (3.80) and taste (3.79) in 5 point scale.In order to overcome the drudgery, a portable onion dicing tool working on the principle of levers was fabricated and compared with manual cutting methods. The tool was capable of making 9 dices each having size 8 X 8 mm. The cutting efficiency of dicing tool was found to be 97.23%. The cost of the dicing tool was worked out to Rs. 5000/ with the average capacity of 60kg/h. It was also recorded a saving in operational cost (44%) and time (71%) over conventional cutting methods.

Title: Extension of storage life of guava using ethylene inhibitors and its integration with modified atmosphere packaging (2021)

Sachin A. J., IARI, Dr. D. V. Sudhakar

Guava is one of the most delicious and nutritious fruits, liked by consumers for its refreshing taste and pleasant flavour. It is a climacteric fruit that ripens very rapidly after harvest under ambient conditions and thus highly perishable. Postharvest life of guava fruits can be enhanced by employing different post- harvest treatments followed by storage at optimum temperature or through manipulation of ripening related genes by recombinant DNA technology. In the present investigation different concentrations of three ethylene inhibitors viz. salicylic acid (SA), sodium nitroprusside (NO donor) and 1-methylcyclopropene (1-MCP) were applied on 'Arka Mridula' guava fruits and stored at three different temperatures 8 □, 12 □ and RT. Among the different post-harvest treatments, 1-MCP (500ppb) treated fruits was found to be effective in extending the storage life of guava fruits for three, four weeks at 12 □ and 8 □ respectively and seven days at ambient storage conditions followed by SNP (1.5mM) and SA (3mM). 1-MCP (500ppb) had exhibited minimum PLW, maximum firmness, with greater retention of green colour and higher quality parameters by the end of storage period at different storage conditions. Concurrently, the effect of different packaging films viz. polypropylene (PP), low density polyethylene (PE) and Cryovac® PD-961 (PD) with and without micro- perforation in extending the shelf life of guava fruits was investigated. The results revealed that, the non perforated polypropylene (PP-NP) packaging had effectively maintained optimum modified atmosphere conditions and resulted in least PLW, higher fruit firmness and had retained all the quality parameters of guava at 12 □ and room temperature conditions. In order to reap benefits of both the technologies, they were integrated and applied at three different storage temperatures. Among all the combinations, 1-MCP treatment integrated with non- perforated PP film was found to be significantly effective in extending the storage life and maintenance of different quality attributes of guava fruits. Gene expression studies with two ethylene mediated ripening genes viz. expansin and ACC synthase has revealed the close association between the ethylene production and ACC synthase activity, and due to 1-MCP action ACC synthase expression was down regulated during 14 days of storage. While expansin expression was down regulated till 14 days of storage, a surge in expansin expression was recorded after 21 days of storage which can be directly correlated with the physical texture breakdown noticed under 12 □ storage.

Plant Physiology & Biochemistry

Title: Isolation and characterization of polygalacturanase inhibitor protein from chillies (*Capsicum annuum* L.) (2004)

C.Thimma Reddy, UAS, Bangalore, Guide: Dr.S.Shivashankar

The experimental study undertaken for "Isolation and characterization of polygalacturonase-inhibiting protein from chillies affected by anthracnose fruit rot" is described in this thesis. Chilli fruit PGIp was purified by ammonium sulfate fractionation, gel-filtration on Sephadex G-150 column and ion-exchange chromatography on DEAE cellulose. The degree of purification achieved was 24.08–fold in resistant variety and 20.96 in susceptible variety. The PGIP preparation was homogenous with one major bandas revealed by native PAGE. The molecular weight of chilli PGIP of both resistant and susceptible variety determined by SDS-PAGE suggested that chilli PGIP is a single polypeptide chain of 37kDa molecular weight. The chilli PGIP was found to be stable in the pH range of 3.0-9.0. The chilli PGIP was maximally active at 60 ºC although the activity was retained up to 90 ºC. By using increasing doses of the purified chilli PGIP, it was possible to inhibit up to 90% of Colletotrichum capsiciii polygalacturonase activity. Chilli PGIP demonstrated high level of specificity for polygalacturonase from Colletotrichum capsicii when assayed against the polygalacturonases from other five fungi. The chilli PGIP from both resistant and susceptible varieties were found to be similar in their physic-chemical characteristics. The high specificity and the degree of inhibition obtained with chilli GPIP are pointers to the effectiveness of PGIP in avoiding pathogen in gress.

Title: Physiological and biochemical basis of internal breakdown in Alphonso mango-a study on the roles of ethylene, calcium and oxidative stress (2006)

J.E.Nagamani, Kuvempu University, Shimoga, Guide: Dr.S.Shivashankar

Reduction in ethylene evolution in the spongy tissue was mainly due to the reduced activity of ACC oxidase leading to the accumulation of ACC. This might have lead to the reduced ripening of the tissues resulting in sponginess. There are many softening enzymes and the major ones are polygalacturonase, pectin methyl esterase and cellulase. Results indicated the lower softening of the tissues in the spongy tissue when compared to the healthy tissues. In climacteric fruits like mango respiratory raise during ripening is very important for proper ripening and development of good aroma. The ethylene hormone strictly controls this. In this direction an attempt has been made to assess the respiratory enzymes to understand whether they are affected due to the formation of spongy tissue. Activities of starch and sugar metabolising enzymes are decreased in spongy tissue leading to the lower sugar formation. Study of antioxidative enzymes in spongy tissues. Oxidative free radicals have been associated with many membrane related disorders. Lipid peroxidation is one of the important effects of free radicals damage. Oxidative free radicals combined with metallic ions like ferrous results in greater damage due to the production of highly reactive hydroxyl radicals. Free radicals are usually scavenged by the antioxidative enzymes like SOD, catalyse, peroxidase, polyphenol oxidase, ascorbate peroxidase, glutathione reductase etc., However, if there is damage to the free radical scavenging mechanism then there will be an accumulation in free radicals resulting in the damage of membrane. As a measure of oxidation products MDA has been analysed and antioxidative enzymes like super oxide dismutase, peroxidase, catalyse, polyphenopl oxidase have been estimated in different samples. Spongy tissue has higher oxidative products and lower activity of antioxidative enzymes indicating the lipid peroxidation of membranes. Minerals are essential for the normal functioning of membranes and also for the maintenance of turgor of the cells and for enzyme activities. In this regard, minerals like Zn, Fe, Ca and Mg are estimated in spongy and healthy tissues. Most of the minerals except Ca did not show any significant differences between the tissues. Calcium showed a marginal reduction in spongy tissue.

Assessment and quantification of the impact of elevated CO2 and temperature on Tomato under different climate change scenarios (2016)

Mamatha H, Jawaharlal Nehru Technological University, Hyderabad, Guide: Dr. N.K. Srinivasa Rao

Tomato is an important. vegetable which meets the dietary nutrient and antioxidant requirements of diverse populations. Being a C3 crop it is likely to be influenced by increased CO 2 concentrations under climate change situation. This study was conducted to investigate the effects of elevated CO2 on overall physiology of tomato (Lycopersicon esculentum Mill) cv. Arka Ashish under normal water supply and under water limiting conditions. The study also comprised of the effect of mild increase in temperature on physiology, growth parameters of tomato hybrid Arka Ananya and Yield prediction of different tomato growing district of Karnataka using INFOCROP simulation model. Increased assimilation rate, decreased stomatal conductance and transpiration rate were observed at elevated CO 2 concentrations. Lower total chlorophyll content was recorded at elevated CO2. Increased number of flowers and fruits together with higher fruit set led to higher fruit yield at both elevated CO2 concentrations. The fruits showed a lower content of phenols, flavonoids, ferric reducing antioxidant potential, total soluble solids, and titratable acidity in plants grown at elevated CO 2 as compared with the control. The plants grown at elevated CO2 had significantly higher Photosynthesis (PN) with decreased stomatal conductance (gs) and leaf transpiration rate (E) compared to plants grown at 380 ppm ambient CO2, irrespective of water supply conditions. Higher SOD and GR activity was observed at elevated CO2 compared to the plants grown at ambient CO 2 concentration. Increased number of fruits and fruit weight per plant were observed at elevated CO2 both at control and water stress condition.There was also a reduction in average fruit weight and total fruit yield per plant as the temperature increased from 27.6°C to 30°C. The data run through INFOCROP simulation model predicted reductions in yield of only 5% during rabi season of 2080, in Bangalore rural and Kolar districts of Karnataka. During 2080 highest yield reductions of 26% was predicted in rainy (Kharif) and summer seasons.

Title: Phenotyping of tomato genotypes for high temperature stress tolerance (2020)

Geeta Biradar, UAS, Bangalore, Guide: Dr. R. H. Laxman

Lycopersicon esculentum Mill., is an important vegetable crop (Tomato) in most regions of the world and affected by high temperature stress at various stages of its growth. Likely increase in periodicity of high temperature episodes under climate change conditions would further affect the tomato production. To sustain productivity and yields under climate change situations, there is an urgent need to develop suitable cultivars as an adaptation strategy. For this endeavour, identification of high temperature (HT) tolerant lines for crop improvement is a prerequisite. Hence the present study comprised three experiments. The first experiment was carried out to screen 52 tomato genotypes at seedling stage using temperature induction response (TIR) technique. Second experiment was carried out by screening 49 tomato genotypes in the poly tunnel under field conditions at whole plant level. Third experiment was carried out by taking relatively tolerant and susceptible genotypes at four true leaf stage identified from the first experiment. Later, the important traits responsible for imparting HT stress tolerance in tomato were identified for further screening and crop improvement programme.In TIR technique two day old seedlings were subjected to an initial induction treatment i.e., gradual temperature increase from 33-43°C for 3 h followed by 50°C for 3 h as challenging temperature. Wide variability was seen for seedling survival and vigour. In genotypes IIHR-2202, Arka Ananya and Arka Rakshak seedling survival was as high as 90%, while IIHR-329, IIHR-371, Vaibhav and IIHR-335 showed least reduction in growth and also had better seedling vigour index. Of the 52 genotypes, 21 were identified as tolerant, 12 moderately tolerant and 19 susceptible. The TIR technique is simple, quick and less expensive than whole plant screening. Hence, it could be used by plant physiologists and plant breeders for screening seedlings at an early stage in the phenotyping and crop improvement programmes.At whole plant level the HT caused reduction in net photosynthesis rate (PN), stomatal conductance (gs), transpiration rate (E) and photochemical efficiency of PSII (Fv/Fm). Under HT condition, changes are observed across genotypes in membranes stability, concentration of osmolytes, relative water content (RWC), light harvesting pigments and yield traits. Further the genotypes were categorized into tolerant, moderately tolerant and sensitive groups based on the physiological and biochemical traits using multivariate analysis such as principle component analysis (PCA) and cluster analysis. The identified tolerant genotypes, IIHR-2330, IIHR-2337, IIHR-369, IIHR-335, IIHR- 2202, Abhinava and Arka Vikas showed higher PN, Fv/Fm, electron transport rate (ETR II), RWC, membrane stability index (MSI), number of fruits per plant and fruit weight per plant. These traits are found to be most important for temperature tolerance there by improved yield. An increase in the activity of superoxide dismutase (SOD), peroxidise (POD) and catalase (CAT) was observed across the genotypes. The accumulation of sugars such as sucrose, inositol, fructose and glucose was higher in all the tomato genotypes subjected to induction treatment. The genotypes Abhinava, Arka Rakshak, Arka Ananya, IIHR-335, IIHR-329 and IIHR-369 showed higher thermotolerance with increase in osmoprotectants and by maintaining a strong antioxidant enzyme system.

Biotechnology

Title: Studies on the beneficial microbial association in Brinjal (*Solanum melongena* L.) (2000)

Jennifer Lolita, Bangalore University, Guide : Dr.Sukhada Mohandas

Nitrogen fixing bacteria were isolated from the endorhizosphere and phylloplane of Solanum melongena L. cultivars Arka Shirish, Arka Keshav, Arka Kisumakar, Pusa Purple long and 17 IIHR accessions. Nitrogen fixation was recorded by acetylene reduction bioassay. The bacterial colonization in the endorhizosphere was recorded by electron microscopy and on the rhizosphere by scanning electron microscope. The bacteria were cyst forming, gram positive, motile and having polar flagellum. Transverse sections of the root of brinjal revealed the colonization of the bacteria in the inter and intracellular spaces of the cortex. On the phylloplane also the bacterial colonies were present in large number. Using several physico-chemical tests and API kit, the bacteria were identified as Bacillus polymyxa which is a nitrogen fixer and phosphate solubiliser Bacteria produced 114.7 pg mole-1of zeatine riboside in culture in 24 hours period. The amount of gibberellins produced was 0.08 ug ml -1 in the same period. Brinjal plants treated with the bacteria produced higher Zeatine riboside (65.66 pg g-1 fresh weight) compared to untreated control plants (16.77 pg g-1 fresh weight) and 61% higher gibberellins than controls. The beneficial effects of the bacterial colonization were tested in pots under sterile conditions by inoculating the same to the crop at seed germination stage. The bacteria improved seed germination, enhanced plant growth, plant height and enhanced flowering, Under field conditions also the inoculation of the bacteria helped in improving plant growth, flowering and yield.

Title: Utilization of VAM fungi for improving the establishment of micropropagated plants (2002)

Sowmya, Bangalore University, Guide : Dr.Sukhada Mohandas

In the present investigation, the utilization of vesicular arbuscular mycorrhizal (VAM) fungi in the establishment of micropropagated plants of Bacopa monnieri (L) Pennell and banana, Musa paradisica. L. cv. Dwarf cavendish was studied. Bacopa monnieri L. Pennell is an important medicinal plant used in Ayurvedic, Siddha, Unani and modern system of medicines. The available reports indicate their importance as memory vitalizer and nervine tonic with special reference to their saponin content. From the present study, the obtained results indicate that, vesicular- arbuscular mycorrhizal fungi Glomus mosseae and Glomus fasciculatum could colonize well in both normally raised and micropropagated plants. The micropropagated plants of Bacopa monnieri responded excellently to the VAM inoculation in the pots which compared with the normal plants. These mycorrhizal plants were compared with uninoculated control plants. The efficiency of Glomus mosseae and Glomus fasciculatum helped the micropropagated Bacopa plants in availing the good growth, improved physiological condition by attaining the better establishment in the pots. The establishment of mycorrhizal plants is expressed by increase in their biomass and bacoside-A content. This is a first report of utilization of VAM fungi in micropropagated Bacopa plants. Banana is an important commercial fruit crop. In the present study the two Glomus species, Glomus fasciculatum and Glomus mosseae benefited the banana plant growth in pots and establishment in the field. Both single inoculation and dual inoculation with PSM, Trichoderma viride gave better results compared to uninocualted control plants. The results of this study clearly indicate that micropropagated banana plantlets showed better establishment when they are raised in the presence of VAM fungi from pots to field condition. By utilizing these VAM fungi there can be improvement in the cultivation of both medicinal and horticultural plants propagated in vitro.

Title:Studies on in vitro propagation of Chrysanthemum (*Dendranthema grandiflora* tzvelev) (2006)

Bindu Panicker, UAS, Bangalore, Guide : Dr.Pious Thomas

The investigations were carried out with the objectives of optimizing an in vitro propagation protocol for the naturally shy propagating chrysanthemum, detecting the presence of any covert endophytic bacteria associated with in vitro chrysanthemum cultures, isolation and identification of covert endophytes, evaluating the effect of plant growth promoting rhizobacteria and VAM during acclimatization and subsequent field performance of micropropagated chrysanthemum, and testing the micropropagated and conventionally propagated plants in the field. The experiments were carried out using chrysanthemum varieties Arka Swarna and Arka Ravi and there were eight major experiments. The salient findings of the study included: (i) Rapid propagation of shy- suckering chrysanthemum varieties Arka Swarna and Arka Ravi was accomplished using shoot tip and nodal microcuttings;), (ii). Higher level of growth regulators reduced the net propagation rate besides causing more rampant bacterial contamination, (iii) Indexing the cultures through could detect the covert contaminants, which was rampant in chrysanthemum cultures, (iv) Endophytic bacteria associated with the cultures of chrysanthemum were isolated and were identified based on 16S rDNA sequence homology analysis. Curtobacterium flaccumfaciens pv. basellae was a common endophyte of Arka Swarna cultures and Enterobacter hormaechei subsp. steigerwaltii and Methylobacterium sp were isolated from Arka Ravi cultures, (v) Cleansing the cultures from covert contaminants was accomplished through disinfection treatment of shoot tips followed by challenge with single antibiotics (gentamycin, streptomycin or cefazoline) at 50-100 mg L-1 for one month, and selection of the clean cultures through repeated indexing of tissue and medium for 2-4 passages; (vi) Among the four bioinoculants (VAM, phosphate solublising bacteria, Azospirillum and Bacillus pumilus) tried singly or in combination, combined inoculation with VAM, Azospirillum and PSB at 40 g Kg-1 enhanced the flower yield per plant in Arka Swarna. In Arka Ravi, single inoculation with VAM at 40 g Kg-1 enhanced the yield per plant. (vii) Bio- inoculants as such did not improve the % survival during acclimatization in both the varieties, (viii) Micropropagated plants showed no deviation in the growth pattern and performance in the field condition.

Title: Generation of Single Chain Antibody Fragments (SCFV) for detection of *Ralstonia solanacearum* causing bacterial wilt of tomato (2006)

K.N.Chandrashekara, Kuvempu University, Shimoga, Guide : Dr. Akella Vani

The bacterial wilt disease is widespread causing severe loss on many economically important solanaceous vegetables in India in general and Karnataka in particular. Wilt symptoms caused by several pathogens such as fungal pathogen (Fusarium, Rhizoactonia and Phythium), insect damage (shoot borer and nematode damage) and bacterial wilt caused by Ralstonia solanacearum show same symptoms. Hence the present study was undertaken to develop a single chain monoclonal antibodies (scFv) which is cost effective and easy to handle both by researchers and farmers to detect the pathogen at very low concentrations. Fifty seven isolates from different host plants viz., tomato, potato, brinjal, bird of paradise, capsicum, coleus and davana from different geographical locations of Karnataka and different states of India (Himachal Pradesh, Andhra Pradesh, Kerala, Maharastra and Orissa) were isolated. This is the first report of Ralstonia solanacearum isolated from davana and coleus crop. Phage Display Technology was used in the present study to generate scFv. ScFv monoclonal antibody was developed against both virulent and avirulent strains of Ralstonia solanacearum with very high specificity. These antibodies detected as few as 10 cells of the bacterium in an infected tissue. This is the first time that single chain antibody were developed against race-1 biovar – III of Ralstonia solanacearum. Amplification with OLI1 & Y2 and Y1 & Y2 primers further confirmed that the isolates were indeed Ralstonia solanacearum. All the 57 isolates were determined as belonging to race-1, biovar-III on the basis of their pathogenicity to infect different plant species and their inability to infect mulberry and banana. Three SSR primers were developed against Ralstonia solanacearum by using the ‘Tandem Repeats Finder Program’ and were used for fingerprinting the bacterium. The primers gave highly polymorphic bands. It was evident that the fingerprinting pattern was unique and suggested that the bacterial genome also carries repeats of genomic segments which were as many as 13 repeats in a single genome. DNA fingerprinting of all 57 isolates was carried out to study variability of the strains with respect to host plant and geographical location. This is also first time that a highly specific dipstick based nucleic acid detection kit was developed for any pathogen.

Title: Isolation, cloning and characterization of chitinase gene from entomogeneous fungus *Nomuraea rileyi /Metarhizium anisopliae* (2006)

C.Suneetha, Kuvempu University, Shimoga, Guide : Dr.J.B.Mythili

Crop losses due to pathogens results in substantial reduction in potential crop production annually. Conventional breeding for resistance to these diseases has not been very successful. Hence genetic engineering approach to introduce specific genes especially chitinase that could offer resistance to various fungal pathogens is being widely used in the development of transgenic crops with enhanced resistance to fungal diseases. Of late, there are reports on the variation in the efficacy of the chitinase genes isolated from various sources and chitinases isolated from the biocontrol fungus Trichoderma harzianum have been shown to be more effective. Keeping this in view, the study was aimed at "Isolation, cloning and characterization of chitinase gene from entomogenous fungi Nomuraea rileyi/Metarhizium anisopliae" Chitinase gene from M. anisopliae, was isolated through RT-PCR using primers designed from the sequences of Metarhizium obtained from NCBI site. The RT-PCR resulted in 1.5 kb product. This was cloned and sequenced. Sub cloning was followed to amplify the middle portion of the gene product. The primers were designed using the sequence data obtained from the forward and reverse sequences and the PCR amplification resulted in 875 bp Product. The sequence with and without introns (1275bp) showed very high homology of 90-99% to chitinase sequences from Metarhizium species while, 70-90% homology with other fungal chitinase sequences including Trichoderma, which have already been deposited in the NCBI database. The full length 1275bp chitinase gene encodes 425 amino acids with the potential chitin binding domain which is conserved across the entomopathogenic fungal species and amongst the class V chitinases of various fungal species. The gene was then cloned into binary vector pBIN by directional cloning method and was mobilized into A. tumefaciens strain LBA 4404 through triparental mating technique. The gene construct containing chitinase gene was used for transformation studies in tobacco. Transgenic tobacco plants confirmed for the presence of transgene were generated. Efficacy of the gene in inhibiting the pathogen growth was demonstrated through in vitro pathogen (Alternaria alternata) inhibition studies from protein extracted from tobacco plants transformed with the gene construct in comparison with the untransformed plants.

Title: In vitro studies on Banana cultivars (2007)

K.Y.Pratibha, Bangalore University, Guide : Dr.Sukhada Mohandas

Banana cvs. Rasthali (AAB) and Neypoovan (AB) are seriously affected by Fusarium wilt and the former is under the threat of extinction. In order to transform the cultivars with disease resistant genes a regeneration protocol using somatic embryogenesis was developed using immature flower buds. Immature flower buds cultured in vitro resulted in embryogenic callus formation in banana cvs. Rasthali (AAB) and Neypoovan (AB). The cv. Rasthali took less time to regenerate plantlets from somatic embryos compared to Neypoovan. Immature flower buds were found to be better to induce embryogenic callus than shoot tip explants in both the cvs. Histological observation of embryogenic callus of Rasthali, revealed the origin of somatic embryos to be multicellular. Interestingly the studies showed many differently shaped embryos at all t stages of development. Histological studies of germinated embryo showed well developed plumule with leaf primordia, coleoptile, cotyledon, provasculature and many root initials. Studies on histochemical changes during somatic embryogenesis in Rasthali showed the presence of higher amounts of biomolecular substances such as insoluble polysaccharides, proteins and nucleic acids during different stages of embryo formation. Direct secondary somatic embryogenesis was observed on the epidermal region of primary somatic embryos of banana cv. Rasthali. Secondary somatic embryos were formed in two different modes on primary embryos. Histochemical observation of secondary somatic embryos showed the presence of higher amount of total insoluble proteins, total polysaccharides and nucleic acids. Morphological studies of commercially propagated in vitro bananas in the field have shown the enormity of the off-types generated through micropropagation. Through field study 25 types of variants were identified and molecular markers for Dwarf variants and bunch variants which were the most common types of off-types causing heavy loss to the farmers were identified. Molecular markers like RAPD, SSR, ISSR, SRAP were used to identify the genetic variations in banana cv. Grand Naine. All the markers tried clearly showed polymorphism between the off types and the normal banana plants. Overall 9-17% polymorphism was observed in variants indicating the level of genetic change. The primers OPS-05 were redesigned as a marker for dwarf off-type and AR-14 for dwarf non-flowering.

Title: Generation of transgenic Tomato carrying Single Chain Antibody Fragments (SCFV) against viral expressed genes of tospovirus (2008)

K.Jagadish, Kuvempu University, Shimoga, Guide : Dr.Akella Vani

To generate transgenic tomato carrying single chain antibody fragments (Scfv) against viral expressed genes of tospovirus for resistance to tospovirus (PBNV) Through Plant body Mediated Approach. In the present study, the nucleocapsid protein gene (n-gene) of peanut bud necrosis virus (PBNV-Bangalore isolate) was amplified by RT-PCR using gene specific primers and was cloned into pUC18 vector for sequencing. The sequence revealed that it had an open reading frame of 831 bp (reported for the first time NCBI ACCESSION AAO17798) Monoclonal scFv antibodies against nucleocapsid protein of PBNV were generated by phage display technology. The antibody could detect PBNV in infected field samples when tested by dipstick assay where NUNC™ immune sticks were used as solid support onto which a capture antibody, scFv PBNVNP- 71 was coated. Arka Vikas by electroporation of apical buds. The transgenic plants obtained in T1 were further analyzed by PCR to check for the presence of scFvPBNVNP gene in tomato genome. Southern Blotting on the genomic DNA of 4 transgenic events revealed that the plants had one copy of the transgene each. Expression studies of single chain variable fragment (scFv) against the nucleocapsid protein of the PBNV were conducted. The plants expressing plant body protein, when challenged with viruliferous thrips, were resistant to PBNV, where as all the control plants were susceptible II) To generate transgenic tomato for resistance to tospovirus (PBNV), TLCV and combined resistance to PBNV and TLCV through pathogen derived resistance approach. In this study, the nucleocapsid gene of peanut bud necrosis virus was amplified by RT- PCR and the replicase gene of TLCV was amplified from infected leaves through PCR. The nucleocapsid gene of PBNV, replicase gene of TLCV and a transcriptionally fused chimeric construct containing the replicase gene and n-gene were individually cloned into pAV vector with plant promoter and transcription terminator. These constructs were transformed into four different cultivars of tomato namely, Arka Vikas, Arka Sourabh, Arka Meghali and Pusa Ruby. The plants, which were resistant for both the viruses showed the integration of both transgenes, when detected with individual probes in a separate experiments in Southern blot. Transgenic plants were also generated with plant expression construct for replicase gene of TLCV alone in order to authenticate the ability of the replicase gene to confer resistance to TLCV. Twenty-three plants out of 29 PCR positive plants in T1 and 32 out of 39 plants in T2 were completely resistant to TLCV when challenged with the viruliferous white flies. Southern blot analysis on four events revealed single copy integration. The PCR positive plants when challenged with the viruliferous white flies were resistant to the virus where as all the non-transgenic plants were susceptible to the virus.

Title: Generation of a transgenic plant carrying single chain antibody (scFv) gene against coat protein of *citrus tristeza* virus (2008)

K.B.Krishna Moorthy, UAS, Bangalore, Guide : Dr.Akella Vani

Acid lime (Citrus aurentifolium) belongs to the family Rutaceae and is one of the most important fruit crops cultivated throughout the world. Generating transgenic citrus for resistance to CTV appears to be the most promising control strategy because, control of vector under field conditions is very difficult.. This ScFv protein retains the antigen-binding potential and consists of only one polypeptide chain. In the present study the coat protein gene of Citrus Tristeza Virus was amplified by RT-PCR using gene specific primers and was cloned into pUC18 and was sequenced. The clone had an open reading frame of 651bp. The scFvCTVCP-41 monoclonal which performed better than other monoclonals, was transcriptionally fused to the gene coding for alkaline phosphate (ALP) to reduce the time required for ELISA. The resulting clone (anti CTVCPALP conjugate) had alkaline phosphatase activity and the antibody domain could detect CTV in infected field samples as well in glass house grown graft inoculated seedlings. The antibody domain could detect CTV in infected field samples when tested by DIBA where nitrocellulose membrane was used as solid support onto which scFvCTVCP monoclonal antibody was coated and CTV antigen was captured. Antibody based dip stick method was standardized for detecting CTV in infected field samples, where NUNCTM immune sticks were used as solid support onto which CTV antigen was captured and it was directly detected with anti CTVCPALP fusion protein. The plantibody construct was developed by subcloning the scFvCTVCP gene into plant expression vectors with NOS promoter and NOS terminator and the construct was electroporated into floral buds of citrus and apical buds of model plant. The T1 transgenic model plants when analysed by PCR showed the presence of scFvCTVCP gene in their genome. The Southern Blotting was carried out for PCR amplified products as well as on the genomic DNA of transgenic plants. A strong hybridization signal was obtained with labeled scFv indicating transgene integration. Expression of plantibody gene by transgenic plants was analysed by ELISA. The scFv plantibody protein was detected in the sap of 6 transgenic events (tomato was used as a model plant) out of 12 PCR positive events, while none of the control plants tested positive, indicating that these antibody fragments were functional.

Title: Biochemical and molecular changes in Banana cv. Neypoovan colonized with AM fungi (*Glomus mosseae*) and Trichoderma in the management of *Fusarium oxysporum* f.sp.cubense causing panama wilt (2008)

R.Manjula, Kuvempu University, Shimoga, Guide : Dr.Sukhada Mohandas

Fusarium wilt is regarded as one of the most devastating diseases of banana, affecting plantations in almost all banana-growing countries of the world. In the present study different BCAs, viz., Glomus mosseae, Trichoderma harzianum and Pseudomonas fluorescens were studied for the effect of their inoculation on Fusarium resistance, in banana cv. Neypoovan. The electron microscopic studies of the banana roots showed the colonization of BCAs in epidermis and cortex regions and were characterized by thick cell wall apposition, high electron dense material and accumulation of dense amorphous material along the cell wall . Colonisation of FOC was seen in the vascular region of the root as bright fluorescent colonies. Reduction in the number of bright fluorescent colonies of FOC was observed in BCA treated plants there by strengthening it. The results of ELISA assay revealed that FOC population had drastically reduced in biocontrol treated plants in both glass house and field conditions. the ten peroxidase isozymes observed in banana roots, biocontrol agent treatments induced PO 4, 5, 6, 8 and 10 isozymes at various stages after inoculation and these bands were not induced in control plant roots. In leaves only six peroxidase isozymes were observed with no significant difference among treatments. In PPO isozyme analysis, the BCAs treatment induced 4, 5, 6 and 7 isozymes in roots compared to untreated control. The intensity of these bands increased when challenged with FOC. In chitinase isozyme analysis, a unique CHIT 1 band was induced in the combination of G. mosseae + T. harzianum treatment which was not present constitutively in control plants and also had an increased intensity of all the isozymes compared to control.The study clearly demonstrated the ability of BCA to impart disease resistance and help in the management of Fusarium wilt of banana. It should be noted here that it was our observation that if Fusarium has already infected the suckers before precolonization with BCAs the plant would succumb to the disease as Fusarium being very aggressive would over power the colonizing organisms. A precolonization with BCAs for 90 days is a pre-requisite for deriving the benefit of structural, biochemical and molecular changes induced by the organism and eliciting defense response in the host plant.

Title: Agrobacterium-mediated transformation in Tomato and Chilli for fungal resistance (2008)

H.J.Rashmi, Kuvempu University, Shimoga, Guide : Dr.J.B.Mythili

Fungal pathogens are potent microorganisms and pose a threat to cultivated crops worldwide. Plant pathogens are known to destroy 12% of world's crops through disease epidemics. Tomato and chilli are the two important vegetable crops grown in the topical and subtropical parts of the world. These crops are attacked by various fungal, bacterial, viral and nematode pathogens and are known to severely affect the economic yields in these crops. As conventional breeding for resistance to early blight in tomato and fruit rot in chilli have met with limited success, alternative methods of diseases control by introduction of genes for disease resistance by novel biotechnological approaches have been tried. The study was aimed at transforming chilli and tomato using chitinase genes from different sources such as baculovirus, Trichoderma harzianum and Metarhizium anisopliae. Chilli, being a recalcitrant crop for regeneration, exhaustive treatments including use of ethylene inhibitors and phenyl acetic acid were tried during standardizing the protocol. Seven putative transformants of chilli with baculovirus chitinase gene were obtained. In tomato, two transformants each with baculovirus, T .harzianum and M. anisopliae chitinase gene were obtained and T .harzianum and M. anisopliae gene constructs gave rise to significantly greater percent of transformants as compared to baculovirus chitinase gene construct. The presence of the transgene was demonstrated through PCR, dot blot and Southern blots. Additionally, the expression of the gene was studied through chitinase and in vitro fungal inhibition assay in the transgenic plants.

Title: Breeding and development of molecular markers linked to bacterial blight (*Xanthomonas axononopodis* pv. dieffenbachiae) resistance in Anthurium (*Anthurium andreanum* Lind.) (2009)

Patil Manjunath Sidlingappa, UAS, Bangalore, Guide : Dr.C.Aswath

Studies on “Breeding and development of molecular markers linked to bacterial blight resistance in Anthurium (Anthurium andreanum) are presented here. Based on evaluation studies and economical characters varieties Sunglow, Simba, Meringue White, Acropolis and Fla Orange were recommended for commercial cultivation. Based on the screening studies IIHR selection Al was found to be moderately resistant recording low PDI (9.83%). IIHR selection A1 can be used as best general combiner for all the characters followed by Tropical. The crosses where IIHR selection Al was involved resulted in maximum spike length, leaf area, number of leaves and increased disease resistance over mid parent and check. Only three crosses (S x AO, T x AO and P x AO) exhibited significantly negative heterosis for disease resistance. DNA extraction yielded 40-1450 ug of DNA per gram fresh weight of leaf. High RAPD polymorphism was observed in the present material. Out of 110 decamer primers screened notably 6 primers (OPB 01, OPB 02, OPB 10, OPB 13, OPB 18 and OPB 20) have generated one or more polymorphic DNA markers and the frequency of polymorphic markers was as high as 74.80 per cent. From the results obtained about molecular markers for Xanthomonas resistance from the bulk segregant analysis, it was found that a marker OPB 01 at 600 bp, OPB 02 at 1200 bp, OPB 10 at 250 bp, OPB 13 at 750 bp and OPB 20 at 250 bp which is linked to bacterial blight resistance in Anthurium can be successfully used for rapid screening and identification of genotypes resistant to bacterial blight of anthurium. A dendrogram based on Squared Euclidian Distances grouped into two major subgroups.The first cluster consisted of resistant parent IIHR selection A 1 and resistant bulk which arouse from same node in the dendrogram while second cluster consisted of susceptible parent Pistache and susceptible bulk placed together in adjacent to the first cluster. This cluster grouping shows that resistance in F1 hybrids has inherited from the parent. Based on the RAPD data, Pair wise Squared Euclidian Distances was calculated for all the hybrids. The Pair wise Squared Euclidian Distances ranged from 13 to 48. A1 and A2 had a distance of 34. AlO and A12 hybrids had minimum Pair wise Squared Euclidian Distances of 13.

Title: Generation of transgenic plants resistant to tospo virus (2011)

S.Rashmi, Kuvempu University, Shimoga, Guide : Dr.Akella Vani

Tospoviruses are the plant disease causing pathogenic viruses, causing huge losses to crops depending on the stage at which infection occurs. They are found all over the world on many plant species, which are economically important. The present investigation was carried out to explore the possibilities of developing transgenic watermelon through recombinant DNA technology to develop resistance to Watermelon Bud Necrosis Virus (WBNV). Watermelon Bud Necrosis Virus, which belongs to serogroup IV of tospovirus, was reported very recently from India for the first time and is known to be spread by insect vector namely Thripsplami. There is no known source of resistance to the virus in the watermelon germplasm. In order to develop transgenics, cultivar Arka Manik, a popular watermelon variety, developed by Indian Institute of Horticulture, Hessaraghatta, Bangalore was used. This variety is reported to be highly susceptible to Watermelon Bud Necrosis virus. Attempt was made in the present study to achieve resistance through either a partial nucleocapsid protein or through its m-RNA which was predicted to be involved in RNA mediated gene silencing. Therefore, studies were carried out in the present investigation using a 583 bp of 3'partial WBNV-ΔN-gene with a high homology to published sequence. From this study, we were able to successfully produce transgenic watermelon plants using the Direct DNA uptake method namely electroporation. Transgenic plants produced in the present study were evaluated for the presence of transgene, its inheritance pattern in different generations, and were scored for resistance to the bud necrosis disease. The PCR products of these transgenic plants were subjected to Dot Blot hybridization analysis using the transgene specific DNA probe. Plants containing the transgene were selfed and homozygous plants were obtained in T 2 as evidenced by PCR of T3 plants. The progenies of 2 events in T2 and T3 plant population containing complete cassette were further analyzed by Southern blot hybridization studies using the labeled DNA probe of WBNV-N-gene for studying the copy number. One event (543-4-36-6) had a single copy and the second event (543-4-30-6) had 2 copies. Transgenic plants containing the complete cassette were studied for resistance to watermelon bud necrosis virus (WBNV) by challenge inoculation with viruliferous thrips collected from infected watermelon. There was a variation in their response to the level of infection in selfed transgenic plant populations. The reasons for variations in resistance have to be studied further. PCR analysis of event 543-4 and 542-12 across different generations showed that the transgene was inherited in a Mendelian fashion and stable homozygous line was obtained in the T2 segregant 543-4-36. T2 plants selections namely 543-4-30 and 543-4-36 and their T3 progeny showed resistance till fruit set, indicating stability of the trait and that the inheritance of pattern of resistance was stable.

Title: Transcriptomic analysis for Fusarium wilts resistance in Banana (2015)

V. Swarupa, Jawaharlal Nehru Technological University Kukatpally, Hyderabad, Guide: Dr. K.V. Ravishankar

Fusarium wilt of banana caused by soil-borne fungus Fusarium oxysporum. f. sp. cubense is a devastating disease of banana. Banana being the most important food crop, the prevalence of the disease in almost all banana growing countries is a great constraint to the banana production. Understanding the defense mechanism of banana on Fusarium wilt infection provides a valuable source of information for a better crop improvement program. The present study was carried out to examine the molecular response to Foc infection in contrasting genotypes of banana viz. 'Calcutta-4'(tolerant) and 'Kadali' (susceptible). Transcriptome analysis was done by constructing forward, reverse subtracted library and DSN (duplex specific nuclease enzyme) based normalized cDNA library, where 83, 56 and 369 unique ESTs were identified, respectively. Gene expression studies revealed changes in the expression of genes involved in various metabolic pathways upon Foc infection. They include mainly R-genes that help in recognition (NBS-LRR disease resistance protein, LRR receptor like serine/threonine-proteinkinase etc.), ROS scavenging (peroxidase, catalase, glutaredoxin, etc.), cell-wall strengthening (peroxidase, chitinase, etc.), cell-wall reorientation (actin, tubulin etc.), Ca^{2+} signalling (calmodulin, C2 domain containing protein, etc.), ubiquitination, photosynthesis and various transcription factors. qPCR results indicated that the level and expression pattern of genes varies in tolerant and susceptible genotypes. The timing and expression of defense genes were the important factors that help to counteract Foc and delineate.

Title: Cultivation dependent and cultivation independent approaches to study endophytic bacteria associated with Banana (2017)

Aparna C Sekhar, Directorate Of Research And Development Jawaharlal Nehru Technological University Hyderabad Guide: Dr. Pious Thomas

Endophytie bacteria associated with shoot-tip tissue of banana were studied employing cultivation-dependent and cultivation- independent approaches. In the cultivation-based method, tissue homogenization and plating from 30 suckers resulted in the isolation and identification of 88 endophytic bacterial isolates. As per 16S rRNA sequence analysis these belonged to 26 genera under the phyla Actinobacteria, Proteobacteria and Firmicutes, including seve ral uncommon bacteria and two isolates that appeared novel organisms. In cultivation-independent method, 799f -1492R primer pair displayed a bias towards Proteobacteria which resulted in the identification of limited diversity, through 16S rRNA gene cloning and ribotyping approach. 16S rRNA rnetagene profiling of the V3-V4 hypervariable region after filtering the chloroplast and mitochondrial sequences unveiled enormous bacterial diversity. Microscopic studies employing stain YTO -9 coupled with epi- fluorescence and confocal laser sc anning microscopy revealed bacterial colonization along the peri -space and in the cytoplasmic matrix. Bacteria colonizing these two niches were designated as ‘Cytobacts’ and ‘Peribacts’, respectively. Agar plate screening trials for antagonistic activity among the endophytic isolates from banana shoot-tips against the Panama wilt pathogen, Fusarium oxysporumf. sp. cubense showed remarkable antagonism against the pathogen by the isolate GNS 13.2a (identified as Pseurlornonas aeruginosa). However, P. aeruginosa, which is a frequently reported endophyte with antagonistic activity against diverse plant pathogens, showed poor survivor under field conditions and imparted a deleterious effect on the native soil bacterial community w hich rendered the organism unfit for biocontrol experiments. The integral Association of a diverse array of endophytic bacteria with the shoot -tip tissue of banana and the possibility of their clonal perpetuation indicate significtant roles played by the organisms in the biology of the host with implications during vegetative propagation and micropropagation.

Title: Genetic structure, aggressiveness and fungicidal sensitivity of phytophthora associated with Chilli (*Capsicum annuum* L.) (2018)

S Madhura, Directorate of Research and Development Jawaharlal Nehru
Technological University Hyderabad, Guide : Dr.P.Chowappa

Chilli (Capsicum annuum L.) is among the extensively grown vegetable crops all over the globe, which is devoured in diverse forms. Gl ob ally, Indi a is a single most immensely colossal grower and exporter of chillies and its farming is mainly intense in Andhra Pradesh, Karnataka, Maharashtra, Gujarat, Tamil Nadu, and Orissa.Among 82 Phytophthora cultures recuperated from disease - exaggerated foliar tissues of chilli from diverse locality of India between 2011 to 201.4, 62 isolates were recognized as P. boehmeriae and 19 isolates as P. capsici isolates, predicated on morphology, a homogeneous attribute search of ITS sequences at GenBank,PCR restrictionfragment length polymorphism patterns, and species concrete PCR utilizing PC1/PC2 and PB1/PB2 primer pairs. In addition, an electrophoretic pattern of total protein and i soenzyme analysis was also carried out to have additional supporting evidence. B ased on these criteria, isolates recovered from hotpepper were identified as P. boehm.eriae and P. copsici, but no differences were found within the isolates of same species. The isolates were additionally considered for metalaxyl compassion, pathogenicity on germplasm of chillies. All cultures of P. capsici isolateswere intermediatein metaxyl sensivit y while P. bohmeriae were susceptible to fungicide metaxyl. Isolates of P. bohmeriae were highly truculent and engendered significantly $(P< 0.01)$ more astronomically immense lesion than those of P. capsici isolates. Hence, P.bohemeriae emergence was responsible for a stringent foliar blight outbreak on hot pepper in South India, albeit P,boehmeriae is not solemn pathogen on any crop in any part of the globe.

Title: Phenotypic plasticity and genetic diversity of Indian Honey bee, *Apis cerana* Fab. (2018)

Sudhagar S., Jain University, Guide: Dr. P.V.R. Reddy

The phenotypic plasticity of Apis cerana was studied by analyzing the morphological characters of worker bees collected from 24 different agro -climatic regions of India; covering 16 states and a Union territory. Significant difference was observed in standard morphometric characters of worker bees of geographically isolated populations. The altitude exhibited significant positive relationship with all the morphometric characters except ReB, NH and PmB which showed significant negative relationship. Hierarchical cluster analysis approach revealed two major morphoclusters (1 and II) along with sub 4 clusters (A, B, C and D). Thirty three polymorphic microsatellite Markers, mitochondrial marker and other nuclear gene marker were used to understand the genetic diversity of A. cerana population collected from different zones. The microsatellite exhibited the allele frequency estimated range from 0.1154 to 0 .9231 with an average value of 0.553.The analysis of molecular variance (AMOVA) showed 86% among population, 0% among individual, 14 % within individual and 100 % total variations. Two major clusters, Cluster I and II were formed at the genetic distance of 0.84 coefficient value. The marginal likelihood comparison among collected populations in this study showed that th e Relaxed Clock Exponential model (RCE) fits best for analysis of time to most recent common ancestors (TMRCAs), using the Bayesian-based coalescent approach with an estimated mean substitution rate of 3.2316x10-3 (95% HPD 0.0102-5.5146x10-6). Twenty s i x populations, With NCBI accession numbers MI-1588650 — MI1588675 which formed 3 major clusters (I, II and III). Forty six isolates of culturable bacteria were identified using 16S rDNA primers from the gut of A. cerana populations collected from different elevations. They mainly belonged to two phyla viz., Proteo bacteria and Firmicutes. Phylogenetic tree was constructed to obtain specific genetic distance in which all the Bacillus sp. clustered together with separate Glade which belonged to phyla Firmicutes, whereas Serratia sp., Klebbsiella sp., Pantoea sp. and Enterobacter sp. clustered into separate clade of phyla y-Proteobacteria. This study has clearly established the evidence of intra specific variation in morphological characters, molecular and gut microbes of Indian honey bee, A. cerana.

Development of multiple virus resistant transgenic tomato (*Solanum lycopersicum* L.) by RNAi mediated gene silencing (2019)

K. Prasad Babu,Jain University, Guide: Dr. M. Mana mohan

Plant viruses are the most devastating pathogens causing substantial yield losses in many crops. Tomato (Solanum lycopersicum L.) is a globally important vegetable crop, and its production is severely limited by many virus groups. In this scenario, RNAi mediated viral resistance has acquired importance. RNA interference is a sequence dependent gene silencing mechanism having huge potential in imparting virus resistance in crop plants. In this study, ihp RNA gene construct against broad spectrum of viruses was designed based on the conserved sequences of seven genes from four different viruses commonly infesting tomato viz., Capsicum chlorosis virus-nucleocapsid (CaCV-N), Groundnut bud necrosis virus-nucleocapsid and non-structural proteins (GBNV- Nand NSs), Overall, TUB, EF1, TIP41-like family protein (TIP4) and ubiquitin 3 (UBI) can be used as stable candidate reference genes for normalization in GBNV, CMV and ChiVMV expression studies.The hpRNAi-MVR transgenic and WT-Control plants were challenge inoculated with GBNV, CMV and ChiVMV inocula in T2 generation. After mechanical inoculation only C-line showed the consistent resistance, the other transgenic and WT-Control plants were susceptible to GBNV, CMV and ChiVMV. The plant height, and fruit yield were comparatively higher in C-line than B-line, M- line and WT-Control plants in GBNV, CMV and ChiVMV inoculated plants.In case of GBNV inoculation the C-line showed nearly 91.3 % resistance, while only 7.6 % resistance observed in WT-Control, B-line and M-lines respectively.The GBNV accumulation of about 87-91% in susceptible plants where very less in case of C-line. The RT-qPCR results showed that the GBNV-N gene expression was nearly 266-2399 folds lower in C-line than the WT-C, B-line and M-line .In case of CMV inoculation, only the C-line showed the resistance, nearly 88.5 %, while it was only 4.7- 6.8 % in WT-Control, B-line and M-lines. DAC- ELISA results revealed nearly 81-94 % of CMV accumulation in WT-Control, B-line and M-line, where very low CMV accumulation observed in C-line. Hence, the RT- qPCR resulted that the CMV-CP expression in C- line showed nearly 2230-7621 folds lower than WT-Control, B-line and M-line respectively. There was nearly 67-75 % decline in fruit yield in WT- Control, B and M transgenic lines, while it was only 9 % in C-line.In ChiVMV inoculation, the average disease incidence of 59.5 % in case of WT-Control, B-line, and M-line, where the C-line showed 100% resistance forChiVMVThe ChiVMV- CP expression level in C-line was nearly +51,026 folds lower than WT- Control, B-line, and M- line. Reduction in fruit yield due to virus infection was very high in WT-Control, B-line and M- lines, while, only 9 % yield loss was recorded in C-line. Overall, against all the three viruses the C- line showed predominant resistant level compared to WT-Control, B-line, and M-line. Thus, this study demonstrated that the broad-spectrum virus resistance couldb e achieved against GBNV, CMV and ChiVMV. This is the first report of developing broad spectrum virus resistance in tomato against three virus groups of tospovirus, cucumovirus and potyvirus.

Title: Molecular and morphological characterization of major Mealybug species (Hemiptera: Pseudococcidae) in selected horticultural crops (2019)

Nagalakshmi.G, , Jain University, Guide: Dr. G Selvakumar

Mealybugs (Hemiptera: Pseudococcodae) are economically significant pests of agricultural and horticultural crops worldwide. Mealy bugs are difficult to identify due to their waxy covering. The present study was aimed at confirming the identity of major mealybug species morphologically and developing molecular diagnostic tools for their quick identification. The major mealybug species of horticultural crops were collected from in and around Bengaluru and certain regions of Karnataka through intensive surveys during 2012-15.A total of 18 species of mealybugs were collected from 58 host plants and identified based on their morphology. For identification, taxonomical key characters were provided for all these species. Natural enemies associated with 13 mealybug species were collected, identified from experts and documented. Among the total 18 mealybug species, 15 species of mealybug were characterized using MT-CO1 and ITS2 gene region. Of which six species were characterized using MT-CO1, three species were characterized using ITS2 and the remaining six species werecharacterized using both MT-CO1 and ITS2 gene regions. The population dynamics with special reference to Rastrococcus iceryoides Green in mango ecosystem was studied. The prediction models were developed for the mealybug R. iceroyoides outbreaks based on a single independent variable (temperature) in organic mango orchard. In 2013-2014 and 2014-2015 while recording the mealybug population, ant species associated were simultaneously recorded. An attempt was made to find, if there was any numerical response between the ants and mealybug R. iceryoides. The distribution of Rastrococus spp. in major mango growing regions of Karnataka were also studied

Title: Study the effect of Nanoparticles on morphological, biochemical and biotechnological aspects of Eggplant (2019)

Tejaswi Thunugunta, Jain University, Guide: Dr. D.C. Lakshmana Reddy

The escalating utilization of nanomaterials and their accumulation in the ecosystem has made essential to study their effects on the environment. The aim of this study was to understand the impact of different concentrations of zinc oxide, titanium dioxide and iron oxide nanoparticles on eggplant at different stages of growth, along with their accumulation in different parts of eggplant. The study was carried out in both in vitro and in vivo conditions to estimate the effects of nanoparticles on eggplant. A number of morphological parameters like seed germination, shoot length, root length, number of lateral roots, root mass were estimated under invitro condition. Similarly, morphological parameters such as number of leaves, leaf length, leaf width,shoot length, number of branches, number of fruits, fruit length and width, fresh weight and dry weights of fruit were estimated and compared with control under in vivo conditions. Gas exchange parameters were recorded at flowering stage. The effect of nanoparticles on eggplant genomic DNA was evaluated by using RAPD and ISSR markers. ESEM is used to study the transport and accumulation of nanoparticles in eggplant. The experimental results indicate that nanoparticles exposed directly to the seeds and seedlings under in vitro conditions, it imparted many adverse effects on eggplant. In contrast, nanoparticles exposure under in vivo conditions enhanced several growth paramters of eggplant. Increase in biochemicals like MDA, H_2O_2, POD and SOD at initial stages of eggplant growth indicates the stress caused by nanoparticles and their decrease in later stages proves the recovery of eggplant. Increase in gas exchange parameters indicated the positive effect of nanoparticles. In contrast bulk ZnO/TiO_2/Fe_2O_3 treatment did not show better growth than nanoparticles treatment. Eggplant exposed to nano and bulk ZnO/TiO_2/Fe_2O_3 at different concentrations did not show negative effect on genomic DNA, since no polymorphic patterns evidenced in RAPD and ISSR marker studies. Irrespective of growth conditions and nanoparticles concentrations, nanoparticles enter eggplant and accumulate in different parts like stem, leaf and root. This provided evidence for the possibility of nanoparticles accumulation in fruits and their effects on living organisms. Thus there is a need for further research on nanoparticles effect on animals.

Title: Molecular characterization and development of formulation of plant growth promoting Rhizobacteria for the bio- management of nematode induced disease complex in Onion (2019)

Priti Khalkho, Directorate of Research and Development Jawaharlal Nehru Technological University Hyderabad, Guide: Dr MS Rao

Plant growth-promoting rhizobacteria fluorescent pseudomonads and B. pumilus are known to be effective biocontrol agents for suppressing plant pathogens, promote plant growth and enhance crop yield. In the present study PGPRs Fluorescent pseudomonads and B. pumilus were isolated, identified and characterized using 16s rRNA marker gene technology. The active compounds were identified by solid- phase microextraction and gas chromatography-mass spectrometry (SPME-GC-MS). P. monteilii (PMS2), P. entomophila (PES2), P. stutzeri (PSS1) and B. pumilus (BPS4) produced 7 antienmatodal, 3 antifungal and 5 plant growth promoting VOCs including Benzaldehyde; Butanethioic acid, S-methyl ester; Cyclohexene, 1- (1,1- dimethylethoxy) -3- methyl; 1,1,4- Trimethylcyclohexane; 3,4,4-Trimethylcyclohexene; 2,3- Butanediol; Pyrazine, methyl-; Pyrazine, 3-ethyl-2,5-dimethyl-; Indole; Phenol; Carbon disulfide and Disulfide Dimethyl. P. monteilii (PMS2) showed ISR effect against M. incognita by producing 2,3- Butanediol.Experiments were conducted in screen house prior to field experiments to evaluate the interaction of PGPRs in onion. A nematode induced disease complex was observed in onion where Fusarium oxysporum f.sp. cepae (FOC) and root-knot nematode (RKN) Meloidogyne incognita showed positive association in screen house experiments.Combination formulations were developed with the PGPRs and fungal bioagent T. harzianum for the bio-management of nematode induced disease complex in onion. The strains were tested for compatibility in vitro and in vivo to ensure the development of a stable formulation. Viability of microbial postulates in the formulation was accessed by studying its shelf life.Experiments were conducted in the field to develop a bio-management strategy fornematode induced disease complex in onion. A successful bio-management strategy requires devising a safe application method to the field. Organic substrates – vermicompost and neem cake were used to proliferate bio-agent prior to field application and the enriched substrate was used for preparation of field for planting. Also priming of the planting material from the seed stage and repeated application by fertigation was found to helpful in effectively controlling the nematode induced disease complex in onion.The bio-management of the disease complex in onion by M. incognita and F. oxysporum f.sp. cepae in the field environment were devised by applying combination formulations of PGPRs fluorescent pseudomonad and B. pumilus with fungal bioagent T. harzianum.

Title: Optimization of sampling size for DNA-based PCR assay forhybrid purity test in brinjal & cauliflower (2019)

Arpita Pattanaik, Jain University, Guide: Dr C. Aswath

Farmers can harness she full potential of any hybrid only when they get genetically pure seeds of the hybrid. The present study was undertaken to identify the SSR markers that could be used to test the hybrid purity of three hybrids [viz. 2 brinjal (Arka Anand and Asha), 1 cauliflower (NBH Tania- 815)] and to optimize the minimum sample size that can be used for purity assessment of the brinjal and cauliflower hybrids.In GOT, purity evaluation was carried out based on ten morphological traits specified in the published descriptors of brinjal and cauliflower. Plants from four different sample sizes (100, 200, 300 and 400) of brinjal hybrids (`Arka Anand'; Visha') and cauliflower hybrid (`NBH-Tania 815') were studied individually to determine if they were true-to- type for ten morphological characters in the GOT. In case of brinjal hybrid `Arka Anand', out of the ten morphological characters analysed; Flower petal no., leaf colour, leaf length, flower petal no., fruit shape and fruit colour exhibited the maximum variation. In case of brinjal hybrid `Asha'; flower colour, flower petal no., calyx spininess, fruit shape, fruit colour, calyx colour and presence of fruit stripes exhibited the maximum variation. In case of cauliflower hybrid (NBH Tania-81 5); plant habit, leaf shape, curd compactness and curd colour exhibited the maximum variation. In PCR- based assay, a total of 120 and 220 SSR markers were screened for a survey of polymorphism between the parents of brinjal and cauliflower hybrids respectively. 21 SSRs clearly distinguished the parental lines of both the brinjal hybrids and 32 markers showed polymorphism between the parental lines of cauliflower hybrid. Each F1 hybrid were screened with shortlisted polymorphic Two SSR markers (eme08D09 & embOlF16) was found to be co-dominant in brinjal; one SSR marker (BrgMS565) was found to be co-dominant in cauliflower. The percentage of hybrid purity was calculated in GOT assay and in PCR based assay. Hence results indicated that instead of 400 sample size, 100 seedlings are enough to confirm the hybrid purity of brinjal & cauliflower as it showed results comparable with higher sample size. In comparison to that, marker analysis showed the consistent result with GOT. The identified co-dominant markers can be used as referral markers for unambiguous identification, seed purity testing and protection of the hybrids. Hence, it is proposed that molecular marker-based hybrid purity assessment may serve as an effective substitute to traditional GOT.

Title: Molecular studies on lycopene content in Tomato (2019)

P. Shilpa Directorate of Research and Development Jawaharlal Nehru Technological University Kukatpally, Hyderabad, Guide: Dr MS Rao

Tomato is an important vegetable crop grown all over the world. It is a good source of antioxidants and vitamin C. Lycopene is one such carotenoid which is present in abundance in red tomatoes. Therefore this study was done to understand molecular mechanism involved in the variation in lycopene content in tomatoes. Gene expression analysis of selected genes from the carotenoid pathway was done at different stages of ripening. We observed that the genes Phytoene synthase and Phytoene desaturase showed increase in the gene expression from initial stage to the ripe stage but the gene Lycopene f3 cyclase showed decrease in expression at the ripe stage in IIHR 249-1(High lycopene line } but there was increase in expression in IIHR 2866 (Low lycopene line).Promoter analysis of Chloroplast specific Lycopene ft cyclase (LCY-B) and Chromoplast specific Lycopene f3 cyclase(CYC-B) was done. We observed a 28bp InDel in the promoter region of CYC-B in IIHR2866 but absent IIHR 249-1. This 28bp InDel consists of a 5' UTR Pyrimidine rich stretch region which confers high transcription levels of the gene and thismight be the reason for increase in expression of Lycopene ft cyclase in IIHR 2866 and lycopene is converted to 3- carotene. Phenotyping of the F2 population showed normal distribution of the traits total carotenoids and lycopene content. This means the trait is polygenic and not solely controlled by single gene. Therefore Lycopene 13 cyclase is not the only gene responsible for lycopene accumulation there may be other linked genes which are involved in lycopene accumulation. Genetic analysis also showed that the PCV was more than GCV and this might also influence the accumulation of lycopene in tomatoes.

Title : Molecular analysis and mapping of Fusarium wilt tolerance in Banana (*Musa spp.*) (2019)

Pavitra Kotari, Jain University, Guide: Dr. A Rekha

Banana being the most important food crop, the prevalence of the disease in almost all banana growing countries is a great constraint to the banana production. The study began with a screening technique involving macropropogation technique, to multiply and screen for the segregating pattern among the F1 mapping population ("Calcutta-4" x "Kadati") and also to estimate the Disease Severity Index(DSI) for the parental lines and mapping population by an artificial inoculation method. Secondly, this study also focused on development of genetic map and identification of associated QTLs using SSR markers, which could facilitate to recognize and map genes underlying the quantifiable traits. These could further help in gene identification / OTLs associated with FW tolerance as well as few phenotypic traits for undertaking extensive molecular breeding in banana. 315 SSR markers were screened for parental polymorphism and 138 were found to be polymorphic among the parents. Of the 138 markers used for mapping sixty two markers were mapped on eleven Linkage groups (LGs) spread across a length of 1819.8 cM with a maximum distance of fifty and six putative QTLs for Fusarium wilt resistance were identified for five traits (Photosynthesis, Transpiration, Stomatal conductance, Leaf s ymptom index and Rhizome discolouration index) with 11.0 to 13.3 % phenotypic effect (R2) and 2.07 to 2.92 LOD values, across three chromosomes (Chrl, Chr6 and ChrS). QTL with highest LOD score (2.92) and maximum phenotypic effect {13.3 %) was detected for leaf symptom index on the chromosome 6.The study revealed the changes in gene expression patterns involved in various functions upon Foc, infection. Which mainly included miRNAs-Targets, Autophagy, Effector and R-genes (defense genes) that were involved in ROS scavenging, cell wall strengthening, Ca 2+ signalling, ubiquitination, photosynthesis and various transcription factors that involve in different signal transduction pathways. The early and increased expression of prominent defense-related genes; maintenance of cell turgor; maintenance of transpiration, photosynthesis and stomatal conductance rate and increased activity of proteins noted in tolerant genotype "Calcutta-4" during Foc infection might be the possible reasons for tolerance nature.

Title: Standardization of different factors on production of adventitious roots in *Withania somnifera* using bioreactors (2019)

R. Sindhu, Jain University, Guide: Dr. C. Aswath

Withania somnifera (Dunal) popularly known as Ashwagandha, “Winter Cherry” and “Indian Ginseng”. Its roots and leaves are used in a number of preparations for their anti-inflammatory and antitumor properties. Ashwagandha contains very high concentration of metabolites like steroidal lactones (Withanolides), alkaloids and flavonoids. The annual requirement of Withania sominifera in India is about 9127 MT whereas the estimated production in India is only 5905 MT. This requirement canbe met by mass cultivation of adventitious roots using bioreactors. Adventitious roots induced by this form are considered to be genetically uniform, true to its type that gives rise to mass production of desired pharmaceutical compound. Seeds of lines likeJawahar Ashwagandh 20 (JA 20), Arka Ashwagandha (AA), IIHR WS-48 and IIHR WS-32 have been raised in in vitro conditions. Adventitious roots were induced from in vitro leaves by varying factors. Growth conditions of half MS supplement with selected auxin combination of 0.25 mg/L IAA and 0.75 mg/L IBA, photoperiod of 16 hours of light and 8 hours of dark period, 3% sucrose and culture period of 15 days at 25±2 °C were found the best conditions for induction of hairy root in W. somnifera when compared with hairy root induction using A.rhizogenes. Comparative estimationof total withanolide content in 15 days adventitious root of all four lines of W. somnifera showed that Arka Ashwaganda line had the highest total withanolide concentration of 0.84 mg/g.Optimization of protocol for proliferation of adventitious root mass in Arka Ashwagandha lines and JA-20 lines by suspension culture led to the results that full strength suspension culture media supplemented without auxins, 3% sucrose with photoperiod of 16 hours light and 8 hours dark period, produced higher results of fresh root weight in Arka Ashwagandha line of W. somnifera compared to JA 20 lines .150 µM SA treatment on 30th day of suspension culture for 4 hours resulted in significantly higher production of total withanolide with withanolide A and B. Hence Arka Ashwagandha line was chosen for proliferation of adventitious rootsin bioreactors. Out of three types of bioreactor, borosilicate air lift glass bioreactor having 5 liter capacities was suitable for adventitious root proliferation. When 1g adventitious roots of Arka Ashwaganda were proliferated in bioreactors the fresh root biomass increased to 40.57g at four weeks with a growth index of 39.57, the root biomass further increased to 71.40 with a growth index of 70.40g at 8 weeks of incubation.

Plant Pathology

Title: Development of integrated disease management package and transgenic technology for the control of powdery mildew (*Leveillula taurica*) in capsicum (*Capsicum annuum* L.) (2007)

A.Manoj Kumar, Kuvempu University, Shimoga, Guide: Dr.Girija Ganeshan

Bell pepper (Capsicum annuum L.) is an important vegetable crop in India and World. Powdery mildew (Leveillula taurica) takes heavy toll under field and greenhouse conditions. The major goal of the study was to develop an Integrated Disease Management (IDM) package for the control of powdery mildew (Leveilula taurica) in bell pepper and development of transgenic bell pepper using Agrobacterium tumefaciens mediated in plant transformation protocol. Arka Mohini recorded maximum yield and minimum disease incidence and F1 hybrid, Indra also performed well reporting high fruit yield and lowest disease incidence. From 58 primers about 219 unambiguous, readable and reproducible bands were produced, 57 (26%) were polymorphic and shared among at least two individuals, 144 (65.8%) were monomorphic common to all the individuals and 18 (8.2%) were polymorphic and unique. The variety grouped under cluster A were high yielding with low disease incidence, indicating that they are hybrids. The varieties grouped under cluster B recorded relatively low yield and high disease incidence.Fungicides viz., Triademifon, Tebuconazole and Dinocap; biological control agent, Ampelomyces quisqualis and plant products neem oil and pongamia oil significantly reduced the powdery mildew disease incidence and increased the fruit yield.. IDM strategy developed including A.quisqualis, T.harzianum, pongamia oil and best fungicide there was a decline in the powdery mildew disease incidence around 93.0 per cent over control in Indra and California Wonder. Transgenic technology was standardized to incorporate disease resistance gene. The total RNA was extracted from the selected plants (TAG-2, TAG-6 and T AG-8 of T1 generation) and was reverse transcribed to single stranded cDNA and the ss cDNA was employed as template in a PCR reaction using uidA (gus) specific primers. Over all the efficiency of transformation was 6.66 per cent. In case of Arka Mohini, 35 To transformants were raised and fruits were harvested. 31 T1 plants were screened using gene specific uidA (gus) (463 bp) primers by PCR amplification. Further, these plants were also screened using hpt II (509 bp) and 35suidA (687 bp) specific primers. In T2 generation, 30 plants were analysed for the presence of trans gene in which 14 plants were PCR positives against uidA (gus), hpt II and 35s-uidA specific primers. Over all the efficiency of transformation was 5.71 per cent.

Title:Mechanism of carbendazim resistance in Fusarium and its management (2019)

Mahesh Kumar Kumawat, Jain University, Guide: Dr. S. Sriram

Carbendazim belonging to benzimidazole group of fungicides is one of the most widely used fungicides for the management of various soil borne and foliar pathogens. Forty-two Fusarium species isolated from horticultural crops were tested for resistance to carbendazim and other benzimidazole fungicides. Ten isolates were tolerant to carbendazim even at 5000 ppm. These resistant isolates were from ornamental crops viz. carnation (7), marigold (1) and gladiolus (2). In seven of these carbendazim tolerant isolates there was cross resistance to benomyl and thiabendazole. Occurrence of multiple resistance to fungicides in Fusarium species was observed in many isolates to different fungicides viz., copper oxychloride (9), tebuconazole (2), bitertanol (2), mancozeb (2), azoxystrobin (1), tebuconazole (1) and propiconazole (1) up to 5000 ppm concentration. However, all isolates were sensitive to captan, pyraclostrobin and chlorothalonil.The cytological observations on nuclear material and germiling morphology indicated no adverse effects on carbendazim resistant Fusarium isolates when treated with carbendazim. The efficacy of alternate fungicides viz., chlorothalonil (0.2%), captan (0.2%), bitertanol (0.2%), pyraclostrobin (0.1%), propiconazole (0.1%), mancozeb (0.2%), tebuconazole (0.1%) was evaluated for wilt incidence in gladiolus and marigold through pot culture. Fungicides captan, mancozeb, bitertanol, pyraclostrobin, chlorothalonil and propiconazole were highly effective in reducing the pathogen population and wilt incidence in marigold and gladiolus. Evaluation of biocontrol agent (Trichoderma harzianum) and fungicides against carbendazim resistant F. solani in marigold indicated that the combination of biocontrol agent (carbendazim tolerant TH-GJ16B isolate) with carbendazim (8.33% wilt) showed best result followed by another isolate of TH-10 which is T. harzianum isolate tolerant to copper oxychloride (16.66% wilt). Treatments with TH-GJ16B isolate with copper oxychloride (16.66% wilt), TH-10 with copper hydroxide (25% wilt) and TH-GJ16B with copper hydroxide (25% wilt) were also found effective in minimizing wilt disease in marigold. Use of alternative fungicides and carbendazim tolerant Trichoderma isolates will not only help in the management of Fusarium wilt in marigold and gladiolus but also in managing the carbendazim resistance by reducing the inoculum level of resistant isolates in soil over a period of time in the target locations where fungicide resistant populations occur.

Title: Proteomic analysis of rose - powdery mildew (*Podosphaera pannosa* (wallr.: Fr.) de Bary) interaction and mining of resistance mechanism (2020)

Neethu K Chandra , Jain University, Guide: Dr. S. Sriram

Rose is amongst the most important ornamental crops worldwide and powdery mildew (Podosphaerapannosa (Wallr.: Fr.) de Bary) is the major disease of rose when grown in polyhouse or open field. Resistance gene analogues (RGAs) were identified in rose genotypes maintained at ICAR-Indian Institute of Horticultural Research (IIHR). One RGA was identified from Rosa indica (resistant) and First red (susceptible). RGA from susceptible variety probably confers resistance to other diseases. Major defense related genes identified were RPP13, TFs, MAP kinases, GLPs, peroxidase, chitinase, glucan endo-1, 3-beta-glucosidase 2, RLKs and R genes from IIHRR13-4. Gene Ontology (GO) term enrichment and pathway analyses revealed that the transcriptome of IIHRR13-4 was enriched more with transcripts coding for plant hormone signal transduction, plant-pathogen interaction, starch and sucrose metabolism, serine and threonine metabolism, compared to that of susceptible cultivar Konfetti. The proteome profiles of IIHRR13-4 and Konfetti at 0 and 36 hai of powdery mildew were studied by 2- dimensional electrophoresis and MALDI-TOF-MS. The number of differential and unique protein at each time point of powdery mildew infection in IIHRR13-4 and Konfetti was analysed and seven protein spots were selected based on their fold expression. The spot 47 in particular from IIHRR13-4, was identified as probable disease resistance protein At1g61300 reported earlier from Arabidopsis thaliana. The results confirm the expression of a disease resistance protein during early stages of powdery mildew infection at IIHRR13-4 and that was not observed in Konfetti. The mechanism of resistance in IIHRR13-4 was confirmed with the expression of RPP13 and disease resistance protein At1g61300 and thereby R gene mediated response to powdery mildew.The transcriptome and proteome results confirm the expression of R gene in IIHRR13-4 during powdery mildew infection process there by preventing the invasion of powdery mildew. The interaction of Avr factor from the powdery mildew to the LRR domain of RPP gene/disease resistance protein initiates the defense cascade during initial powdery mildew infection and disease resistance might be established in IIHRR13-4. The results of this study confirms gene for gene interaction in IIHRR13-4 genotype by the presence of RPP13 gene or disease resistance protein and new insights for breeding for disease resistance in rose. The genomic, transcriptomic and proteomic information generated from this study give better understanding of disease resistance against powdery mildew in IIHRR13-4.

Entomology
& Nematology

Title: Investigations on the root-knot nematode (*Meloidogyne incognita*) (Kofoid & White, Chitwood) resistance in cowpea (*Vigna unguiculata*, L.) walp (1983)

D.B.Singh, UAS, Bangalore, Guide : Dr.P.Parvatha Reddy

Resistance to M. incognita in cowpea selections IC 9642-B and TVU 2430-P was associated with reduced larval invasion, root galling, egg mass production and fecundity; delayed development of larvae to adult female stage coupled with high concentration of magnesium. Histological studies revealed that was a direct correlation between the number of cork layers and resistance to M. incognita. Cortical sclereids were noticed in resistant selections, while they were absent in the susceptible cultivars. There was more number of starch grains in the cortex susceptible cultivars than in that of resistant selections. Histopathological investigations revealed that there was less number of giant cells which were smaller in size with less number of nuclei in resistant selections as compared to susceptible cultivars. Death of cells (hypersensitive reaction) around infecting M. incognita larvae occurred in the roots of resistant selection IC 9642-B. Histochemical studies revealed that there were more of insoluble polysaccharides, proteins and nucleic acid in susceptible cultivars as compared to the resistant selections of cowpea. Cowpea selections IC 9642- B and TVU 2430-P (resistant to M. incognita were crossed with commercial cultivars S-288 and S-488 (susceptible). The mode of root-knot nematode inheritance in F1's, F2's and back cross generations indicated a Mendelian pattern of segregation. The F1 plants were all resistant. The F2 populations segregated as expected assuming monogenic control and complete dominance with resistant and susceptible plants occurring in a 3 to 1 ratio. The back crosses generations of these crosses with the susceptible parents segregated in the ratio of 1 resistant to 1 susceptible. Hence it was concluded that resistance to M. incognita in IC9642-B and TVU 2430-P selections of cowpea is conditioned by a dominant allele at a single locus.

Title: Aphid (Aphididae: homoptera) vectors of papaya ringspot virus (prsv) disease and their management (2006)

C.M.Kalleshwara Swamy, UAS, Bangalore, Guide: Dr. Abraham Verghese & Dr.N.K.Krishna Kumar

A. gossypii, A. craccivora and M. persicae are the dominant aphid species in yellow funnel traps. Among these, A. gossypii was observed to be the pre-dominant species in terms of number in yellow funnel trap catches compared to A. craccivora and M. persicae. A number of A. gossypii trapped in yellow funnel trap was higher between March and April and from December to Second fortnight of February. Fresh PRSV infection was higher in April-May. Fresh incidence of PRSV (%) coincided with alates caught in yellow funnel traps in the fourth previous week suggesting the strong relationship between aphid number and PRSV incidence. Multiple regression models point to total number of alates caught in traps, maximum and minimum temperature in influencing the PRSV incidence. The model developed for 2004-5, when validated for 2005-6 explained 80%(R2=0.80) variation by a combination of three factors (total of three species of aphid vectors, maximum temperature and minimum temperature) which indicates the strength of the model developed. The cropping pattern also has bearing on higher trap catches. In south Karnataka, cultivation of cucurbits has an influence on PRSV epidemiology. Alate production of A. gossypii is dependent on the density of apterous forms and age of the plant. A gossypii a dominant vector in terms of number is also an efficient vector and can inoculate PRSV to a number of plants (at least four) once acquired the PRSV. Leaf – disc assay is the first of its kind to use for PRSV vector efficiency of aphids and opens a window of opportunity for studying virus-vector relationship. Time of infection was observed to influence total yield. Avoiding early PRSV infection was crucial to enhance yield. The plants which were infected prior to flowering (9 months after planting) yielded very less fruits compared to plants infected later.

Title: Biodiversity and seasonal incidence of lepidopteran pestcomplex of mango with special reference to mango leaf webber (*Orthaga exvinacea* Hampson) in Karnataka (2019)

Soumya B. R., Jain University, Guide: Dr. Verghese Abraham

Mango is the most important fruit crop of India, with pests, including lepidopterans limiting its yield. Hence the present study was started with a view to examine the dynamics of lepidopteran population across seasons in three commercial varieties of mango viz., Totapuri, Alphonso and Banganapalli. The field work was carried out from July 2013 to June 2015 at ICAR-Indian Institute of Horticultural Research, Bengaluru.A total of 29,160 individuals of lepidopterans comprising of 15 species were recorded during two years of study period. In the vegetative phase, lepidopterans viz., O. exvinacea, D. aprobola, C. transversa, C. euthysticha, A.syngramma, P. jocosatrix, P. scintillans, E. fraterna, T. falsaria, Hypotima sp. werefound on Totapuri. The species richness of lepidopterans during flowering comprised of D. aprobola, C. transversa, C. euthysticha, P. scintillans, Hypotima sp., Anarsia sp., Nanaguna sp., P. illepidaria and O. australis postica. Higher species diversity indicated by Shannon-Wiener index especially between October to December indicated higher probability of intervention for dominant pests. Prediction models were obtained by using correlation matrix of insects with weather or phenology parameters (as crop phenology mainly affected by changes in weather parameters) to forecast lepidopteran occurring onmango well in advance, to help in taking management decisions especially the serious ones. Various distribution parameters showed that O. exvinacea followed an aggregation pattern on mango panicles in all three varieties. As the different segments of the tree viz., the four directions and canopies showed east direction and upper canopy had significant differences in mean densities when compared to other segments, east upperis the best sampling zone. MtCOI gene of insects was selected as prime region for molecular identification through barcoding.Of the 13 lepidopterans barcoded, five (O. exvinacea, A. syngramma T. falsaria,Hypotima sp. and P.illepidaria) were identified up to species level and eight werefound similar with their respective sequences in GenBank, NCBI (USA).

Soil Science & Agricultural Chemistry

Title: Behavior of metalaxyl and mancozeb residues in soils and tomato (1996)

T.H.Hanumantha Raju, UAS, Bangalore, Guide: Dr.M.D.Awasthi

The present investigation on “Behaviour of metalaxyl and mancozeb residues in soil and tomato” was taken up with the main objectives of finding the extent of adsorption and degradation of fungicide residues in soils, their uptake and persistence in tomato plants. The studies were conducted on a systemic fungicide metalaxyl and a contact fungicide mancozeb along with its major metabolite ETU interacting with tomato plant and three main types of soil from Bangalore, Chettalli and Hiriyur representing the different textural classes. Metalaxyl adsorption in soils decreased in the order of Hiriyur> Chettalli> Bangalore, which is also the order of decreasing clay content. The degradation pattern of metalaxyl, mancozeb and ETU residues indicated a close correspondence to first order exponential degradation kinetics in soils and mainly influenced by soil moisture and temperatures. Slower degradation of metalaxyl was noticed in the soils and their half – life values were higher than mancozeb and ETU as evident by wide range of half – life values from 41.24 to 165.11 days. In case of metalaxyl Hiriyur soil was found to be superior in degrading the metalaxyl. In mancozeb treated soils, the ETU formation was increased up to 30 days of incubation and thereafter it declined. The plant studies have indicated that maximum concentration of metalaxyl and ETU residues in tomato plants following uptake from soil was attained after 15 and 20 days of soil application respectively. The degradation of soil retained fungicide residues followed the first- order exponential reaction (R2>0.9) and metalaxyl persistence was higher than mancozeb. The half-life values for metalaxyl for different treatments. The rapid disappearance of metalaxyl and mancozeb residues to the extent of 59.2 to 72.4 and 3.81 to 48.3% was found within 10 days of fungicide applications at the two application rates. Metalaxyl residues dissipated at higher rate of residue decay in foliage as compared to fruits. A reverse order on dissipation of mancozeb residues was found in foliage and fruits. The persistence of ETU in foliage continued beyond 40 days but fruits were devoid of any detectable residues. The rate of loss of residues were almost same from the two application rates upon washing followed by cooking while the intensity of dislodging the residues being severe from washing followed by cooking. Decontamination processes of washing followed by cooking removed as high as 78.3 to 78.86% metalaxyl; 74.6 to 78.4% mancozeb and 44.5 to 48.3% ETU residues.

Title: Soil and nutrient management studies in *Coleus vettiveroides*. Jacob (2009)

Dr. T.N. Shivananda, Mamatha. B, University of Agricultural Sciences, Bangalore, Guide:

Four field trials and four pot culture trials were conducted during 2007-2008 and 2008-2009 at Indian Institute of Horticultural Research, Bangalore for soil and nutrient management studies in Coleus vettiveroides. Application of 100:50:50 NPK kg ha-1 recorded significantly higher plant growth (50.86 cm), biomass accumulation (32.75 t ha-1), and nutrient uptake (uptake of 50.60 kg N, 7.21 kg P, 126.04 kg K ha-1) of C. vettiveroides at 116 days after planting (DAP). C. vettiveroides plants grown in 18 inch diameter with 30 inch length PVC column produced significantly higher total root yield (315.2 g plant-1) and biomass accumulation (3597.2 g plant-1) at 121 DAP. Growth media comprising of sand and soil mixed in equal proportion (100 kg) added with 0.5 kg Farm Yard Manure (FYM) recorded significantly higher biomass accumulation (782.34 g plant-1 and 1653 g plant-1) of C. vettiveroides in cement pots and PVC columns respectively at 135 DAP. Application of FYM. (282.80 g plant-1) or inorganic fertilizer (312.73 g plant-1) along with bio-fertilizer recorded higher biomass accumulation of C. vettiveroides as compared with sole application of FYM (210.49 g plant- 1) or inorganic fertilizer (261.56 g plant-1) at 130 DAP. Significantly higher root yield (3.16 t ha-1), biomass accumulation (49.66 t ha-1) and nutrient uptake (uptake of 50.13 kg N, 7.75 kg P, 119.11 kg K ha-1) of C. vettiveroides recorded with application of recommended FYM (10 t ha-1) + recommended NPK (100:50:50 kg ha-1) at 140 DAP. Application of Mucuna mulch 10 t ha-1 recorded significantly higher plant growth (51.74 cm) and application of FYM mulch 10 t ha-1 recorded higher biomass accumulation (33.37 t ha-1) and nutrient uptake (uptake of 49.30 kg N, 9.41 kg P, 148.74 kg K ha-1) of C. vettiveroides at 139 DAP. The different chemical constituents identified in oil of root of C. vettiveroides are hydrocarbons (β-Himachalene etc), oxygenated compounds like alcohols (Vellerdiol, Isothujol etc), aldehydes (β-Cyclocitral, etc), esters (Sabinyl acetate, etc), ketones (β-lonone, Traseolide etc).

Title: Development of protocols for the production of liquid formulations of *Paecilomyces lilacinus* and Trichoderma spp. for eco-friendly management of root-knot nematode *Meloidogyne incognita* (2020)

Gummala Nuthana Grace, Jain University, Guide: Dr. T. N. Shivananda

Root-knot nematode (Meloidogyne spp.) is a major pest on plants causing huge losses on host crops worldwide.. Trichoderma and Paecilomyces species are the two potential biocontrol agents that have been extensively used. In this study liquid formulations were standardized and their bio- efficacy on root-knot nematodes and their shelf life are reported. Paecilomyces lilacinus and Trichoderma harzianum were isolated, identified and characterized from soil samples of 5 districts of Karnataka. Four strains from each of P. lilacinus and T. harzianum were selected and tested for virulence against Meloidogyne incognita under in vitro conditions. Results from these studies suggested that PL IV from P. lilacinus and TH IV from T. harzianum were found to be the most virulent strains. PL- IV recorded 95.48% of egg hatching inhibition and 96.42% of juvenile mortality whereas92.13% and 94.53% by TH IV respectively. Four liquid formulations were standardized for each of the most virulent strain of P. lilacinus and T. harzianum.. Results based on monthly spore count suggested that these bio-agents can be stored at room temperature up to 16 months without any loss of virulence on M incognita. A total of 9 treatments consisted of untreated control, a chemical nematicide carbofuran applied at 3.33g/pot, and bio-agents enriched with vermicompost at different concentrations. Tuberose, tomato and okra recorded significantly better plant growth parameters in T5 (200g of vermicompost enriched with 0.5 ml of T. harzianum strain F IV) and T6 (200g of vermicompost enriched with 0.5 ml of P. lilacinus strain TH IV) treatments in both the seasons of the study which was on par with carbofuran treatedpots. In tuberose, root gall index (RGI) was 1.5 and 1.9 in T5 and T6 respectively. RGI in okra was 1.9 and 1.5 in T5 and T6 respectively. The density of bio-agents in soil at the end of the trial in T5 and T6 was 5.1x104 and 4.8x104 respectively. Studies in tuberose suggested that plant yield parameters and root colonization of P. lilacinus and T. harzianum were significantly superior in T5 (enrichment of 2 tons of vermicompost with 5 liters of liquid formulation of T. harzianum strain TH IV) and T6 (enrichment of 2 tons of vermicompost with 5 liters of liquid formulation of P. lilacinus strain PL IV) which was on par with chemical nematicide carbofuan used at 1 kg a.i./ha. The density of bio-agent in soil was 4.8 x104 and 4.5 x104 in T5 and T6 respectively.

Title: Study of the behaviour of fluopyram and tebuconazole in tomato, capsicum, Pomegranate, soil and water (2020)

Nagapooja Y. M., Jain University, Guide: Dr. Soudamini Mohapatra

Fluopyram and tebuconazole combination formulation was primarily introduced for resistance management of fungal pathogens. Fluopyram benzamide is a major metabolite of fluopyram and it included as fluopyram for risk assessment purpose. The behaviour of these two fungicides was studied in tomato, capsicum, pomegranate, soil and water. The extraction of fluopyram, fluopyram benzamide and tebuconazole from fruit, leaves, stem, root of tomato and capsicum plant, soil was carried out by QuEChERS analytical method; pomegranate fruit matrices by ethyl acetate based extraction method; LLE method used for water. The method validation was carried out as per SANTE (2017) guidelines. Selectivity, linearity, accuracy, precision, LOD and LOQ of the methods were evaluated and the results obtained were within satisfactory limits. The uptake study in tomato and capsicum plants was carried out by soil drench application of the formulated product fluopyram 17.7% + tebuconazole 17.7% (Luna experience 400 SC), at 0.5 mL L-1 water. Fluopyram and tebuconazole analysis in tomato and capsicum tissues was carried by QuEChERS analytical method in conjunction with LC-MS/MS. The method LOQ thus obtained was 0.005 mg kg-1, which is less than the MRL of both compounds in tomato and capsicum. Fluopyram and tebuconazole were rapidly absorbed by tomato and capsicum plants from their soil drench application. The pomegranate field study was conducted to study the movement of fungicides within the fruit i.e., outer peel, inner peel, aril. The highest residue was found in outer peel followed by inner peel and below LOQ in arils at all sampling days. A sandy loam soil and high organic content soil was taken to study the persistence of fluopyram and tebuconazole under laboratory conditions. The half-life of fluopyram in sandy loam soil at room temperature with field capacity and flooded condition were 223 and 230 days, whereas at 400 C temperature it was 217 and 228 days at field capacity moisture and flooded condition, respectively. In high organic content soil the PHI was 237 days at field capacity moisture and 247 days under flooded conditions at room temperature; 233 days and 239 days at 40oC under field capacity and flooded conditions. Tebuconazole half-life was 176 and 200 days under field capacity moisture and flooded conditions at room temperature; 173 days at field capacity and 194 days under flooded conditions at 40oC in sandy loam soil. Tebuconazole degradation half-life in high organic content soil was 186 days (field capacity) and 213 days (flooded) at room temperature; 181 and 202 days at 40oC from field capacity moisture and flooded conditions The dissipation study of fluopyram and tebuconazole was carried out in three different types of water i.e., acidic water (pH 5), neutral water (pH 7) and alkaline water (pH 9).The results of the studies carried out on the behaviour of fluopyram and tebuconazole in plant, soil and water can be utilize, while employing these two fungicides in plant protection programs for control of fungal diseases of tomato, capsicum and pomegranate.

Microbiology

Title: Development of a microbial consortium for compost production from horticultural wastes (2017)

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Traditionally cow dung has been used as a compost starter to prepare composts, but in recent times the scarcity of cow dung especially in the peri-urban areas and its bulkiness, have led to the use of alternatives such as microbial bioconversion starters for the composting of 'horticultural wastes.The present study was therefore conducted with aim of developing a starter consortium containing potential bioconversion agents for the bioconversion of different groups of horticultural crop. Twenty five bacterial and seventy fungal isolates covering the entire bioconversion spectrum viz., cellulolytic bacteria, cellulolytic fungi, xylanolytic fungi, tannin degrading fungi, pectinolytic fungi and lignolytic fungi. The Consortium-1 comprising (A.spergillus sp. TMLF-1, Aspergillus oryzae CP-2, Trichoderma hamatum FLF-13 and Aspergillu,s sp. TL-8) produced the best quality compost from mango leaf litter (C:N ratio of 15.52, humification index of 4.1, humic like carbon/Fulvic like carbon ratio of 3.3, radish seed germination index of 371.58) and grape pruning's (C:N ratio of 14.4, humification index of 5.2, humic like carbon/Fulvic like carbon ration of 3.4, radish seed germination index of 431.51),The Consortium-2 comprising (Bacillus endophyticus FLCB-1 1, Aspergillus .sp. CF-11, Xylaria sp. TF-4 and Penicilhum chrysogenum VCLF-1) produced the best quality compost from chilli stalks (C:N ratio of 16.13, humification index of 6.25, humic like carbon/fulvic like carbon ratio of 6.09, radish seed germination index of 308.2) .When the prepared composts were evaluated under polyhouse conditions on tomato hybrid UNIK-38, it was observed that the mango leaf litter, brinjal stalks and grape pruning's composts prepared using the Consortium-1, significantly improved the vegetative and harvest parameters of tomato, while the Dolichos stover and chilli stalks composts prepared using Consortium-2 were superior in improving the vegetative and harvest parameters of tomato.Consortium-2 comprising (Bacillus endophyticus FLCB-11, Aspergillus sp. CF-11, Xylaria sp. TF-4 and Penicillium clnysogenum VCLF-1) is more suitable for the bioconversion of a wide range of horticultural crop residues, while the Consortium-1 comprising (Aspergillu.s. sp. TMLF- 1 , Aspergillus olyzae CP-2, 7)1c/rodent/a hamatum FLF-13 and Aspergillms sp. TL-8) is more suited for bioconversion of mango leaf litter and grape pruning's.

Title: Rhizobacterial mediated alleviation of water stress in To mato (*Solanum lycopersicum* L.) (2018)

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Plants are subjected to biotic and abiotic stresses which have a direct bearing on plant productivity throughout all growth stages.. The present study was therefore conducted with the objective of developing a microbial consortium having drought stress alleviation traits. The isolates were identified as Bacillus amyyloliquefaciens (P-72), Pseudomonas sp. (CP-3), Bacillus sp. (CP-2, G-4, and R-7), Enterobacter sp. (P-39, P-41, P-46,P-68, and P-76) and the aetinobaeterial isolate Citricococcus zhociaensis (B-4).While the isolate Bacillus amyloliquefaciens P-72 exhibited significant phosphate solubilisation activity under osmotic stress conditions, the isolates EnterobacterP-68, Bacillus amyloliquefaciens P-72 and Bacillus sp. G-4, exhibited significant ACC deaminase activity under osmotic stress conditions. Growth hormones like IAA, GA3 and cytokinins were analyzed by high performance liquid chromatography(HPLC).The GA3 production ranged from 166.1-906. l ng/mL Under water stressed conditions plants inoculated with the isolates Enterobect.er P-68, Enierobacter P-46, Ent.erohacier P-39 and Bacillus G-4 recorded the highest activity levels of the enzymes peroxidase, superoxide dimutase, catalase and glutathione reductase respectively, while plants inoculated with Bacillus amyloliquef'uciens P- 72 recorded the highest levels of in plant levels of proline. Two elite strains viz., B.amyloliquifaciens and C.zhacaiensis were formulated and the shelf life of the formulation was estimated under normal and refrigerated (40C) conditions. The ability of the actinobacterial strain C.zhacaiensis B -4 and the spore forming B.amyloliquefaciens P-72 were evaluated for their abilities to alleviate the deficit irrigation stress effects and improve plant growth at 100,50 and 25% water holding capacity (WHC) of the soil. Compared to the uninocullated controls, inoculation with the actinobacterium C.zhacaiensis resulted in 24 and 9% higher yields, while plants inoculated with B. amyloliquefaciens recorded 42.0 and 12.7% higher marketable fruit yields at 50 and 25% WHC besides recording higher activities of physiological parameters during different plant phemologial stages. This study thereby reinforces the strategy of utilizing osmotolerant plant growth promoting microbes for alleviation of deleterious effects of drought stress in tomato.

Plant Genetic Resource

Title: Ex situ conservation and physiological studies in some threatened medicinal plant species (2003)

P.E.Rajasekharan, Bangalore Univerisity, Guide: Dr.S.Ganeshan

Research investigations involving endangered medicinal plant species of south India (Coleus forskohlii, Kaempferia galanga, K. rotunda, Rouvolfia serpentina and Tylophora indica) were carried out to design suitable conservation strategies. In all species, regeneration was normal in vitro resulting in large no. of vitro plants. Attempts to conserve the regenerated in vitro plantlets by lowering the incubation temperature, media constituents and osmoticum resulted in development of protocols, which could be used to conserve these species. Artificial seeds which resulted in regeneration of normal plantlets were formed by encapsulation of explants using sodium alginate and subsequent storage at low temperature. In vitro plants regenerated from these five species could be successfully conserved in vitro for durations ranging from 9-18 months reducing the intervening sub-culture frequency. Such material was capable of regenerating normal in vitro plants when they are recultured in regular medium under SCC. The conserved vitro plants thus regenerated could be established extra vitrum in pots containing "soil rite" prior to establishment in Field Gene Bank. Cryopreservation of nodal and apical explants resulted in <15% vitro plant recovery profiles. (Further investigations are required for obtaining optimal recovery of cryopreserved vitro plants.) out of 9 experiments in 3 species and 3 for Kaempferia galanga involving rapid freezing techniques carried out, only few vitro plants could be recovered and from these there was no survival extra vitrum in pots with "soil rite". Conservation of gene pool components like pollen and seed was successful in Tylophora indica and to a certain extent in Rauvolfia serpentina. Plants were also domesticated and conserved in Field Gene Bank, exclusively established for these species. The physiological and bio chemical studies on phenolics, total alkaloids, saline soluble proteins and PAGE (Poly Acrylamide Gel Electrophoresis) using two species namely Kaempferia galanga and Tylophora indica revealed no perceivable changes occurring due to conservation at low temperature and reduced light. Eco- rehabilitation studies using these species Kaempferia galanga, Rauvolfia serpentina and Tylophora indica were successful and the plants could be re established in their respective place of collection

Title: Ex situ conservation strategies for the threatened medicinal plant species Acorus calamus Linn and *Adhatoda beddomeii* c.b. Clarke (2006)

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An effective ex situ conservation strategy was developed for establishment of FGB followed by in vitro conservation using tissue culture techniques for two red listed plant species Adhatoda beddomeii C.B. Clarke & Acorus calamus Linn. Adhatoda beddomeii C.B. Clarke is a critically endangered endemic shrub used in medicinal preparations for its antieemetic and haemostatic properties. Acorus calamus Linn. Is a non-endemic critically endangered used to cure diarrhea, dysentery digestion abdominal obstruction and colic. In two plant species collected from different region were successfully acclimatized and established in FGB without any mortality. A perennial problem regarding the true identity and existence of Adhatoda beddomeii has been solved by reporting it as a variant of A. vasica and true A. beddomeii merged with A. gingiana based on the morphological evidences which showed variation. The molecular characterization of the above through RAPD analysis followed by electrophoresis of PCR products and the banding patterns emerged was scored. The resulting dendrogram revealed two clusters that is A. beddomeii one and A. vasica and A. gingiana another which is a clear indication that A. beddomeii cannot be considered synonymous with A. gingiana. Phonological events showed variation with regard to few morphological traits in A. beddomeii and Acorus calamus accessions established in FGB. For both the species morphological characterization were reported with about 20 quantitave and 25 qualitative characteristics in A. beddomeii and 9 quantitative and 22 qualitative characteristics for A. calamus. Cytological studies attempted to ascertain the ploidy level and somatic chromosomes number in both which showed 2n= 34 and 4n=44 in Adhatoda beddomeii an Acorus calamus respectively. TLC and HPLC were carried out to estimate the active principles and vasicine and asarone were identified in A. beddomeii and A. calamus respectively. In vitro regeneration was observed in both species under SCC. A. beddomeii could be maintained for a short duration of 1 year at SCC and A. calamus could be maintained for period of 1 year without sub culture. Encapsulation of A. beddomeii and A. calamus were attempted for long term storage by cryopreservation technique using liquid nitrogen. Along with pollen germination studies the pollen cryopreservation enabled the storage for Integrated PGR conservation program.

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