GENETIC VARIABILITY IN CHINESE POTATO (*Solenostemon rotundifolius* (Poir) J.K. Morton) FOR YIELD AND NEMATODE TOLERANCE

by

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(2017-11-044)

THESIS

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DECLARATION

I, hereby declare that this thesis entitled **"Genetic variability in Chinese potato (*Solenostemon rotundifolius* (Poir) J.K. Morton) for yield and nematode tolerance"** is a bonafide record of research work done by me during the course of research and the thesis has not previously formed the basis for the award to me of any degree, diploma, associateship, fellowship or other similar title, of any other University or Society.

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CERTIFICATE

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Ankitha M O.

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LIST OF ABBREVIATIONS AND SYMBOLS USED

ANOVA	Analysis of Variance
ANCOVA	Analysis of Covariance
cc	Cubic centimetre
CD	Critical Difference
cm	Centimetre
CRD	Completely Randomized Block Design
CTCRI	Central Tuber Crop Research Institute
cv	Cultivar
DAP	Days after planting
df	Degrees of freedom
et al.	And others
F_1	First filial generation
Fig.	Figure
G	Gram
GAM	Genetic advance as per cent of mean
gcc^{-1}	Gram per cubic centimetre
GCV	Genotypic Coefficient of Variation
hr	Hour
kg	Kilo gram
k cal	Kilo calorie
ml	Millilitre
No.	Number

PCV	Phenotypic Coefficient of Variation
Plant^{-1}	Per plant
S. E	Standard Error
Sl.	Serial
sp. or spp.	Species (Singular and Plural)
t	tonnes
tha^{-1}	Tonnes per hectare
viz.	Namely

INTRODUCTION

1. INTRODUCTION

Tuber crop species produce large quantities of dietary energy and have stable yields under difficult environmental conditions. The most important tuber crops are cassava, sweet potato, yam and the aroids, sharing important common traits such as bulkiness, post-harvest perishability and vegetative propagation.

Coleus (*Solenostemon rotundifolius* (Poir) J.K. Morton), commonly known as Chinese potato, or 'poor man's potato' is a minor tuber crop of the tropical regions of India, Indonesia, Malaysia, Sri Lanka and Africa. It is considered as a native of central or east Africa where its cultivation is mostly confined to the southern states. In Kerala, it is commonly known as "*koorka*" or "*cheevakizhangu*". It is a small herbaceous annual, 1-2 feet high, prostrate or ascending with succulent stem and aromatic thick leaves which belongs to the family Lamiaceae (syn. Labiatae). The plant is a polyploid with 2n=6x=72 (Sreekumari and Abraham, 1985). The crop produces small dark brown, aromatic tubers in clusters at the base of the stem which is consumed as a vegetable-cum tuber. The crop prefers a hot humid climate for a luxuriant vegetative growth. Further, low night temperature is essential for proper tuberization. Due to the same reasons, in Kerala, it is cultivated in the rice fallows during summer and in the uplands during rainy season (CTCRI, 1987). Due to photosensitivity for tuberization, the availability of the tubers in the market is seasonal. The normal season is confined to the months of July to November when the market will be flooded with the tubers.

Chinese potato tuber contains 20.1 to 30.0 per cent dry matter, 14.7 to 20.8 per cent starch, 0.04 to 0.31 per cent protein and 0.57 to 0.9 per cent sugar (Sreekumari and Abraham, 1985). Since ancient times, *Coleus* spp. have been used in Ayurvedic medical practice. The major uses are in heart diseases, abdominal colic, respiratory disorders , insomnia and convulsions. They are also used for the treatment of dysentery and certain eye disorders (Ammon and Muller, 1985).

Assessing the available genetic variability and partitioning it into heritable and non-heritable components is a basic step to the planning of any breeding programme. Lush (1940) and Johnson *et al.* (1955) devised an accurate procedure for calculation of genetic advance under specified intensity of selection. Hamson *et al.* (1956) proposed the mathematical relationship of various estimates on computation of heritability. In asexually propagating plants such as Coleus, any combination of genetic factors that yield a superior genotype can be multiplied through clonal propagation and can be used directly as a variety.

Root knot nematode, *Meloidogyne incognita* (Kofoid and White) Chitwood is a serious pest of *S. rotundifolius*. Due to nematode attack conspicuous gall like swellings are formed in roots resulting in malformation of tubers making it unfit for consumption as well as storage. Overdependence on pesticides harmful to the environment can be avoided if a variety resistant to *M. incognita* is identified. Hence varieties tolerant to *M. incognita* infestation are the need of the hour.

Considering the above mentioned facts, in the present scenario, collection and evaluation of Chinese potato genotypes with high yield which can tolerate nematode infection is important. So the current study has been proposed with the main objective of assessing the available genetic variability for yield and nematode tolerance in Chinese potato.

REVIEW OF LIERATURE

2. REVIEW OF LITERATURE

Chinese potato (*Solenostemon rotundifolius* (Poir) J.K. Morton) is one of the important minor tuber crop species grown for its edible tubers, which is a vegetable cum tuber crop. *Solenostemon rotundifolius* is synonymous with *Plectranthus rotundifolius, Coleus parviflorus* Benth and *Coleus tuberosus* (Blume) Benth.

The genus *Coleus* belonging to the family Lamiaceae syn. Labiatae has over 3000 spp. which includes both annuals and perennials. The generic name *Coleus* is derived from the Greek word *Koleos* meaning sheath. The members of the genus have four didynamous dedinate stamens whose filaments unite as a sheath at the base (Morton, 1962 and Codd, 1971). Coleus is supposed to be a native of central or East Africa and it has come to India at an early period. It has adapted well in South East Asia including India and Sri Lanka (Purseglove, 1974).

2.1 GROWTH AND QUALITY ATTRIBUTES OF CHINESE POTATO

The plant is a small herbaceous annual, 15-30 cm high, with a succulent stem and somewhat thick leaves having a characteristic aroma. Flowers, small and pale violet, are produced on racemose cymes with pairs of very caducous floral leaves. The colour of the two lipped calyx and corolla are greenish brown and violet, respectively. Anther and stigma are violet. Complete pollen sterility exists due to highly irregular meiosis (Ramachandran, 1967) and hence seed setting is absent. Flowering starts 50-60 days after planting and continues for about two months. Small, dark brown tubers are produced in clusters at the base of the stem.

The nutritive status of this crop compares favourably with many of the major tuber crops. Coleus tuber, with its characteristic flavour has a special preference among consumers. Compared to other tuber crops, it fetches premium price in the market, although it is known as poor man's potato. Fresh coleus tuber contains 20.1- 30.0 per cent dry matter, 14.7 - 20.8 per cent starch, 0.04- 0.31 per cent protein and 0.57-0.96 per cent sugar. Hundred gram dry weight of tuber

contains: carbohydrate 91 per cent, protein 1.4per cent; fat 1per cent, ascorbic acid 4.8 mg; calcium 60.4 mg; iron 7.2 mg and energy 392 k cal (Rajmohan, 1988).

Coleus is a season bound crop. First week of October was found to be the optimum time for planting coleus for getting maximum yield (Singh and Mandal, 1976). Vasudevan and Jos (1990) reported that coleus is a strictly seasonal crop and tuber production is found in July to September planting. Vimala (1994) also opined that coleus is season bound.

Very low variability exists in this species, mainly due to pollen sterility and problems of seed set. Meiotic abnormality may be the reason for pollen sterility. Isolated attempts have been made to study the seed setting of this crop. Thoppil and Jose (1995) analysed the chromosomal constitution of *C. parviflorus* and reported that it is a polyploid with (2n= (6x)= 72). Karyomorphometrical data revealed their symmetrical and primitive karyotype, which seems to be correlated with their essential oil composition and chemical characterization. Major essential components found in *C. parviflorus* are beta thujone and alpha farnesene (Thoppil and Jose, 1995).

Sandhya (1996) studied the antioxidant activity of total flavonoid preparation from *Solenostemon rotundifolius* in normolipidemic and hyperlipidemic rats. The elevated levels of glutathione and stimulated activities of antioxidant enzymes in the experiment animal account for the antioxidant activity of these flavonoids.

2.2. BIOMETRIC CHARACTERS

Variability within coleus was reported by Sreekumari and Abraham (1985). Variation in morphology, especially three whorled phyllotaxy may be considered physiologically significant since it leads to more biomass production as compared to ordinary plants.

2.2.1. Days to Flowering

Sixty genotypes of coleus were evaluated by Abraham (2002) and the results revealed that days to flowering ranged from less than 100 days to more than 130 days.

Thirty seven genotypes of *Coleus forskohlii* were assessed in which days to 50per cent flowering had an average value of 84.73 and the value fluctuated between 65 and 95 days. (Kavitha *et al.*, 2007).

2.2.2. Days to Tuberization

Variability study conducted by Abraham (2002) revealed that days to tuberization ranged from 107.5 to 130 days among the thirty genotypes. The average days to tuberization was 126.63.

2.2.3. Point of Tuberization

Accessions of Chinese potato were evaluated and point of tuberization was observed both at base of the stem and at leaf nodes. The values for point of tuberization ranged from 2 to 3 with an average of 2.28 (Abraham 2002).

2.2.4. Number of Tubers Plant^{-1}

Number of marketable tubers produced in the coleus variety Sreedhara was found to be 13.69 (Archana,2001). Among sixty genotypes of coleus, Abraham (2002) reported that the range of number of tubers plant^{-1} varied from 25.30 to 89.20 with an average of 54.31. Maximum number of tubers plant^{-1} was produced in the genotype Peringallur local.

The mean performance of number of tubers per plant was nine for *S. rotundifolius* cv. *bola innala* (Prematilake, 2005). Thirty seven *Coleus forskohlii* genotypes were subjected to diversity analysis by Kavitha *et al.* (2007). The number of tubers plant^{-1} ranged from 16.12 to 45.77.

An experiment was conducted in *Coleus forskohlii* Briq. ecotype Garmai by Velmurugan (2009) who briefed that the value for number of tubers plant^{-1} was

24.5.A study conducted by Jayapal (2012) revealed that the variety Sreedhara produced considerably more number of marketable tubers plant^{-1} (12.61).

Exo- morphological study was conductd in *Solenostemon rotundifolius* (Poir) J. K. Morton and *Plectranthus esculentus*. The results showed that number of tubers per plant ranged from 87.67 in *S. rotundifolius* var. *alba* and 88.33 in *S. rotundifolius* var *nigra*. (Agyeno *et al.*, 2014).

Time of planting and nutrient management for off-season production of Chinese potato was studied by Anju *et al.* (2015) who stated that number of tubers varied from 8.17 to 12.10 when the variety Suphala was planted in the off season.

2.2.5. Tuber Girth

An experiment was done by Abraham (2002) to assess variability among the sixty Chinese potato genotypes, in which the tuber girth ranged from 3.3 cm to 6.6 cm and the mean tuber girth was 4.90 cm. Maximum tuber girth was reported in the accession IC 85703.

Eighty six genotypes of sweet potato were studied by Anshebo *et al.* (2004) to assess genetic variability and character association and described that average value of tuber girth was found to be 3.7 cm.

Studies on induced variability and *in-vitro* regeneration were conducted in *S. rotundifolius cv. bola innala* genotype by Prematilake (2005) who reported that the value of average tuber diameter was 3.4 cm.

In *Coleus forskohlii* Briq. ecotype Garmai, correlation studies were made by Velmurugan *et al.* (2009). The findings of the study revealed that average girth of tuber was 3.45 cm

A study conducted by Agyeno *et al.* (2014) revealed that tuber diameter for *S. rotundifolius* var. *alba* was 11.80 whereas *S. rotundifolius* var *nigra* exhibited 7.97 cm.

2.2.6. Tuber Volume

In a study conducted by Abraham (2002), tuber volume ranged from 2.45cc to 10.70cc. The genotype Parlikad Local showed the highest tuber volume of 10.70 cc.

2.2.7. Average Weight of Tubers

Variability analysis among sixty genotypes of Chinese potato was conducted by Abraham (2002) and stated that average weight of tubers ranged from 2.70 g to 14.07 g with a mean value of 6.44 g.

The value of average tuber weight was found to be 9.4 g in a study conducted by Velmurugan *et al.* (2009) to assess correlation and path analysis among the mutants of *S. rotundifolius* cv. *bola innala.*

2.2.8. Tuber Density

Tuber density of sixty Chinese potato accessions ranged from 1.00 gcc^{-1} to1.4 gcc^{-1}. The genotype Trivandrum local recorded maximum tuber density of 1.4 gcc^{-1} (Abraham, 2002).

2.2.9. Tuber Yield $Plant^{-1}$

Vimala (1994) reported that there was no significant difference in yield between most of the different accessions of Chinese potato maintained in the germplasm at CTCRI. However one accession CP-58 gave a comparatively higher yield and was released as 'Sreedhara'. In a study conducted in Sreedhara, the tuber yield $plant^{-1}$ observed was 208.33 (Archana, 2001).

Sixty coleus genotypes were subjected to variability study in which the tuber yield $plant^{-1}$ ranged from 47.5 to 500 g. The average tuber yield was 224.71. The highest tuber yield of 500g was recorded in the genotype Madakkathara Local (Abraham, 2002).

Correlation and path analysis conducted by Velmurugan *et al.* (2009) stated that the fresh tuber yield per plant of *Coleus forskohlii* Briq. ecotype was 510 g.

The variety Suphala produced an average yield of 20.99 t ha^{-1} when it was planted during the season of July to October (Jayapal *et al.,* 2013). A study by Anju *et al.* (2015) revealed that 14.89 t to 10.71 t ha^{-1} of tuber yield could be produced by the variety Suphala during the off season.

2.2.10. Biological Yield

Variability studies in coleus by Abraham (2002) reported that the value for biological yield varied from 275.00 g to 1443.75 g with an average of 667.83 g.

Genetic variability of another important tuber crop, sweet potato on yield and yield related traits was studied by Demelie and Aragaw (2016) who stated that biological yield ranged from 120 to 500g.

2.2.11. Plant Height (cm)

Plant height of variety Sreedhara at different stages of growth such as 30 DAP, 60 DAP, 90 DAP, 120 DAP and at harvest was noted by Archana (2001), and plant height at harvest was 45.25 cm.

Abraham (2002) detailed the range of plant height of Chinese potato from 56.65 cm to 140.90 cm with an average of 98.54 cm. Maximum plant height was recorded by the accession IC 65725.

Analysis of variability for qualitative and quantitative traits in *Coleus forskohlii* Briq. was investigated by Kavitha (2007). The results revealed that the average plant height was 31.07 cm among the 37 genotypes studied. Velmurugan *et al.* (2009) analysed *Coleus forskohlii* Briq. ecotype Garmai and pointed out that plant height was 63.50cm, 180 days after planting.

In a study conducted by Jayapal (2012), the coleus variety Sreedhara recorded a plant height of 18.66 cm whereas Suphala had 22.99 cm, one month after planting.

Data on quantitative characters studied by Agyeno *et al.* (2014) showed that plant height ranged between 19.52 cm in *S. rotundifolius* var. *alba* and 66.48 cm in *S. rotundifolius* var *nigra.*

2.2.12. Harvest Index

The value of harvest index of sixty Chinese potato genotypes stretched in between 0.06 and 0.57 with an average of 0.28 (Abraham, 2002).

Harvest index of sweet potato cultivars ranged from 0.3 to 0.7 and the average value was 0.5. (Gurmu *et al.*, 2018).

2.3. STATISTICAL CHARACTERS

2.3.1. Genetic Parameters *viz.*, PCV, GCV, Heritability and Genetic Advance

Harvest index is closely associated with yield (Sinclair, 1998). Kawano *et al.* (1978) had reported that there was enormous genetic variation for harvest index in seedling populations of cassava and by virtue of its high heritability could be effectively used as an indicator for seedling selection. In cassava, heritability of harvest index was much higher than that of root yield and total plant weight under both very high yielding and low yielding environments.

Vimala and Lakshmi (1991) assessed high heritability estimates for vine weight, tuber girth, tuber length and tuber weight, which indicates additive genetic variance in sweet potato. Low heritability estimates were reported for number of leaves per plant, vine girth, vine length, petiole length and number of tubers.

Naskar *et al.* (1991), by studying the performance of F_1 populations of cassava reported high heritability estimates and genetic advance for plant height, stem diameter, number of tubers and tuber yield indicating their efficiency in selection.

By genetic analysis of 12 characters in 25 accessions of taro, Pillai and Unnikrishnan (1991) reported high heritability and genetic advance estimates for characters like weight of cormels per plant and number of cormels per plant.

In a study involving 76 genotypes of cassava, Sunthirapandian *et al.* (1994) reported that the highest genetic advance was noticed for number of leaves. Among the economic characters, highest genetic advance was noticed for tuber yield plant^{-1} followed by number of tubers, single tuber weight and tuber length.

In taro, estimate of genotypic and phenotypic variance coupled with high heritability was noticed for length and diameter of cormel. All the characters showed heritability exceeding 60 per cent. This indicates the scope for attaining high yielding clones from local population of taro (Apte *et al.,* 1994).

A study on variability of sweet potato cultivars reported high phenotypic and genotypic coefficients of variation for average tuber weight, number of tubers per plant and tuber yield per plant. Estimates of heritability and genetic advance were maximum for tuber yield per plant, average tuber weight and number of tubers per plant. (Hossain *et al.,* 2000).

Maximum PCV was shown by the character days to flowering and it had a low GCV of 1.33. The other characters such as tuber yield, mean weight of tuber, mean volume of tuber and biological yield also exhibited high PCV as well as GCV values. High heritability estimates were obtained for the characters mean weight of tuber, tuber yield, tuber density, plant height, biological yield and harvest index. High genetic gain was revealed for the characters such as harvest index (81.09per cent), biological yield (77.99 per cent), tuber weight (70.81 per cent), tuber yield (72.34 per cent) and tuber volume (69.30 per cent), whereas low values of genetic gain was detected for nematode susceptibility (21.94 per cent), tuber girth (12.14 per cent), point of tuberization (7.89 per cent), tuber density (8.49 per cent), days to tuberization (0.85per cent) and days to flowering (0.16per cent) (Abraham 2002).

Genetic variability and correlation studies in sweet potato was performed by Anshebo *et al.* (2004) who stated that characters such as number of branches per plant, length of tuber , girth of tuber and weight of single tuber presented high magnitude for phenotypic and genotypic coefficients of variation whereas number

of tubers per plant displayed the minimum values of GCV and PCV. The characters such as number of branches per plant, girth of tuber, weight of single tuber, and length of tuber exhibited high heritability estimates linked with high genetic advance specifying the existence of additive gene effect.

Genetic diversity and interrelationship of qualitative and quantitative traits in sweet potato was analysed by Solankey *et al.*(2014) who pointed out that PCV and GCV were the highest for tuber yield per plant, starch content, fresh weight of tubers per plant and number of branches per plant. Heritability and genetic advance as per cent of mean estimates, were highest for fresh weight of tubers per plant followed by total carotene content, tuber yield per plot, starch content and total sugar content.

In a study conducted in taro cultivars by Mukherjee *et al.* (2016), it has been found that the characters such as dry matter percentage, weight of cormels per plant and number of cormels per plant had high GCV values and also had a good share of respective PCV values. Both heritability and genetic advance were very high for number of cormels per plant (84.90 per cent and 81.19 per cent)

Variability study in sweet potato pointed out that the highest value of PCV and GCV was observed for yield per plot followed by yield per plant, leaf area, vine length, petiole length, number of tubers per plant, number of branches per plant, tuber girth and internode length. Highest heritability was shown by yield per plot followed by vine length, leaf area, yield per plant, petiole length, internode length, number of branches per plant, tuber girth, tuber length and number of tubers per plant. High heritability coupled with high genetic advance as per cent of mean was observed for yield per plot (Narasimhamurthy *et al.,* 2018).

2.3.2. Correlation Analysis

Mohankumar *et al.* (1990) indicated that mean weight of cormel, number of cormels per plant and leaf area index was positively and significantly correlated with yield. Correlation studies for 7 characters in cassava, showed that tuber yield

was positively and significantly correlated with all the characters except petiole length (Naskar *et al.*, 1991).

Nanda (1994) reported that in sweet potato, marketable tuber yield was positively and significantly correlated with number of tubers per plant but neck length was negatively correlated with yield.

In sweet potato vine length, number of branches, number of leaves and tuber yield showed high genotypic and phenotypic coefficient of variation from data on eight quantitative characters in 25 genotypes of sweet potato (Kumar *et al.*, 1996).

In a study conducted by Hossain *et al, (*2000), the results revealed that root yield was positively and significantly correlated with root diameter ($r = 0.756$), average tuber weight ($r = 0.729$) and number of tubers per plant ($r = 0.635$).

Genetic variability and correlation studies in sweet potato revealed that characters such as weight of single tuber, girth of tuber, length of tuber and number of branches per plant showed a strong positive correlation with tuber yield. However, length of vine expressed a strong negative correlation with it. Selection based on weight of single tuber, length of tuber and number of branches per plant can be effective for genetic improvement of sweet potato (Anshebo *et al.*, 2004).

Character association studies were done by Choudhary (2011) in taro. The results indicated that cormel yield was positively correlated with number of leaves (r=0.69), corm length (r=0.98), number of cormels (r=0.74) and cormel weight (r=0.97). Thus the screening of genotypes based on these traits either in combination or alone would be beneficial to enhance yield potential.

Sweet potato varieties for yield and yield contributing parameters were studied by Mekonnen *et al.* (2015). The outcome of correlation analysis indicated that root diameter was positively correlated with marketable tuberous root yield and total tuberous root yield. Similarly number of tuberous roots per plant had positive correlation with marketable tuberous root yield and total tuberous root

yield. Also marketable tuberous root yield was highly significantly and positively correlated with total tuberous root yield.

Character association indicated that tuber yield per hectare was positively and significantly associated with number of tubers per plant, tuber yield per plant and β carotene content at phenotypic and genotypic correlation levels and tuber yield per plant was positively and significantly associated with vine length, vine internodal length, leaf area and tuber girth at both phenotypic and genotypic levels (Mohanty *et al.*,2016).

2.3.3. Path Coefficient Analysis

Abraham (2002) reported that characters such as harvest index, tuber girth and tuber weight showed positive direct effect on tuber yield whereas negative influence was exerted by characters such as point of tuberization, tuber volume, tuber density, plant height and nematode susceptibility. Maximum indirect positive effect was exerted by tuber volume through tuber weight (0.798). Point of tuberization showed indirect positive effects on yield through tuber volume (0.024), days to tuberization (0.206) and plant height (0.153). Tuber volume exerted indirect positive effect on yield through tuber density (0.035), biological yield (0.020), plant height (0.150), and harvest index (0.193). Nematode susceptibility recorded indirect positive influence on yield through tuber weight (0.356) and plant height exerted its indirect positive effect through tuber volume (0.226).

The path analysis of different traits on yield of coleus mutants revealed positive direct influence through the characters such as plant height (0.979), number of tubers plant-1 (0.169), tuber girth (0.048) and tuber length (0.386). The direct effect was the highest for plant height (0.979) (Velmurugan *et al.*, 2009).

Choudhary *et al*, (2011) analysed taro accessions and pointed out that highest direct effect among characters was observed with cormel weight (1.2158).

Other characters such as number of cormels (0.8538), plant height (0.5385) and number of leaves (0.4977) also significantly influenced the yield.

Path coefficient analysis in sweet potato cultivars indicated the highest positive direct effect on fresh weight of tubers per plant at the genotypic level was due to dry matter content (2.50) via starch content and days to maturity followed by moisture content (1.74) via number of tubers per plant and total sugar content. (Solankey *et al.,* 2014).

A study on genetic variability, character association and path co-efficient analysis on morphological and yield attributing characters of taro by Mukherjee *et al.*,(2016) revealed that weight of cormels per plant possessed the highest direct effect on tuber yield. Weight of cormels per plant also showed highly significant positive correlation with tuber yield per plant. Yield attributes like number of cormels per plant and weight of corm per plant showed very little direct effect on tuber yield per plant.

Studies on character association and path analysis of sweet potato revealed that number of branches per plant, number of roots per plant, root yield per plant, root length, starch and reducing sugar exerted a high positive direct effect on root yield per hectare (Mohanty *et al.,* 2016)

The result of path-coefficient analysis of selected genotypes of sweet potato by Gurmu *et al.,*(2018) revealed that number of roots per plant and individual root weight had high values of positive direct effects (0.776 and 0.821) on fresh root yield whereas the number of roots per plant exhibited an indirect negative influence on fresh root yield through individual root weight (−0.373) and days-to-maturity (−0.217).

2.3.3. Genetic Divergence

The D^2 analysis of 43 accessions of coleus by Muralidharan *et al.* (1985) indicated some varietal differences between the accessions.

Mannan *et al.* (1993) carried out divergence analysis of Panikachu (*Colacasia esculenta* (L) Schott.) and information on genetic diversity was generated from multivariate analysis of divergence among 39 genotypes for eight yield contributing characters. Using Mahalanobis D^2 method the genotypes were assembled into four clusters. Plant height, length of stolons and number of stolons per plant contributed most towards total diversity.

Information on genetic divergence of sweet potato was derived from data on eight quantitative characters in 18 genotypes using Mahalanobis D^2 method. Naskar and Kurup (1996) grouped sweet potato genotypes into seven different clusters.

In a study conducted by Abraham (2002) sixty coleus genotypes were grouped into ten clusters. The calculated D^2 values ranged from 2.839 to 57.244 presenting high divergence among the genotypes. The highest inter-cluster distance was between clusters VI and IX (D^2 = 57.244) and the minimum inter-cluster distance was between clusters V and I (D^2 = 6.51). The highest intra cluster distance was in cluster VI representing that variability exists between the genotype of the same cluster.

Thirty potato genotypes were grouped into six clusters by Haydar *et al*, (2007). The inter cluster distances were higher than the average intra cluster distances, which indicated wide genetic diversity among the genotypes of different groups than those of same cluster. The highest inter cluster distance was observed between clusters II and VI (26.334) followed by clusters I and V (22.926) and the lowest between cluster II and cluster III (4.226). The highest intra-cluster distance was observed for the cluster VI and minimum for the cluster II.

Thirty one genotypes of potato were grouped into five different clusters. The maximum inter-cluster divergence was observed between the clusters I and V, and it was minimum between clusters II and III. The maximum intra-cluster distance was observed in cluster V and minimum in cluster I. The characters such

as plant height, number of stems per plant, tuber girth per plant, individual tuber weight per plant, tuber dry-matter content and weight loss due to respiration 150 days after harvest had contributed largely to the total divergence (Mondal *et al.*, 2007).

The cluster analysis in sweet potato by Solankey *et al*, (2014) revealed the existence of two major groups, 1 and 2 with low genetic variability of 0.52. Number of roots, weight of roots, fresh weight/plant and dry matter content differed significantly among and within agro-ecological zones. Landraces Lubisi from southern highlands zone had the highest number of roots (12 per plant) and Shinamugi from Eastern zone had highest dry matter content of 39.4 per cent.

Cluster analysis resulted in two major groups of sweet potato Group A and Group B. Group A had11sub-groups consisting of 66 genotypes whereas Group B had 5 subgroups with 30 genotypes. The analysis showed a genetic diversity of 0.54 among test genotypes. Clustering of sweet potato genotypes into groups showed a lack of association between origin of collection and genotypes. However most of the test genotypes from all the three geographical areas were clustered in Group A. Genetic similarities between and within groups and sub-groups of characterized sweet potato genotypes ranged from 0.66 to 0.91 with the mean similarity value of 0.85. (Kagimbo *et al.,* 2017).

2.4. POT CULTURE STUDY FOR IDENTIFICATION OF NEMATODE TOLERANT CHINESE POTATO GENOTYPES WITH HIGHER YIELD

Root-knot nematode, (*Meloidogyne incognita*) is a serious pest of coleus. Root knot infestation in coleus from Kerala was reported by *Sathyarajan et al.* (1966). Conspicuous gall like swellings are formed in the roots due to the attack of *M. incognita* resulting in malformation of tubers, which makes it unfit for immediate consumption as well as for storage.

Patnaik and Das (1986) observed significant reduction in coleus tuber yield with 100 nematodes per pot onwards. The crop loss due to root-knot nematode

was 92 per cent (in terms of fresh weight of tubers) at an inoculum level of 10,000 *M incognita* larvae per pot (Sosamma, 1988).

Mohandas and Ramakrishnan (1997) stated that an initial inoculum level of 100 juveniles of *M. incognita* per plant resulted in significant reduction in tuber yield and fresh and dry fibrous root weight of *Dioscorea rotundata* Poir.

Effects of *Meloidogyne incognita* on growth and storage root formation of cassava revealed that the root-gall index of inoculated plants varied from 1.5 to 4.8 and was maximum for plants inoculated with 1000 juveniles at 14 DAP (Makumbi-Kidza *et al.,* 2000).

Five sweet potato cultivars (Beauregard, Hernandez, Jewel, Porto Rico and Excel) were evaluated for resistance to *M. arenaria* race 2, *M. incognita* race 3 and *M. javanica.* Ten thousand eggs were injected into the soil to infest each plant. The number of eggs per gram of root system produced by *M. incognita* race 3 was higher in 'Beauregard' (1,214 eggs) and in 'Porto Rico' (1,571 eggs), compared to the other 3 cultivars (20 eggs). *M. incognita* race 3 caused significant galling in 'Porto Rico' and 'Beauregard', but not in the other 3 cultivars. Galling ranged from 0 to 20% of the root system affected, with 'Porto Rico' having the higher value (Cervantes-Flores, 2001)

Response of wild and cultivated potato clones to *Meloidogyne spp* was investigated by Di Vito *et al* (2003). Significant differences were found among evaluated accessions in terms of both egg mass index and gall index. Among the *S. tuberosum* clones studied, CS8617 exhibited mean gall indices of 1, 0, 0 and 0.4 when inoculated with *M. arenaria*, *M. hapla*, *M. incognita* and *M. javanica* respectively.

Variety Sreedhara differed significantly from other accessions recording the minimum number of larvae (40.00 per five g root). Variety Nidhi and CTCRI line-74, reported mean larval population of 55.33 and 58.33 per five g root respectively. The performance of CTCRI lines 64 and 79 was on par recording mean larval population of 67.67 and 76.67 respectively (Nisha, 2005).

Responses of some Chinese potato cultivars to root-knot nematode *Meloidogyne javanica* (Treub) Chitwood was examined by Jada *et al.*, (2007). Six cultivars of Chinese potato were subjected to infection by 500 second stage juveniles (J2) of root-knot nematode. The results indicated that all the six cultivars had galling index of greater than 3.5.

Olabiyi (2007) studied susceptibility of three local cultivars of sweet potato namely, Red Nancy, White Star and Puerto-Rico to root knot nematode. All the varieties screened were moderately susceptible to root knot nematode attack. Gall index was maximum in the cultivar Red Nancy (3.8) followed by Puerto-Rico (3.1) and White Star (3.7).

Studies were conducted in *Coleus forskohlii* (Willd.) Brig by Sreenivasn and Devarajan (2008) who assessed that the initial nematode population in 1100 cc soil was 83 and it increased to 865 at harvest.

Six population levels of 0, 1000, 2000, 3000, 4000 and 5000 eggs replicated five times were inoculated to Chinese potato seedlings. At a nematode population of zero (0) the maximum number of clean tubers were obtained and no nematode symptoms were observed whereas the least number of tubers were found at a nematode population of 5000 eggs which also had the highest nematode incidence symptomized by heavy galling on the roots and on the tubers. The number of tubers significantly decreased as the nematode population increased. Higher soil nematode population was also observed from plots inoculated with 5000 eggs (Anyalewechi *et al.*, 2009).

Relatively higher damage was observed on *D. rotundata* roots and tubers whereas low damage was observed on *D. alata* roots and tubers. The galling damage increased with increase in nematode inoculum level in all cultivars but damage was significantly higher only in plants inoculated with 1000 and/or 3000 juveniles of *Meloidogyne spp.* Nematode eggs were most abundant in both moderately and severely galled tubers. Relatively higher population densities of

all nematode stages were recovered in severely galled than moderately galled tubers (Mudiope *et al.*, 2012).

Nisha and Sheela (2015) reported that coleus variety Sreedhara was relatively tolerant to *M. incognita* infestation showing reduced number of larvae, females, egg masses and eggs per egg mass in root. This variety also recorded the minimum root knot index of one.

Osunlola and Fawole (2015) evaluated pathogenicity of root knot nematode on sweet potato and found that the mean gall index fluctuated significantly at various inoculum densities. Plants inoculated with 90,000 nematode eggs having mean gall index of 3.3 followed by those inoculated with 60,000 eggs (2.9) were significantly higher than those inoculated with 30,000 eggs (2.3) and control (0.0). The highest gall index was observed on cultivar TIS 4400 – 2 (2.4) followed by cv Kayode (2.1) and then cv TIS -70357 (1.8) in the first trial conducted in 2003.

MATERIALS AND METHODS

3. MATERIALS AND METHODS

The experiment entitled 'Genetic variability in Chinese potato (*Solenostemon rotundifolius* (Poir) J.K. Morton) for yield and nematode tolerance' was conducted at the Department of Plant Breeding and Genetics, College of Agriculture, Vellayani during 2017-19. The study was conducted as two experiments. The first experiment was field evaluation of Chinese potato genotypes for yield and nematode tolerance and the second experiment was pot culture study for varietal reaction to root knot nematode.

3.1. EXPERIMENTAL DETAILS

3.1.1. Collection of Chinese potato Genotypes

The experimental material consisted of 30 (Table 5) Chinese potato genotypes which were collected from CTCRI ,Sreekariyam, local markets and farmer's fields of major Coleus growing tracts of Kerala.

3.1.2. Evaluation of Chinese potato genotypes

Before starting the field experiment, the seed tubers collected from various sources were multiplied in a primary nursery and 45 day old cuttings from the top having 15 cm length with four internodes were used for planting in the main field for evaluation at College of Agriculture, Vellayani.

3.1.3. Location

Field experiment was conducted at College of Agriculture, Vellayani, situated at 8°5' N latitude and 76°9'E longitude and at an altitude of 29 m above mean sea level.

3.1.4. Season

The first experiment was conducted from August 2018 to January 2019 with thirty Chinese potato genotypes and the second experiment from July 2018 to September 2018.

Table 1. List of Chinese potato (*Solenostemon rotundifolius* (Poir) J.K. Morton) genotypes used in the study

Genotype No.	Name of the genotypes	Sources
T1	Kuruppanthara local	Kottayam district
T2	Kattappana local	Idukki district
T3	Ponkunnam local	Kottayam district
T4	Thodupuzha local 1	Idukki district
T5	Thodupuzha local 2	Idukki district
T6	Thuravur local	Alapuzha district
T7	Parassala local 1	Thiruvananthapuram district
T8	Parassala local 2	Thiruvananthapuram district
T9	Keezhuparambu local	Kozhikode district
T10	Thottamkulam local	Palakkad district
T11	Pattambi local	Palakkad district
T12	Mangalamkunnu local	Palakkad district
T13	Kallumazhi local	Palakkad district
T14	Valancherry local	Malappuram district

T15	Edayur local	Malappuram district
T16	Sreedhara	Variety released from CTCRI, Sreekariyam
T17	Kenichira local	Wayanad district
T18	Suphala	Variety released from KAU
T19	Mullankolli local	Wayanad district
T20	Nidhi	Variety released from RARS, Pattambi
T21	CP1	CTCRI, Sreekariyam
T22	CP2	CTCRI, Sreekariyam
T23	CP3	CTCRI, Sreekariyam
T24	CP4	CTCRI, Sreekariyam
T25	Thopramkudy local	Idukki district
T26	Balussery local	Kozhikode district
T27	CP7	CTCRI, Sreekariyam
T28	CP8	CTCRI, Sreekariyam
T29	CP9	CTCRI, Sreekariyam
T30	CP10	CTCRI, Sreekariyam

Plate 1. Chinese potato plants in the nursery two weeks after sowing

Plate 2. Chinese potato genotypes in the nursery two months after sowing

Plate 3. Field view of the first experiment

Kuruppanthara local

Kattappana local

Ponkunnam local

Plate 4. Thirty genotypes of Chinese potato used in the study

Thodupuzha local 1

Thodupuzha local 2

Thuravur local

Plate 4 (Continued). Thirty genotypes of Chinese potato used in the study

Parassala local 1

Parassala local 2

Keezhuparambu local

Plate 4 (Continued). Thirty genotypes of Chinese potato used in the study

Thottamkulam local

Pattambi local

Mangalamkunnu local

Plate 4 (Continued). Thirty genotypes of Chinese potato used in the study

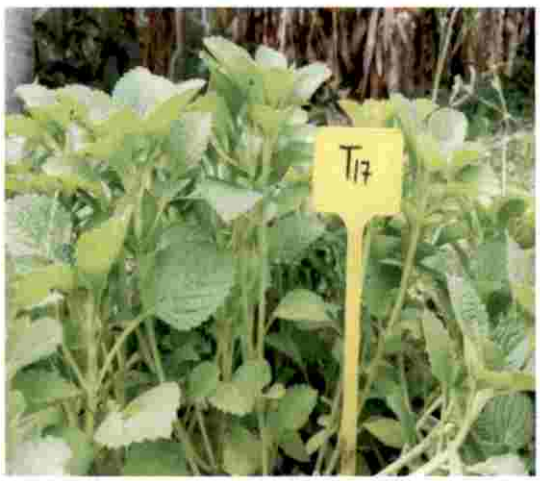
Kallumazhi local

Valancherry local

Edayur local

Plate 4 (Continued). Thirty genotypes of Chinese potato used in the study

Sreedhara



Kenichira local

Suphala

Plate 4 (Continued). Thirty genotypes of Chinese potato used in the study

Mullankolli local

Nidhi

CP 1

Plate 4 (Continued). Thirty genotypes of Chinese potato used in the study

CP 2

CP 3

CP 4

Plate 4 (Continued). Thirty genotypes of Chinese potato used in the study

Thopramkudy local

Balussery local

CP 7

Plate 4 (Continued). Thirty genotypes of Chinese potato used in the study

CP 8

CP 9

CP 10

Plate 4 (Continued). Thirty genotypes of Chinese potato used in the study

3.1.5. Layout of the Experiment

Experiment No. I

Design : RBD

Treatments : 30

Replications : 3

Spacing : 60 cm×30 cm

Plot size : 2.16 m^2

Experiment No. II

Design : CRD

Treatments : 30

Replications : 3

3.2. MORPHOLOGICAL CHARACTERIZATION

Experiment No. I

Five plants were randomly taken from each plot and tagged for recording biometric characters.

3.2.1. Biometric Characters

3.2.1.1. Days to Flowering

The number of days taken from planting till the appearance of the first open flower was recorded as the days to flowering. This was recorded at 15 days interval till 50 per cent of the plants in the plot flowered.

3.2.1.2. Days to Tuberization

Initiation of tuberization was observed at 15 days interval, after 90 days of planting .

3.2.1.3. Point of Tuberization

This parameter was employed to denote the point of tuber formation on the plant. Tuberization was at the base of the stem or at leaf nodes or both. Scores were assigned as follows to denote this character.

Base of stem alone	- 3
Base of stem + Leaf nodes	- 2
Leaf nodes only	- 1

3.2.1.4. Number of Tubers Plant^{-1}

The average number of tubers obtained from the five selected plants excluding aerial tubers was recorded as number of tubers per plant.

3.2.1.5. Tuber Girth (cm)

It was recorded as the average girth of 10 tubers randomly selected from each treatment and expressed as centimeters. The girth was measured using a cord and a meter scale.

3.2.1.6. Tuber Volume (cc)

The volume of 10 randomly selected tubers from each treatment was recorded by water displacement using measuring jar. Mean volume was expressed in cubic centimeter (cc).

3.2.1.7. Average Weight of Tubers (g)

The mean weight of 10 tubers selected from each treatment were taken and expressed in grams.

3.2.1.8.Tuber Density (g cc-^{1})

Density of tubers was calculated as the ratio of tuber weight in grams to the tuber volume in cc.

3.2.1.9. Tuber Yield (g)

Fresh weight of tubers from five randomly selected plants was recorded using a top pan weighing balance after removing under developed tubers and soil particles. The average yield was expressed in grams.

3.2.1. 10. Biological Yield (g)

The weight of plant tops was recorded from five selected plants at random and average was worked out.

3.2.1.11. Plant Height (cm)

The length of the shoot was measured at harvest as the height from the ground level to the tip of the top most leaf. The average of five plants was computed and expressed in cm.

3.2.1.12. Harvest Index

It is computed from five selected plants as the ratio of economic yield to total biomass.

3.2.1.13. Susceptibility to Nematode Infestation

3.2.1.13.1. Initial and Final Nematode Population in Soil

Soil samples (200cc) were collected from the rhizosphere of coleus plants for the estimation of nematode population before planting and at the time of harvest. Nematodes were extracted from the representative soil samples following Cobb's sieving and decanting technique (Cobb, 1918) and modified Baermann's method (Schindler,1961). The nematodes thus extracted were counted under a stereo zoom microscope .

3.2.1.13.2. Nematode Population Characteristics in Root

Main items of observations taken were number of larvae (5g root), root knot count (5g root), number of females (5g root), number of egg masses (5g root) and number of eggs per egg mass.

3.3. STATISTICAL ANALYSIS

3.3.1. Analysis of Variance (ANOVA) and Covariance (ANCOVA)

Per replication mean value of each treatment is used to work out Analysis of Variance (Panse and Sukhatme, 1967).

Anova table

Sources of variation	d.f	Sum of squares	Mean squares	F ratio
Replications	t-1	SSR	MSR	MSR/MSE
Treatment	r-1	SST	MST	MST/MSE
Error	(t-1)(r-1)	SSE	MSE	
Total	rt-1			

Where r= number of replications

t= number of treatments

SSR= sum of squares for replication

SST= sum of squares for treatments

SSE= sum of squares for error

Critical Difference, CD= $t_{\alpha}\sqrt{\frac{2MSE}{r}}$

Where t_{α} is students't table value distribution at error d.f with level of significance α (5% or 1%).

Ancova Table

Source	df	SS			Adj SS	Adj df	MSS adj	F
		Xx	Yy	Xy				
Blocks	r-1	B_{xx}	B_{yy}	B_{xy}				
Treatments	t-1	SST_{xx}	SST_{yy}	SST_{xy}	E_1 - E	t-1	MST	MST/MSE
Error	(t-1) (r-1)	SSE_{xx}	SSE_{yy}	SSE_{xy}	E	(t-1) (r-1)-1	MSE	
Treatment + error	(t-1) (r-1) +v-1	E_{1xx}	E_{1yy}	E_{1xy}	E_1	(t-1) (r-1) +v-1-1		
Regression	1	bE_{xy}			1		bE_{xy}	bE_{xy} / MSE

3.3.2 Estimation of Genetic Parameters

a. Coefficient of Variation

Genotypic, Phenotypic and Environmental Coefficient of Variation were estimated from VP, VG and VE, expressed in percentage for each trait.

i. Genotypic coefficient of variation, GCV $= \frac{\sqrt{VG}}{X} \times 100$

ii. Phenotypic coefficient of variation, PCV $= \frac{\sqrt{VP}}{X} \times 100$

iii. Environmental coefficient of variation, ECV $= \frac{\sqrt{VE}}{X} \times 100$

Where, X= Grand mean

Sivasubrahmanian and Menon (1973) reported following categories for the range of variation.

High: >20 percent

Medium: 10-20 percent

Low: <10 percent

b. Broad Sense Heritability

Ratio of genotypic variance to the total observed variance in the population and calculation expressed in percentage.

$$H^2 = \frac{VG}{VP} \times 100$$

Range of Heritability estimation (Johnson *et al.*, 1955)

High: >60 percent

Medium: 30-60 percent

Low: <30 percent

c. Genetic Advance

The expected genetic gain or improvement in the next generation by selecting superior genotype under certain amount of selection pressure. Genetic advance estimated by using Burton (1952) formula.

$GA = KH^2 \sqrt{VP}$

Where K= selection differential

At 5% selection intensity K=2.06

H^2= Heritability

Vp= Phenotypic variance

d. Genetic Advance as Percent of Mean

GAM= GA/X ×100

GA= Genetic Advance

X= Grand Mean

Ranges of genetic advance by Johnson *et al.* (1955).

High= >20 percent

Medium= 10-20 percent

Low= 10 percent

3.3.3. Estimation of Correlation

Degree and direction of association between two variables refers the correlation. Genotypic and phenotypic correlations were calculated by using Falconer (1964) formula.

Genotypic coefficient of correlation (r_g) = $r(x_i.x_j)_g = \frac{Cov((xi.xj)g}{\sqrt{v(xi)g.v(xj)g}}$

Phenotypic coefficient of correlation (r_p) = $r(x_i.x_j)_p = \frac{Cov((xi.xj)p}{\sqrt{v(xi)p.v(xj)p}}$

Error coefficient of correlation (r_e) = $r(x_i.x_j)_e = \frac{Cov((xi.xj)e}{\sqrt{v(xi)e.v(xj)e}}$

3.3.4. Path Coefficient Analysis

It is a standardized partial regression coefficient which separates the correlation coefficients into direct and indirect effects (Dewey and Lu, 1959).

$r_{1y} = P_{1y}\, r_{11} + P_{2y}r_{12} + P_{3y}r_{13} \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots + P_{ny}r_{1n}$

$r_{2y} = P_{2y}\, r_{21} + P_{2y}r_{22} + P_{3y}r_{23} \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots + P_{ny}r_{2n}$

$r_{ny} = P_{1y}\, r_{n1} + P_{2y}r_{n2} + P_{3y}r_{n3} \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots + P_{ny}r_{nn}$

Where,

1,2……..n = independent variables

y = dependent variable

$r_{1y}, r_{2y} \ldots\ldots\ldots r_{ny}$ =coefficient of correlation between independent variables

1 to n on dependent variable y.

P_{1y}, P_{2y}.....P_{ny} =direct effect of character 1 to n on character y.

The above equation can be written in matrix form

$$\begin{bmatrix} r_{1y} \\ r_{2y} \\ . \\ . \\ . \\ r_{ny} \end{bmatrix} \qquad \begin{bmatrix} 1 & r_{12} & r_{13} & . & . & r_{1n} \\ r_{21} & 1 & r_{23} & . & . & r_{2n} \\ . & . & . & . & . & . \\ . & . & . & . & . & . \\ . & . & . & . & . & . \\ r_{n1} & r_{n2} & r_{n3} & . & . & 1 \end{bmatrix} \qquad \begin{bmatrix} P_{1y} \\ P_{2y} \\ . \\ . \\ . \\ P_{ny} \end{bmatrix}$$

Then $B=C^{-1}A$ where $C^{-1}=\begin{bmatrix} C_{11} & C_{12} & C_{13} & . & . & C_{1n} \\ C_{21} & C_{22} & C_{23} & . & . & C_{2n} \\ . & . & . & . & . & . \\ . & . & . & . & . & . \\ . & . & . & . & . & . \\ C_{n1} & C_{n2} & C_{n3} & . & . & C_{nn} \end{bmatrix}$

Direct effects:

$P_{1y}= \sum_{i=1}^{k} c_{1i}\ r_{iy}$

$P_{2y} = \sum_{i=1}^{k} c_{2i} r_{iy}$

$P_{ny} = \sum_{i=1}^{k} c_{ni} r_{iy}$

Residual effect $PR_y= \sqrt{1-r^2}$

Where, $r^2 = (P_{1y}r_{1y} + P_{2y}r_{2y} + P_{3y}r_{3y} \dots\dots\dots\dots\dots\dots\dots\dots + P_{ny}r_{ny})$

P_{iy} = direct effect of X_i on y

r_{iy} = correlation coefficient of X_i on y

i = 1,2,3.....n

3.3.5. Divergence Analysis

The assessment of genetic variability present among different genotypes is one of the potent tools of measuring genetic divergence in various breeding materials. Genetic diversity arises due to geographical separation or due to genetic barriers of crossability. The genetic divergence of the ecotypes was studied using Mahalanobis D^2 statistics. The D^2 statistic measures the forces of differentiation at intra-cluster and inter-cluster levels (Mahalanobis, 1936). The genotypes were grouped into distinct clusters using their relative distances from each other (D^2 values). The accessions were clustered by Tocher's method.

3.4. POT CULTURE STUDY FOR IDENTIFICATION OF NEMATODE TOLERANT CHINESE POTATO GENOTYPES WITH HIGHER YIELD

3.4.1. Nematode Population Characteristics in Root

3.4.1.1. Number of Larvae in Root (5g)

Roots were taken and washed thoroughly in a flow of tap water. Five gram of root sample was weighed and cut into small bits of 2-3 cm length and placed above tissue paper supported by wire guage placed on petriplate. The nematode suspension was collected after 24 hr, pooled and counted under a stereo zoom microscope.

3.4.1.2. Root Knot Count (5g)

The number of galls per 5 g of root was counted and the root-knot index was fixed as per the modified method of Heald *et al.* (1989) as detailed below

Number of galls or Root-knot index	Root-knots per plant	Reaction
0	0	Highly resistant
1-25	1	Resistant
26-50	2	Moderately resistant
51-75	3	Moderately susceptible
75-100	4	Susceptible
>100	5	Highly susceptible

3.4.1.3. Number of Females (5g root)

Root sample (5 g) of tomato was cut into small bits of 2 - 3 cm length and stained by differential staining method using acid fuschsin-lactophenol mixture. Lacto phenol was prepared by mixing liquid phenol (500 mL), lactic acid (500 mL), glycerine (100 mL) and distilled water (500 mL). Stock solution of acid fuchsin was prepared by dissolving 3.5g acid fuchsin in 250 mL of acetic acid and 750 mL of distilled water. Working solution of the stain was prepared by adding one mL of the stock solution of the stain into 100 mL of lacto phenol solution. The stain was boiled in a beaker on a hot plate. The infected roots of each treatment were immersed in the boiling stain for one min. rinsed with tap water and then destained in lacto phenol solution until the maximum contrast between the nematodes and the root tissue was obtained. The processed roots were pressed between glass slides, teased with a clean needle and observed under a microscope to count the number of females.

3.4.1.4. Number of Egg Masses (5g root)

To estimate the number of egg mass per five gram of root, the root sample was cut into small bits of two to three cm length, stained and observed under the microscope.

3.4.1.5. Average Number of Eggs per Egg Mass

For the estimation of average number of eggs per egg mass, the sterile egg mass was kept between glass slides, crushed thoroughly, stained and examined under the microscope to count the eggs.

3.4.2. Nematode Characteristics in Soil (200 cc)

Soil samples (200cc) were collected from the rhizosphere of coleus plants for the estimation of nematode population at the time of harvest. Nematodes were extracted from the representative soil samples following Cobb's sieving and decanting technique (Cobb, 1918) and modified Baermann's method (Schindler,1961). The nematodes thus extracted were counted under a stereo zoom microscope .

RESULTS

4. RESULTS

4.1. EVALUATION OF CHINESE POTATO GENOTYPES FOR YIELD AND NEMATODE TOLERANCE

4.1.1. Variability

Thirty genotypes of Chinese potato were evaluated for 13 biometric characters. Performance of each genotype showed significant difference except for two of the characters under study.

4.1.1.1. Mean Performance

Mean performance of the 30 genotypes is tabulated (Table 2).

Days to flowering was noticed to be maximum for the genotype T2 (80.47). The minimum value for days to flowering was observed for the genotype T17(66.53), which was on par with eight other genotypes such as T7(67.20), T20 (67.27), T18 (67.33), T19 (68.33), T30 (68.33), T15(68.40), T10(68.87) and T12 (69.07).

Maximum days to tuberization was recorded for the genotype T3 (88.73) which was on par with genotypes T2 (88.53), T24 (86.40) and T22 (86.07). The genotype T1 (76.27) exhibited minimum days to tuberization and it was on par with the 12 genotypesT17 (76.47), T8 (76.53), T4 (76.93), T7 (77.07), T20 (77.47), T12(77.67), T15 (77.80), T14 (77.93), T6 (78.20), T10 (78.33), T18(78.53) and T19 (78.60).

Out of the thirty genotypes, tuberization was observed both at base of the stem and leaf nodes for seven genotypes (T7, T9, T12, T15, T21, T18 and T26). In all other genotypes tuberization was observed at base of the stem only.

Number of tubers per plant ranged from 6.73 to 14.27. The maximum number of tubers per plant was recorded by the genotype T17 (14.27) which was on par with the five genotypes T9(13.00), T23 (12.87), T2 (12.67), T26 (12.60) and T13(12.53). The genotype T10 had the lowest number of tubers per plant

Table 2. Mean performance of 13 biometric characters of 30 genotypes of Chinese potato

Sl No.	Genotypes	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13
1	T1	69.80	76.27	3	6.87	10.87	32.23	33.18	1.03	163.35	909.10	85.13	0.18	1
2	T2	80.47	88.53	3	12.67	8.82	19.38	19.45	1.00	208.53	993.93	74.63	0.21	1
3	T3	79.20	88.73	3	7.80	7.17	18.18	20.37	1.12	123.88	1027.40	85.5	0.12	1
4	T4	69.47	76.93	3	8.53	8.17	19.17	20.25	1.06	155.52	909.53	81.4	0.17	1
5	T5	76.47	85.20	3	9.40	8.00	21.19	22.19	1.05	173.68	873.67	77.73	0.20	1
6	T6	71.47	78.20	3	8.80	11.33	23.46	24.93	1.06	142.03	943.40	82.17	0.15	4
7	T7	67.20	77.07	2	7.20	10.13	31.53	32.17	1.02	179.43	774.27	77.4	0.23	1
8	T8	70.07	76.53	3	11.87	10.63	22.5	22.6	1.00	215.03	849.50	72	0.25	5
9	T9	69.47	80.00	2	13.00	7.57	15.93	17.33	1.09	205.07	928.97	71.6	0.22	5
10	T10	68.87	78.33	3	6.73	12.97	26.07	27.88	1.07	123.32	944.67	83.07	0.13	1
11	T11	72.07	82.13	3	9.53	11.63	21.73	22.07	1.01	163.30	957.83	81.67	0.17	5
12	T12	69.07	77.67	2	10.40	12.07	27.7	28.04	1.01	241.75	804.27	68.67	0.30	3
13	T13	71.73	80.60	3	12.53	10.63	18.27	18.4	1.01	196.67	815.67	76.33	0.24	1
14	T14	69.07	77.93	3	10.20	11.53	27.63	28.2	1.02	225.02	831.37	71.33	0.27	1
15	T15	68.40	77.80	2	11.33	12.5	27.63	31.57	1.14	231.43	826.00	72.77	0.28	1

X1- Days to flowering, X2- Days to tuberization, X3- Point of tuberization, X4- Number of tubers plant^{-1}, X5- Tuber girth (cm), X6- Tuber volume (cc), X7- Average weight of tubers(g), X8- Tuber density(gcc^{-1}), X9- Tuber yield plant^{-1} (g), X10-Biological yield(g), X11- Plant height (cm), X12- Harvest index, X13- Susceptibility to nematode infestation

Table 2. Continued…

Sl. No	Genotypes	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13
16	T16	70.27	81.00	3	10.73	7.17	16.87	17.23	1.02	136.62	1051.33	62.33	0.13	2
17	T17	66.53	76.47	3	14.27	13.1	23.57	26.57	1.13	295.37	626.70	67.67	0.47	1
18	T18	67.33	78.53	2	11.27	11.17	22.46	23.63	1.05	258.10	625.67	67.13	0.41	1
19	T19	68.33	78.60	3	11.47	11.63	22.59	24.9	1.10	211.62	875.20	72.67	0.24	1
20	T20	67.27	77.47	3	12.27	8.67	21.83	21.87	1.00	221.40	833.67	71.33	0.27	2
21	T21	73.20	82.60	2	9.33	11.77	29.93	32.07	1.07	245.60	720.87	67.33	0.34	4
22	T22	76.60	86.07	3	9.40	10.83	23.67	26.23	1.11	211.85	882.00	72.33	0.24	2
23	T23	69.67	81.67	3	12.87	10.67	22.15	23.93	1.08	252.63	653.83	65.33	0.39	3
24	T24	75.80	86.40	3	9.33	11.67	26.58	27.97	1.05	205.30	883.17	73	0.23	2
25	T25	71.60	81.47	3	9.53	9.83	25.85	27.23	1.05	176.20	1014.97	76.33	0.17	1
26	T26	73.33	83.80	2	12.60	7.5	15.03	17.8	1.18	239.17	778.00	70	0.31	2
27	T27	70.60	80.67	3	11.60	12.73	28.5	31.13	1.09	243.07	681.33	69	0.36	3
28	T28	70.40	82.27	3	9.33	13.57	32.02	32.06	1.00	254.05	637.33	67.67	0.40	1
29	T29	72.27	82.67	3	11.40	11.03	25.16	26.63	1.06	261.67	616.00	68.33	0.42	2
30	T30	68.33	79.67	3	7.87	13.17	29.08	32.84	1.13	182.68	1038.87	76.67	0.18	3
	Mean	**71.14**	**80.71**	**2.77**	**10.34**	**10.62**	**23.93**	**25.36**	**1.06**	**204.78**	**843.62**	**73.62**	**0.26**	**2.07**
	S.E(m)	**0.91**	**1.03**		**0.64**	**0.25**	**0.34**	**0.36**	**0.01**	**5.54**	**7.51**	**3.92**	**0.01**	
	CD(0.05)	**2.57**	**2.93**	**NS**	**1.82**	**0.70**	**0.96**	**1.02**	**0.018**	**15.69**	**21.25**	**11.11**	**0.018**	**NS**

X1- Days to flowering, X2- Days to tuberization, X3- Point of tuberization, X4- Number of tubers plant^{-1}, X5- Tuber girth (cm), X6- Tuber volume (cc), X7- Average weight of tubers (g), X8- Tuber density (gcc^{-1}), X9- Tuber yield plant^{-1} (g), X10-Biological yield (g), X11- Plant height (cm), X12- Harvest index, X13- Susceptibility to nematode infestation.

(6.73) which was on par with the genotypes T1 (6.87), T7 (7.20), T3 (7.80) and T30 (7.87).

The genotype T28 reported highest tuber girth (13.57 cm) and it was on par with the genotypes T30 (13.17 cm), T17 (13.3 cm) and T10 (12.97 cm). Minimum tuber girth was noticed in two genotypes T3 and and T16 (7.17 cm) which was on par with the six genotypes T26 (7.5 cm), T9 (7.57 cm), T5 (8.00 cm), T4 (8.17 cm), T20 (8.6 cm) and T2 (8.82 cm).

The highest tuber volume was noticed in the genotype T1 (32.23 cc) which was on par with the genotypes T28 (32.02 cc) and T7 (31.53cc). The genotype T9 (15.93 cc) was on par with the genotype T26 (15.03 cc) which recorded the minimum tuber volume.

The average tuber weight varied from 17.23g to 33.18g.The genotype T1 exhibited highest value (33.18g) which was on par with the genotypes T30 (32.84g) and T7 (32.17g). The lowest tuber weight was observed in the genotype T16 (17.23g) which was on par with the genotypes T9 (17.33g) and T26(17.8g).

Tuber density was maximum for the genotype T26 (1.18 gcc^{-1}). Minimum tuber density was recorded by the genotypes T20, T28 and T2 (1.00gcc^{-1}).

Highest tuber yield was obtained from the genotype T17 (295.37g). Minimum tuber yield was reported in the genotype T10 (123.32g) which as on par with the genotypes T3 (123.88g) and T16 (136.62g).

Biological yield was maximum for the genotype T16 (1051.33g) which was on par with the genotype T30 (1038.87g). The genotype T29 had the minimum biological yield (616 g) which was on par with the genotypes T18 (625.67g) and T17 (626.70g).

The genotype T3 recorded the highest plant height (85.5 cm) which was on par with the eleven genotypes T1 (85.13 cm), T10 (83.07 cm), T6 (82.17 cm), T11 (81.67 cm), T4 (81.40 cm), T5 (77.73 cm), T2 (74.63 cm),T7 (77.4 cm), T13 (76.33 cm), T25 (76.33 cm) and T30 (76.67 cm). Minimum plant height was

observed in the genotype T16 (62.33 cm) which was on par with the seventeen genotypes T23 (65.33 cm), T18(67.13 cm), T21(67.33 cm), T17 (67.67 cm), T28 (67.67 cm), T29 (68.33 cm), T12 (68.67 cm), T27 (69 cm), T26 (70 cm), T20 (71.33 cm), T14 (71.33 cm), T9 (71.6 cm), T8 (72 cm), T22 (72.33 cm), T19 (72.67 cm), T15 (72.77 cm) and T24 (73 cm).

Harvest index ranged from 0.12 to 0.47. Harvest index was the highest for the genotype T17 (0.47) and the genotype T3 (0.12) exhibited the minimum harvest index.

4.2. STATISTICAL ANALYSIS

4.2.1. Analysis of Variance

Analysis of variance was conducted for all the characters studied and the results showed significant variation among the thirty genotypes except for two characters (point of tuberization and susceptibility to nematode infestation) used in the experiment (Table 3). Analysis covariance was carried out for the 11 characters and the result showed that there exists statistically significant difference between all the characters on tuber yield plant^{-1} (Table 4).

4.2.2. Genetic Parameters

The phenotypic and genotypic coefficient of variation, heritability and genetic advance were worked out and shown in Table 5.

4.2.2.1. Coefficient of Variation

4.2.2.1.1. Phenotypic Coefficient of Variation

The phenotypic coefficient of variation (PCV) ranged from 4.60% for tuber density to 37.34% for harvest index. High PCV was observed for harvest index (37.34%), tuber yield (21.97%), number of tubers (21.22%) and tuber volume (20.07%). The characters such as average tuber weight (19.89%), tuber girth (18.39%), biological yield (15.61%) and plant height (11.18%) showed moderate phenotypic coefficient of variation. Low PCV was recorded for the characters

Table 3 : Analysis of variance of 13 characters in 30 Chinese potato genotypes

Sl No.	Characters	Mean squares	
		Genotypes	Error
1	Days to flowering	37.1680**	2.4630
2	Days to tuberization	38.4010**	3.2050
3	Point of tuberization	0.555172^{NS}	2.45E-16
4	Number of tubers per plant	11.9480**	1.2410
5	Tuber girth	11.0700**	0.1810
6	Tuber volume	68.4810**	0.3460
7	Average weight of tubers	75.5770**	0.3890
8	Tuber density	0.0070**	0.0001
9	Tuber yield	5886.6770**	92.206
10	Biological yield	51666.9250**	169.065
11	Plant height	111.0840**	46.198
12	Harvest index	0.0271**	0.0001
13	Susceptibility to nematode infestation	5.572414^{NS}	2.45E-15

Table 4. Analysis of covariance for the 11 characters of Chinese potato

Characters	Treatment mean sum of squares and product										
	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11
X1	37.16										
X2	34.67	38.40									
X3	-2.02	-0.066	11.95								
X4	-7.93	-6.89	-1.35	11.07							
X5	-15.16	-15.40	-13.95	20.29	68.48						
X6	-15.90	-14.90	-13.91	22.04	70.21	75.57					
X7	0.013	0.071	0.032	0.005	-0.112	0.035	0.007				
X8	-112.24	-43.85	176.83	97.61	121.41	146.33	0.923	5886.67			
X9	455.74	278.75	-323.05	-303.58	-533.65	-562.91	-.890	-14534.9	519666.92		
X10	15.02	1.07	-23.73	-3.82	2.59	2.12	-0.019	-603.66	1373.05	111.08	
X11	-0.292	-0.128	0.324	0.226	0.307	0.356	0.002	12.03	-35.36	-1.23	0.027

X1- Days to flowering, X2- Days to tuberization, X3- Number of tubers plant^{-1}, X4- Tuber girth (cm), X5- Tuber volume (cc), X6- Average weight of tubers (g), X7- Tuber density (gcc^{-1}), X8- Tuber yield plant^{-1} (g), X9-Biological yield (g), X10- Plant height (cm), X11- Harvest index

such as days to flowering (5.27%), days to tuberization (4.79%) and tuber density (4.60%).

4.2.2.1.2. Genotypic Coefficient of Variation

The value of genotypic coefficient of variation (GCV) ranged from 4.24% for days to tuberization to 37.09% for harvest index. The characters such as harvest index (37.09%) and tuber yield (21.46%) showed the high genotypic coefficient of variation. Moderate GCV values were observed for the characters, tuber volume (19.92%), average tuber weight (19.74%), number of tubers (18.28%), tuber girth (17.94%) and biological yield (15.53%). The characters like plant height (6.32%), days to flowering (4.78%), tuber density (4.47%) and days to tuberization (4.24%) recorded low values of genotypic coefficient of variation.

4.2.2.2. Heritability

High heritability was observed for biological yield (99.03%) followed by harvest index (98.67%), tuber volume (98.50%), average tuber weight (98.47%), tuber yield (95.44%), tuber girth (95.25%), tuber density (94.61), days to flowering (82.45%), days to tuberization (78.55%) and number of tubers (74.20%). Moderate heritability was observed for the character plant height (31.89%).

4.2.2.3. Genetic Advance (as Percentage of Mean)

The highest estimate of genetic advance recorded was 75.89 % for harvest index followed by tuber yield (43.19%), tuber volume (40.72%), average tuber weight (40.35%), tuber girth (36.08%), number of tubers (32.43%) and biological yield (31.84%). The characters such as tuber density (8.96%), days to flowering (8.94%), days to tuberization (7.75%) and plant height (7.35%) showed low values of genetic advance.

Table 5. Genetic parameters of 11 characters of Chinese potato genotypes

Characters	GCV	PCV	Heritability	Genetic advance (as % of mean
Days to flowering	4.78	5.27	82.45	8.94
Days to tuberisation	4.24	4.79	78.55	7.75
No of tubers plant^{-1}	18.28	21.22	74.20	32.43
Tuber girth	17.94	18.39	95.254	36.08
Tuber volume	19.92	20.07	98.50	40.72
Average weight of tubers	19.74	19.89	98.47	40.35
Tuber density	4.47	4.60	94.61	8.96
Tuber yield plant^{-1}	21.46	21.97	95.44	43.19
Biological yield	15.53	15.61	99.03	31.84
Plant height	6.32	11.18	31.89	7.35
Harvest index	37.09	37.34	98.67	75.89

4.2.3. Correlation Analysis

Genotypic, phenotypic and environmental correlation coefficients were studied to know the relationship between two characters. The results of correlation are presented here.

4.2.3.1. Genotypic Correlation Coefficient

The genotypic correlation coefficients are given in Table 6.

Days to flowering had positive correlation with days to tuberization (0.974) and biological yield (0.342). Days to flowering was negatively correlated with tuber girth (-0.414), tuber volume (-0.314), average weight of tubers (-0.313) and harvest index (-0.305).

Negative correlation was recorded for days to tuberization with tuber girth (-0.345), tuber volume (-0.316) and average tuber weight (-0.290).

The interrelationship of number of tubers per plant with tuber yield (0.702) and harvest index (0.599) were found to be having significant positive correlation. Tuber volume

(-0.518), average tuber weight (-0.495), biological yield (-0.436) and plant height (-0.939) had significant negative correlation with number of tubers per plant.

Tuber girth was positively correlated with tuber volume (0.745), average tuber weight (0.770), tuber yield (0.387) and harvest index (0.415). Significant negative correlation was found with biological yield (-0.406) for tuber girth.

Tuber volume had significant positive correlation with average tuber weight (0.976) and negative correlation with biological yield (-0.285). Significant negative correlation was reported for average tuber yield with biological yield (-0.286).

Tuber yield was positively correlated with harvest index (0.952). Biological yield (-0.844) and plant height (-0.991) had negative correlation with tuber yield.

Table 6. Genotypic correlation coefficient among the characters of Chinese potato

Characters	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11
X1	1.000										
X2	0.974**	1.000									
X3	-0.120	0.000	1.000								
X4	-0.414**	-0.345**	-0.132	1.000							
X5	-0.314**	-0.316**	-0.518**	0.745**	1.000						
X6	-0.313**	-0.290**	-0.495**	0.770**	0.976**	1.000					
X7	0.027	0.151	0.106	0.018	-0.163	0.047	1.000				
X8	-0.256*	-0.110	0.702**	0.387**	0.193	0.221*	0.145	1.000			
X9	0.342**	0.206	-0.436**	-0.406**	-0.285**	-0.286**	-0.048	-0.844**	1.000		
X10	0.268*	-0.029	-0.939**	-0.153	0.042	0.029	-0.043	-0.991**	0.753**	1.000	
X11	-0.305**	-0.138	0.599**	0.415**	0.226*	0.249*	0.131	0.952**	-0.946**	-0.928**	1.000

*Significant at 5% **Significant at 1%

X1- Days to flowering, X2- Days to tuberization, X3- Number of tubers plant^{-1}, X4- Tuber girth, X5- Tuber volume, X6- Average weight of tubers, X7- Tuber density, X8- Tuber yield plant^{-1}, X9-Biological yield, X10- Plant height, X11- Harvest index.

Biological yield had significant positive correlation with plant height (0.753). Negative correlation was found for biological yield with harvest index (-0.946). Plant height was negatively correlated with harvest index (-0.928).

4.2.3.2. Phenotypic Correlation Coefficient

Phenotypic correlation coefficients are given in Table 7.

The interrelationship of days to flowering was positive with the characters days to tuberization (0.827) and biological yield (0.307). Tuber girth (-0.350), tuber volume (-0.278), average tuber weight (-0.277) had significant negative correlation with days to flowering.

Days to tuberization had significant negative correlation with tuber girth (-0.317) and tuber volume (-0.275).

Positive correlation was recorded for number of tubers per plant with tuber yield (0.611) and harvest index (0.518). Tuber volume (-0.438), average tuber weight (-0.411), biological yield (-0.371) and plant height (-0.401) were negatively correlated with number of tubers per plant.

Tuber girth had significant positive association with tuber volume (0.721), average tuber weight (0.746), tuber yield per plant (0.373) and harvest index (0.403). Negative correlation was found between tuber girth and biological yield (-0.393).

Positive correlation was found for tuber volume with average tuber weight (0.975) and negative correlation with biological yield (-0.282). Tuber yield per plant recorded positive association with harvest index (0.945). Biological yield (-0.812) and plant height (-0.536) were negatively correlated with tuber yield per plant.

Biological yield had positive correlation with plant height (0.420) and negative association was reported with harvest index (-0.935). Plant height was negatively correlated with harvest index (-0.517).

Table 7. Phenotypic correlation coefficient among the characters of Chinese potato

Characters	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11
X1	1										
X2	0.827**	1									
X3	-0.058	-0.008	1								
X4	-0.350**	-0.317**	-0.095	1							
X5	-0.278**	-0.275**	-0.438**	0.721**	1						
X6	-0.277**	-0.254*	-0.411**	0.746**	0.975**	1					
X7	0.023	0.119	0.119	0.023	-0.164	0.051	1				
X8	-0.212*	-0.062	0.611**	0.373**	0.187	0.217*	0.145	1			
X9	0.307**	0.184	-0.371**	-0.393**	-0.281**	-0.282**	-0.046	-0.812**	1		
X10	0.212	0.062	-0.401**	-0.068	0.018	0.018	0.001	-0.536**	0.420**	1	
X11	-0.265*	-0.104	0.518**	0.403**	0.223*	0.247*	0.129	0.945**	-0.935**	-0.517**	1

*Significant at 5% **Significant at 1%

X1- Days to flowering, X2- Days to tuberization, X3- Number of tubers plant^{-1}, X4- Tuber girth, X5- Tuber volume, X6- Average weight of tubers, X7- Tuber density, X8- Tuber yield plant^{-1}, X9-Biological yield, X10- Plant height, X11- Harvest index.

4.2.4. Path Coefficient Analysis

Path coefficient analysis splits correlation coefficient into direct and indirect effects. The estimate of direct and indirect effects of component characters on yield was determined by path coefficient analysis.

The path correlation coefficients representing the direct and indirect effects are given in table 8.

Days to flowering showed a direct positive effect on tuber yield plant^{-1} (0.121). A negative indirect effect was showed through plant height (-0.035) ,number of tubers plant^{-1} (-0.082), biological yield (-0.120), average weight of tubers (-0.167). Tuber girth (0.021) and harvest index (0.005) showed positive indirect effect on tuber yield plant^{-1}.

Number of tubers plant^{-1} had direct positive effect on tuber yield plant^{-1} (0.682). A positive indirect effect was recorded through number of tubers plant^{-1}(0.682), biological yield (0.153), plant height (0.148) and tuber girth (0.007). Indirect effect through harvest index (-0.010), days to flowering (-0.015) and average weight of tubers (-0.263) were negative.

The direct effect of tuber girth on tuber yield plant^{-1} was negative (-0.051). A negative indirect effect was showed through harvest index (-0.007), days to flowering (-0.050), tuber girth (-0.051) and number of tubers plant^{-1} (-0.090). Indirect effect through average tuber weight (0.410), biological yield (0.142) and plant height (0.033) were positive.

The direct effect of average tuber weight on tuber yield plant^{-1} was positive (0.532). A negative indirect effect was observed through harvest index (-0.004), days to flowering (-0.038), tuber girth (-0.039), and number of tubers plant^{-1} (-0.337). Biological yield (0.101) and plant height (0.007) showed positive indirect effect on tuber yield plant^{-1}.

The direct effect of biological yield on tuber yield plant^{-1} was negative (-0.351). A negative indirect effect was showed through plant height (-0.122),

Table 8. Direct and indirect effects of correlated characters of Chinese potato on tuber yield plant^{-1}

Characters	X1	X2	X3	X4	X5	X6	X7	Genotypic correlation
X1	0.121	-0.082	0.021	-0.167	-0.120	-0.035	0.005	-0.256
X2	-0.015	0.682	0.007	-0.263	0.153	0.148	-0.010	0.702
X3	-0.050	-0.090	-0.051	0.410	0.142	0.033	-0.007	0.387
X4	-0.038	-0.337	-0.039	0.532	0.101	0.007	-0.004	0.221
X5	0.041	-0.297	0.021	-0.152	-0.351	-0.122	0.016	-0.844
X6	0.028	-0.657	0.011	-0.025	-0.278	-0.154	0.017	-0.991
X7	-0.037	0.409	-0.021	0.133	0.332	0.153	-0.017	0.952

X1- Days to flowering, X2- Number of tubers per plant, X3- Tuber girth, X4- Average weight of tubers, X5-Biological yield, X6-Plant height, X7- Harvest index.

average weight of tubers (-0.152) and number of tubers plant^{-1}(-0.297). Days to flowering (0.041), tuber girth (0.021) and harvest index (0.016) showed positive indirect effect on tuber yield plant^{-1}.

Plant height had negative direct effect on tuber yield plant^{-1} (-0.154). A positive indirect effect was observed through days to flowering (0.028), harvest index (0.017) and tuber girth (0.011).Average tuber weight (-0.025), biological yield (-0.278) and number of tubers plant^{-1} (-0.657) exerted negative indirect effect on tuber yield plant^{-1}.

Harvest index showed direct negative effect (-0.017) on tuber yield plant^{-1}. Tuber girth (-0.021) and days to flowering (-0.037) recorded negative indirect effect on tuber yield plant^{-1}. A positive indirect effect was exerted through number of tubers plant^{-1} (0.409), biological yield (0.332), plant height (0.153) and average weight of tubers (0.133).

4.2.4. Divergence analysis

The multivariate analysis using Mahalanobis' D^2 statistic provides a useful statistical tool for measuring the genetic diversity in germplasm collections with respect to the characters considered together. It also provides a quantitative measure of association between geographic and genetic diversity based on generalized distance. Further, the problem of selecting diverse parents for hybridization programme can be narrowed, if one can identify the characters responsible for the discrimination between the populations.

The data collected on yield and its contributing characters *viz.,* days to flowering, number of tubers per plant, tuber girth, average weight of tubers, biological yield, plant height and harvest index for 30 genotypes of Chinese potato were subjected to multivariate analysis. The quantitative assessment of genetic divergence was made by Mahalanobis' D^2 statistics for yield and its contributing characters.

4.2.4.1. Grouping of genotypes into various clusters

Thirty genotypes were grouped into ten clusters based on D^2 values using the Tocher's method (Rao 1952) such that the genotypes belonging to same cluster had an average smaller D^2 values than those belonging to different clusters. The distribution of genotypes into various clusters is shown in table 9. Out of the ten clusters, cluster I was the largest comprising of seven genotypes followed by cluster II, cluster III and cluster V with four genotypes, cluster IV and cluster VI with three genotypes, cluster VII with two members. Cluster VIII, cluster IX and cluster X were the smallest with one genotype each.

Biological yield contributed maximum (60.46%) to the divergence among the genotypes and it was followed by average weight of tuber (31.49%), tuber girth (4.83), harvest index (1.84%), days to flowering (1.15%), and tuber yield per plant (0.23%) (Table 10).

4.2.4.2. Average intra and inter cluster distances

The average intra and inter cluster D^2 values were presented in Table 11. Intra-cluster D^2 values ranged from zero (cluster VIII, cluster IX, cluster X) to 114.105 (cluster V). Maximum intra cluster distance was observed in cluster V (114.105), followed by cluster VI (97.379), cluster I (97.367), cluster III(89.743), cluster VII (82.519), cluster II (80.994) and cluster IV (68.387).

The inter cluster distances varied from 199.084 (cluster I and IX) to 2421.004 (cluster IV and VII). The maximum cluster distance (2421.004) was observed between clusters IV and VII followed by clusters II and VII (2393.518), clusters II and X (1851.068), clusters VII and IX (1698.049), clusters II and III (1447.345), clusters VI and X (1317.723), clusters IV and X (1312.694), clusters IV and V (1293.582), clusters II and V (1264.553), clusters II and VIII (1225.689), clusters III and IV (1191.733), clusters I and VII (1125.458), clusters VII and VIII (1058.442), clusters VI and VII (1028.141), clusters VII and X (887.569), clusters V and X (883.236), clusters VI and VIII (822.010), clusters V and IX (807.852), clusters IX and X (798.601), clusters IV and VI

Table 9: Clustering pattern of Chinese potato genotypes by Tocher's method

Cluster No	No of genotypes	Name of genotypes
I	7	T22, T24, T19, T14, T8, T12, T15
II	4	T18, T23, T29, T17
III	4	T6, T11, T25, T10
IV	3	T21,T27, T28
V	4	T4,T5,T9,T2
VI	3	T13,T20,T26
VII	2	T3, T16
VIII	1	T1
IX	1	T7
X	1	T30

Table 10. Relative contribution (%) of each character to the genetic diversity for yield and it's components in Chinese potato

Sl No.	Character	No. of times ranked first	Contribution (%)
1	Days to flowering	5	1.15
2	No of tubers plant^{-1}	0	0.00
3	Tuber girth (cm)	21	4.83
4	Average weight of tubers (g)	137	31.49
5	Tuber yield plant^{-1} (g)	1	0.23
6	Biological yield (g)	263	60.46
7	Plant height (cm)	0	0
8	Harvest index	8	1.84

Table 11: Average intra and inter cluster distance among ten clusters formed by Tocher's method in Chinese potato

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	Cluster IX	Cluster X
Cluster I	97.367 (9.86)	629.406 (25.09)	382.992 (19.57)	417.335 (20.43)	415.332 (20.38)	303.112 (17.41)	1125.458 (33.55)	269.481 (16.41)	199.084 (14.11)	628.061 (25.06)
Cluster II		80.994 (9.00)	1447.345 (38.04)	252.640 (15.89)	1264.553 (35.56)	651.543 (25.53)	2393.518 (48.92)	1225.689 (35.01)	685.707 (26.19)	1851.068 (43.02)
Cluster III			89.743 (9.47)	1191.733 (34.52)	322.735 (17.96)	659.345 (25.68)	418.155 (20.45)	265.584 (16.30)	672.174 (25.93)	245.075 (15.65)
Cluster IV				68.387 (8.27)	1293.582 (35.97)	793.796 (28.17)	2421.004 (49.20)	699.977 (26.46)	274.568 (16.57)	1312.694 (36.23)
Cluster V					114.105 (10.68)	263.848 (16.24)	393.071 (19.83)	656.021 (25.61)	807.852 (28.42)	883.236 (29.72)
Cluster VI						97.379 (9.87)	1028.141 (32.06)	822.010 (28.67)	592.492 (24.34)	1317.723 (36.30)
Cluster VII							82.519 (9.08)	1058.442 (32.53)	1698.049 (41.20)	887.569 (29.79)
Cluster VIII								0.000 (0.00)	217.704 (14.75)	210.421 (14.51)
Cluster IX									0.000 (0.00)	798.601 (28.26)
Cluster X										0.000 (0.00)

(793.796),clusters IV and VIII (699.977), clusters II and IX (685.707), clusters III and IX (672.174), clusters III and VI (659.345), clusters V and VIII(656.021), clusters II and VI (651.543), clusters I and II (629.406), clusters I and X (628.061), clusters VI and IX (592.492), clusters III and VII (418.155), clusters I and IV (417.335), clusters I and V (415.332), clusters V and VII (393.071), clusters I and III (382.992), clusters III and V (322.735), clusters I and VI (303.112), clusters IV and IX (274.568), clusters I and VIII (269.481), clusters III and VIII (265.584), clusters V and VI (263.848), clusters II and IV (252.640), clusters III and X (245.075), clusters VIII and IX (217.704), clusters VIII and X (210.421) and clusters I and IX (199.084).

4.2.4.3. Cluster means of the characters

The cluster means for each of eight characters are presented in Table 12. From the data it can be seen that considerable differences existed for all the characters under study. Cluster II had high mean value for tuber yield plant^{-1}(266.943), and harvest index (0.423). Cluster VI had highest number of tubers plant^{-1}(12.467). Cluster VII showed highest biological yield (1039.365). Cluster VIII had highest average tuber weight (33.18) and maximum plant height (85.13). Cluster IX exhibited least days to flowering (67.20). Cluster X recorded maximum tuber girth (13.17).

4.3. POT CULTURE STUDY FOR IDENTIFICATION OF NEMATODE TOLERANT CHINESE POTATO GENOTYPES WITH HIGHER YIELD

Second stage juveniles of *Meloidogyne incognita* obtained from pure culture were inoculated at the rate of 1000 juveniles per plant 15 days after planting of cuttings of Chinese potato genotypes in the pot.

4.3.1. Nematode Population Characteristics in Root

Analysis of Variance was carried out for all the characters studied and the results showed significant variation among the thirty genotypes for all the characters studied under the pot culture experiment (Table 13).

Table 12 : Mean values of ten clusters obtained by Tocher's method in Chinese potato genotypes

Cluster No.	Days to flowering	No. of tubers plant^{-1}	Tuber girth (cm)	Average tuber weight (g)	Tuber yield plant^{-1} (g)	Biological yield (g)	Plant height (cm)	Harvest index
Cluster I	71.049	10.57	11.55	27.073	220.286	850.216	71.824	0.259
Cluster II	68.95	12.453	11.493	25.19	266.943	630.55	67.115	0.423
Cluster III	71.003	8.648	11.44	25.528	151.213	965.168	80.81	0.155
Cluster IV	71.40	10.087	12.69	31.753	247.573	679.843	68	0.367
Cluster V	73.97	10.90	8.14	19.805	185.70	926.525	76.34	0.20
Cluster VI	70.77	12.467	8.93	19.357	219.08	809.113	72.553	0.273
Cluster VII	74.735	9.265	7.17	18.80	130.25	1039.365	73.915	0.125
Cluster VIII	69.80	6.87	10.87	33.18	163.35	909.10	85.13	0.18
Cluster IX	67.20	7.20	10.13	32.17	179.43	774.27	77.4	0.23
Cluster X	68.33	7.87	13.17	32.84	182.68	1038.87	76.67	0.18

Table 13. Analysis of Variance for six characters of 30 genotypes under pot culture experiment.

Sl No.	Characters	Mean squares	
		Genotypes	Error
1	Number of larvae in root	116.962**	1.132
2	Root knot count	28.427**	0.143
3	Number of females	94.878 NS	0.080
4	Number of egg masses	29.666**	0.157
5	Average number of eggs per egg mass	101.105**	3.561
6	Nematode population in soil	37.336**	0.079

** Significant at 1%

Data on reaction of different accessions of Chinese potato to *Meloidogyne incognita* are given in Table 14.

4.3.1.1. Number of Larvae in Root (5g)

There was statistically significant variation in the number of larvae (per 5 g root) in all the treatments. Number of larvae was highest in the genotype T11 (612.67). The genotype T5 recorded minimum number of larvae (12.00) which was statistically on par with the eight genotypes T17 (15.00), T28 (15.00), T4 (19.33), T10 (20.33), T19 (21.67), T1 (23.33), T18 (25.33) and T14 (26.67).

4.3.1.2. Root Knot Count (5g)

Root knot count ranged from 3.00 to 154.00. The genotype T11 (154.00) reported maximum root knot count (per 5g root). The minimum root knot count was recorded by the genotype T5 (3.00) which was on par with the genotypes T17 (3.67), T4 (4.67) and T19 (5.33).

4.3.1.3. Number of Females (5g root)

Number of females in five g root varied from 9 to 531.67. Number of females was maximum in the genotype T11 (531.67) followed by T8 (459.00) and T9 (350.33) The genotype T5 showed minimum number of females (9.00).

4.3.1.4. Number of Egg Masses (5g root)

The number of egg masses per 5g root varied from 1.67 to 98.67. The maximum number of egg masses was found in the genotype T11 (98.67). The genotype T28 reported minimum number of egg masses (1.67) and it was statistically on par with the five genotypes T4 (2.00), T5 (2.33), T17 (2.33), T1 (3.33) and T14 (3.67).

4.3.1.5. Average Number of Eggs per Egg Mass

Maximum number of eggs per egg mass was observed in the genotype T8 (269.67). The genotype T3 recorded minimum number of eggs per egg mass

Table 14: Reaction of different accessions of Chinese potato to *Meloidogyne incognita*

Sl. No	Genotypes No.	Number of Larvae (5g root)	Root knot Count (5g)	Number of Females (5g root)	Number of Egg Masses (5g root)	Average number of Eggs per egg mass
1	T1	23.33 (4.79)	5.67 (2.36)	27.67 (5.25)	3.33 (1.79)	145.67 (12.07)
2	T2	41.33 (6.35)	10.67 (3.23)	34.67 (5.88)	4.33 (2.06)	244.00 (15.62)
3	T3	40.33 (6.31)	10.33 (3.20)	18.33 (4.28)	4.67 (2.14)	135.67 (11.65)
4	T4	19.33 (4.37)	4.67 (2.13)	22.00 (4.69)	2.00 (1.38)	155.67 (12.48)
5	T5	12.00 (3.40)	3.00 (1.69)	9.00 (2.98)	2.33 (1.47)	137.33 (11.72)
6	T6	340.67 (18.45)	82.33 (9.07)	225.33 (15.01)	18.67 (4.30)	230.00 (15.17)
7	T7	83.67 (9.14)	20.67 (4.54)	159.00 (12.61)	7.33 (2.70)	183.00 (13.53)
8	T8	527.67 (22.96)	134.00 (11.57)	459.00 (21.42)	24.33 (4.92)	269.67 (16.42)
9	T9	463.00 (21.52)	119.67 (10.94)	350.33 (18.72)	20.33 (4.50)	207.33 (14.40)
10	T10	20.33 (4.477)	5.67 (2.37)	25.67 (5.06)	4.33 (2.03)	147.00 (12.12)
11	T11	612.67 (24.75)	154.00 (12.41)	531.67 (23.06)	98.67 (9.93)	238.33 (15.44)
12	T12	253.33 (15.90)	63.67 (7.97)	205.33 (14.33)	26.67 (5.16)	193.00 (13.89)
13	T13	49.00 (6.97)	12.33 (3.50)	80.33 (8.96)	10.00 (3.16)	176.33 (13.27)
14	T14	26.67 (5.13)	6.67 (2.56)	35.33 (5.94)	3.67 (1.87)	157.33 (12.54)
15	T15	51.33 (7.11)	12.67 (3.53)	62.67 (7.91)	4.67 (2.13)	150.67 (12.27)

16	T16	115.67 (10.72)	28.67 (5.33)	129.67 (11.38)	12.33 (3.49)	145.67 (12.07)
17	T17	15.00 (3.82)	3.67 (1.90)	26.67 (5.16)	2.33 (1.47)	180.00 (13.42)
18	T18	25.33 (4.97)	6.00 (2.41)	36.33 6.02)	4.33 (2.04)	155.33 (12.46)
19	T19	21.67 (4.61)	5.33 (2.27)	32.67 (5.71)	11.67 (3.40)	169.67 (13.03)
20	T20	119.33 (10.91)	30.33 (5.50)	132.33 (11.50)	11.00 (3.28)	144.00 (12.00)
21	T21	322.33 (17.95)	80.67 (8.98)	283.00 (16.82)	30.67 (5.54)	234.50 (15.23)
22	T22	133.33 (11.55)	33.67 (5.80)	160.67 12.68)	16.33 (4.03)	205.67 (14.34)
23	T23	258.33 (16.07)	64.67 (8.04)	265.67 (16.30)	25.33 (5.03)	242.50 (15.48)
24	T24	166.67 (12.90)	41.67 (6.45)	225.67 (15.02)	17.33 (4.16)	192.50 (13.80)
25	T25	61.33 (7.83)	15.33 (3.91)	86.33 (9.29)	9.67 (3.10)	140.67 (11.86)
26	T26	178.33 (13.35)	44.67 (6.68)	216.00 (14.70)	19.33 (4.39)	222.00 (14.79)
27	T27	246.67 (15.70)	61.67 (7.85)	270.00 (16.43)	23.33 (4.83)	254.00 (15.83)
28	T28	15.00 (3.82)	3.33 (1.79)	18.67 (4.30)	1.67 (1.24)	156.67 (12.52)
29	T29	97.67 (9.20)	37.67 (6.12)	175.33 (13.24)	20.33 (4.49)	216.33 (14.71)
30	T30	226.67 (15.05)	58.33 (7.63)	260.67 (16.14)	24.33 (4.92)	207.50 (14.20)
	SE (m)	0.607	0.218	0.161	0.29	0.153
	CD (0.05)	1.737	0.648	0.462	0.644	0.434

(Figures in the parenthesis are the data after square root transformation)

(135.67) and it was on par with the five genotypes T5 (137.33), T25 (140.67), T20 (144.00), T1 (145.67), T16 (145.67).

4.3.2. Nematode Population Characteristics in Soil

Data on nematode population characteristics in soil are given in Table 15.

4.3.2.1. Nematode Population in Soil (200 cc)

Nematode population in 200 cc soil ranged from 68.67 to 421.33. Maximum nematode population was found in T8 (421.33) followed by T6 (388.33), T11 (380.67) and T26 (365.33). The minimum nematode population was reported in T5 (68.67).

4.3.3. Varietal Reaction to Root Knot Nematode Under Pot Culture

Varietal reaction to root knot nematode was estimated using the scoring method of Heald *et al.* (1989) and it is given in Table 16.

Fifteen Chinese potato genotypes were found to be resistant to *M. incognita.* The genotypes T1, T2, T3, T4, T5, T7, T10, T13, T14, T15, T17, T18, T19, T25 and T28 reported root knot index of one and it is categorized as resistant to root knot nematode. Moderately resistant genotypes are T16, T20, T22, T24, T26 and T29 with a root knot index of two. The genotypes T12, T23, T27 and T30 were moderately susceptible to root knot nematode having a root knot index of three. Susceptible genotypes were T26 and T21 with a root knot index of four. There were three genotypes (T8, T9 and T11) which were highly susceptible to nematode infestation, showing a root knot index of five.

Table 15. Nematode population in 200 cc soil

Sl No.	Genotypes	Nematode population in soil (200 cc)
1	T1	145.00 (12.03)
2	T2	243.67 (15.61)
3	T3	242.33 (15.57)
4	T4	110.67 (10.52)
5	T5	68.67 (8.28)
6	T6	388.33 (19.71)
7	T7	324.00 (18.00)
8	T8	421.33 (20.53)
9	T9	345.33 (18.58)
10	T10	284.33 (16.86)
11	T11	380.67 (19.51)
12	T12	352.67 (18.78)
13	T13	242.33 (15.57)
14	T14	169.67 (13.02)
15	T15	240.67 (15.51)
16	T16	310.33 (17.62)
17	T17	84.00 (9.16)
18	T18	175.67 (13.25)
19	T19	141.67 (11.90)
20	T20	324.67 (18.02)
21	T21	351.00 (18.73)
22	T22	327.67 (18.10)
23	T23	364.00 (19.08)
24	T24	355.00 (18.84)
25	T25	279.33 (16.71)
26	T26	365.33 (19.11)
27	T27	352.33 (18.77)
28	T28	86.67 (9.30)
29	T29	343.00 (18.52)
30	T30	325.67 (18.04)
	SE (m)	0.161
	CD (0.05)	0.458

(Figures in the parenthesis are the data after square root transformation)

Table 16 : Varietal reaction to root knot nematode

Sl No	Treatments	No of galls	Root-knot index	Reaction
1	T1	5.67	1	Resistant
2	T2	10.667	1	Resistant
3	T3	10.33	1	Resistant
4	T4	4.67	1	Resistant
5	T5	3.00	1	Resistant
6	T6	82.33	4	susceptible
7	T7	20.67	1	Resistant
8	T8	134.00	5	Highly susceptible
9	T9	119.67	5	Highly susceptible
10	T10	5.67	1	Resistant
11	T11	154.00	5	Highly susceptible
12	T12	63.67	3	Moderately susceptible
13	T13	12.33	1	Resistant
14	T14	6.67	1	Resistant
15	T15	12.67	1	Resistant

16	T16	28.67	2	Moderately resistant
17	T17	3.67	1	Resistant
18	T18	6.00	1	Resistant
19	T19	5.33	1	Resistant
20	T20	30.33	2	Moderately resistant
21	T21	80.67	4	Susceptible
22	T22	33.67	2	Moderately resistant
23	T23	64.67	3	Moderately susceptible
24	T24	41.67	2	Moderately resistant
25	T25	15.33	1	Resistant
26	T26	44.67	2	Moderately resistant
27	T27	61.67	3	Moderately susceptible
28	T28	3.33	1	Resistant
29	T29	37.67	2	Moderately resistant
30	T30	58.33	3	Moderately susceptible

Kuruppanthara local

Kattappana local

Ponkunnam local

Thodupuzha local 1

Thodupuzha local 2

Thuravur local

Plate 5. Root knot formation on thirty genotypes of Chinese potato

Parassala local 1

Parassala local 2

Keezhuparambu local

Thottamkulam local

Pattambi local

Mangalamkunnu local

Plate 5 (Continued). Root knot formation on thirty genotypes of Chinese potato

Kallumazhi local

Valancherry local

Edayur local

Sreedhara

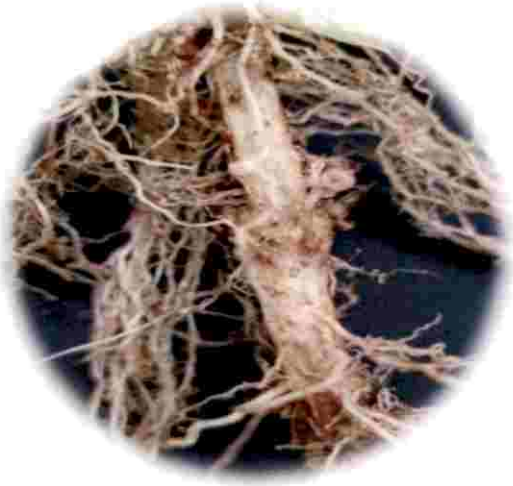
Kenichira local

Suphala

Plate 5 (Continued). Root knot formation on thirty genotypes of Chinese potato

Mullankolli local

Nidhi



CP 1

CP 2

CP 3

CP 4

Plate 5 (Continued). Root knot formation on thirty genotypes of Chinese potato

Thopramkudy local

Balussery local

CP 7

CP 8

CP 9

CP 10

Plate 5 (Continued). Root knot formation on thirty genotypes of Chinese potato

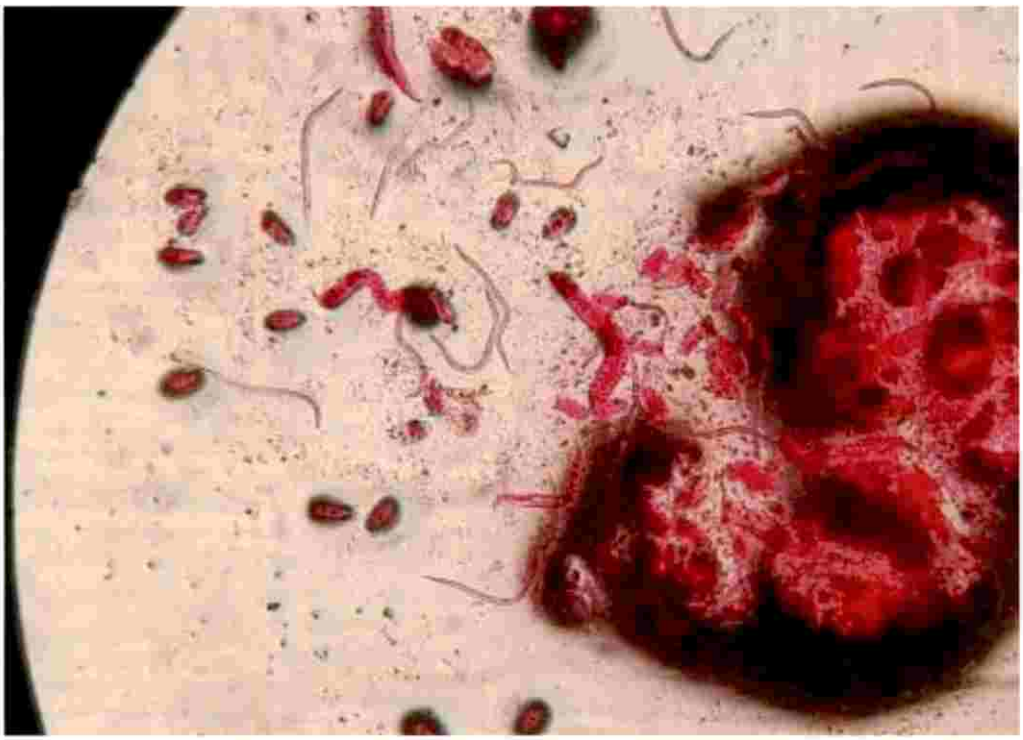


Plate 6. Larvae of root knot nematode

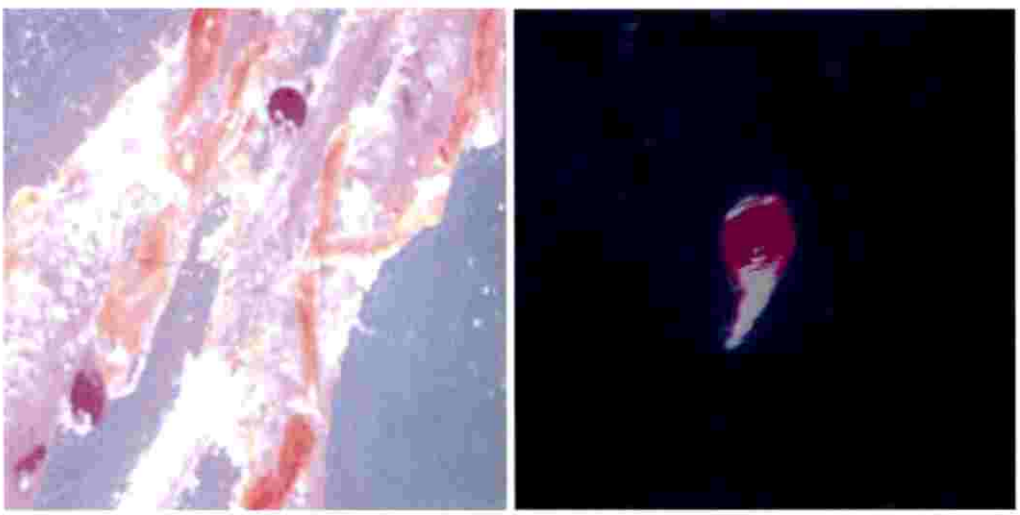


Plate 7.Females of root knot nematode

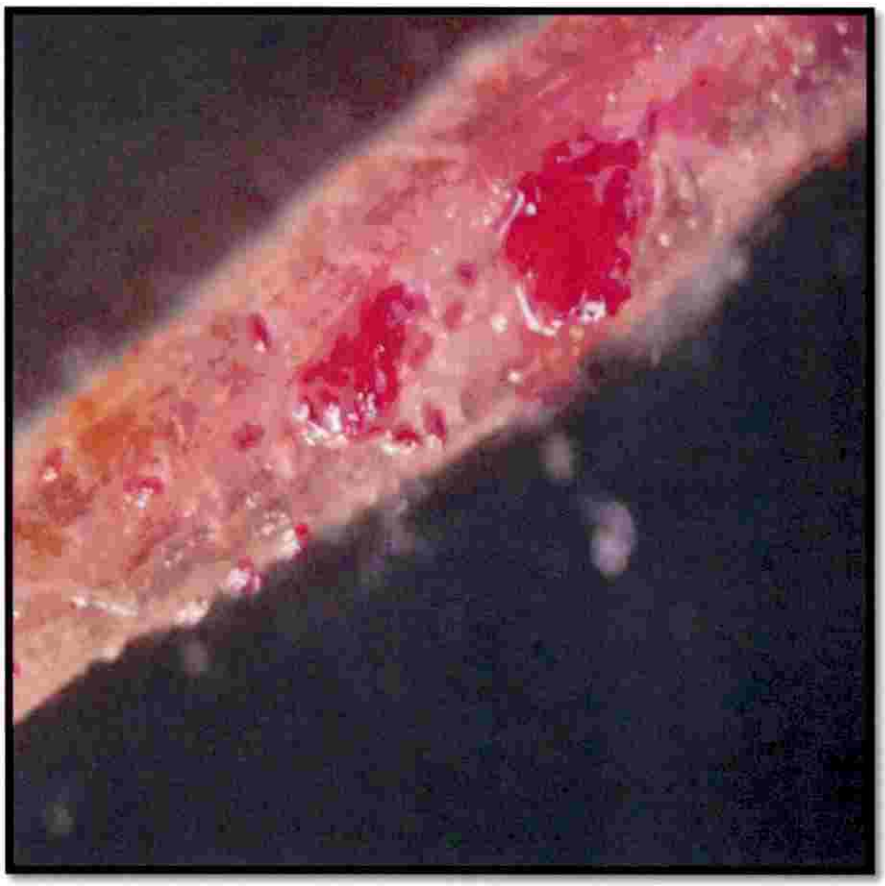


Plate 8. Egg masses of root knot nematode

DISCUSSION

5. DISCUSSION

Chinese potato is an under exploited tuber crop of the tropics. Not much work has been done on crop improvement in coleus and only few distinct varieties have been released so far. An attempt has been made here through studies on variability, character association, genetic diversity and screening for root knot nematode tolerance to identify superior genotypes with higher yield and nematode resistance.

The present study was conducted as two experiments for evaluation of Chinese potato genotypes and for identification of root knot nematode tolerant genotypes with high yield at the Department of Plant Breeding and Genetics, College of Agriculture, Vellayani.

In the present investigation, thirty diverse *Solenostemon rotundifolius* (Poir) J.K. Morton germplasm collected from CTCRI Sreekariyam, local markets and farmer's fields of major coleus growing tracts were evaluated for yield and nematode tolerance under field conditions. These accessions were used for pot culture study for varietal reaction to root knot nematode in the second experiment. The promising nematode tolerant genotypes with higher yield identified in the study can be advanced through further yield trials for promotion as varieties.

5.1. VARIABILITY ANALYSIS

5.1.1. Mean performance

In the present study, thirteen biometric characters were analysed for thirty genotypes. Except for the two characters (point of tuberization and susceptibility to nematode infestation) all others showed considerable variation among the genotypes studied. The wide range of variation noticed in all the eleven characters confirmed that the materials selected were genetically diverse and that they were appropriate for the study. Variability for different characters has been previously observed by several workers such as Sarkar *et al.* (1992), Sreekumari and

Abraham (1985), Khairwal and Babu (1985), Amalraj *et al.* (1989) and Abraham (2002).

Significant variation was observed in days to flowering which ranged from 66.53 to 80.4. Minimum days to flowering (66.53) was observed in the genotype T17 (Kenichira local), which is a suitable attribute for developing short duration varieties. The variation observed for days to flowering in the present study was in accordance with the findings of Abraham (2002) and Kavitha (2007), although the duration to flowering was much larger in both situations.

Days to tuberization ranged from 76.27 (Kuruppanthara local) to 88.73 (Ponkunnam local) in the present study. Much longer days to tuberization was reported by Abraham (2002).

Out of the thirty genotypes, tuberization was observed both at base of the stem and leaf nodes for seven genotypes Parassala local 1, Keezhuparambu local, Mangalamkunnu local, Edayur local, Suphala, CP 1 and Balussery local. In all the other genotypes tuberization was observed at base of the stem only. Formation of aerial tubers which are not harvestable is an undesirable character due to which the underground tuber yield will get reduced and photosynthates are unnecessarily wasted.

A significant variation in number of tubers plant^{-1} was noticed among the Chinese potato genotypes studied. Number of tubers per plant ranged from 6.73 to 14.27. The maximum number of tubers^{-1} plant was recorded by the genotype Kenichira local(14.27). The genotype Thottamkulam local had the lowest number of tubers plant^{-1} (6.73). The results were in accordance with the studies conducted by Archana (2001) where Sreedhara produced 13.69 marketable tubers. Jayapal (2012) also reported similar results where Sreedhara produced 12.61 marketable tubers and in the findings of Anju *et al.*(2015) where Suphala planted in off season produced 8.17 to 12.10 tubers. In the present study suphala gave a comparable yield of 11.27 tubers plant^{-1} and Sreedhara 10.73 tubers plant^{-1}.

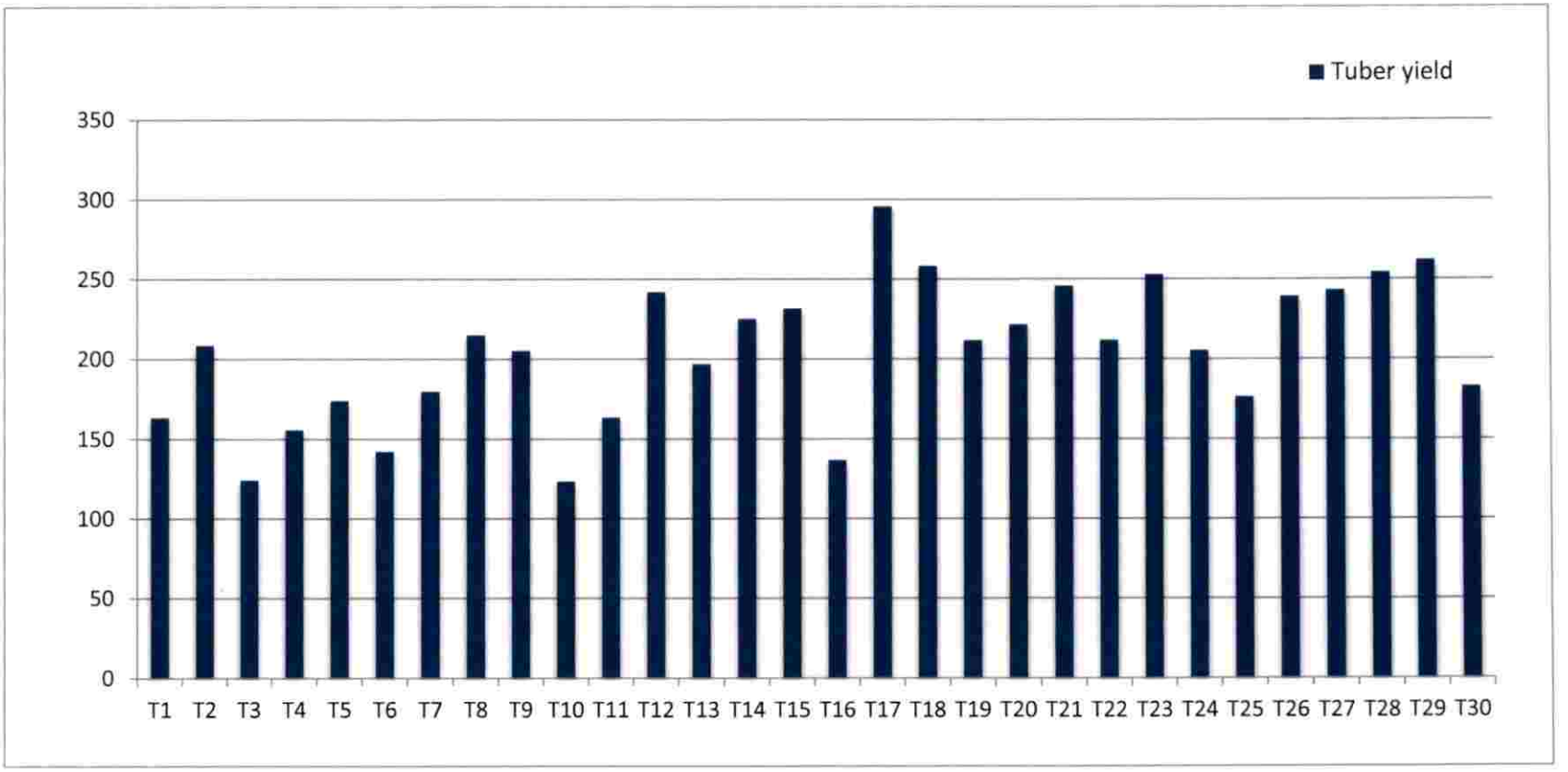


Fig.1. Comparative mean yield performance of 30 Chinese potato genotypes

In the present study, tuber girth showed significant variation ranging from 7.17 cm for Ponkunnam local and Sree Dhara to 13.7 cm for CP 8 with an average value of 10.62 cm. The observation of the current study is supported by the findings of Agyeno *et al.* (2014) where tuber girth ranged from 7.97 to 11.80 cm between varieties. Lower tuber girth was reported in various studies conducted by Abraham (2002), Prematilake (2005) and Velmurugan *et al.*(2009), the mean values being 4.9 cm, 3.4 cm and 3.45 cm respectively.

The lowest tuber volume among the thirty Chinese potato genotypes was recorded in Balussery local (15.03 cc) which was on par with the genotype Keezhuparambu local. The highest tuber volume was noticed in the genotype Kuruppanthara local (32.23 cc). Highest tuber volume of 10.70 cc was reported by Abraham (2002).

The average tuber weight varied from 17.23g to 33.18g.The genotype Kuruppanthara local exhibited the highest value (33.18g) which was on par with the genotypes CP 10 (32.84g) and Parassala local 1(32.17g). Similarly, variations in average tuber weight was reported by Abraham (2002) and Prematilake (2005) also but the values were lower being 2.70 - 14.07 g and 3.1 – 23.7 g respectively.

Tuber density was maximum for the genotype Balussery local(1.18 gcc^{-1}). Minimum tuber density was recorded by the genotypes Nidhi, CP 8 and Kattappana local (1.00gcc^{-1}). This result was in agreement with the findings of Abraham (2002) where the density ranged from 1.00 to 1.4 gcc^{-1}.

The present study reported tuber yield $plant^{-1}$ ranging from 123.32g to 295.37g. Comparative yield performance of all the genotypes is given in Fig.1. Highest tuber yield was obtained from the genotype Kenichira local (295.37g). Minimum tuber yield was reported in the genotype Thottamkulam local (123.32g). The average value for tuber yield $plant^{-1}$ was 204.778. Similar results for average tuber yield $plant^{-1}$was reported by Archana (2001) and Abraham (2002), being 208.33g and 224.71g respectively.

The greatest variability was recorded for biological yield which could be used as a selection criterion for crop improvement in Chinese potato. Biological yield was the highest for the genotype Sreedhara(1051.33g). The genotype CP9 had the lowest biological yield (616 g) and the average was 843.62 g. Variation for this character was in accordance with the earlier reports of Abraham (2002) reporting n average biological yield of 667.83 g.

Plant height ranged from 62.33 cm to 85.5 cm with an average of 73.61 cm. The genotype Ponkunnam local recorded the highest plant height (85.5 cm) in the present study. Supporting evidences were given by Abraham (2002), where the plant height ranged from 56.65 – 140.90 cm among the 60 genotypes with an average of 98.54 cm. Kavitha (2007) obtained an average plant height of 31.07 cm among the 37 genotypes studied.

Harvest index was the highest for the genotype Kenichira local (0.47) and the genotype Ponkunnam local (0.12) exhibited the lowest harvest index. The variations observed in the present study were in accordance with the findings of Abraham (2002) ranging from 0.06 to 0.57. in coleus and Gurmu (2018) in Sweet potato (0.3 to 0.7)

5.1.2 Variability Components

The variability available in a population could be partitioned into heritable and non-heritable components with the aid of genetic parameters such as genotypic coefficient of variation (GCV) heritability, (H^2) and genetic advance (GA) which can be used as reliable guidelines for selection. PCV measures the extent of total variation while GCV is effective in providing the range of genetic diversity of the quantitative traits. Moreover, GCV and PCV helps to separate out environmental influence on the genotype from the total variability. These parameters are estimated and the results are discussed here (Fig.2)

The value of genotypic coefficient of variation was smaller than phenotypic coefficient of variation, but small difference was recorded between PCV and GCV indicating that environment had less contribution towards trait

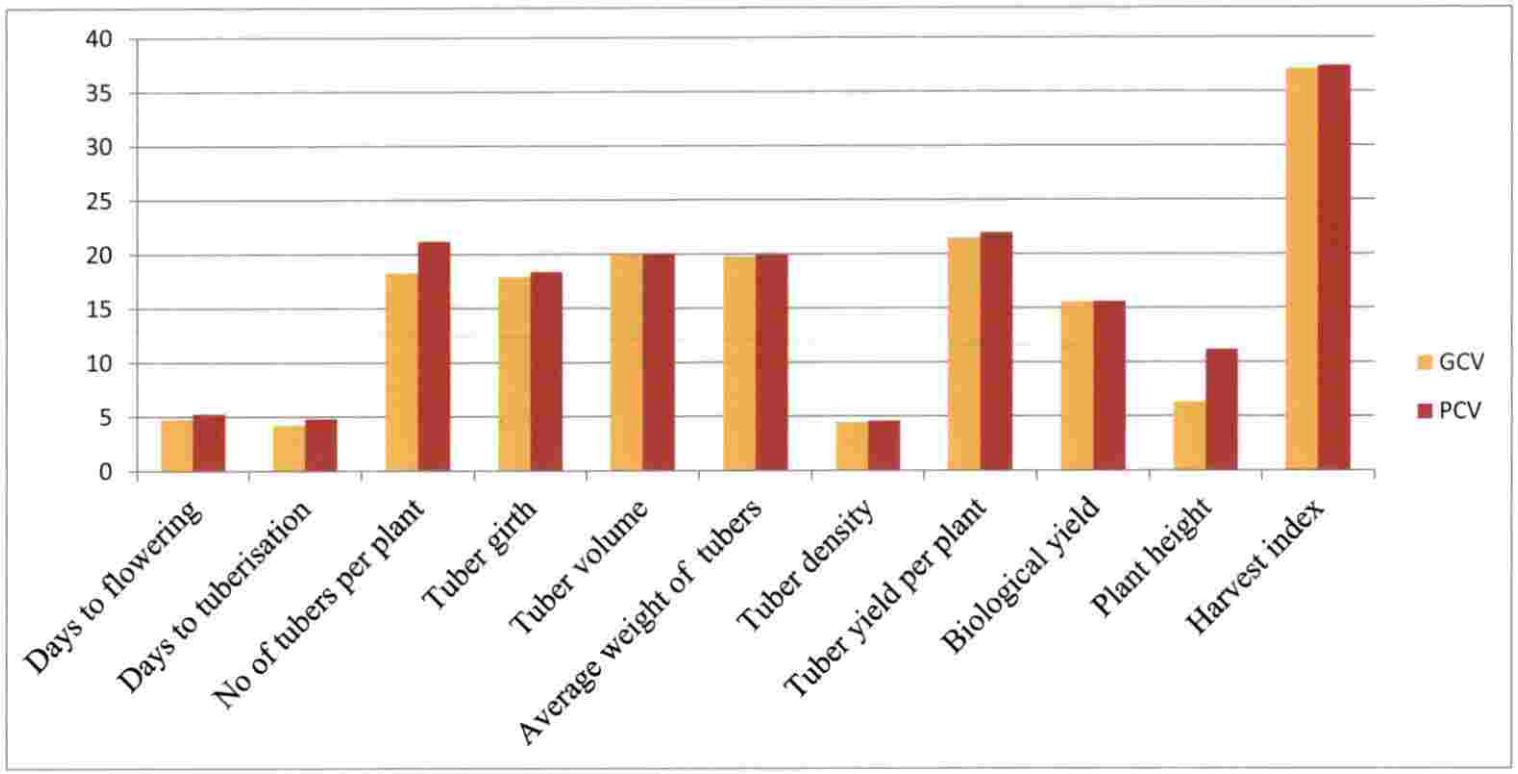


Fig. 2. GCV and PCV for the characters of Chinese potato genotypes

expression. Similar result was reported by Abraham (2002) in (*Coleus parviflorus* Benth.), Anshebo *et al.* (2004), Solankey *et al* (2014) and Demelio and Aragaw (2016) in sweet potato.

The values of GCV ranged from 4.24per cent for days to tuberization to 37.09per cent for harvest index. High GCV and PCV were observed for the characters harvest index and tuber yield which revealed that total variation present in genotypes were contributed by genetic component. Therefore, selection could be done for these characters. High GCV and PCV values were observed for tuber yield, harvest index, mean volume of tuber, mean weight of tuber and biological yield in a study conducted by Abraham (2002). The results of the present study were also in accordance with the findings reported in cassava by Naskar *et al.* (1991), Kumar *et al.* (1996), Alam *et al.* (1998) and Choudhary *et al.*(1999) in sweet potato.

Moderate GCV and PCV was recorded for average weight of tuber, tuber girth and biological yield which indicated that the variation present in the germplasm for these characters was moderately contributed by genetic constitution of genotypes. Moderate GCV and PCV was observed for tuber girth in coleus by Abraham (2002). The minimum PCV and GCV values were recorded for the characters days to flowering, days to tuberization and tuber density. Similar findings were reported by Abraham (2002)

Moderate GCV and high PCV were observed for number of tubers plant^{-1} and tuber volume. Low GCV and moderate PCV was recorded for the character plant height.

5.1.3 Heritability and Genetic Advance

Heritability is the heritable portion of the phenotypic variance of the characters. It indicates the degree at which a character is transmitted from the parent to its offspring. The estimates of heritability help the plant breeder in selection of elite genotypes from diverse genetic populations. Higher broad sense

heritability value of the character indicates the greater proportion of genotypic variance on the heritable character rather than phenotypic effect.

In the study, heritability estimates ranged from 31.89 per cent for plant height to 99.03 per cent for biological yield. High heritability was observed for biological yield (99.03 per cent) followed by harvest index (98.67 per cent), tuber volume (98.50 per cent), average tuber weight (98.47 per cent), tuber yield (95.44 per cent), tuber girth (95.25 per cent), tuber density (94.61), days to flowering (82.45 per cent), days to tuberization (78.55 per cent) and number of tubers (74.20 per cent). Moderate heritability was observed for the character plant height (31.89 per cent) (Fig.3).

Average weight of tubers, tuber yield plant^{-1}, tuber density, biological yield and harvest index ^{1} showed high heritability in the broad sense, in accordance with the results of Abraham (2002) in coleus and Kamalam (1991) in sweet potato. Apte *et al.* (1994) reported that in taro, cormel girth had high values for heritability and similar result was reported by Narasimhamoorthy *et al.* (2018) in sweet potato. High heritability for number of cormels plant^{-1} was reported by Mukherjee *et al.* (2016) in taro and Narasimhamoorthy *et al.*(2018) in sweet potato. This indicates that heritability of these characters is due to additive gene effects and hence the observed variability is heritable with negligible influence of environment. So selection may be effective in improving these traits.

However in contradiction to the present results Abraham (2002) reported high heritability for plant height.

Heritability values alone may not provide clear predictability of the breeding value. Heritability in conjugation with genetic advance over mean is more effective and reliable in predicting the effectiveness of selection.

In the present investigation, highest estimate of genetic advance recorded was 75.89 per cent for harvest index followed by tuber yield (43.19per cent), tuber volume (40.72per cent), average tuber weight (40.35per cent), tuber girth (36.08per cent), number of tubers (32.43per cent) and biological yield (31.84per

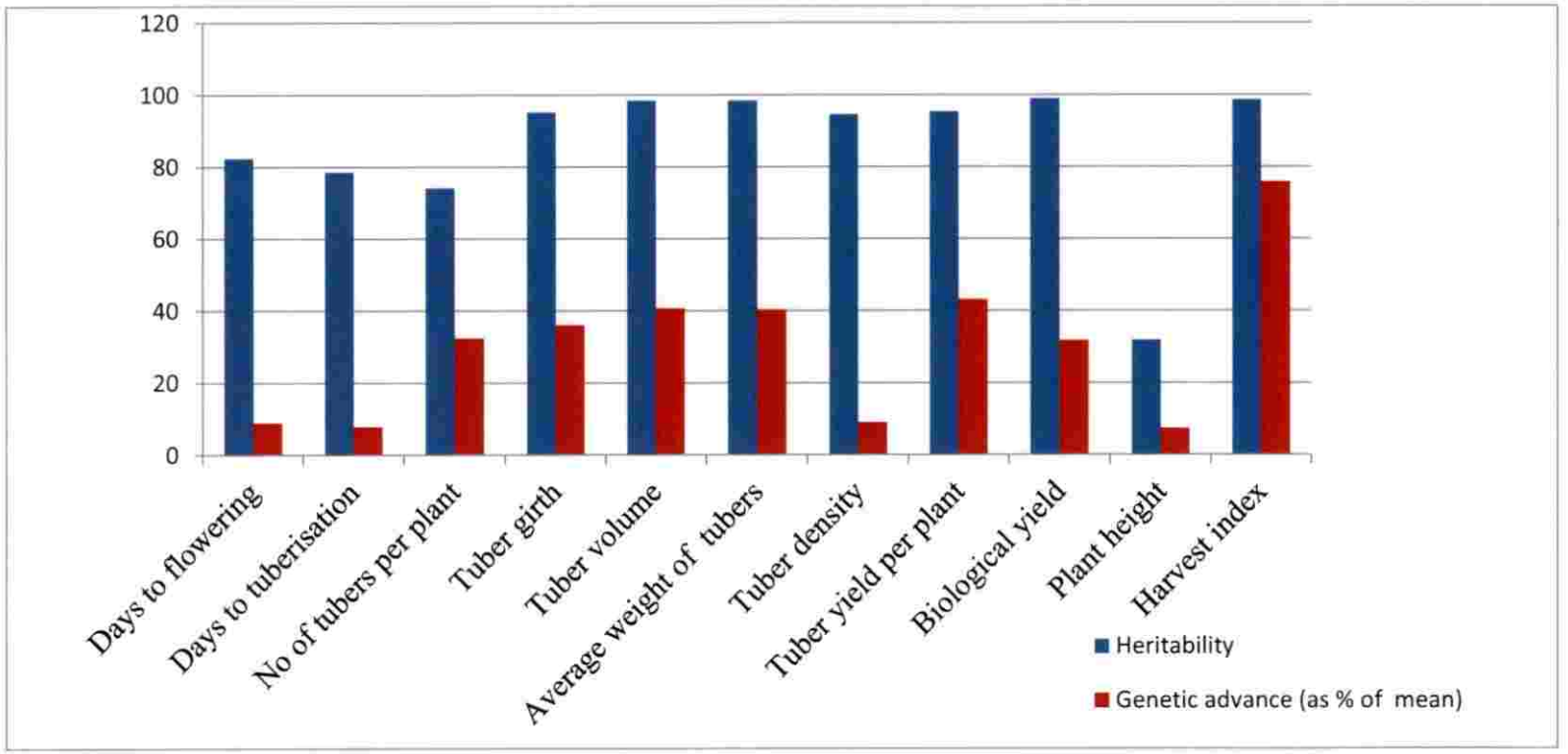


Fig. 3. Heritability and Genetic Advance for the characters of Chinese potato genotypes

cent).High genetic advance for biological yield and tuber yield plant^{-1} was reported in coleus by Abraham (2002) and Kamalam (1991) in sweet potato. High genetic advance of the characters such as tuber girth, average tuber weight and number of tubers plant^{-1} was in line with the findings of Hossain *et al.* (2000).

High heritability coupled with high genetic advance was observed for the traits namely biological yield, harvest index, tuber volume, average tuber weight, tuber yield plant^{-1}, tuber girth and number of tubers plant^{-1}. Occurrence of high heritability and high genetic advance together may be ascribed to the conditioning of the characters by additive gene action which could be improved upon by direct selection. High heritability and high genetic advance was reported for the traits tuber yield plant^{-1} and biological yield by Abraham (2002) and for average weight of tubers and number of tubers plant^{-1} in a study conducted by Hossain *et al* (2000). High heritability with low genetic advance was observed for the characters tuber density, days to flowering and days to tuberization. This indicted that even though traits are highly heritable the improvement over mean population is less because of the presence of non-additive effects. Moderate heritability with low genetic advance was observed for the character plant height in the present investigation.

5.1.4 Correlation Studies

Correlation measures the degree and direction of association between two or more variables. Knowledge of correlations studies helps the plant breeder to ascertain the real components of yield and to provide an effective basis for selection. It may be positive or negative correlation which depends on the nature of the traits. When selection is carried out for a trait of interest in a population, it is associated with the improvement of other traits associated with the trait of interest. This helps in simultaneous improvement of more than one character which moves in the same direction of selection.

In the present study, genotypic and phenotypic correlations were worked out for 11 quantitative characters of Chinese potato genotypes. Correlation

analysis between the characters revealed that genotypic correlation coefficients were higher than the corresponding phenotypic correlation coefficients due to the presence of environmental influence on two traits. Moreover, the difference between phenotypic and genotypic correlations were lesser, which detailed the environment had a minute effect on those characters.

Number of tubers plant^{-1} ,tuber girth, average weight of tubers and harvest index had a significant positive correlation with tuber yield plant^{-1}. Due to positive correlation, improvement in any one of these characters will simultaneously result in improvement of the dependent character. Similar correlated responses were observed in the studies conducted by Abraham (2002) in coleus, Hossain (2000) in sweet potato and Choudhary (2011) in taro.

The genotypic correlation between the characters provides a reliable measure of genotypic association between characters and helps to differentiate the vital associations useful in breeding from non-vital ones. (Falconer,1981). On analysing the genotypic correlation among 11 quantitative characters in Chinese potato the trait harvest index showed significant positive correlation with most of the characters except days to flowering, days to tuberization, tuber density, biological yield and plant height. Abraham (2002) studied 60 Chinese potato genotypes and reported positive genotypic correlation of harvest index with tuber yield, tuber volume, average weight of tubers and days to flowering. Comparable correlations were also reported by Sreekumari and Abraham (1985) in coleus and Gurmu *et al.* (2018) in sweet potato.

Number of tubers plant^{-1} was positively correlated with tuber yield plant^{-1} and harvest index. Similar reports were also made by Gurmu *et al.* (2018).

Tuber volume was positively and significantly correlated with tuber girth, average weight of tubers and harvest index. . The result of the present study was supported by the findings by Abraham (2002).

Average weight of tubers was positively correlated with tuber yield plant^{-1} tuber volume and harvest index. Abraham (2002) reported similar findings.

Biological yield and plant height were negatively correlated with tuber yield plant^{-1}. This apparent negative correlation at genetic level would have arisen from repulsion linkage of gene(s), controlling the direct and indirect effects. Similar results were achieved by Lakshmi and Amma (1980) in Asian greater yam, Abraham (2002) in coleus and Demelie and Aragaw (2016) in sweet potato.

The present study clearly revealed that direct selection for tuber yield alone will not help because the character is influenced both by environment as well as associated traits. This is in conformity with the findings of Sreekumari and Pillai (1993) in taro and Abraham (2002) in coleus.

5.1.5 Path Analysis

Correlation coefficient indicates the degree of relationship between characters but that alone does not give a clear picture of the measure of association between yield and its components. Path analysis was done to confirm whether the correlation of component characters with the dependent character was due to their direct effect or due to indirect effect through some other character. Path coefficient divides the correlation coefficients into direct and indirect effects which contribute to yield (Dewey and Lu, 1959). If the correlation between tuber yield and a component character is due to direct effect, it indicates true direct association between these traits. Thus, direct selection for this component character can be rewarding to attain improved tuber yield. If the correlation is due to indirect effect of the component character through another component character, then the plant breeder should go for selection of the latter character through which the indirect effect was influencing the tuber yield.

From the genotypic correlation the correlated yield components such as days to flowering, number of tubers plant^{-1}, tuber girth, average weight of tuber, biological yield, plant height and harvest index were taken as independent characters for path coefficient analysis for better interpretation. This measures the direct and indirect contribution of independent characters on dependent character (Fig.4).

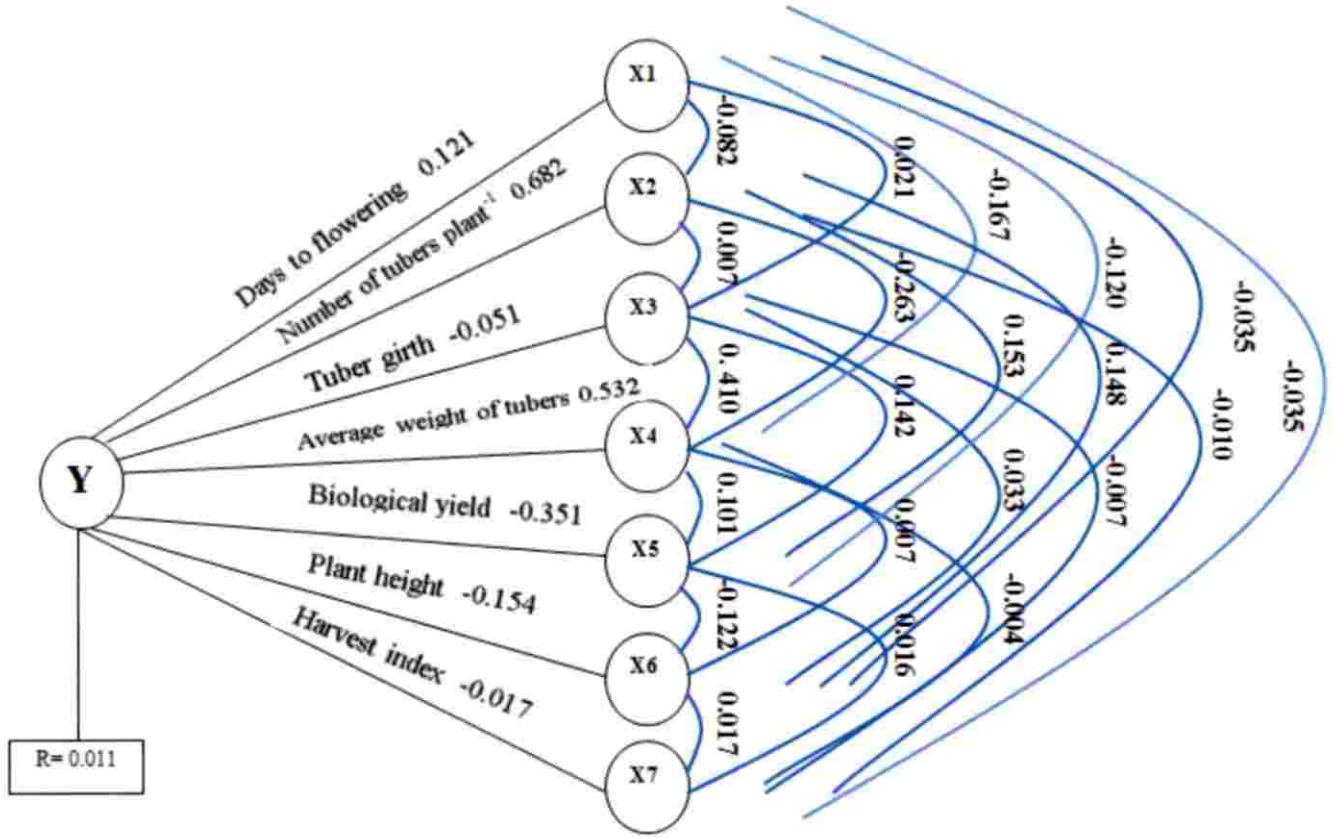


Fig. 4. Path diagram showing direct and indirect effect of different characters of Chinese potato on tuber yield plant^{-1}

In the present study, the highest positive direct effect on tuber yield plant^{-1} was shown by the trait number of tubers plant^{-1} followed by average weight of tubers and days to flowering. The two characters namely number of tubers plant^{-1}, and average weight of tubers were found to have direct and significant positive correlation towards tuber yield plant^{-1}. This indicated that selection for the above traits will result in improvement of tuber yield in Chinese potato genotypes. In accordance with the present study Choudhary *et al.*,(1999) reported that cormel weight and number of cormels had highest direct effect on cormel yield of sweet potato. Similar findings were reported by Mukherjee *et al.*(2016) in taro and Gurmu *et al.*(2018) in sweet potato.

The traits biological yield and plant height exhibited direct, significant negative correlation towards tuber yield, indicating that selection for this character will result in reduction of tuber yield in Chinese potato genotypes. This result was supported by the findings of Abraham (2002).

Days to flowering had direct positive effect on tuber yield plant^{-1} but the correlation was negative. In such situations, direct selection for such traits should be practised to reduce the undesirable indirect effect.

The characters tuber girth and harvest index showed a negative direct effect on yield plant $^{-1}$ and positive genotypic correlation indicated the indirect effect through the other independent variable. Negative direct effect and significant positive correlation of tuber girth on tuber yield^{-1} was in line with the findings of Mohanty *et al.* (2016) in sweet potato.

All the traits included in the study explained almost all variability towards yield which could be concluded from the low residual effect.

5.1.6. Divergence Analysis

Multivariate analysis using Mahalanobis D^2 statistics is a valuable tool for obtaining quantitative estimates of divergence between biological populations. For an effective breeding programme, information concerning the extent and

nature of genetic diversity within a crop species is essential. It is found to be a powerful tool in the hands of the plant breeder to assess the degree of dissimilarity among the genotypes and consequently to group them based on their phenotypic expression. The variability can be further expanded through induced mutation in representative samples taken from these clusters.

D^2 analysis using a combined classification approach in respect of eight selected characters led to the discovery that the 30 genotypes studied could be grouped into ten clusters. The clustering specified that some genotypes belonging to the same locality got separated into different clusters and certain genotypes from different places got assembled in the same cluster. This leads to the conclusion that factors other than geographical diversity may be accountable for such clustering and that there was no parallelism between genetic diversity and geographic distribution. A similar interpretation of non-parallelism of genetic divergence with geographical distribution has been conveyed by Roy and Panwar (1993) and Mannan *et al.* (1993) in taro. These results agree with the suggestions made by Raut *et al.* (1980) that genetic drift and human selection could cause greater diversity than geographic distance.

In the present study out of the ten clusters, cluster I was the largest comprising of seven genotypes followed by Cluster II, Cluster III and Cluster V with four genotypes, Cluster IV and Cluster VI with three genotypes and Cluster VII with two members. Cluster VIII, Cluster IX and cluster X were the smallest with one genotype each. Clusters with maximum number of genotypes comprise of members collected from distant districts.

Maximum intra cluster distance was observed in cluster V, which shows that there exists significant variability among the genotypes of that cluster. Selection within a cluster might also be exercised based on the highest mean performance of the genotypes for desirable traits such as tuber yield plant^{-1}, girth of tuber, harvest index and plant height. Maximum cluster distance was observed between clusters IV and VII (Fig 5). The greater the distance between clusters the

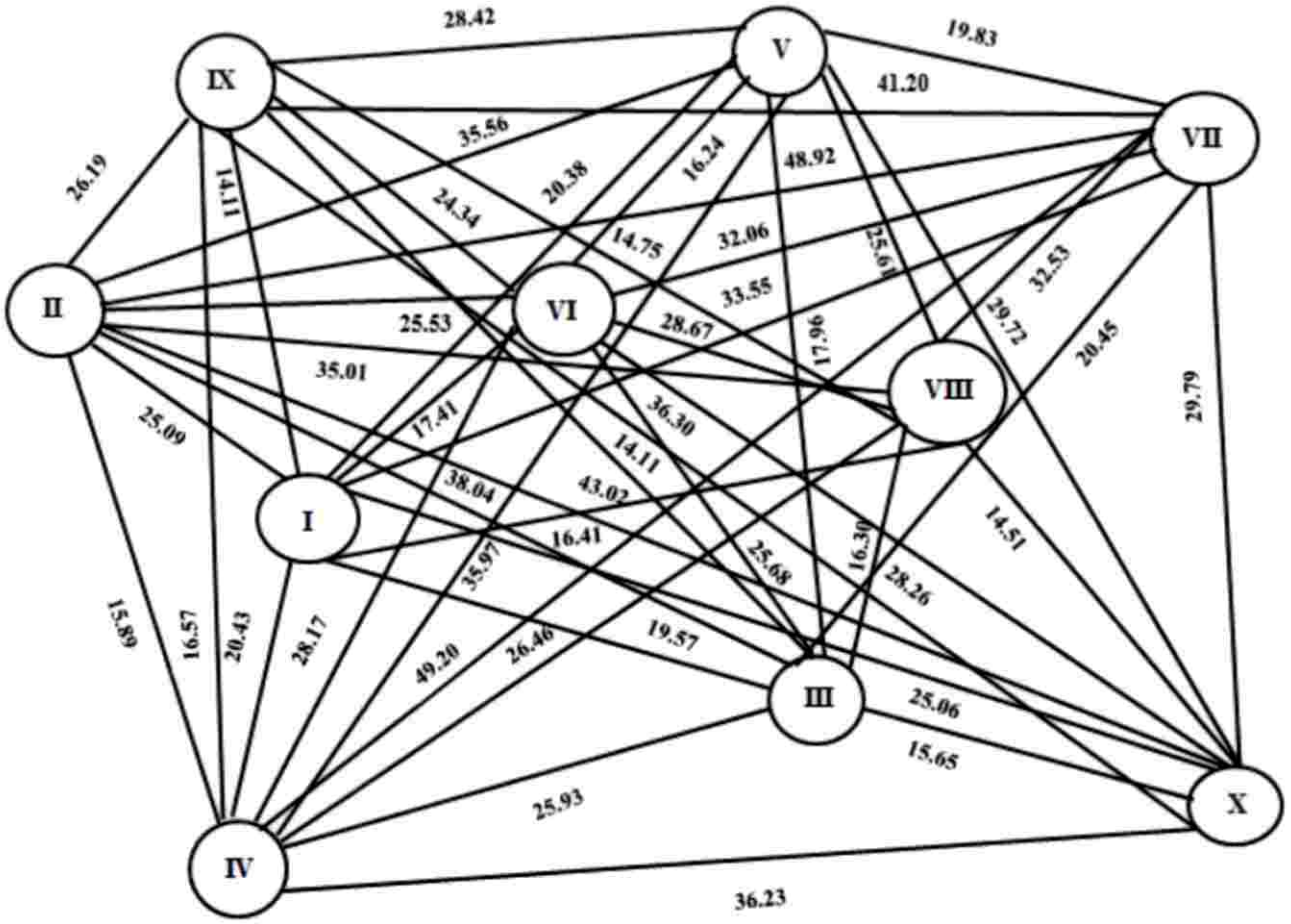


Fig. 5.Cluster diagram showing intra and inter cluster distances and clustering pattern

wider will be the genetic distance between the member genotypes. Biological yield contributed maximum to the divergence among the genotypes and it was followed by average weight of tuber. This finding is reinforced by earlier findings of Haydar *et al.* (2007).

Cluster II had high mean value for tuber yield plant^{-1}and harvest index. Cluster VI had highest number of tubers plant^{-1}. Cluster VII showed highest biological yield. Cluster VIII had highest average tuber weight and maximum plant height. Cluster IX exhibited least days to flowering. Cluster X recorded maximum tuber girth. The results indicated that selection of genotypes having high values for particular trait could be made and used in crop improvement programmes.

5.2. IDENTIFICATION OF NEMATODE TOLERANT CHINESE POTATO GENOTYPES WITH HIGHER YIELD

Root knot nematode, *Meloidogyne incognita* (Kofoid and White) Chitwood is a serious pest of *S. rotundifolius*. Due to nematode attack conspicuous gall like swellings are formed in roots resulting in malformation of tubers making it unfit for consumption as well as storage. Overdependence on pesticides harmful to the environment can be avoided if a variety resistant to *M. incognita* is identified. Hence varieties tolerant to *M. incognita* infestation are the need of the hour. The resistance reaction of the varieties / lines / accessions, a major component in integrated nematode management strategy was taken care of, in this study. Hence the present study was conducted to identify genotypes tolerant to root knot nematode.

Pot culture studies were conducted to evaluate the varietal reaction to root knot nematode. The same thirty genotypes used in the first experiment were raised in pots. Each pot was artificially inoculated with 1000 number of second stage juveniles of *Meloidogyne incognita.* Comparative reaction of the genotypes was evaluated in terms of nematode characteristics in root and soil.

5.2.1. Nematode Characteristics in Root

Number of larvae, root knot count and number of females were highest in the genotype Pattambi local whereas the genotype Thodupuzha local 2 recorded minimum values. Similarly maximum root gall index was produced in cassava when the plants were inoculated with 1000 juveniles at 14 DAP (Makumbi-Kidza *et al.*, 2000). This result was also in accordance with the findings of Mudiope *et al.*(2012). The difference in level of plant response may depend on factors such as the ratio between the number of nematodes and the food resources supplied by the plant. The amount of galling in roots varies depending on the species of both plant and nematode involved in the host-parasite relationship.

Activation or repression of plant pathways involved in the synthesis of polyphenols plays a key-role in plant defence mechanism against nematode infection. Specific activities of plant resistance-related enzymes, namely peroxidase (POX), polyphenol oxidase (PPO) and phenylalanine ammonia lyase (PAL) also determine the intensity of galling on roots. On inoculation with the nematode, resistant variety induces phenylalanine ammonia-lyase activity, while a nematode susceptible variety decreases it (Wuyts, 2006).

In the present study number of larvae, root knot count, number of females and number of egg masses were found to be maximum for the genotype Pattambi local but number of eggs per egg mass was significantly low. Limited food and space, probably, produced detrimental effects on the maximum development of the nematode and consequently on egg production. Insufficient nutrition might be the cause of less number of eggs. This inference is in line with the findings of Bird (1974).

Nematode eggs were most abundant in genotypes which were having severely galled roots. This result was supported by earlier findings of Mudiope *et al.* (2012).

5.2.2. Nematode Characteristics in Soil

Maximum nematode population was found in the genotype Parassala local 2 and minimum was found in Thodupuzha local 2. An increase in nematode population in the soil at the time of harvest was reported by Sreenivasan and Devarajan (2008). The number of larvae in both soil and root were the lowest in Thodupuzha local. According to Nisha (2005) nematode population in soil (200 cc) and root was 557.50 and 468.00 respectively when coleus plants were inoculated with 1000 juveniles of the root knot nematode. This result is in accordance with the current study.

5.2.3. Varietal Reaction to Root Knot Nematode

Though all the genotypes exhibited galling, degree of reaction to root knot nematode varied from resistant to highly susceptible. Fifteen genotypes were found to be resistant, six genotypes were moderately resistant, four of them were moderately susceptible, two genotypes were susceptible and three genotypes showed high susceptibility to nematode infestation. Similar scoring for varietal reaction to root knot nematode was made by Nisha (2005). According to Nisha (2005), two varieties Sreedhara and Nidhi were resistant. But in the current study both the varieties were found to be moderately resistant. This could be due to the progressive increase in the virulence of the nematode after prolonged selection on these resistant genotypes.

Differences in reaction of genotypes to root knot nematode could be due the interaction between nematodes and the plant secondary metabolites. Tolerant genotypes may have higher level of secondary metabolites like phenylpropanoids. Higher levels of these compounds have been found to increase resistance against hydrolytic enzymes secreted by nematodes during the infection process.

Comparative yield performances of the tolerant genotypes are given in fig.6. The number of larvae, root knot count and number of females were the lowest in the genotype Thodupuzha local 2 but the yield performance was poor. Although 15 genotypes showed tolerant to root knot nematode, all of them were

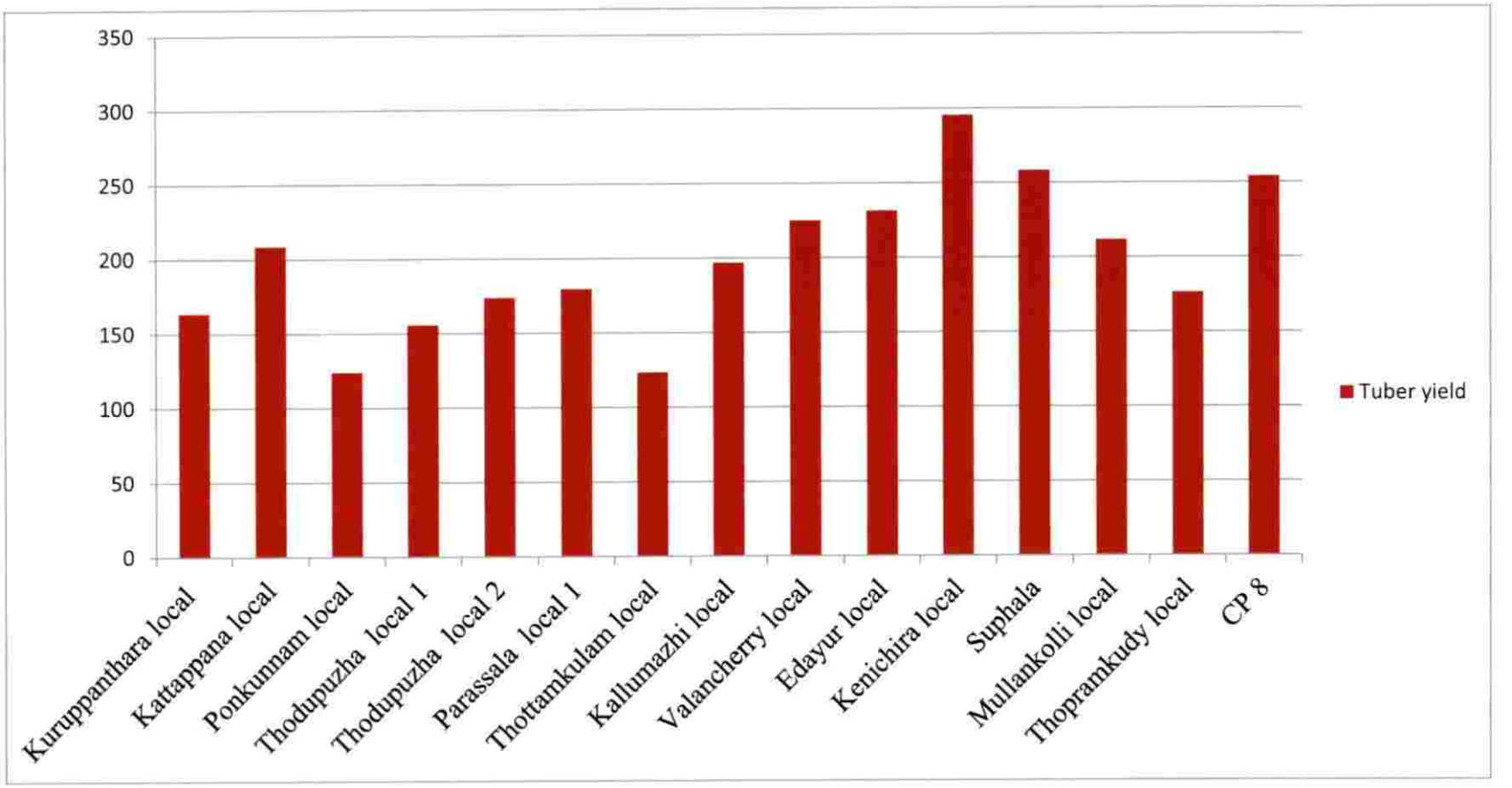


Fig.6. Comparative yield performance of 15 tolerant genotypes

not high yielders. The genotypes Kenichira local, Suphala, CP 8 and Edayur local were found to be having high yield with nematode tolerance.

The identified genotypes with higher yield and nematode tolerance can be forwarded to further yield trials for variety development.

SUMMARY

6. SUMMARY

The present study on Genetic variability in Chinese potato (*Solenostemon rotundifolius* (Poir) J.K. Morton) for yield and nematode tolerance was conducted at the Department of Plant Breeding and Genetics, College of Agriculture, Vellayani, during 2017-19. An attempt has been made here through studies on variability, character association, genetic diversity and screening for root knot nematode tolerance to identify superior genotypes with higher yield and nematode tolerance.

The present study was conducted as two experiments. The first experiment was done with thirty genotypes of Chinese potato which were collected from ICAR - CTCRI Sreekariyam, local markets and farmers' fields of major coleus growing tracts of Kerala were evaluated in the field in a Randomized Block Design (RBD) with three replications during 2018-19. The Chinese potato tubers were raised in the nursery. Two month old cuttings were planted to the main field with a spacing of 60 x 30 cm and the plot size was 2.16 m^2. A total of 12 plants were maintained in each plot and each genotype was considered as each treatment.

In the first experiment the thirteen biometric characters of 30 genotypes were observed and all the genotypes showed significant variation except for point of tuberization and susceptibility to nematode infestation. The genotype Kenichira local (T17) recorded the highest tuber yield $plant^{-1}$ (295.37g) followed by CP 9 (261.67g), Suphala (258.10g) and CP 8 (254.05g) which were on par with each other whereas the lowest yield of 123.32g was recorded by Thottamkulam local (T10).

The mean performance of all the characters studied of the 30 genotypes showed that the genotype Kenichira local (T17) recorded minimum days to flowering (66.53), maximum number of tubers $plant^{-1}$(14.27) and maximum harvest index (0.47). Tuberization was observed both at base of the stem and at leaf nodes. Seven genotypes produced tubers both at base of the stem and leaf

nodes which is an undesirable character. Tuber girth was highest for the genotype CP 8 (13.7). Highest values of tuber volume (32.23 cc) and average weight of tubers (33.18g) were recorded by the genotype Kuruppanthara local. Tuber density was maximum for the genotype Balussery local (1.18 gcc^{-1}). The genotype Sreedhara recorded highest biological yield (1051.33g) whereas the genotype Ponkunnam local showed maximum plant height (85.5 cm).

The value of genotypic coefficient of variation was smaller than phenotypic coefficient of variation, but small difference was recorded between PCV and GCV indicating that environment had less contribution towards trait expression. The character harvest index recorded highest GCV (37.09 per cent) and PCV (37.34 per cent). High GCV and PCV were observed for harvest index and tuber yield $plant^{-1}$ which revealed that total variation present in genotypes were contributed by genetic component. Therefore selection could be done for these characters. High PCV was also observed for the characters number of tubers $plant^{-1}$ and tuber volume. Moderate PCV and GCV were observed for tuber girth, average weight of tubers and biological yield. Days to flowering, days to tuberization and tuber density recorded lowest GCV and PCV. The minimum PCV and GCV values were recorded for the characters days to flowering, days to tuberization and tuber density.

In the study, heritability estimates ranged from 31.89 per cent for plant height to 99.03 per cent for biological yield. High heritability was observed for biological yield (99.03 per cent). Highest estimate of genetic advance recorded was 75.89 per cent for harvest index. High heritability coupled with high genetic advance was observed for the traits namely biological yield, harvest index, tuber volume, average tuber weight, tuber yield $plant^{-1}$, tuber girth and number of tubers $plant^{-1}$. Occurrence of high heritability and high genetic advance together may be ascribed to the conditioning of the characters by additive gene action which could be improved upon by direct selection

Genotypic and phenotypic correlations were worked out for 11 quantitative characters of the Chinese potato genotypes. Correlation analysis between the characters revealed that genotypic correlation coefficients were higher than the corresponding phenotypic correlation coefficients due to the presence of environmental influence on two traits. Moreover the difference between phenotypic and genotypic correlations were lesser, which detailed the environment had a minute effect on these characters. Yield plant^{-1} was significantly and positively correlated with number of tubers per plant, tuber girth, average weight of tubers and harvest index both at genotypic and phenotypic levels. Due to positive correlation, improvement in any one of these characters will simultaneously result in improvement of the dependent character. Days to flowering, biological yield and plant height exhibited significant negative correlation with tuber yield plant^{-1}.

Path analysis was done to confirm whether the correlation of component characters with the dependent character was due to their direct effect or due to indirect effect through some other character From the genotypic correlation the correlated yield components such as days to flowering, number of tubers plant^{-1}, tuber girth, average weight of tuber, biological yield, plant height and harvest index were taken as independent characters for the path coefficient analysis for better interpretation. Path analysis revealed that days to flowering, number of tubers plant^{-1} and average weight of tubers had maximum positive direct effect on yield plant^{-1} whereas the characters biological yield, plant height, tuber girth and harvest index had negative direct effect on tuber yield plant^{-1}.

Thirty genotypes were grouped into ten clusters based on D^2 values indicating the genetic diversity among them. Out of the ten clusters, Cluster I was the largest comprising of seven genotypes followed by Cluster II, Cluster III and Cluster V with four genotypes, Cluster IV and Cluster VI with three genotypes, Cluster VII with two members. Cluster VIII, Cluster IX and Cluster X were the smallest with one genotype each. Biological yield and average weight of tuber contributed maximum to the total divergence.

Maximum intra Cluster distance was observed in Cluster V, which shows that there exists significant variability among the genotypes of that Cluster. Maximum Cluster distance (2421.004) was observed between Clusters IV and VII. The greater the distance between Clusters the wider will be the genetic distance between the genotypes. Cluster II had high mean value for tuber yield plant^{-1} and harvest index. Cluster VI had highest number of tubers plant^{-1}. Cluster VII showed highest biological yield. Cluster VIII had highest average tuber weight and maximum plant height. Cluster IX exhibited least days to flowering. Cluster X recorded maximum tuber girth.

Second experiment was pot culture study for artificial screening of genotypes for resistance to root knot nematode. The same thirty genotypes evaluated in the first experiment were raised in pots. The experiment was laid out in Completely Randomized Design (CRD) during July, 2018 to September, 2018. Each plant was inoculated with 1000, second stage juveniles of *Meloidogyne incognita,* 15 days after planting of cuttings.

Analysis of Variance was carried out for all the characters studied and the results showed significant variation among the thirty genotypes for all the characters studied under the pot culture experiment. Number of larvae was highest in the genotype T11 (612.67). The genotype T11 reported maximum root knot count (154.00) and number of egg masses (98.67) per 5g root. Maximum number of eggs per egg mass was observed in the genotype T8 (269.67). Number of larvae, root knot count and number of females were highest in the genotype Pattambi local whereas the genotype Thodupuzha local 2 recorded minimum values.

Varietal reaction to root knot nematode was estimated using the scoring method of Heald *et al.* (1989). Fifteen Chinese potato genotypes were found to be tolerant to *M. incognita.* The genotypes T1, T2, T3, T4, T5, T7, T10, T13, T14, T15, T17, T18, T19, T25 and T28 reported root knot index of one and it is categorized as tolerant to root knot nematode. Moderately resistant genotypes are

T16, T20, T22, T24, T26 and T29 with a root knot index of two. The genotypes T12, T23, T27 and T30 were moderately susceptible to root knot nematode having a root knot index of three. Susceptible genotypes were T26 and T21 with a root knot index of four. There were three genotypes (T8, T9 and T11) which were highly susceptible to nematode infestation, showing a root knot index of five.

The results of the present study showed that T17 (Kenichira local) was superior in yield performance (295.37g) with nematode tolerance followed by the genotype T18 (Suphala),T28 (CP8) and T15 (Edayur local). The genotypes identified from the study can be forwarded to further yield trials for variety development.

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Genetic variability in Chinese potato (*Solenostemon rotundifolius* (Poir) J.K. Morton) for yield and nematode tolerance.

by

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Abstract of the thesis
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ABSTRACT

The present study entitled "Genetic variability in Chinese potato (*Solenostemon rotundifolius* (Poir) J.K. Morton) for yield and nematode tolerance" was carried out in the Department of Plant Breeding and Genetics, College of Agriculture, Vellayani during 2017-2019, with the objective to identify high yielding Chinese potato genotypes having nematode tolerance. Chinese potato is a minor tuber crop of the tropics in which heavy yield loss occurs due to root knot nematode infestation.

The study comprised of two experiments. In the first experiment thirty accessions of *Solenostemon rotundifolius* (Poir) J.K. Morton, collected from ICAR - CTCRI Sreekariyam, local markets and farmers' fields of major coleus growing tracts were evaluated for yield and nematode tolerance under field condition. These accessions were evaluated in Randomized Block Design (RBD) with thirty treatments and three replications during August 2018- January, 2019.

Analysis of variance was conducted for all the thirteen characters studied. For all characters except for point of tuberization and susceptibility to nematode infestation, ANOVA revealed significant differences among all the genotypes evaluated. The genotype Kenichira local (T17) recorded the highest tuber yield plant^{-1} (295.37g) followed by CP9 (261.67g), Suphala (258.10g) and CP 8 (254.05g) which were on par; whereas the lowest yield of 123.32g was recorded by Thottamkulam local (T10). Minimum days to flowering, maximum number of tubers plant^{-1} and maximum harvest index were observed for the genotype Kenichira local (T17).

High genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were observed for tuber yield plant^{-1} and harvest index. Thus, selection for these characters would result in improvement of the genotype. High heritability coupled with high genetic advance was observed for number of tubers plant^{-1}, tuber girth, tuber volume, average tuber weight, tuber yield plant^{-1}, biological yield and harvest index. These characters, if selected for, would improve over generations.

Tuber yield plant^{-1} was significantly and positively correlated with number of tubers plant^{-1}, tuber girth, average weight of tubers and harvest index both at genotypic and phenotypic levels. So an improvement in these characters would enhance the tuber yield plant^{-1}. Path coefficients were found out using tuber yield plant^{-1} as the dependent character and other correlated characters as independent variables. Path analysis revealed that number of tubers plant^{-1}, average weight of tubers and days to flowering had positive direct effect on tuber yield plant^{-1}.

Mahalanobis' D^2 statistics was employed to study genetic divergence among the 30 genotypes which were grouped into ten clusters on the basis of relative magnitude of D^2 values using Tocher's method. Cluster I accommodated maximum number of genotypes and in sequence Clusters were having 7, 4, 4, 3,4, 3, 2, 1, 1 and 1genotypes respectively. The maximum inter-Cluster distance was observed between Clusters IV and VII. No close correspondence between geographical distribution and genetic divergence was observed.

The second experiment was pot culture study for varietal reaction to root knot nematode. The same thirty genotypes evaluated in experiment I were raised in Completely Randomized Design with three replications during July, 2018 to September 2018. All the pots were artificially inoculated with second stage juveniles of *Meloidogyne incognita* obtained from pure culture, at the rate of 1000 juveniles plant^{-1}.

Nematode characteristics in both soil and root samples were studied. Maximum nematode population in soil was found in the genotype T8 (Parassala local 2). Root-knot index was calculated for each genotype based on scoring method suggested by Heald *et al.* (1989). According to this scoring method, the genotypes having 0-25 root knots per five gram of root was categorized as resistant. Fifteen genotypes were found to be in the category resistant. The genotype T11 (Pattambi local) showed highest mean values for number of larvae, root knot count, number of females and number of egg masses per five g root.

The results of the current study showed the presence of wide range of variability in the thirty Chinese potato genotypes. Characters such as number of tubers plant^{-1} and average weight of tubers had positive significant correlation and

direct association with tuber yield plant^{-1}. Considering superior yield with nematode resistance, Kenichira local ranked first. It was followed by Suphala, CP8 and Edayur local. Kenichira local, CP 28 and Edayur local can be forwarded for further yield trials for variety development.