

Identification of Resistant Sources against Wilt Disease of Chilli (*Capsicum annuum* L.)

Syeda Farwah
(2017-H-191-M)



Division of Vegetable Science

Faculty of Horticulture

**Sher-e-Kashmir University of Agricultural Sciences &
Technology of Kashmir
2020**

**Identification of Resistant Sources against Wilt Disease
of Chilli (*Capsicum annuum* L.)**

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Thesis

Submitted to

The Faculty of Horticulture

Sher-e-Kashmir

**University of Agricultural Sciences & Technology of Kashmir
in partial fulfilment of requirements for the award of the degree of**

**Master of Science in Horticulture
(Vegetable Science)**

2020

DEDICATE MY THESIS TO
“MY BELOVED PARENTS”
“Parents”

*Someone who holds us in arms as we enter this world
Someone who encourages all our efforts and appreciate us wholeheartedly
Someone who listens patiently to our never ending doubts
Some who's eyes shine with pride and happiness at our every little achievement
Someone who helps us to smile instead shedding a tear
Someone who is our life-long friend*

AND TO MY ADVISOR “**Dr. Khursheed Hussain**”.

Sher-e-Kashmir
University of Agricultural Sciences & Technology of Kashmir
Faculty of Horticulture Division of Vegetable Science

Name of the student : **Ms. Syeda Farwah**
Registration No. : 2017-H-191-M
Major Subject : Vegetable Science
Minor Subject : Genetics & Plant Breeding/Plant Pathology.
Major Advisor : **Dr. Khursheed Hussain**
Assistant Professor
Division of Vegetable Science,
SKUAST-Kashmir, Shalimar
Title of the Thesis : **“Identification of Resistant Sources against
Wilt Disease of Chilli (*Capsicum annuum* L.)”**

ABSTRACT

The present investigation entitled “Identification of resistant sources against wilt disease of chilli (*Capsicum annuum* L.)” was carried out at Experimental Field, Division of Vegetable Science and Mycology and Forest Pathology Laboratory, Division of Plant Pathology, Sher-e-Kashmir University of Agricultural Science & Technology of Kashmir, Shalimar, Srinagar. The experiment was laid out in randomized complete block design (RCBD) with three replications. On the basis of morphological and pathological characteristics and DNA barcoding, the pathogen associated with the disease was identified as *Fusarium solani*. The pathogen on artificial inoculation produce symptoms characteristic of the disease. Of the One hundred and seven chilli genotypes screened under field conditions, one genotype(SKAU-193) showed immune reaction, twenty two genotypes showed resistant reaction and remaining all exhibited moderately resistant, susceptible or highly susceptible reaction. In order to validate the field resistance of 51 genotypes (1-immune, 21-resistant, 17-moderately resistant, 12-susceptible) they were further screened under artificially inoculated controlled conditions. The results confirmed the immune reaction of one genotype (SKAU-193), twenty one genotypes were found resistant while seventeen genotypes showed moderately resistant reaction and remaining twelve genotypes showed susceptible reaction. DUS traits were recorded on forty two traits as per guidelines of PPV & FR authority (PPV&FR, 2003) exhibited a wide range of variation for the traits. Observations were recorded on twenty two quantitative and qualitative traits. Analysis of variance revealed significant differences among genotypes for all the traits studied. A wide range of variation was observed among the different genotypes for all the traits under study. Maximum range was recorded for fruit yield ha⁻¹ (23.90-239.43 q), followed by vitamin C (43.86-201.16 mg100g⁻¹), number of fruits plant⁻¹ (29.66-99.86),

capsanthin content (66.24-125.83 ASTA units), plant spread (44.33-86.64 cm) plant height (49.16-86.00cm), and number of branches plant⁻¹ (14.26-48.93), while minimum range was observed for fruit pedicel diameter (0.21-0.44 cm), capsaicin (0.29-0.75 mg g⁻¹) and fruit diameter (0.78-1.92 cm). The highest phenotypic and genotypic coefficients of variation were observed for fruit yield hectare⁻¹ (56.34, 56.32), number of fruits plant⁻¹ (31.44, 31.41), fruit length (20.49 and 20.16), fruit diameter (20.37, 16.82), fruit weight (38.73, 38.67) and number of branches plant⁻¹ (25.35, 25.32). In general PCV was marginally higher than the corresponding GCV indicating the less influence of environment in the expression of traits under study. High heritability coupled with high genetic advance as percentage of mean was observed for almost all traits except fruit diameter (cm) indicating that most of the traits studied were mainly controlled by additive gene effect and thus selection may be effective. Correlation coefficients revealed that the fruit yield per hectare exhibited significant positive association plant height, no. of branches plant⁻¹, days to flower initiation, days to fruit initiation, days to harvesting, fruit diameter, fruit weight, fruit length, fruit pedicel length, fruit pedicel diameter, number of fruits plant⁻¹. Estimates of divergence among 60 chilli genotypes revealed that significant divergence existed among them. The genotypes under study were grouped into 4 clusters as per Mahalanobis D² (1928) analysis employing Tochers method with maximum number of genotypes in cluster II (25) followed by cluster I (20), cluster III (14) and cluster IV was monogenotypic. Maximum intercluster distance was observed between II and III (14621.56) while maximum intracluster distance was observed in cluster III (5177.30). The per cent contribution towards the total genetic divergence revealed that fruit yield (q/hac), number of fruits per plant, vitamin C content, dry matter, days to harvesting, days to flower initiation were the main contributing characters towards total genetic divergence. The crosses between the genotype of cluster IV with those of I, II and III are likely to exhibit high heterosis and produce recombinants with desired traits in segregating generations. Three genotypes viz; SKAU-193, SKAU-173 and SKAU-163 showed yield potential of 239.43 qhac⁻¹, 206.02 qhac⁻¹ and 186.24 qhac⁻¹ is significantly higher than Kashmir Long-1 (184.54 q ha⁻¹) and were found resistant to chilli wilt during screening. These genotypes selected on the basis of *per se* performance of fruit yield, yield contributing and quality traits can be used in chilli improvement programme as elite germplasm lines or may be recommended for commercial cultivation after testing them over years and locations.

Keywords: *Capsicum annum* L., Correlation, DNA barcoding, *Fusarium solani*, Genetic divergence, Screening.

Signature of Student
Dated:

Signature of Major Advisor
Dated:

ACKNOWLEDGEMENT

First of all my humble and devoted prostration to Almighty Allah who enlightens me and leads me to right way, with his mercy I reached to this stage

It is my proud privilege to humbly place on record my profound sense of gratitude, indebtedness and heartfelt thanks to my chairman of the advisory committee – Dr. Khursheed Hussain, Assistant Professor, Division of Vegetable Science, SKUAST-Kashmir Shalimar. I am immensely grateful to him for his genuine guidance, constant fomenting, selfless and sustained interest and above all his affectionate way of dealing with the things throughout the course of my investigation, which helped me to consummate the research work,

I extend my sincere thanks to my Advisory Committee Members, Dr. Kouser Parveen, Prof and Head Division of Vegetable Science; Dr. Zahoor Ahmad Dar, Professor cum chief scientist, Dryland (Karewa) Agriculture Research Station, Dr. Shakeel Ahmed Mir, Prof and Head Division of Agri-Statistics, Dr. Zahoor Ahmad Bhat, Assistant Professor, Division of Plant Pathology, Dr. Mohammad Maqbool Mir (Dean P.G Nominee) Assistant Professor, Division of Fruit Science for their valuable suggestion and advice during the study programme and for the finalization of manuscript.

I owe a special debt of gratitude to Dr. Zahoor Ahmad Bhat, Assistant Professor, Division of Plant Pathology, SKUAST-K, Shalimar, for her constant and relentless guidance, earned suggestion and going through the manuscript.

I am highly grateful to all the Faculty members of Division of Vegetable Science particularly Dr M.A.Chato, Dr Faheema Mushtaq, Dr. Sumati Narayan, Dr. Shehnaz Mufti, Dr. Baseerat Afroza, Dr. Ummiyah Masoodi, Dr Aijaz A. Malik, Dr Nayeema Jabeen for their support, valuable suggestion and advice during the study programme.

Special thanks to Dr. Khalid Masoodi, Assistant Professor Division of Plant Biotechnology, SKUAST-Shalimar, for helping me during the course of research work,

Sincere thanks to Mr. Fayaz Ahmad Mir, Breeding Assistant for his valuable suggestions and concern. I am highly thankful to field staff members especially Mr. Maqbool Ahmad, Mr. Mohammad Shafi, Mr. Masood Ahmad for their help and assistance during my research work in the field.

I am highly indebted to Dr. Gowhar Ali, Assisatnt Professor, Division of Genetics and Plant Breeding for getting my data analyzed.

I find myself hard pressed for words to reciprocate the affection, moral support, good wishes and sustained help rendered to me by my beloved Father Mr. Syed Nazir Rizvi and Mother Mrs. Syeda Bilqueesa, who nourished and educated me well in spite of their hardships and difficulties. Whenever anything fascinated my eyes, I never received a "No" from them. Help, support and assistance during entire course of my study and research work, extended to me by my brothers Syed Suhail, Syed Qammar and Syed Meesum and by my siblings Saima, Shakir, Sakib, Shuhaib, Sana and Shafia is simply unforgettable.

Indeed the words in my lesson are not sufficient either in form or in thought to express my deep sense of gratitude and indebtness to Syed Mazahir Hussain who has been instrumental in the successful completion of my research work. Whenever I was in need of anything during my research work, he was always there by my side.

To me, there is nothing better than having good friends, so great pride is with me while thanking my friends Seerat Rizvi, Aatifa wani, Sana Saleem and Shaila din who gave me courage and boosted up my patience, believed in me and stood up by me When I needed.

Cheerful acknowledgement is also expressed to my colleagues Waseem Yousuf, Misbah, Sana, Najmah, Majid Rashid, Afroza Akhter, Azra, Ambreen, Insha, Danishta, Srinavasullu, Muzamil, for their cooperation, appreciation and camaraderie during the course of this study. My sincere thanks are also due to all the non teaching staff members of the Division of Vegetable Science particularly, Mrs. Shahnaz, Mrs Pushvinder Kaur, Ms. Laliya, Mrs. Saleema and Mr. Mohammad Yaseen Bhat for their sincere help in laboratory work during quality analysis which led to successfully completion of my research programme.

I express my sincere thanks to the Head, Central Library SKUAST-K and supporting staff for extending full cooperation in collecting the pertinent literature. The cooperation of ARIS and CAB staff is duly acknowledged.

Syeda Farwah

Place : Shalimar, Srinagar

Dated :

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Chapter-1

INTRODUCTION

Chilli (*Capsicum annuum* L.) ($2n=2x=24$) belongs to the family Solanaceae (Nightshade). The genus name *Capsicum* is derived from the Latin word ‘capsa’ meaning chest or box because of the shape of fruit which encloses seeds very neatly, as in the box. The genus *Capsicum* has more than 30 species of which only five viz., *C. annuum* L., *C. chinense* Jacq., *C. frutescens* L., *C. baccatum* L. and *C. pubescens* are domesticated and cultivated (Bosland and Votava, 2000). Due to the existence of many species, it is difficult to identify intermediary forms resulting from natural interspecific crosses, the former three species (*C. annuum* L., *C. chinense* Jacq., *C. frutescens* L.) are now treated as one species (*C. annuum* L.) with four major cultivars groups that are: *chinense* group (West Indies chilli), *frutescens* group (bird chilli), *annuum* group (hot chilli) and *baccatum* group (sweet pepper).

It is native of Tropical America and West Indies and is believed to have been introduced to India by the Portuguese in the seventeenth century. Since then it has gained importance as an inevitable condiment and vegetable. Its production and consumption has steadily increased worldwide during 20th century due to its use as both vegetable and spice and is an important component of diverse cuisines in the world.

It is the leading spice-cum-vegetable crop grown commercially throughout the world. Its fruit appear in different shapes, sizes and colours. It is highly valued for its green or red ripe fruits with characteristic pungency, colour and flavour. It is consumed as fresh, dried or in powder form (El-Ghoraba *et al.*, 2013; Pujar *et al.*, 2017). The fruits are an excellent source of health-related phytochemical compounds, such as vitamin C (143.7µg), vitamin A (292.04 IU) vitamin E (0.69 mg), vitamin K (14 µg) per 100g, minerals like Calcium, Phosphorus and Iron of fruits, alkaloid capsaicin/capsicutin ($C_{18}H_{27}NO_3$) and red pigment Capsanthin

(C₄₀H₅₆O₃). The capsaicinoids that are very important in preventing chronic diseases such as cancer, asthma, toothache and cardiovascular diseases (El-Ghoraba *et al.*, 2013; Wahyuni *et al.*, 2013; Kerketta *et al.*, 2018). The alkaloid capsaicin/capsicutin (C₁₈H₂₇NO₃) present in placenta of the chilli fruit responsible for its pungency has diverse prophylactic and therapeutic uses in Allopathy and Ayurveda and can directly scavenge various free radicals (Bhattacharya *et al.*, 2010). It has also acquired a great importance because of the presence of ‘oleoresin’(Fruits contain a fixed oil which is non-pungent and yield 20-25 per cent alcoholic extract called oleoresin), which permits better distribution of colour and flavour in foods. It has antioxidant, anti-mutagenesis, hypocholesterolemic and immunosuppressive properties (El-Ghoraba *et al.*, 2013), inhibits bacterial growth and platelet agglomeration (Wahyuni *et al.*, 2013) and facilitates starchy food digestion (Bhattacharya *et al.*, 2010). At global level, chilli is one of the spices that generate huge revenues for producers and therefore contributes to poverty alleviation and improvement of women’s social status (Karungi *et al.*, 2013).

The crop is grown throughout the world including tropics, subtropics and temperate regions (Pickersgill, 1997). As per latest statistics it is grown over an area of 366 thousand hectares with an average production of 3737 thousand metric tonnes in India (FOA, 2018-19). In Kashmir it is grown on an area of 3,200 hectares with an annual production of 64,800 tonnes (NHB, 2017). The major chilli growing states of India are Andhra Pradesh, Karnataka, Maharashtra, Orissa, Tamil Nadu, Madhya Pradesh, West Bengal and Rajasthan. India has a great potential to increase the production and productivity in order to promote export, besides meeting the domestic requirement. However, despite continuous efforts at various levels, the chilli productivity has not gained momentum. This could be attributed to a number of limiting factors of which disease incidence and lack of superior genotypes are of prime concern.

The chilli yield in Kashmir is miserably low compared to that of other states such as Tamil Nadu, Andhra Pradesh, Karnataka, Bihar, Punjab and Gujrat, which along with many other factors is mainly attributed to multitude of diseases affecting the crop primarily of fungal origin. Of these fungal disease, the more destructive are damping-off [*Pythium aphanidermatum* (Eds.) Fitzp.], leaf and fruit blight [*Phytophthora capsici* Leon.], anthracnose and die back [*Colletotrichum capsici* (Syd.) Butler and Bisby], leaf spot [*Cercospora capsici* Heald & Wolf and *Alternaria alternata* Fr. Keissler] and wilt. Chilli wilt occurs in epiphytotic form in several chilli growing areas of the valley and has forced chilli cultivators to abandon its cultivation. The disease has been reported to cause approximately 45 to 60 per cent yield loss of chilli in Kashmir valley alone (Najar, 2001) and as such posing a serious threat to its profitable production. The practise of monoculture and cultivation of susceptible chilli cultivars (Foaster and Walker, 1947; Matta and Garibaldi, 1972; Huber and Watson, 1974; Williams, 1979; Dar and Mir, 1995; Verma and Sharma, 1995) seem to have given fillip to the development and spread of this disease. The chilli wilt was first reported from New Mexico in the year 1919 (Leonian, 1919) and since then it has been reported from Peru and Arizona (Brown and Gibson, 1926), West Indies (Ciferri, 1926), India (McRae, 1932), Spain (Benlloch and Dominguez, 1934), Argentina (Marchionatto, 1935), Uganda (Hansford, 1940), Brazil (Chaves, 1947), Turkey (Copcu and Saydam, 1974), Chile (Fernandez, 1983), Iraq (Sarhan and Sharif, 1986), Cuba (Camino *et al.*, 1987), Tunisia (Moens and Benaicha, 1990). In India, the disease has been reported in alarming proportions from Karnataka (Khan *et al.*, 1979), Tamil Nadu (Vidhyasakaran and Thiagarajan, 1981), Haryana (Srivastava and Diwakar, 1987), Kerala (Jyothi *et al.*, 1993), Punjab (Kaur, 1993), Kashmir (Dar and Mir, 1995), West Bengal (Chatterjee *et al.*, 1997) and Himachal Pradesh (Singh and Singh, 1998).

Chilli wilt is characterized by brown vascular discolouration along with withering and chlorosis of leaves and subsequent death of the plant (Wani, 1994).

The disease is reported to be induced by a complex of soil borne pathogens (Madi *et al.*, 2017). Pathogens of fungal and bacterial origin have been found associated with the disease in different parts of the world. Wilt is characterised by wilting of the plant and upward and inward rolling of the leaves. The leaves turn yellow and die. Generally appear in localised areas of the field where a high percentage of the plants wilt and die, although scattered wilted plants may also occur. Disease symptoms are characterised by an initial slight yellowing of the foliage and wilting of the upper leaves that progress in a few days into a permanent wilt with the leaves still attached. By the time above ground symptoms are evident, the vascular system of the plant is discoloured, particularly in the lower stem and roots (Belwansi, 2012). Different species of *Fusarium* (Moens and Benaicha, 1990; Koleva and Vitanov, 1990; Hashmi, 1989; Thind and Jhooty, 1985; Kaur, 1993; Wani, 1994), *Phytophthora capsici* (Fernandez, 1983; Palloix, 1986; Jia, 1992; Hartman and Hwang, 1993; Hwang and Kim, 1995; Xie *et al.*, 1999), *Rhizoctonia solani* (Alavi *et al.*, 1986; Mushtaq and Hashmi, 1997; Najar, 2001), *Sclerotium rolfsii* (Wanghiliar *et al.*, 1988; Mathur and Gurjar, 2001), *Ralstonia solanacearum* (Jyothi *et al.*, 1993; Chatterjee *et al.*, 1997) , *Fusarium solani* (Thoyajakshi Bai *et al.*, 2018) have been ascribed to chilli wilt disease. Najar (2001) found *F. pallidoroseum* and *R. solani* cause of chilli wilt from Kashmir division of Jammu and Kashmir State. The complex nature of disease renders most of the management practices ineffective. The most efficient and economical method to mitigate the menace of soil borne diseases is the use of resistant varieties, however, the chilli cultivars being grown under Kashmir conditions are more or less susceptible to the disease. Moreover, there are limited resistant sources available in the chilli germplasm throughout the world (Naik *et al.*, 2007).

DNA barcoding is a fast, accurate, and standardized method for species level identification, by using short DNA sequences. DNA barcoding is a taxonomic method in which a short genetic marker to identify DNA to which organisms or a particular species it belongs. It helps to identify an unknown

sample in terms of a preexisting classification. This marker is different for various species like CO1 cytochrome c oxidase 1 for animals, matK and rbcL for plants and Internal Transcribed Spacer (ITS) for fungus. Ideal DNA barcode should be normally a uniform short sequence of DNA (400-800bp), able to be simply generated and used to characterize all the living organisms (Savolainen *et al.*, 2005).

In the crop improvement programmes, efforts are being made to develop high-yielding, disease-resistant and stable cultivars. Morphological descriptions of many cultivars are in vague. Further, characterization of chilli genotypes is also required for their protection under Plant Variety Protection (PVP) legislation, because varietal testing for distinctiveness, uniformity and stability (DUS) is the basis for grant of protection of new plant varieties under the protection of Plant Varieties and Farmer's Right Act 2001 (PVR &FR Act 2001).The act has provision to compare the candidate variety with the varieties of common knowledge on a set of relevant characteristics prescribed in the 'Minimal Descriptors of Vegetable Crops' for chilli (Srivastava *et al.*, 2001). As far as development of superior genotype(s) is concerned, it is an often cross pollinated crop, exhibits wide variability for different qualitative and quantitative traits and breeding methods of both self and cross pollinated crops could be employed for its genetic improvement. Yield is an ultimate criterion for a plant breeder to evolve improved cultivars in any crop. The success of breeding program depends on the availability of the genetic variability present in the available germplasm. Study of biological parameters of the crop are often considered useful in the study of genetic variability. Since most of the plant characters of economic importance are polygenic in nature and are highly influenced by environment, it is therefore necessary to workout whether the observed variability is heritable or due to environment. Thus, there is an imperative need to workout the phenotypic variation into heritable and non-heritable components. Realising the economic

potential of the crop, there is an urgent need to isolate such breeding lines which have desirable traits, better quality coupled with high yield potential.

Unlike the qualitative traits which are discrete in nature and show clear-cut classes, most of the horticulturally important characters including yield are polygenically controlled and are highly influenced by environmental factors. High phenotypic coefficient of variability (PCV), genotypic coefficient of variation (GCV), heritability estimates coupled with high genetic gain indicate the existence of wide range of variability and offers good scope for improvement through selection. Genetic parameters, therefore, help in partitioning the overall variability into heritable and non-heritable components. Since yield is a complex trait and depends on several components, selection on yield alone is not likely to be efficient. The component characters are interrelated among themselves and also influence the yield. Correlation coefficient tells whether the mutual relationship between a pair of traits is positive or negative. Estimation of correlation coefficient among the yield contributing variables is necessary to understand the direction of selection and to maximize yield in shortest period of time. Genetic correlation indicates the relative importance of trait(s) on which greater emphasis should be made in selection for yield. Johnson *et al.* (1955) found that genotypic correlation coefficients provide a measure of association between various traits and help to identify the traits that may be useful in selection. The correlation coefficients, however, measure the nature and magnitude of association between different traits. Component analysis of this relationship reveals the importance of most important traits towards the yield.

Genetic divergence analysis among genotypes is helpful to screen the genetically diverse parents that are likely to produce high heterotic effects among crosses and also generate large spectrum of variability during segregation and recombination of genes at heterozygous polygenic blocks. Multivariate technique using D^2 statistics (Mahalanobis, 1928) is a powerful tool in quantifying the degree of divergence among the genotypes. This would help to identify putative

parents for executing an effective breeding strategy to obtain high heterotic response and transgressive segregants. Estimation of genetic divergence helps in reducing the large data of genotypes to manageable proportions. It is assumed that the parents showing wide genetic divergence are best suited for being used in the hybridization programme. In the process of formulating the chilli improvement programme through hybridization and creating variability for the improvement of yield and other desirable traits, it is essential to understand the nature and degree of genetic divergence present in the available germplasm. Though a few studies have been made in India to study genetic divergence in chilli, but no such effort has been made under temperate conditions of Kashmir. In this regard, the proposed investigation on “Identification of Resistant Sources against Wilt Disease of Chilli (*Capsicum annuum* L.)” were conducted with the following objectives:

Objectives:

- Isolation and identification of causal pathogen associated with chilli wilt disease.
- Screening of available chilli genotypes against the wilt disease, including qualitative and quantitative traits.

Chapter- 2

REVIEW OF LITERATURE

The brief resume of research work done in India and abroad on various aspects relevant to present investigation entitled “Identification of Resistant Sources against Wilt Disease of Chilli (*Capsicum annuum* L.)” has been reviewed and presented under following headings:

2.1 Causal organism

The wilt disease of chilli has been reported to be caused by different pathogens. Pathogens of fungal and bacterial origin have been found associated with the disease in different parts of the world. Different species of *Fusarium* such as *F. annuum* (Crawford, 1934), *F. oxysporum* (Garofalo, 1957), *F. solani* and *F. equisti* (Moens and Benaicha, 1990; Koleva and Vitanov, 1990), *F. moniliformae*, *F. oxysporum* and *F. solani* (Hashmi, 1989) and *F. pallidoroseum* (Thind and Jhooty, 1985; Kaur, 1993; Wani, 1994; Najar, 2001) have been associated to chilli wilt disease. *Phytophthora capsici* has been also associated as causal agent of wilt of peppers (Fernandez, 1983; Palloix, 1986; Jia, 1992; Hartman and Hwang, 1993; Hwang and Kim, 1995; Xie *et al.*, 1999). Alavi *et al.* (1986) reported *Rhizoctonia solani* as cause of wilt and death of chilli plants in Central Iran. In Pakistan, *R. solani* was also one of the predominant fungi isolated from roots and stems of infected plants of bell pepper showing symptoms of wilting (Mushtaq and Hashmi, 1997). Wanghiliar *et al.* (1988) observed *Sclerotium rolfsii* causing collar/root rot of chilli in Maharashtra. The fungus was also reported as a threat to chilli in Rajasthan by Mathur and Gurjar (2001). Verticillium wilt of capsicum has been reported from Canada (Woolliams *et al.*, 1962), Turkey (Copcu and Saydam, 1974), China (Lu *et al.*, 1984) and USA (Gonzalez and Bosland, 1993). *Fusarium oxysporum*, *F. solani*, *F. moniliforme* and *F. pallidoroseum* have been reported as the wilt causing agents from chilli growing areas but *F. oxysporum* and *F. solani* are the most prevalent species of *Fusarium* found associated with wilt of

chilli in India (Naik, 2006). Chatterjee *et al.* (1997) also reported *R. solanacearum* as causal agent of chilli wilt in West Bengal. Najar (2001) found *F. pallidoroseum* and *R. solani* as cause of chilli wilt from Kashmir division of Jammu and Kashmir. Tariq (2005) found association of *F. oxysporum*, *P. capsici*, *R. solani* and *S. rolfsii* with chilli wilt disease from Jammu division of Jammu and Kashmir. Jabeen (2006) reported *F. pallidoroseum* as causal agent of chilli wilt in Kashmir. Faisal *et al.* (2013) isolated and found soil borne fungi viz., *R. solani*, *Macrophomina phaseolina*, *F. oxysporum*, *F. solani* and *Pythium sp.* as the cause of chilli root rot in Pakistan. Toyyaba *et al.* (2014) found three microbial agents viz., *R. solanacearum*, *F. oxysporum* and *R. solani* out of eight isolated organism as the cause of wilting in chilli. Mekonnen *et al.* (2015) reported bacterium *R. solanacearum* and four fungal pathogens viz., *R. solani*, *Fusarium spp.*, *Pythium spp.* and *Verticillium spp.* as the cause of wilt disease in hot pepper in Ethiopia. Raghu *et al.* (2016) reported *Fusarium solani* as the cause of chilli wilt in Karnataka, Andhra Pradesh and Maharashtra. Thoyajakshi Bai *et al.* (2018) isolated and reported *Fusarium oxysporum* and *Fusarium solani* as the cause of chilli wilt in Andhra Pradesh.

2.2 Molecular Characterization

Ferniah *et al.* (2014) identified fungi by its internal transcribed space regions (ITS regions). One pathogenic strain was isolated from Tawangmangu, Karanganyar and was identified molecularly as *F. oxysporum*. Tembhurne *et al.* (2017) reported molecular diversity assessment in M₃ chilli mutant genotypes using RAPD markers revealed high variability among the genotypes at molecular level and high divergence among these genotypes.

Anjos *et al.* (2019) collected tissue samples of plants with wilt symptoms. The DNAs of the *Fusarium* species were extracted, and subjected to polymerase chain reaction, using the primers ITS1 (5'TCCGTAGGTGAACCTGCGG-3') and ITS4 (5'-TCCTCCGCTTATTGATATGC-3'). Subsequently, the sequencing

revealed five *Fusarium* species viz., *F. solani*, *F. oxysporum*, *F. equiseti*, *F. incarnatum*, *F. chlamydosporum*, predominating *F. solani* and *F. equiseti*.

2.3 Germplasm screening

Kelaiya and Parakhia. (2000) screened twenty varieties of chilli in Gujarat Agriculture University, Junagadh against most virulent isolate of *Fusarium solani* and reported only two genotypes viz., GC-9 and GC-2 as resistant, five genotypes viz., HC-9, HC-1, PBS 86-1 and PBS-86-2 moderately resistant; eleven genotypes HC-4, HC-10, HC-12, HC-13, HC-15, HC-11, HC-2, HC-3 and HC-6 susceptible and two genotypes Reshmaputto and Gholar as highly susceptible.

Madhukar *et al.* (2002) in CPCRI Kasargod identified HR-3018 as resistant line against *Fusarium* wilt of chilli by seed inoculation and rapid-root-dip-transplanting technique, DS-1 and LCA-206 as moderately resistant and the remaining all were highly susceptible. Kaur *et al.* (2004) in Pantnagar screened one hundred and fifty chilli genotypes comprising of hybrids, commercial cultivars and breeding lines for identification of resistance. No cultivar or hybrid was found to be immune or highly resistant under field condition. Two cultivars PBC-408 and PBC-199 were donors for resistance in breeding programme. Some cultivars such as Punjab Lal, Punjab Rurkh, Punjab Guchhedar and MF-14-1-1-1 possessed good degree of field resistance.

Naik *et al.* (2008) evaluated thirty chilli genotypes in College of Agriculture Raichur, Karnataka, and screened against *Fusarium* wilt under laboratory condition by three different inoculation techniques viz; seed inoculation, rapid-root dip transplanting method and sick pot method. Among thirty genotypes IHR-3018 showed consistently reaction in both seed inoculation and root dip transplanting method. DS-1 and LCA-206 were moderately resistant and remaining genotypes were found to be susceptible to highly susceptible. However, in sick pot method high percentage of mortality was noticed due to

consideration of both pre and post emergence infection, as a result even IHR-3018 and LCA-312 were categorized under moderately resistant genotypes.

Jabeen *et al.* (2009) in SKUAST Shalimar, evaluated two resistant and six susceptible chilli genotypes and their twelve F₁ hybrids showing variable degree of resistance to *Fusarium* wilt were analyzed for phenols and phenolic enzymes, under both uninoculated and inoculated conditions at different growth stages. There existed a positive correlation between the host resistance and the amount of phenols and increased enzyme activities while it was almost the opposite in susceptible lines.

Pawaskar *et al.* (2014) evaluated thirty three genotypes of chilli in Agricultural University, Dapoli, Maharashtra and reported that none of the genotypes was found immune to bacterial wilt incited by *Ralstonia solanacearum*, eleven genotypes viz., Kokan Kirti, LCA-334, BSS-273, BC-28, Pb. Guchhedar, BC-24, Pant-C-3, LCA-283, LCH-206, LCA-312, CO-4 were moderately resistant, nine genotypes viz., RHR-16-5, DPL-C-1, DPL-C-2, DPL-C-3, Chivar-8, Chivar-5, Chivar-4, Chivar-2, Chivar-1 were susceptible and Jayanti and RHR-CLU Pendulus were highly susceptible. CS-9818, Jwala, RHR-57, Sel-2, Phule Tejas, DPL-C-4, DPL-C-5, KA-2, Chivar-7, Chivar-6, Chivar-3 were moderately susceptible.

Maruti *et al.* (2014) evaluated chilli genotypes against *Fusarium solani* at University of Agricultural sciences, Raichur, Karnataka and screened about fifty six restorer lines and thirty eight F₁ hybrids under laboratory conditions. Among the fifty six genotypes, none of them were immune or resistant. However, only one genotype viz; P3 was found moderately resistant in both seed inoculation and rapid root dip transplanting techniques. However, out of thirty eight two hybrids viz; JNA2×ACB1 and Rajaput×P3 showed resistance under sick pot culture.

Singh *et al.* (2017) evaluated chilli cultivars against *Fusarium oxysporum* causing wilt in chilli under in vitro conditions by water culture technique and

found that out of the twenty-two chilli genotypes, most of the genotypes were susceptible to the disease. Among the twenty-two cultivars screened, only one cultivar CO-4 showed resistant reaction (6.67% disease incidence), whereas, six cultivars viz., HC-1, GC-1, GC-2, Kashi Gaurav, Ajeet-6 and DKC-8 were moderately resistant with disease incidence of 15.56 to 24.44 per cent. Three cultivars viz., Pant C-1, Punjab Lal and Kashi Sinduri were moderately susceptible with 33.33 to 48.99 percent disease incidence and remaining twelve cultivars/varieties were either susceptible (>50 percent disease incidence) or highly susceptible (>75 percent disease incidence). The cultivars Pusa Sadabahar and Arka Abhir were highly susceptible to wilt disease with 100 per cent disease incidence.

Tembhurne *et al.* (2017) screened chilli genotypes at College of Agriculture, Raichur during *kharif* resistant to *Fusarium* wilt in M₂ and M₃ generation. Among sixty two selected genotypes twenty six genotypes showed resistance, thirty two genotypes showed moderately resistant and three genotypes registered susceptible reaction in M₂ generation. However, only one genotype recorded highly susceptible reaction to *Fusarium* wilt.

Tembhurne *et al.* (2017) screened M₃ generation consists of seventy three genotypes of chilli viz., P3 T1-1, P3 T1-3, P3 T1-5, P3 T1-9, P3 T1 -12-10, P3 T1-18, P3 T1-20, P3 T1-24, P3 T1-26, P3 T2-5-4, P3 T2-5-6, P3 T2-7, P3 T2-8-7, P3 T2 -10, P3 T2 -15-4, P3 T2 -16, P3 T2 -17, P3 T2 -18, P3 T2 -19, P3 T2 -20-4, P3 T2 -20-5, P3 T2 -21-6, P3 T2 -21-7, P3 T2 -23-4, P3 T2 -23-5, P3 T2 -25, P3 T2 -26, P3 T2 -27, P3 T3 -1, P3 T3- 14, P3 T3 -11-10, P3 T3 -5-2, P3 T1 -4, P3 T1 -12-3, P3 T1-13, P3 T1-15, P3 T1-16, P3 T1-19-2, P3 T1-19-8, P3 T1-22-4, P3 T1-22-6, P3 T1-23-2, P3 T1-23-4, P3 T1-27, P3 T1-29-6, P3 T1-3, P3 T2 -2-4, P3 T2 -2-9, P3 T2 -4, P3 T2 -8-3, P3 T2- 6, P3 T2 -11, P3 T3 -2-3, P3 T3 -2-8, P3 T3 -3, P3 T3 -5-6, P3 T3 -8, P3 T3 -9-2, P3 T3 -9-5, P3 T3 -11-3, P3 T3 -13, P3 T1 -6-1, P3 T1 -6-8, P3 T1 -7, P3 T1 -8-7, P3 T1 -8-8, P3 T1 -10, P3 T1 -11, P3 T1 -28, P3 T1 -29-1, P3 T1 -31, P3 T2-15-6, P3 T3-4 and reported thirty

two genotypes showed resistant, twenty nine genotypes were found to be moderately resistant and twelve genotypes exhibited susceptible reaction.

2.4 DUS Characterization

DUS characterization of chilli genotypes conducted by Farhad *et al.* (2010) showed wide range of variation among the chilli genotypes for several morphological, fruit and quality characters. Among the different characters, all genotypes showed white corolla colour followed by single flower per axil, pigmentation at node and green fruit colour. Predominance of single descriptor state was found in more than 50 per cent genotypes for fifteen characters.

Datta and Das (2013) characterized fifty three genotypes of chilli (*Capsicum annuum* L.) for twenty three characters. These genotypes upon cataloguing showed distinct variations for vegetative, inflorescence, fruit and quality characters. A wide range of variation was also observed among the genotypes for several morphological, fruit and quality characters. Among the different characters, white corolla colour showed 100% frequency and higher frequency was also recorded in single flower per axil (86.79%), pigmentation at node (83.02%) and green fruit colour (69.81%) at intermediate stage.

Zhani *et al.* (2015) characterized five local accessions of chilli pepper (*Capsicum frutescens* L.) and reported that the pepper accessions were significantly different ($p < 0.01$) in many morphological characters studied. Three accessions produced plants with erect and short habit, small and lanceolate leaves and grouped flowers whereas rest of the accessions had dichotomous branching with bushy secondary stems, large and oval leaves and for flowers, all accessions were having solitary flowers with the same form and colour. The fruits had enrobing calyx, narrow triangular shape, dark red colour at maturity and a smooth to slightly wrinkled surface. In addition to this difference in attitude, sinuation of pericarp at basal part, surface texture, and glossiness was also observed.

Padma *et al.* (2017) studied thirty chilli genotypes for identification of thirty three morphological characters. Among them, only eight qualitative morphological characters viz., Intensity of anthocyanin coloration of nodes, stem pubescence, plant growth habit, leaf color, leaf pubescence, flower position, anther colour and calyx annular constriction and three qualitative characters viz., plant height, leaf length and leaf width were found important morphological characters for identification. Other characters viz., Seedling: Anthocyanin colouration of hypocotyl, hypocotyl pubescence, Stem colour, Plant: Anthocyanin etc., were of secondary importance for identification of varieties.

Rahman *et al.* (2017) conducted experiment using sixty genotypes of chilli to characterize the germplasm based on morphological traits. Distinct variation among the germplasm was observed in all the qualitative parameters except cotyledonous leaf shape and fruit persistence. The maximum variation was observed in fruit colour both at mature and immature stage. Fruit colour was observed in four categories, namely green, black, green with blackish blush and dark green. The germplasm AMS-42, AMS-45, RI-35 and AH-5 showed black coloured fruit indicating their high carotenoid content. Leaf pigmentation was found in AMS-39, AMS-44, AMS-45, AH-1 and RI-2 germplasm. Purple coloured corolla observed in AMS-42, AMS-45, AH-1 and AH-2 showing their high pollen fertility.

Morphological characteristics of a plant are used for genotype identification and distinctiveness of one cultivar from the other (Simmonds and Shepherd, 1955 and Oka, 1958). Amit *et al.* (2014) evaluated twenty three genotypes of chilli for genetic variability. Maximum plant height was attained in Surajmukhi (120.23 cm) which was statistically at par with Pusa Sadabahar (116.40 cm) while, minimum plant height was recorded in DCL-352 (52.40 cm), Pusa Sadabahar (10.62) recorded maximum number of branches closely followed by Pusa Jawala (10.47), whereas, PCP-08-CH (4.70) recorded minimum number of branches per plant. The genotype PUP-CH-08 took minimum number of days

(58.83 days) for initiation of first flowering which was statistically at par with Kashmir Long (60.20 days), CPC-08-E (60.31 days) and CH-1 (60.38 days), whereas, DCL-352 took maximum number of days for first flowering (86.30 days), 50 per cent of flowering was noticed earlier in Kashmir Long (70.53 days) closely followed by PUP-CH- 08 (72.05 days), whereas, DCL-352 took maximum number of days for 50 per cent of flowering (94.13 days), Surajmukhi took minimum number of days to harvest (101.26 days) green chilli fruits which was statistically at par with CH-1 (102.60 days), PUP-CH-08 (102.96 days) and Kashmir Long (103.38 days). However, PCP-CH-4-08 took maximum number of days to harvest (124.11 days) green chillies , Surajmukhi (198.25) registered maximum number of fruits per plants closely followed by Pusa Jawala (194.26), whereas, CCH-05(66.64) registered minimum number of fruits per plant. The genotype LCA-357 registered maximum fruit weight (5.19 g) which was statistically at par with Pusa Jawala (5.16 g), CH-1 (5.12 g) and Kashmir Long (5.08 g), whereas, K-1 had lowest fruit weight (1.71 g), maximum fruit length (14.70 cm) in LCA-357 and minimum fruit length (4.16 cm) in K-1 out of twenty three genotypes evaluated, maximum fruit diameter (2.80 cm) in LCA-357 and minimum fruit diameter (0.88 cm) in PH-08 out of twenty three genotypes evaluated and maximum fruit yield of green mature chillies was recorded in CH-1 (854.64 g) which was statistically significant. However, minimum green fruit yield was recorded in AG-08 (258.85 g).

An experiment conducted by Jabeen *et al.* (2007) to identify the resistant genotypes of chilli against *Fusarium pallidorozeum* (Cooke) Sacc. at Division of Vegetable Science, SKUAST-Kashmir. The results indicated, that there exists a positive correlation between resistant hosts and higher amount of phenols and increased enzymes while it was almost reverse in susceptible ones. It was concluded that the positive association of higher phenols and enzymes with resistance could be of immense value for early identification of resistant genotypes during artificial screening of segregating populations.

Herison *et al.* (2014) evaluated growth and yield performance of chilli hybrids. Twelve new hybrids and one commercial hybrid cultivar prada as a control, were evaluated. In the greenhouse experiment, H₂₃ and H₂₀ showed better vegetative growth compared to the other hybrids and control. Hybrid H₁₇ showed the highest yield, followed by H₅, H₄ and H₆ hybrids.

Janaki *et al.* (2015) evaluated sixty three chilli genotypes for ten quantitative traits. The analysis of variance revealed significant differences among the genotypes for all the ten characters indicating the presence of genetic variability among the genotypes. Among sixty three genotypes, the genotype LCA-720 recorded maximum plant height whereas the genotypes, Pusa Sadabahar and Pandava recorded the highest number of primary branches plant⁻¹. The genotype LCA-709 recorded earlier flowering while maximum fruit set per cent was observed for LCA-746. The genotype LCA-706 recorded maximum fruits plant⁻¹, whereas the maximum fruit length was observed for the genotype LCA-740. The genotype Warangal Chapatta recorded highest fruit diameter, dry fruit weight and number of seeds fruit⁻¹, whereas the genotype LCA-625 recorded highest dry fruit yield per plant.

Rahman *et al.* (2017) conducted experiment using sixty genotypes of chilli to characterize the germplasm based on morphological traits. The germplasm was collected and evaluated for twenty two qualitative and five quantitative characters. Distinct variation among the germplasm was observed in all the qualitative parameters except cotyledonous leaf shape and fruit persistence. The maximum variation was observed in fruit colour both at mature and immature stage. Fruit colour was observed in four categories, namely green, black, green with blackish blush and dark green. The germplasm AMS-42, AMS-45, RI-35 and AH-5 showed black coloured fruit indicating their high carotenoid content. Leaf pigmentation was found in AMS-39, AMS-44, AMS-45, AH-1 and RI-2 germplasm. Purple coloured corolla observed in AMS-42, AMS-45, AH-1 and AH-2 showing their high pollen fertility. The highest quantitative variation was

observed in yield plant⁻¹ suggesting that the evaluated germplasm could be used in developing high yielding variety. Considering the yield and yield contributing parameters the germplasm AI-1, AI-2 and RI-2 were found better among the sixty germplasm.

Kumar *et al.* (2018) evaluated thirty seven advanced lines of green chilli for important yield and yield related traits. The data pertaining to yield characters revealed that genotype ST-16 recorded higher yield plant⁻¹ (939.30 g), followed by ST-33 (879.37 g) and ST-13 (882.27 g). The genotype ST-16 (26.46 kg) recorded significantly higher yield plot⁻¹ followed by ST-13 (25.18 kg) and ST-33 (24.29 kg). The genotype ST-28 recorded higher plant height (84.46 cm) and plant spread (58.51cm) while genotype ST-37 (4.40) for number of primary branches and higher number of secondary branches plant⁻¹ recorded in ST-36 (9.60). The genotype ST-07 has taken minimum number of days (22.50) for first flowering and also days to 50 per cent flowering. Number of fruits plant⁻¹ recorded maximum in genotype ST-33 (198), fruit length in ST-25 (12.62cm) and fruit diameter in ST-20 (1.59 cm), whereas maximum fruit weight was recorded in ST-14 (7.85 g), lowest stalk length in ST-22 (1.80 cm) of stalk to fruit ratio in ST-01 (0.021).

2.5 Variability

The study of genetic variability was made for the first time by great biologist Fisher (1918) and subsequently, the estimation of genotypic and phenotypic variations were used to predict the expected genetic response. Manju and Sreelathakumary (2002) evaluated thirty-two accessions of chilli to estimate the genetic variability. Higher phenotypic and genotypic coefficients of variation were observed for fruits plant⁻¹, fruit yield plant⁻¹, seeds fruit⁻¹ and fruit weight. High estimates of heritability coupled with high genetic gain were also observed for these characters, indicating that they could be effectively improved through selection.

A field study was undertaken by Sreelathakumary and Rajamony (2004) on thirty-five chilli (*Capsicum annuum* L.) genotypes to assess genetic variability. Higher phenotypic and genotypic coefficients of variation were observed for leaf area, fruits plant⁻¹, fruit weight, fruit length, fruit girth and fruit yield plant⁻¹. High heritability coupled with high genetic gain observed for these characters imply the potential for crop improvement through selection.

Prasath *et al.* (2007) analyzed twenty-seven accessions of chilli from different eco-geographical regions for different quality traits. The results indicated large genetic diversity for colour and pungency among the germplasm collections from different parts of India. Accessions numbers 22 and 23 showed high colour and low pungency and were therefore considered promising parents for breeding high-yielding accessions with extractable colour.

Patel *et al.* (2009) evaluated thirty eight genotypes of chilli for different morpho-metric and qualitative characters. The analysis of variance indicated presence of considerable amount of variability among the genotypes studied. The highest GCV was observed for number of fruits plant⁻¹ and green fruit yield plant⁻¹.

Ajjapplavara and Channagoudra (2009) carried a study on variability, heritability and genetic gain in chilli and indicated that the moderate to high genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were observed for most of the characters except days to 50 per cent flowering.

Sarkar *et al.* (2009) evaluated forty-nine genotypes of chilli to study the genetic variability as well as association for twelve growth and fruit characters. A significant variation among the genotypes was observed. Fruit yield plant⁻¹, number of fruits plant⁻¹, fruit length, placenta length, fruit weight, number of seeds fruit⁻¹ and plant height showed high values of GCV and PCV.

Padhar and Zaveri (2010) revealed a significant genotypic difference in chilli accessions for all the traits studied. The estimates of genotypic (GCV per cent) and phenotypic (PCV per cent) coefficient of variation were high for number of fruits plant⁻¹, fresh fruit yield plant⁻¹, dry fruit yield plant⁻¹, pulp: seed ratio, girth of fruit and length of fruit.

Datta and Jana (2010) carried an experiment on genetic variability, heritability and correlation in chilli genotypes and recorded estimates of GCV and PCV on the basis of pooled value for growth and yield characters. The study revealed that the contribution of those characters towards final phenotypic expression were mostly of genetic rather than environmental factors. The high GCV value was observed for capsaicin content in green fruit, number of fruits plant⁻¹, extractable fruit colour, fruit length and individual fruit weight.

Singh and Chaudhary (2011) observed considerable amounts of GCV and PCV for capsaicin content, number of fruits plant⁻¹, fruit length, fruit diameter, leaf area and total fresh yield plant⁻¹ indicating the existence of greater diversity for these characters.

Rego *et al.* (2011) evaluated sixty nine accessions of chilli for fourteen qualitative and quantitative traits. The accession numbers 33, 44 and 41 showed maximum values for dry matter content and total soluble solids. While on the other hand the accession number 48 showed maximum values for fresh weight, major fruit length and fruit width. The accession 33 belonging to *Capsicum frutescens* species were found with high vitamin C content.

Basavaraja *et al.* (2012) studied genetic variability in sixteen different indigenous genotypes of chilli for five important characters viz., plant height, number of branches, number of fruits plant⁻¹, plant yield plot⁻¹, and fruit yield hectare⁻¹. The analysis of variance revealed significant and high degree of variability for all the characters studied. Phenotypic variance showed higher value than the genotypic variance indicating greater influence of environment. The

higher estimates of genotypic and phenotypic coefficient of variation were observed for fruit yield plot⁻¹ (42.71 and 57.49 kg) and fruit yield hectare⁻¹ (59.55 and 77.69 t) which indicated presence of considerable variability and good of scope for selection.

Datta and Das (2013) revealed wide range of variability for all the characters studied. High heritability along with higher genetic gain was found in capsaicin content in fruit, number of fruits plant⁻¹, yield plant⁻¹ and primary branches plant⁻¹. These characters may be considered as reliable selection indices as they are possibly governed by additive gene effect.

Janakii *et al.* (2015) studied sixty three genotypes of chilli (*Capsicum annuum* L.) to estimate the genetic variability, heritability and genetic gain for ten quantitative traits. Analysis of variance revealed significant differences among the genotypes for all the traits studied indicating the presence of sufficient variability in the studied material. High magnitude of PCV and GCV were observed for per cent fruit set, number of fruits plant⁻¹, fruit diameter, average dry fruit weight, number of seeds fruit⁻¹ and yield plant⁻¹. High heritability coupled with high genetic gain was observed for all the characters except days to 50% flowering indicating the predominance of additive gene action making the simple selection more effective.

Maurya *et al.* (2015) evaluated thirty genotypes of chilli in a field study to access genetic variability, heritability and genetic gain. Analysis of variance revealed significant differences among the genotypes for the traits studied indicating the presence of sufficient variability in the studied material. The phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) and the difference between PCV and GCV was narrow for most of the characters revealing little influence of the environment in the expression of these traits. Higher phenotypic and genotypic coefficients of variation were observed for days to 50% flowering, number of fruits plant⁻¹, fruit

length, number of seeds fruit⁻¹, weight of seeds fruit⁻¹, seed husk ratio, average dry fruit weight and dry fruit yield plant⁻¹.

Patel *et al.* (2015) studied forty diverse genotypes of chilli to access genetic variability. The analysis of variance revealed the significant differences among the genotypes for all the characters studied which indicating that presence of great deal of genetic variability for different traits. The high estimates of GCV and PCV were obtained for number of primary branches plant⁻¹, number of secondary branches plant⁻¹, number of fruits plant⁻¹, average fruit length (cm), average fruit girth (cm), fruit shape index, average fruit weight (g), green fruit yield plant⁻¹(g), chlorophyll content (mg100g⁻¹), ascorbic acid content (mg100g⁻¹) and capsaicin content (mg g⁻¹), while it was low for moisture content (%). The characters like days to flowering (days), plant height (cm), number of primary branches plant⁻¹, number of secondary branches plant⁻¹, number of fruits plant⁻¹, average fruit length (cm), average fruit girth (cm), fruit-shape index, average fruit weight (g), green fruit yield plant⁻¹ (g), chlorophyll content (mg100g⁻¹), ascorbic acid content (mg100g⁻¹) and capsaicin content (mg g⁻¹) exhibited high genetic gain coupled with high heritability, indicating better scope for improvement of these traits by an effective selection programme. The results of correlation studies indicated that genotypic correlation coefficients were higher in magnitude than their corresponding phenotypic correlation coefficients for all the traits. Green fruit yield plant⁻¹ had high, significant and positive association with number of fruits plant⁻¹, average fruit weight, moisture content and chlorophyll content at both genotypic and phenotypic levels which indicating that these traits were main yield attributing traits.

Singh *et al.* (2017) evaluated eighteen genotypes of chilli (*Capsicum annum* L.) to estimate the genetic variability and heritability and genetic gain for thirteen quantitative traits. Analysis of variance revealed highly significant difference among the genotypes for all the characters studied. In general the PCV values was higher than the corresponding GCV values for all the traits. High

magnitude of PCV and GCV were observed for number of fruit plant⁻¹ followed by average fruit weight, fruit yield plant⁻¹, while it was low for number of branches plant⁻¹.

Pandiyaraj *et al.* (2017) evaluated thirty three chilli lines to estimate genetic variability, heritability and genetic gain of twelve quantitative and four qualitative traits. The overall values of GCV were lower than the PCV for all the traits. High magnitude of PCV and GCV were recorded for carotene content and followed by red pod yield plant⁻¹, dry pod yield plant⁻¹ and capsaicin. High values of GCV are an indication of high genetic variability among the germplasm.

Mahantesh *et al.* (2017) evaluated fifty accessions of chilli for genetic variability, heritability, genetic gain and genetic gain as a percent over mean. High degree of variation was observed for all characters. The difference between PCV and GCV were found to be narrow for most of the traits.

Nahak *et al.* (2018) evaluated eleven genotypes of chilli in order to determine the magnitude of variability. Through analysis of variance, a highly significant difference was found for almost all characters indicating a greater opportunity to exploit variability. Genotypic and phenotypic variances were highest for fruit yield plant⁻¹ followed by fruit weight and number of fruits plant⁻¹. Phenotypic co-efficient of variation (PCV) and Genotypic co-efficient of variation (GCV) were maximum in case of number of plants affected by leaf curl plot⁻¹ followed by fruit weight and number of wilted plants plot⁻¹.

2.6 Heritability and genetic gain

Heritability has been widely used in determining the degree to which a character may be transmitted from parents to off springs. It is a measure of the genetic relationship between parents and progeny. The concept of heritability was presented by Lush (1940), who described heritability in broad sense as the proportion of genetic variation to the total phenotypic variation. Robinson *et al.* (1949) defined heritability as the additive genetic variance in per cent of the total

variance. High heritability along with high genetic gain are important for making effective selections. Johnson *et al.* (1955) pointed out that without genetic gain the estimates of heritability would not be of practical importance in selection based on phenotypic appearance and therefore genetic gain should be considered along with heritability in streamlining the coherent selection breeding programme.

In chilli fruit yield and its component traits like fruit length, fruit weight, fruit diameter, number of fruits plant⁻¹ were reported to have high heritability coupled with high genetic gain as percent of mean (Mohammed *et al.*, 2001; Prasath *et al.*, 2007; Patel *et al.*, 2009; Singh *et al.*, 2009); Sarkar *et al.*, 2009; Rego *et al.*, 2011; Diwakar *et al.*, 2012; Basavaraja *et al.*, 2012; Janaki *et al.*, 2015; Maurya *et al.*, 2015; Mahantesh *et al.*, 2017). Similar findings were obtained for plant height, plant spread (Sarkar *et al.*, 2009; Varalakshmi and Haribabu (1991); Sreelathakumary and Rajamony (2002); Khurana *et al.*, 2003; Verma *et al.*, 2004 and Janaki *et al.*, 2015).

High heritability coupled with high genetic gain were observed for leaf area, number of fruits plant⁻¹, fruit weight, fruit length, fruit girth and yield plant⁻¹ in chilli, implying the potential for crop improvement through selection (Sreelathakumary and Rajamony, 2004).

High heritability coupled with high genetic gain was recorded for green fruit yield plant⁻¹, number of fruits plant⁻¹ and fruit weight suggesting that phenotypic selection for these traits would be effective for improvement (Patel *et al.*, 2009). High heritability coupled with high genetic gain was also reported by Singh *et al.* (2009) for marketable fresh and dry yield plant⁻¹, average fruit weight, numbers of marketable fruit, fruit diameter, and oleoresin and capsaicin content, which indicated the role of additive gene action for the inheritance of these traits and their response better to selection. High heritability coupled with high genetic gain was recorded for fruit yield plant⁻¹, number of fruits plant⁻¹, fruit length, days to 50% flowering and plant height indicating that these characters were controlled by additive gene action (Sarkar *et al.*, 2009).

Farhad *et al.* (2008) evaluated forty five chilli (*Capsicum annuum* L.) genotypes for variability, association and direct and indirect effects present among themselves. Fourteen quantitative characters viz., days to 50% flowering, time between fruit set and maturity, plant height, primary branches plant⁻¹, number of secondary branches plant⁻¹, fruit length, fruit girth, fruit weight, number of fruits plant⁻¹, seeds per fruit, 100 seed weight, fruit pedicel length, vitamin-C content and dry fruit yield plant⁻¹ were taken into consideration. Higher genotypic as well as phenotypic coefficient of variations were reported for vitamin C content, number of secondary branches plant⁻¹, number of primary branches plant⁻¹ and fruit yield plant⁻¹. Heritability estimates were higher for all the characters except days to 50% flowering and pedicel length. High heritability coupled with high genetic gain were reported for number of seeds fruit⁻¹ and plant height.

Jyothi *et al.* (2008) studied genetic variability, heritability and genetic gain as per cent mean in chilli on eight characters viz., plant height, plant spread and number of fruits plant⁻¹, fruit length, fruit girth, number of seeds fruit⁻¹, ripe chilli yield and dry chilli yield. Significant differences were observed among genotypes in respect of all the characters studied. High heritability coupled with high genetic gain as per cent mean, was observed for ripe chilli yield, dry chilli yield, number of fruits plant⁻¹, number of seeds fruit⁻¹ and fruit length.

High heritability and high genetic gain were noticed for average fruit weight, fruit yield plant⁻¹, fruit diameter, number of lobes fruit⁻¹, days to first harvest, leaf area and ascorbic acid content (Sharma *et al.*, 2010) and for capsaicin content in green fruit, number of fruits plant⁻¹, extractable fruit color, individual fruit weight, plant height and days to flowering and these may be considered as reliable selection indices as reported by Datta and Jana (2010). While high amount of heritability and genetic gain was observed for number of fruits plant⁻¹, fresh fruit yield plant⁻¹, dry fruit yield plant⁻¹, pulp: seed ratio, girth of fruit and length of fruit, indicating the scope for their improvement through selection as reported by Padhar and Zaveri (2010).

A study carried out by Singh and Chaudhary (2011) on chilli indicated that heritability (b.s) was found appreciably high (>90%) for number of primary branches, leaf area, fruit length, number of fruits plant⁻¹, total fresh yield plant⁻¹ and the total dry yield plant⁻¹. High heritability coupled with high degree of genetic gain was noted for total fresh yield plant⁻¹, number of fruits plant⁻¹ and ascorbic acid content in both, the F₁'s and parents. High heritability coupled with high genetic gain and genetic coefficient of variation reflected that the above characters were under the control of additive gene effects, and selection methods could be relied upon for yield improvement.

Basavaraja *et al.* (2012) revealed high heritability along with high genetic gain as percent mean was found for fruit yield plot⁻¹ and fruit yield hac⁻¹ (55.20 and 63.49 kg) and (59.55 and 94.10 tons) respectively which indicates the additive gene effect regulating their inheritance. The character number of fruits plant⁻¹ showed medium to high genetic coefficient of variation (40.74), phenotypic coefficient of variation (58.56), heritability (48.40) with genetic gain as percent mean of 58.38 indicating the additive and dominant gene effect and scope for simple selection for hybridization.

Surya *et al.* (2014) evaluated ninety four paprika accessions for seventeen different characters for variability, heritability, genetic gain as percent of mean and genetic divergence. Higher phenotypic and genotypic coefficient of variation, heritability and genetic gain was observed for number of fruits plant⁻¹ including fresh fruit yield plant⁻¹, dry fruit yield plant⁻¹, 100 seed weight, number of seeds fruit⁻¹, capsanthin, capsaicin and oleoresin content. Plant height, plant spread, and fruit diameter exhibited moderate PCV and GCV.

A study by Janaki *et al.* (2015) revealed high heritability with high genetic gain for all the characters in chilli germplasm, except days to 50% flowering indicating the predominance of additive gene action making the simple selection more effective.

Meena *et al.* (2016) carried out a study to find out the genetic variability, heritability and genetic gain in chilli. The observations were recorded on five plants plot⁻¹ for days to flowering, plant height, number of branches plant⁻¹, number of fruits plant⁻¹, leaf area, pedicel length, fruit length, fruit width, days to first harvest and fruit yield plant⁻¹. The genotypes Azad Mirch-1, Sel-16 and Sel-7919 performed better in terms of leaf area with maximum value (116.38), succeeded by red ripe fruit yield plant⁻¹ (85.40), fruit width (38.23), number of branches plant⁻¹ (34.43), days to 50% flowering (32.46), days to first harvest (27.83), pedicel length (27.78), fruit yield plant⁻¹ (17.73), fruit length (16.64) and plant height (12.76).

Chakrabarty *et al.* (2017) carried out a study to estimate the genetic variability and character association in chilli germplasm. Significant differences were observed among the genotypes for all the fifteen traits for twenty chilli genotypes. The highest GCV and PCV were found for ten edible fruit weight, number of fruits plant⁻¹, fruit yield plant⁻¹, ten dry fruit weight, fruit length, fruit width, and weight of seeds fruit⁻¹. High heritability coupled with very high genetic gain as per cent of mean was observed for ten edible fruit weight, ten dry fruit weight, fruit length, number of fruits plant⁻¹, and fruit yield plant⁻¹.

High estimates of heritability was found by Mahantesh *et al.* (2017) for plant spread (N-S) at 60 days (64.27%) and 120 days (65.47%) and (E-W) at 60 days (60.56%) after transplanting , number of fruits plant⁻¹ at first picking (98.20%) and early yield (94.67%).

In a study, Pandiyaraj *et al.* (2017) concluded that the traits like carotene content, red pod yield plant⁻¹, dry pod yield plant⁻¹ and mean pod weight with high phenotypic coefficient of variation, genotypic coefficient of variation, heritability and genetic gain as percent of mean, indicating that these characters are under additive gene effects and more reliable for effective selection.

Singh *et al.* (2017) noticed high heritability coupled with high genetic gain as percentage of mean for average fruit weight, number of fruit plant⁻¹ suggesting that the predominance of additive gene action indicating better scope for improvement of these traits by an effective selection programme.

Nahak *et al.* (2018) observed heritability (bs) was highest for fruit weight followed by number of fruits plant⁻¹. The maximum genetic gain (% of mean) was observed in case fruit weight. Genotypic coefficient of variation, heritability and predicted genetic gain were high for the characters fruit weight, number of fruits plant⁻¹ suggesting that additive gene action is responsible for expression of these characters.

2.7 Correlation coefficients analysis

The expression of character in a plant is a consequence of a chain of interactions among characters either directly or through other events. In any crop, fruit yield is a complex character being influenced by several other traits. Selection for such traits may not necessarily lead to its improvement unless the unfavourable linkages among such components are favourably altered through hybridization. The correlation characters may be due to genetic linkage or pleiotropy (Harland, 1939).

The correlation coefficient analysis measures the mutual relationship between various characters and it determines the component traits on which selection can be relied upon to effect the improvement. There are three types of correlations *viz.*, phenotypic, genotypic and environmental correlations.

Phenotypic correlation is the observable correlation between two variables and includes both genotypic and environmental effects. Genotypic correlation on the other hand, is the inherent association between two variables may be either due to pleiotropic action of genes or linkage, more likely both are developmentally induced relationships. A brief review of the nature of association of character in chilli investigated by several workers is presented below:

Smitha *et al.* (2006) evaluated forty chilli genotypes for variability, heritability genetic gain and correlation studies. Correlation studies revealed that, importance should be given to number of fruits plant⁻¹, fruit weight, number of primary branches, fruit length, fruit diameter and plant height during selection process, because these characters are going to contribute directly towards the yield.

Bharadwaj *et al.* (2007) carried out study on genetic variability and association of component characters for yield in chilli. Fruit yield was positively associated with number of branches plant⁻¹ and number of fruits plant⁻¹. Number of branches plant⁻¹ were also positively correlated with fruit width, number of fruits plant⁻¹, capsaicin content and fruit yield. Though selection for improvement of fruit yield is possible through positively correlated yield contributing characters. However, these characters are influenced by environment. Therefore, selection of genotypes for improvement of fruit yield through number of branches plant⁻¹ and number of fruits plant⁻¹ is appropriate in the present set of material since these characters are not much influenced by environment.

Vani *et al.* (2007) reported that fruit yield plant⁻¹ was significantly and positively correlated with all yield attributes, except for stalk weight. High positive direct effect of yield attributing characters such as fruit length, stalk weight and fruit weight resulted in significant correlation with yield. Number of fruits plant⁻¹ and average fruit weight also contributed indirectly through all characters, which made the correlation significant.

Jabeen *et al.* (2009) carried an investigation on character association in chilli and revealed that the fruit yield plant⁻¹ exhibited highly significant correlation with number of fruits plant⁻¹, number of branches plant⁻¹ and height of the plant, indicating the usefulness of these traits for improving upon fruit yield in chilli.

Pandit *et al.* (2009) revealed significant positive correlation of fruit yield plant⁻¹ with fruit length, fruit pedicel length, number of fruits plant⁻¹, fruit weight and 1000-seed weight. Fruit weight was significantly positively correlated with number of seeds fruit⁻¹ and 100-seed weight. Fruit yield plant⁻¹ was positively correlated with number of fruits plant⁻¹ and fruit length.

Patel *et al.* (2009) reported that the green fruit yield per plant showed highly significant and positive correlation with primary branches plant⁻¹, secondary branches plant⁻¹, number of fruits plant⁻¹, fruit length, fruit girth and fruit weight.

The correlation studies by Singh *et al.* (2009) in chilli indicated that average fruit weight, number of total and marketable fruits plant⁻¹, and fruit length contributed to marketable fresh yield. Average dry fruit weight, number of total and marketable fruits plant⁻¹, seed weight fruit⁻¹, and harvest duration played a predominant role for predicting dry yield. Among quality traits, capsanthin was significantly and positively correlated with yield. Ascorbic acid and capsaicin content were positively associated with total soluble solids at green and red stage, respectively.

Wilson and Philip (2009) recorded higher genotypic correlation coefficient and phenotypic correlation coefficient. Yield plant⁻¹ exhibited significant positive association with fruits plant⁻¹, fruit length, fruit weight, 100-seed weight, plant height and negative correlated with 50% flowering.

Sharma *et al.* (2010) studied that number of fruits plant⁻¹ exhibited the highest positive direct effect followed by average fruit weight, number of branches plant⁻¹, pedicel length and harvest duration at genotypic level on yield of chilli.

Shweta *et al.* (2018) evaluated forty two genotypes of chilli for correlation among growth and yield contributing characters. The results revealed that plant

height had positive and significant correlation with number of secondary branches, fruit length, green fruit weight and green fruit yield plant⁻¹.

Vidya *et al.* (2018) evaluated twenty genotypes in chilli (*Capsicum annum* L.) for fourteen different qualitative and quantitative characters. Correlation coefficients at genotypic and phenotypic level indicated that plant spread, fruit length, fruit diameter, fruit stalk length showed highly significant and positive genotypic and phenotypic correlation coefficient with fruit yield plant⁻¹. Reducing and non-reducing sugar showed highly significant and positive genotypic and phenotypic correlation coefficient with total sugar.

2.8 Genetic divergence

Genetic divergence existing in the population helps in the selection of suitable parents for utilization in chilli crop breeding programs. Inter-specific hybridization is possible, though it is not common. Identification and characterization of desirable parental combinations provide the basis for selection in the follow-up breeding process for exploitation of heterosis.

Genetic variability and character association in chilli have been previously studied by various workers. The morphological characterization, evaluation of genetic diversity, documentation and submission to a gene bank are essential to maintain an active basis for the exploration of the genetic variability in breeding programs (Viana *et al.*, 2006; Arriel *et al.*, 2007 and Lannes *et al.*, 2007). Collection and maintenance of the genetic diversity are therefore important to avoid the genetic erosion.

Diversity analysis conducted by Karad *et al.* (2002) revealed good amount of variation among the genotypes studied. D² values ranged between 0.1032 and 8.7702. The 40 genotypes were grouped into eight clusters. Cluster I was the largest containing 23 genotypes, followed by cluster II (4 genotypes), cluster III (3 genotypes), cluster IV (3 genotypes), cluster VII (3 genotypes) and cluster VI (2 genotypes). The clusters V and VIII were mono genotypic. Inter-cluster distance

(D^2) ranged between 7.45 (clusters II and V) and 1.15 (clusters III and VII). The variance of cluster means revealed that fresh fruit weight and fruits plant⁻¹ had the highest contribution towards divergence.

Senapati *et al.* (2003) using Mahalanobis D^2 statistic studied divergence for eleven characters in a collection of 20 diverse chilli genotypes. Based on D^2 values, the genotypes were clustered in six clusters. Cluster I was largest with 13 genotypes, followed by clusters III and IV with two genotypes each. Clusters II, V and VI had single genotype each only. Cluster II showed maximum genetic distance from cluster VI, suggesting wide diversity between these groups. Four characters, namely fresh fruit weight, fruit girth, fruit length and fruit number plant⁻¹ were the chief contributors towards genetic divergence.

Sudre *et al.* (2005) used multivariate techniques to evaluate the genetic divergence among fifty six accessions of chilli and sweet pepper (*Capsicum* spp.). Eleven quantitative descriptors proposed by International Plant Genetic Resources Institute were utilized. Generalized Mahalanobis distance (D^2) was used as dissimilarity measure. Canonical variated analysis, cluster analysis using Tocher's optimization method and distances in the plan were applied. The variables viz., fruit length, fruit diameter, number of seeds fruit⁻¹, fruit average weight, plant height, plant canopy width, 1000-seed weight, days to flowering, days to fruiting, number of fruit plant⁻¹ and fruit weight plant⁻¹ were evaluated. There were significant differences among accessions for all descriptors evaluated. General agreement among all multivariate techniques used was observed and it was possible to separate the accessions in eight distinct groups, indicating that there is genetic variability for the evaluated traits. The highest generalized distance of Mahalanobis was 266.42. Hence, these accessions have the potential to be used as parents in artificial crosses to obtain progenies with higher heterosis.

Smitha and Basavaraja (2006) while studying genetic divergence in forty genotypes of chilli grouped them into eight clusters (A-H). Cluster A included ten genotypes, cluster B seventeen, cluster C five, cluster E four, clusters D, F, G and

H one each. The maximum intra and inter-cluster distance were observed for cluster A and between clusters E and H, respectively, indicating their suitability for heterosis breeding with respect to few important characters. The maximum relative contribution to the total divergence was recorded for number of fruits (28.08%), fruit yield (21.15%), number of primary branches (15.00%), number of secondary branches (10.00%), seeds fruit⁻¹ (10.00%), plant spread (6.67%), fruit width (5.26%) and fruit length (3.44%), confirming the existence of ample amount of divergence in the genotypes with respect to the trait

Gogate *et al.* (2006) carried a study on genetic divergence in chilli and indicate the existence of large variability among the genotypes for all the characters. Total eleven clusters were made based on D² values. The genotypes were distributed randomly irrespective of geographic origin. The grouping of genotype did not show any relationship between genetic divergence and geographic diversity. The intra-cluster distances ranged from 0.00 to 875.95. Number of fruits plant⁻¹, chlorophyll content, green fruit yield and ascorbic content largely influenced genetic discrimination of genotypes. The genotypes viz., Jwala, RHRC 16-5, ACG 349, ACS 98-8, ACS 92-4, S 49 and ACS 2000-02 were identified as promising parents for future breeding programme.

Genetic divergence using Mahalanobis's D² statistic was studied for nine characters in a collection of thirty chilli genotypes by Mankar *et al.* (2007). Based on D² values, the genotypes were clustered into four groups. Cluster II was the largest with sixteen genotypes. Cluster I and III had five genotypes each and Cluster IV consisted of four genotypes. The maximum inter-cluster genetic distance was observed between cluster I and cluster IV suggesting wide diversity between genotypes of these groups. Red chilli yield plant⁻¹ contributed maximum towards the genetic divergence. This was also confirmed by both canonical variate and cluster mean analysis.

Prasath *et al.* (2007) analysed twenty-seven accessions of chilli (twenty six belonging to *Capsicum annuum* and one to *Capsicum baccatum*) from different

eco-geographical regions for different quality traits. The total extractable colour ranged from 32.82 to 208.56 ASTA units, with a mean value of 117.05 ASTA units. Six genotypes exhibited high capsaicin percentage (>1), while three genotypes showed low capsaicin value (<0.20). Plant height and number of fruits plant^{-1} were more variable, ranging from 53.10 to 112.85 cm and 4.15 to 257.50, respectively. Six genotypes possessed individual fruit weight of more than 10 gram. Thirteen accessions recorded higher yields than the arithmetic mean ($324.01 \pm 104.47 \text{ g plant}^{-1}$). The maximum fruit yield plant^{-1} was observed for Accession 27 (797.10), followed by Accession 16 (684.55) and Accession 22 (530.05). The Euclidean distance values ('d'), which reflected the divergence for quantitative traits among genotypes, ranged from 0.397 to 2.530. The results indicate that there is a large genetic diversity for colour and pungency between the germplasm collected from different parts of India.

While evaluating fifty-five accessions of chilli for fifteen quantitative characters, Vani *et al.* (2007) reported that plant height and fruit yield plant^{-1} , showed maximum contribution towards diversity. D^2 analysis grouped all the genotypes into fourteen clusters with ten solitary clusters, and the D^2 values varied between 14.38 and 85.01. Cluster I was the largest containing thirty two genotypes, followed by clusters II and IV with five genotypes each. The maximum intra-cluster distance was reported in cluster I, whereas inter-cluster distance was maximum between clusters VII and XI. Cluster means showed that solitary clusters, i.e. cluster XI (IC-32), cluster XII (Pusa Jwala) and cluster XIV (IC-16), were having high mean values for fruit yield plant^{-1} , average fruit weight, seeds fruit^{-1} and fruit length.

Pandit *et al.* (2010) evaluated forty nine diverse materials of chilli for twelve characters in each genotype through multivariate analysis for estimation of genetic divergence using D^2 statistic. The genotypes were grouped into seventeen clusters with cluster 1 having the maximum number of genotypes (nine genotypes) and Cluster 12, 13, 14, 15, 16, 17 contain one genotype each,

indicating wide range of diversity among the genotypes. The intra and inter-cluster distance represent the index of genetic diversity in clusters. The intra-cluster distance was low, revealing homogeneity in the genotypes in a particular cluster for expression of the twelve characters under consideration. The inter-cluster divergence was maximum between cluster 11 and 16 (32.40), suggesting wide diversity between them. The difference between PCV and GCV were found to be narrow for most of the traits except number of primary and secondary branches, tertiary branches, fifty per cent flowering, early and late fruit yield plant⁻¹ (Krishna *et al.*, 2007). The three characteristics that played the greatest role in differentiation are fruit diameter, number of fruits plant⁻¹, and leaf diameter, which can be utilized as conventional or morphological markers for the improvement of chilli yield and obtaining good segregants in chilli breeding programs (Thul *et al.*, 2009). Considerable diversity within and between clusters was noted and it was observed that number of branches, fruit thickness, number of fruits plant⁻¹ and yield plant⁻¹ were, the potent factors in differentiating the germplasm of chilli (Singh and Singh, 1976).

Kumar *et al.* (2010) conducted a study on genetic diversity in twenty five chilli genotypes for various characters and revealed substantial differences for all the traits. Based on D² values, the genotypes were clustered into eight constellations. Cluster I contained nine genotypes followed by cluster-II (four genotypes), cluster IV and cluster V (two genotypes each). The maximum inter-cluster distance (12.75) was observed between cluster VI and cluster VIII. The cluster IV recorded maximum intra-cluster distance (5.91). Intercrossing among the genotypes belonging to cluster III, IV and I was suggested to develop high yielding varieties with other desirable characters or may be used as potential donors for future hybridization programme to develop better chilli variety with good fruit yield.

Singh and Singh (2010) assessed genetic diversity in fifty germplasm lines of chilli and reported that all the fifty genotypes grouped in four and three clusters

in first year and second year, respectively. Highest intra-cluster D^2 values (468.96) and genetic distance (21.85) in first year was estimated for cluster III followed by cluster II (427.41 and 20.67) and cluster I (202.64 and 14.24). Maximum inter-cluster D^2 values (984.71) and genetic distance (31.38) were recorded between cluster II and III followed by cluster I and III (816.43 and 28.57), cluster III and IV (725.44 and 26.93), cluster II and IV (562.34 and 23.71), cluster I and II (546.70 and 23.38) and cluster I and IV (490.66 and 22.10). In second year cluster I had intra-cluster D^2 values and distance of 121.00 and 11.00, respectively. Maximum inter-cluster D^2 values (824.91) and genetic distance (28.72) were recorded between cluster II and III, followed by cluster I and II (747.37 and 27.34) and cluster I and III (169.00 and 13.00).

Farhad *et al.* (2010) conducted a study on genetic divergence with forty five lines of chilli. The analysis of variance revealed remarkable variability among the genotypes for the character concerned. Cluster analysis was used for the grouping the genotypes which got grouped into six clusters. Cluster II had highest ($D= 4.91$) intra-cluster distance and cluster I had lowest ($D= 3.41$) intra-cluster distance. The characters viz., plant height and number of secondary branches plant⁻¹ contributed maximum towards the divergence.

A study of genetic diversity involving twenty five chilli genotypes for various characters was carried out by Kumar *et al.* (2010) which revealed substantial differences for all the traits. Based on D^2 values, the genotypes were clustered into eight constellations. Cluster I contained nine genotypes followed by cluster-II (four genotypes) cluster IV and V (two genotypes each). The maximum inter cluster distance (12.75) was observed between cluster VI and cluster VIII. The cluster IV recorded maximum intra-cluster distance (5.91). Intercrossing among the genotypes belonging to cluster III, IV and I was suggested to develop high yielding varieties with other desirable characters or may be used as potential donors for future hybridization programme to develop better chilli variety with good fruit yield.

Datta and Jana (2011) grouped sixty five genotypes of chilli into eleven clusters. Cluster I and III comprised forty five and eleven genotypes, respectively while rest of the clusters consisted of only one genotype in each case. The clustering pattern revealed that there was no association of species and geographical distribution for the formation of cluster in genetic divergence. The characters namely, number of primary branches plant⁻¹, days to flowering, ascorbic acid content in fruit and extractable fruit colour were contributing maximum to divergence and supposed to play important role in the improvement of chilli. On the basis of cluster mean, intra and inter cluster distance and *per se* performance, cluster V (CA-29) and cluster X (CA-60); cluster VIII (CA-55) and cluster X (CA-60); cluster VIII (CA-55) and XI (CA-58) cluster VIII (CA-55) and cluster DC (CA-59) may be used for their desirable characteristics in breeding program of chilli improvement.

Hasanuzzaman and Golam (2011) conducted an experiment on selection of parents in chilli (*Capsicum annuum* L.). Based on the degree of divergence among genotypes, the twenty accessions were grouped into six clusters. Cluster I consisted of solitary individual genotype, cluster II and cluster III of three accessions, cluster IV of two genotypes cluster V of maximum seven genotypes while cluster VI consisted of four genotypes. The highest intra-cluster divergence (1.7153) for cluster VI was invariably smaller than the lowest inter-cluster divergence between cluster III and cluster VI (3.247), thus authenticating the clustering pattern formed in this study. The intra-cluster divergence ranged from 0.00 and 0.07288 to 1.7153, whereas the inter-cluster divergence ranged from 3.247 to 12.677 between clusters III and VI and clusters I and V respectively. The four characteristics that played the greatest role in differentiation were fruit yield plant⁻¹, plant height, days to 50% flowering and number of fruits plant⁻¹.

Hasan *et al.* (2015) investigated thirteen genotypes of chilli (*Capsicum annuum* L.) to understand the extent of genetic diversity through six yield attributing characters. Genetic diversity was estimated using Mahalanobis's D²

statistics. The genotypes were grouped into five different clusters by non-hierarchical clustering. The cluster I had the maximum number (5 genotypes) while cluster IV and V each contained only one genotype. The highest inter-cluster distance was observed between cluster I and IV (24.483) and the lowest inter-cluster distance was observed between the clusters II and V (11.633). The results indicated that fruits plant⁻¹ contributed maximum (35.8%) to the total divergence followed by fruit length (21.6%) and fruit yield plant⁻¹ (21.1%). Cluster IV produced highest mean for fruit weight (4.48), number of fruits plant⁻¹ (149.90) and fruit yield plant⁻¹ (676.03). Cluster V produced highest mean for fruit length (10.23), pedicel length (4.94) and fruit diameter (10.36). Cluster I and III recorded minimum mean for almost all characters. Therefore, genotypes belonging to the cluster IV and cluster V may be used as potential parents for future hybridization programme to develop superior chilli variety with desired traits.

Pujar *et al.* (2017) studied sixty three chilli genotypes which included germplasm accessions, local cultivars, and released varieties. The experiment was undertaken to study genetic diversity and selection of suitable genotypes for future hybridization program. Twenty six characters were studied for the better assessment of genetic diversity present between sixty three genotypes. Using Mahalanobis D² statistics, sixty three genotypes were grouped into five divergent clusters with considerable diversity. The magnitude of D² values, which ranged from 25.45 to 64.66. These sixty three genotypes were grouped into five clusters based on similarity of D² values. It was suggested that genotypes from clusters having high inter-cluster distance and with high fruit yield should be selected as parents in the recombination breeding programmes.

Chapter – 3

MATERIALS AND METHODS

The present investigation entitled “**Identification of Resistant Sources against Wilt Disease of Chilli (*Capsicum annuum* L.)**” was conducted at the Experimental Field, Division of Vegetable Science and Mycology and Forest Pathology Laboratory, Division of Plant Pathology, Sher-e-Kashmir University of Agricultural Science & Technology of Kashmir, Shalimar, Srinagar during the year 2018. The experimental field is situated within the premises of university campus, about 12.5 km from main city, at 34° N latitude and 74.9° E longitude. During the experimentation period the average maximum temperature recorded was 25.3°C and the average minimum temperature recorded was 10.9°C. The total precipitation of 800.8 mm was received during 2018. The details of experimental material used and methodologies adopted in achieving the set objectives of the study are described as under:

3.1 Isolation, purification and maintenance of pathogen

3.1.1 Isolation

The chilli plants showing characteristic symptoms of wilt disease were collected and attempted for the isolation of associated pathogen. The stem portions of affected plants were washed in running tap water, cut into segments of 5 mm in length and used immediately for isolation of fungal pathogen into pure culture. The bits were surface sterilized by dipping in 0.1 per cent mercuric chloride for one minute followed by three consecutive rinses in sterilized deionised water. The bits were blotter dried and then aseptically transferred to potato dextrose agar (PDA) medium in sterile petri-plates and incubated at 25±1°C. The plates were observed regularly and outgrowing mycelia were subcultured immediately.

3.1.2 Purification

The culture so obtained was purified by single spore isolation technique (Johnston and Booth, 1983). Spore suspension of fungus was prepared by flooding 10 days old culture plate with 10 ml of sterilized distilled water and serially diluted to 1:1000. Three drops of spore suspension were evenly spread on the surface of plain agar medium in petri-plates for germination. The petri-plates incubated at $25\pm 1^{\circ}\text{C}$ were examined under compound microscope for spore germination. The germinating spores along with agar disc were lifted with the help of sterilized scalpel, transferred to PDA medium plates under aseptic conditions and incubated at $25\pm 1^{\circ}\text{C}$ to maintain its growth.

3.1.3 Maintenance of pathogens

The pure culture so developed was maintained on PDA slants by regular sub-culturing.

3.2 Identification

3.2.1 Morphological identification

Morphological and cultural characters in pure culture of the isolated fungus associated with chilli wilt disease were studied for its identification. Colony characters such as colour and status of the mycelium were studied from the medium visually. For morphology of the fungus, the wet mounts in lactophenol and cotton blue of 15 days old culture were examined under a microscope and the observations with respect to different morphological characters were recorded. The identification of the pathogen was made with the help of descriptions given by Booth (1977) and Booth and Sutton (1984).

3.3 DNA Extraction

DNA extraction was done using 400 μl extraction buffer. This buffer is same as that described by (Cenis, 1992) containing 200mM Tris Hcl pH 8.5, 250mM NaCl, 25 mM EDTA (Ethylene di-amine tetra acetic acid), 0.5% SDS (Sodium

dodecyl sulphate). The fungal mycelium was crushed in extraction buffer using mortar and pestle to make a slurry. The mixture was transferred to a sterilized 2ml microfuge tube and incubated at 65°C in a water bath for 1 hour. After incubation, 4 µl of RNase (20 mg ml⁻¹) was added to cell suspension and again incubated for 10 minutes at 65° with intermittent mixing. After that, 130 µl of 3M sodium acetate, pH 5.2 was added, and the tube was incubated at -20 C for 10 min. The lysate was then centrifuged at 4,000 rpm at 4°C for 15 min and supernatant was transferred to a clean microfuge tube. DNA was precipitated by the addition of 650 µl of isopropanol, pelleted at 4000 rpm for 10 minutes and washed with ice cold 70% ethanol to remove salt contaminants, air dried for 30 minutes and resuspended in 100 µl of Tris-EDTA buffer, pH 8.0.

3.4 Primer Design

Primers were designed using manually Oligocalc (<http://biotools.nubic.northwestern.edu/OligoCalc.html>), ClustalW(<http://www.ebi.ac.uk/Tools/msa/clustalo/>) and Blast (<http://blast.ncbi.nlm.nih.gov/Blast.cgi>) online software shown in detail below in Table -1.

Table 1: Primers used for amplification

S.No.	Primer Name	Primer Sequence	Tm °C
1.	K-Lab-FusOxy-ITS1F2 Primer	5'CCTGCGGAGGATCATT A 3'	63.7
2.	K-Lab-FusOxy-ITS4R2 Primer	5'TCCTCCGCTTATTGAT3'	53.6

3.5 PCR Reaction Mixture

PCR amplification was carried out in a reaction volume of 25 µl in 0.2 ml PCR microfuge tubes. The reaction mixture contents are given in Table 2.

Table 2: PCR reaction mixture used for amplification

Constituents	Volume
Autoclaved water	17.8 μ l
PCR buffer (1 X)	2.5 μ l
MgCl ₂ (25 mM)	1 μ l
dNTPs (25 mM)	0.4 μ l
Forward primer (10 μ M)	1 μ l
Reverse primer (10 μ M)	1 μ l
Taq Polymerase (5 U/ μ l)	0.3 μ l
DNA sample	1 μ l
Total volume	25 μl

3.5.1 PCR cycle conditions

The amplification reaction was carried out in thermocycler (*Applied Biosystems*). The cycling conditions are shown in Table- 3.

Table 3: Thermal cycling conditions used for amplification

Steps	Temperature (°C)	Time	Number of cycles
1. Initial denaturation	94	5 minutes	1
2. Denaturation	94	30 seconds	
3. Annealing	55	30 seconds	35
4. Extension	72	2 minutes	
5. Final extension	72	30 minutes	1

3.5.2 Gel Electrophoresis

The amplified product was electrophoresed on 1% agarose gel in TAE run at 100 volt for 45 minutes and compared with 100 bp DNA ladder.

3.6 Sequencing

30 µl PCR product amplified by ITS1F2 and ITS4R2 primers were put in 1.5ml microfuge tubes along with 50µl primer in separate microfuge tubes having a concentration of 10mmol/µl and were outsourced for sequencing to Agri Genomics Labs, Kerala.

3.7 Bioinformatic analysis

The sequenced data was analysed using various bioinformatics tools like: BLAST, CLASTALW and OLIGOCALC for comparative sequence analysis between query sequences and database sequences. The sequences unique to the sample were marked. Sequence similarity with already existing sequences in the GenBank was done using BLAST N similarity search. Sequence similarity between various sequences obtained through sequencing and sequences already present was done using CLUSTAL W.

3.8 Pathogenicity

The pathogenicity of the isolated organism was established on potted chilli plants (cv. Kashmir Long-1) by confirming postulates of Koch. The method as adopted by Najar (2001) was followed.

3.8.1 Preparation of inoculum and inoculation

The pathogen inoculum was multiplied on sand maize meal agar medium. The medium was prepared by autoclaving 90 g dry sieved sand and 10 g maize meal with 40 ml of distilled water at 1.05 kg cm⁻² pressure for half an hour for three consecutive days. The sterilized medium was then inoculated with the test fungi and incubated for three weeks at 25±1°C. During incubation, the flasks were shaken manually for a few minutes daily to get uniform growth. The inoculums so

prepared was incorporated in pots containing sterilized sand soil (2:1) potting mixture @ 10 per cent (w/w) by mixing it thoroughly in pots and allowed for 7 days to infest soil. The pots were irrigated with tap water regularly to maintain adequate moisture.

3.8.2 Planting of seedlings

Forty five days old chilli seedlings (cv. Kashmir Long-1), raised by growing surface sterilized seeds in sterilized sand soil (2:1) potting mixture were gently uprooted and transplanted in the sterilized potting mixture incorporated 7 days before with test pathogen (Section 3.8.1). The seedlings transplanted in uninoculated sterilized soil served as check.

3.9 Screening of available chilli genotypes against the disease

3.9.1 Screening under field conditions

Chilli germplasm set of 107 lines, were screened against wilt disease under naturally infested soil conditions at the Experimental Field, Division of Vegetable Science, SKUAST-Kashmir, Shalimar Srinagar, during *Kharif* 2018. The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications of each accession following all the recommended practices, except plant protection measures.

The observations on per cent wilt incidence of all the test genotypes were recorded up to harvesting time. The per cent disease incidence was calculated as per the following formula:

$$\text{Disease incidence (\%)} = \frac{\text{No. of diseased plants}}{\text{Total no. of plants observed}} \times 100$$

The per cent disease incidence calculated was used to assess the level of resistance and susceptibility of genotypes as per the disease rating scale of Kesavan and Chaudary (1977) with slight modifications, where:

Table 4: List of chilli genotypes screened under field conditions

S.No.	Chilli Genotypes	Source	S.No.	Chilli Genotypes	Source
1.	SKAU-32	SKUAST-K	27.	SKAU-148	SKUAST-K
2.	SKAU-36	SKUAST-K	28.	SKAU-153	SKUAST-K
3.	SKAU-38	SKUAST-K	29.	SKAU-157	SKUAST-K
4.	SKAU-40	SKUAST-K	30.	SKAU-160	SKUAST-K
5.	SKAU-43	SKUAST-K	31.	SKAU-163	SKUAST-K
6.	SKAU-45	SKUAST-K	32.	SKAU-167	SKUAST-K
7.	SKAU-52	SKUAST-K	33.	SKAU-173	SKUAST-K
8.	SKAU-58	SKUAST-K	34.	SKAU-177	SKUAST-K
9.	SKAU-62	SKUAST-K	35.	SKAU-181	SKUAST-K
10.	SKAU-68	SKUAST-K	36.	SKAU-188	SKUAST-K
11.	SKAU-73	SKUAST-K	37.	SKAU-191	SKUAST-K
12.	SKAU-77	SKUAST-K	38.	SKAU-193	SKUAST-K
13.	SKAU-80	SKUAST-K	39.	SKAU-195	SKUAST-K
14.	SKAU-84	SKUAST-K	40.	SKAU-198	SKUAST-K
15.	SKAU-89	SKUAST-K	41.	SKAU-208	SKUAST-K
16.	SKAU-91	SKUAST-K	42.	SKAU-211	SKUAST-K
17.	SKAU-96	SKUAST-K	43.	SKAU-216	SKUAST-K
18.	SKAU-106	SKUAST-K	44.	SKAU-218	SKUAST-K
19.	SKAU-109	SKUAST-K	45.	SKAU-221	SKUAST-K
20.	SKAU-111	SKUAST-K	46.	SKAU-224	SKUAST-K
21.	SKAU-118	SKUAST-K	47.	SKAU-227	SKUAST-K
22.	SKAU-122	SKUAST-K	48.	SKAU-231	SKUAST-K
23.	SKAU-128	SKUAST-K	49.	SKAU-233	SKUAST-K
24.	SKAU-132	SKUAST-K	50.	SKAU-237	SKUAST-K
25.	SKAU-139	SKUAST-K	51.	SKAU-243	SKUAST-K
26.	SKAU-141	SKUAST-K	52.	SKAU-247	SKUAST-K

53.	SKAU-249	SKUAST-K	81.	IC-413048	NBPGR
54.	SKAU-251	SKUAST-K	82.	IC-362021	NBPGR
55.	SKAU-253	SKUAST-K	83.	IC-505203	NBPGR
56.	SKAU-255	SKUAST-K	84.	IC-561622	NBPGR
57.	SKAU-257	SKUAST-K	85.	IC-561615	NBPGR
58.	SKAU-259	SKUAST-K	86.	IC-344727	NBPGR
59.	SKAU-261	SKUAST-K	87.	IC-391082	NBPGR
60.	SKAU-263	SKUAST-K	88.	IC-505242	NBPGR
61.	SKAU-265	SKUAST-K	89.	IC-572480	NBPGR
62.	SKAU-267	SKUAST-K	90.	IC-343448	NBPGR
63.	SKAU-269	SKUAST-K	91.	IC-344650	NBPGR
64.	SKAU-271	SKUAST-K	92.	IC-362010	NBPGR
65.	SKAU-273	SKUAST-K	93.	IC-302026	NBPGR
66.	SKAU-275	SKUAST-K	94.	IC-565072	NBPGR
67.	SKAU-277	SKUAST-K	95.	IC-347044	NBPGR
68.	SKAU-285	SKUAST-K	96.	IC-278298	NBPGR
69.	SKAU-287	SKUAST-K	97.	IC-284648	NBPGR
70.	SKAU-289	SKUAST-K	98.	IC-561701	NBPGR
71.	SKAU-291	SKUAST-K	99.	IC-561721	NBPGR
72.	SKAU-293	SKUAST-K	100.	IC-561634	NBPGR
73.	SKAU-295	SKUAST-K	101.	IC-505276	NBPGR
74.	SKAU-297	SKUAST-K	102.	IC-276117	NBPGR
75.	SKAU-299	SKUAST-K	103.	IC-390033	NBPGR
76.	SKAU-302	SKUAST-K	104.	IC-561617	NBPGR
77.	SKAU-305	SKUAST-K	105.	Local Kashmiri Chilli-1	KUPWARA
78.	SKAU-310	SKUAST-K	106.	Arka Lohit	IIHR
79.	SC-104	SKUAST-K	107.	KL-1	SKUAST-K
80.	SC-1019	SKUAST-K			

Table 5: Wilt incidence scale

S.No.	Wilt Incidence (%)	Reaction type
1.	0	Immune
2.	0.1-10	Highly resistant
3.	10.1-30	Resistant
4.	30.1-50	Moderately resistant
5.	50.1-80	Susceptible
6.	80.1-100	Highly susceptible

3.9.2 Screening of genotypes under artificially inoculated controlled conditions

Genotypes found immune, highly resistant to moderately resistant under field screening were further screened under artificially inoculated controlled conditions in order to validate field reaction.

3.9.2.1 Preparation of inoculum and inoculation

The method as adopted for pathogenicity test, described in section 3.8 was used for the preparation of inoculum and inoculation of test genotypes. The wilt incidence was recorded after 30 days of sowing to assess the level of resistance and susceptibility of each test entry as per the disease rating scale given in Table 5.

3.10 Characteristics used for observation

Observations on 42 descriptors as mentioned in Table 6 were recorded at different growth stages as per DUS test guidelines of PPV & FR Authority, New Delhi (2001).

Table 6: Table of characteristics

S. No.	Characteristics	States	Note	Stage of observation	Type of assessment
01.	Plant: Habit	Spreading	3	50	VG
		Semi-upright	5		
		Upright	7		
02.	Plant: Length of main stem (cm)	Short (up to 5)	3	50	MS
		Medium (5.01-10)	5		
		Long (>10)	7		
03.	Plant: Length of first internode (on primary branches in cm)	Very short (up to 1)	1	50	MS
		Short (1.01-2)	3		
		Medium (2.01-4)	5		
		Long (4.01-6)	7		
		Very long (>6)	9		
04.	Plant: Anthocyanin colouration of nodes	Absent	1	30	VG
		Present	9		
05.	Plant: Intensity of anthocyanin colouration of nodes	Weak	3	30	VG
		Medium	5		
		Strong	7		
06.	Plant: Height (cm)	Short (<40)	3	50	MS
		Medium (40.01-80)	5		
		Tall (>80)	7		
07.	Plant: Spread (cm)	Narrow (<50)	3	50	MS
		Medium (50.01-100)	5		
		Broad (>100)	7		
08.	Stem: Pubescence (hairiness)	Absent	1	40	VG
		Present	9		
09.	Stem: Intensity of pubescence (hairiness)	Sparse	3	40	VG
		Medium	5		
		Strong	7		
10.	Stem: Shape	Round	3	40	VG
		Angled	5		
		Flat	7		

S. No.	Characteristics	States	Note	Stage of observation	Type of assessment
11.	Leaf: Length of blade (measured from leaf base to leaf tip in cm)	Short (<4)	3	40	MS
		Medium (4.01-8)	5		
		Long (>8)	7		
12.	Leaf: Width of blade (measured on the widest part of the leaf in cm)	Narrow (<3)	3	40	MS
		Medium (3.01-5)	5		
		Broad (>5)	7		
13.	Leaf: Colour	Green	3	40	VG
		Purple	5		
		Green with purple Tinge	7		
		Purple with green Tinge	9		
14.	Leaf: Intensity of green colour	Light	3	40	VG
		Medium	5		
		Dark	7		
15.	Leaf: Intensity of purple colour	Light	3	40	VG
		Medium	5		
		Dark	7		
16.	Leaf: Shape	Lanceolate	3	40	VG
		Ovate	5		
		Broad elliptic	7		
17.	Leaf: Undulation of margin	Weak	3	40	VG
		Medium	5		
		Strong	7		
18.	Leaf: pubescence (hairiness)	Absent	1	40	VG
		Present	9		
19.	Leaf: Intensity of pubescence (hairiness)	Sparse	3		
		Medium	5		
		Strong	7		
20.	Flower: Petal colour	White	3	30	VG
		Yellowish green	5		
		Purple	7		
		Others (specify)	9		

S. No.	Characteristics	States	Note	Stage of observation	Type of assessment
21.	Flower: Anther colour	Yellow	3	30	VG
		Pale blue	5		
		Purple	7		
		Others (specify)	9		
22.	Flower: Days to 50% flowering (from the date of sowing)	Early(<70 days)	3	30	MS
		Medium (70-90)	5		
		Late (>90)	7		
23.	Flower/ Fruit: Orientation	Drooping	3	30/40	VG
		Semi drooping	5		
		Erect	7		
24.	Fruit: Bearing habit (No. of fruits/ node)	1 (Solitary)	3	40	VG
		2-3	5		
		>3 (Cluster)	7		
25.	Fruit: Colour (at mature unripe stage)	White	3	40	VG
		Cream	5		
		Green	7		
		Purple	9		
26.	Fruit: Intensity of colour (at mature unripe stage)	Light	3	40	VG
		Medium	5		
		Dark	7		
27.	Fruit: Length (cm)	Very short (<2)	1	40	MS
		Short (2.01-5.0)	3		
		Medium (5.01-10)	5		
		Long (10.01-15)	7		
		Very long (>15)	9		
28.	Fruit: Diameter (fruits measured at the widest point in cm)	Narrow (<0.8)	3	40	MS
		Medium (0.81-1.5)	5		
		Broad (>1.5)	7		
29.	Fruit: Curvature	Absent	1	40	VG
		Present	9		
30.	Fruit: Curvature intensity	Low	3	40	VG
		Medium	5		
		High	7		

S. No.	Characteristics	States	Note	Stage of observation	Type of assessment
31.	Fruit: Neck at basal end	Absent	1	40	VG
		Present	9		
32.	Fruit: Sinuation of pericarp	Weak	3	40	VG
		Medium	5		
		Strong	7		
33.	Fruit: Texture of surface	Smooth	3	40	VG
		Slightly rough	5		
		Rough	7		
34.	Fruit: Colour (at ripe maturity)	Yellow	1	40	VG
		Orange	2		
		Red	3		
		Brown	4		
		Others (specify)	5		
35.	Fruit: Intensity of colour (at maturity)	Light	3	50	VG
		Medium	5		
		Dark	7		
36.	Fruit: Shape at the base	Acute	3	50	VG
		Round	5		
		Sunken	7		
37.	Fruit: Shape of apex	Acute	1	40	VG
		Blunt	3		
		Depressed	5		
		Depressed & Acute	7		
		Others (specify)	9		
38.	Fruit: Calyx cover	Non-enveloping	1	40	VG
		Enveloping	9		
39	Fruit: Calyx margin	Smooth	1	40	VG
		Dented	9		
40.	Fruit: Calyx Constriction	Absent	1	40	VG
		Present	9		
41.	Fruit: Pedicel Attachment	Weak	1	40	VG
		Strong	9		
42.	Fruit: Blossom end appendage	Absent	1	50	VG
		Present	9		

3.11 Characters studied and observational procedures

Observations were recorded on various yield and quality traits to study the magnitude of genetic variability existing in the experimental material under study. Five competitive plants were selected at random from each replication and tagged for recording the biometrical observations. Mean values for all the characters were worked out. Observations were recorded at the appropriate developmental stages of plant growth as per description below:

3.11.1 Growth parameters

3.11.1.1 Plant height (cm)

The height of five tagged plants was measured in centimeters from the ground level to the tip of the plant when the first fruit in 50% of the plants began to ripe and the average was worked out.

3.11.1.2 Plant spread (cm)

Plant spread was measured simultaneously with height in centimeters as the average spread from North to South and East to West directions and the average of five plants was worked out.

3.11.1.3 Number of branches plant⁻¹

Branches arising from the main stem (primary branches) and those arising from primary (secondary branches) were counted from five selected plants at the end of flowering and the average was worked out.

3.11.1.4 Days to flower initiation

The days to the appearance of first flower set on each tagged plants was recorded from the date of transplanting of seedlings and the average was worked out.

3.11.1.5 Days to fruit initiation

The days to the appearance of first flower set on each tagged plants was recorded from the date of transplanting of seedlings and the average was worked out.

3.11.1.6 Days to harvesting

The days to harvesting was recorded from date of transplanting of seedlings to the first ripe fruit harvest and the average of five plants was worked out.

3.11.1.7 Fruit length (cm)

Fruit length of five randomly selected fruits from each plant was measured from base of the fruit to the tip of fruit (leaving the stalk) and were average was worked out.

3.11.1.8 Fruit diameter (cm)

The fruits used for recording length were also used for measuring diameter. The girth of five fruits from each plant was measured from the middle portion of the fruit with the help of digital vernier caliper and average was worked out.

3.11.1.9 Fruit weight (g)

Fruit weight was calculated in grams by dividing the total fruit yield plant^{-1} by total number of fruits.

3.11.1.10 Fruit pedicel length (cm)

It was recorded as average of five fruits at maturity when the fruits reached marketable stage.

3.11.1.11 Fruit pedicel diameter (cm)

It was also recorded as the average of five fruits at maturity.

3.11.1.12 Number of fruits per plant

The number of fruits from each picking was pooled and the total number of fruits plant⁻¹ was noted.

3.11.1.13 Fruit yield per plant (g)

The total weight of red ripe fresh fruits obtained from each picking of the tagged plants was pooled and the average fruit yield plant⁻¹ was worked out.

3.11.1.14 Fruit yield per hectare (q)

The total weight of red ripe fresh fruits obtained from each picking of the tagged plants was pooled and the average fruit yield hectare⁻¹ was worked out.

3.11.2 Quality parameter

3.11.2.1 Dry matter (%)

The mature fruits from five randomly selected plants were harvested and 100 gram sample weighed on electronic balance. The sample was kept in oven (60°C±2°C) for drying. The sample was then dried. Their weight was recorded in grams after drying when samples exhibited constant weight and average computed.

$$\text{Dry matter content (\%)} = \frac{\text{Dry weight}}{\text{Fresh weight}} \times 100$$

3.11.2.2 Ascorbic acid at green stage (mg100g⁻¹)

A known weight of sample was titrated with 2, 6-dichlorophenol indophenol dye using metaphosphoric acid as stabilizing agent as per A.O.A.C (1984) method of titration.

Five gram sample was ground in a pestle and mortar with stabilizing medium (1:5) and the homogenate was centrifuged. Supernatant was taken and volume was made up to 50 ml with stabilizing medium and filtered. 10ml aliquot

was titrated against 2, 6-dichloro phenol indophenol dye and titre value was noted (i.e., amount of dye added till the appearance of permanent pale yellow colour).

5 ml of 3% HPO_3 was added to 5ml of 10/100 standard ascorbic acid and titrated with the dye solution to a pink colour. The dye factor i.e., mg of ascorbic acid per ml of dye was determined by using the following formula:

$$\text{Dye factor} = 0.5/\text{titre}$$

The vitamin C content of the sample was calculated by using the following formula:

$$\text{Ascorbic acid (mg/100 mg)} = \frac{\text{Titre value} \times \text{Dye factor} \times \text{Volume made up}}{\text{Total weight of the sample} \times \text{Aliquot of sample}} \times 100$$

3.11.2.3 Capsaicin (mg g^{-1})

Capsaicin content was estimated by Phospho molybdic acid method.

Reagents:

- 0.4% Sodium hydroxide (NaOH)
- 3% Phosphomolybdic acid
- Dry acetone (25g of anhydrous sodium sulphate was added to 500 ml acetone one day before use).

A sample weighing 0.5g of dry chilli powder was taken in a volumetric flask and 10ml of dry acetone was added. The solution was shaken for three hours in mechanical shaker. 1ml supernatant was taken in a test tube and evaporated to dryness in hot water bath till residue was left. After this, 5ml of 0.4% NaOH and 3ml of 3% phospho molybdic acid were added to the residue. The contents were shaken and allowed to stand for one hour and the solution was filtered. The clear blue coloured solution was transferred into cuvette directly and absorbance was read at 650 nm with the help of spectrophotometer against dry acetone as blank.

$$\text{Capsaicin (\%)} = \frac{X \times \text{Dilution factor} \times 100}{\text{Weight of sample (g)} \times 1000}$$

Where, X = μg of capsaicin in sample from standard curve using OD value.

3.11.2.4 Capsanthin (ASTA units)

The procedure adopted for the estimation of capsanthin content in chilli is described as follows:

100 mg of chilli powder was transferred to 250 ml volumetric flask and volume was made to 100 ml with acetone. The contents in flask were shaken and the particles were allowed to stand for 16 hours at room temperature in dark. The flask was shaken again and the particles were allowed to settle for 2 minutes, and then a portion of the extract was transferred to cuvette and absorbance was recorded at 460 nm with acetone as blank.

$$\text{ASTA colour value} = \frac{\text{A at 460 nm} \times 16.4 I_f}{\text{g test portion}}$$

Where, A = Absorbance at specific wave length; g = Quantity of test portion; I_f = correction factor.

3.11.2.5 Total phenols (mg 100g⁻¹)

Total phenols were determined by Spectrophotometric measurement of blue coloured complex by the reaction of phenols with phosphomolybdic acid in Folin ciocalteu reagent in alkaline medium (Bray and Thorpe, 1954).

Reagents:

- 80% ethanol
- Folin Ciocalteu reagent (FCR)
- 28% Na₂CO₃: 20g of sodium carbonate was added to 80 ml of distilled water and filtered the solution through Whatman filter paper. Keep the solution a bit warm to prevent solidification.

Method:

A dried fruit sample weighing 1 gram was taken and in a pestle and mortar in 10-times volume of 80% ethanol. The homogenate obtained was centrifuged at 10,000rpm for 20 minutes. The supernatant was saved and the residue re-extracted

with five times the volume of 80% ethanol, centrifuged again to pool the supernatants. The supernatant was transferred to a beaker and kept on hot water bath for evaporation till residue is left. The residue was dissolved in a known volume of distilled water (10 ml). 0.1 ml aliquot was taken and made volume to 3 ml by adding distilled water. 0.5 ml of Folin-Ciocalteu reagent was added to it. After 3 minutes 2 ml of 20% Na₂CO₃ was added to each tube, mixed thoroughly and the tubes were placed in a boiling water for exactly one minute and later cooled. The absorbance was measured at 650nm against a reagent blank. Total phenols (mg g⁻¹ dry weight) were calculated from the standard curve prepared with catechol as reference.

3.11.2.6 Instrumental colour (L*, a*, b*)

The surface colour of chilli in terms of Hunter *L*, *a*, *b* values and yellowness index (Yi) were determined using Hunter lab Miniscan XE plus colorimeter (Model No. 45/0-L, Hunter lab, USA). ‘*L*’ denotes the lightness or darkness, ‘*a*’ green or redness and ‘*b*’, blue or yellowness of the samples. Yellowness index is a derived parameter from *L*, *a*, *b* and was noted directly from the digital colorimeter. Before measuring the colour, the colorimeter was standardized with black and white calibration tiles provided with the instrument. The nose cone of colorimeter was positioned at the chilli surface in such a way that leakage of light thrown by the colorimeter was minimized.

3.12 Statistical and biometrical analysis

The data recorded during the present investigation was subjected to the following statistical and biometrical analysis.

- Analysis of variance and estimation of the components of variance,
- Estimation of heritability and genetic gain,
- Estimation of phenotypic and genotypic correlation coefficients and
- Divergence analysis.

3.12.1 Analysis of variance and estimation of the components of variance

3.12.1.1 Analysis of variance

Analysis of variance for all the characters in randomized complete block design was carried out to test the significance of variation among the treatments. The analysis of variance was done as per procedure described by Panse and Sukhatme (1967).

The analysis of variance table was set up as under:

Source of variation	d.f	SS	MSS	F ratio	Expected mean Square
Replication	r-1	SS (R)	SS (R)/r – 1	MS (R)/MSE	-
Genotypes	t-1	SS (T)	SS (T)/t-1	MS (T)/MSE	$\sigma^2_e + r\sigma^2_g$
Error	(r-1) (t-1)	SS (E)	SS (E)/(r-1) (t-1)		σ^2_e

Where, d.f = Degree of freedom

SS = Sum of squares

MSS = Mean sum of squares

r = Number of replications

t = Number of treatments

σ^2_e = Error variance

σ^2_g = Genotypic variance

The significance of differences was tested by F-test comparing calculated F-value with tabulated F-value at 5 and 1 per cent level of significance at appropriate degree of freedom. When calculated F values were greater than corresponding F tabulated values, the treatments were considered to be significant.

Standard error of differences between treatment mean was calculated as

$$S.E \text{ (diff)} = [2MS (E)/R]^{1/2}$$

Critical difference (C.D. at 5%) = Standard error of difference SE (d) $\times$ t (5%) at error d.f.

$$= (2MS (E)/r)^{1/2} \times t (5\%) \text{ at error d.f.}$$

Where,

MS (E) = Error mean square

R = Number of replications

3.12.1.2 Genotypic variance

Genotypic variance was calculated using the method suggested by Johnson *et al.* (1955).

$$\hat{\sigma}^2_g = \frac{MSG - MSE}{r}$$

Where,

$\hat{\sigma}^2_g$ = Genotypic variance,

MSG = Mean sum of squares due to genotypes,

MSE = Mean sum of squares due to error, and

R = Number of replications

3.12.1.3 Phenotypic variance

Phenotypic variance was calculated as per the procedure given by Johnson *et al.* (1955).

$$\hat{\sigma}^2_p = \hat{\sigma}^2_g + \hat{\sigma}^2_e$$

Where,

$\hat{\sigma}^2_p$ = Phenotypic variance

$\hat{\sigma}^2_g$ = Genotypic variance, and

$\hat{\sigma}^2_e$ = Error variance

3.12.1.4 Phenotypic and genotypic co-efficient of variation

The magnitude of phenotypic co-efficient of variation (PCV) and genotypic co-efficient of variation (GCV) existing in a trait was worked out by the formula given by Burton (1952):

$$PCV = \frac{\sqrt{\hat{\sigma}^2 p}}{\bar{X}} \times 100$$

Where,

$\hat{\sigma}^2 p$ = Phenotypic variance, and

$\bar{X}$ = Grand mean of the trait studied

$$GCV = \frac{\sqrt{\hat{\sigma}^2 g}}{\bar{X}} \times 100$$

Where,

$\hat{\sigma}^2 g$ = Genotypic variance, and

$\bar{X}$ = grand mean of the trait studied

PCV, GCV were categorized as low, moderate and high by following Sivasubramanian and Menon (1973) as follows:

0- 10%: Low

10 – 20%: Moderate

Above 20%: High

3.12.2 Estimation of heritability genetic gain and expected genetic gain

3.12.2.1 Heritability (Broad sense)

It was estimated as per the procedure presented by Burton and Devane (1953), Johnson *et al.* (1955) and Hanson *et al.* (1956).

$$h^2 = \frac{\sigma^2 g}{\sigma^2 p}$$

Where,

h^2 = Estimate of heritability in broad sense,

σ^2_g = Genotypic variance, and

σ^2_p = Phenotypic variance

The heritability percentage was categorized as low, moderate and high as suggested by Robinson *et al.* (1949):

0-30%: Low

30-60%: Moderate

60% and above: High

3.12.2.2 Genetic gain

Genetic gain at 5 per cent selection intensity was worked out by using the formula given by Lush (1949) and Johnson *et al.* (1955).

$$GA = \frac{\sigma^2_g}{\sigma^2_p} \times (\sigma^2_p)^{0.5} \times K$$

Where,

GA = Genetic gain of the trait,

σ^2_g = genotypic variance of the trait,

σ^2_p = phenotypic variance of the trait, and

K = selection differential; (K= 2.06 at 5 per cent selection intensity)

3.12.2.3 Expected genetic gain (genetic gain as per cent of mean)

It was estimated as per the method suggested by Johnson *et al.* (1955).

$$\text{Genetic gain} = \frac{GA}{\bar{X}} \times 100$$

Where,

G.A. = Genetic gain of the trait, and

$\bar{X}$ = mean of the trait

The GA as per cent of mean was categorised as low, moderate and high by following Johnson *et al.* (1955).

0-10%: Low

10-20%: Moderate

Above 20%: High

3.12.2.4 Range

Range is the differences between the least and the greatest terms of a series of observation and thus provides the information about the variability present in the genotype.

3.12.2.5 Mean

Mean of the character was estimated by summing up of all the observation and dividing the sum by the number of observations.

$$\bar{X} = \sum X_i / N$$

Where,

$\sum X_i$ = Summation of all the observation,

N = Number of observations

3.12.3 Estimation of genotypic and phenotypic covariances and correlation coefficients

Covariance analysis followed the same pattern as the variance analysis. The genotypic and phenotypic covariances between two characters were obtained in the same fashion as corresponding variances. Estimate of genotypic and phenotypic variances and covariances were substituted in the following formula

suggested by Panse and Sukhatme (1985) to calculate correlation co-efficient between all possible pairs of characters.

Genotypic correlation co-efficient

$$r_{xy} (g) = \frac{\hat{\sigma}^2_{xy} (g)}{\sqrt{\hat{\sigma}^2_x (g) \hat{\sigma}^2_y (g)}}$$

Phenotypic correlation coefficient

$$r_{xy} (p) = \frac{\hat{\sigma}^2_{xy} (p)}{\sqrt{\hat{\sigma}^2_x (p) \hat{\sigma}^2_y (p)}}$$

Where,

$r_{xy} (g), r_{xy} (p)$ = Genotypic and phenotypic correlation coefficients, respectively, between a pair of characters x and y

$\hat{\sigma}^2_{xy}(g), \hat{\sigma}^2_{xy}(p)$ = Genotypic and phenotypic covariances, respectively, for a pair of characters x and y

$\hat{\sigma}^2_x(g), \hat{\sigma}^2_y(g)$ = Genotypic variance for characters x and y, respectively, and

$\hat{\sigma}^2_x(p), \hat{\sigma}^2_y(p)$ = Phenotypic variance for character x and y, respectively.

Test of significance

The significance of a correlation co-efficient was tested by the following formula:

$$t = \frac{r (n - 2)^{0.5}}{(1 - r^2)^{0.5}}$$

Where,

R = Correlation coefficient and

N = number of observations

Any value ($\pm$) exceeding the table value of t at $n-2$ d.f is significant.

3.12.4 Estimates of genetic divergence

The genetic divergence was computed using the procedure as described by Rao (1952) and Singh and Choudhary (1985). The details of analysis are described under the following heads:

- i. Test of Wilk's criterion,
- ii. Transformation of correlated variables
- iii. Computation of D^2 values,
- iv. Relative contribution of individual characters towards total divergence, and
- v. Group constellation

3.12.4.1 Test of Wilk's criterion

Variances and covariances were obtained from analysis of variance and covariance tables and the following analysis of dispersion table was constructed:

Analysis of dispersion

Dispersion due to	d.f.	Matrix due to			
		Sum of squares		Sum of products	
		X^2_1	$X^2_{2,.....}$	$X_1 X_2$	$X_1 X_{3,.....}$
Replications	$r-1$	a	b	c	$d,.....$
Between treatments (q)	q	a'	b'	c'	$d',.....$
Within treatments (W)	By subtraction n	$A - (a+a')$	$B - (b+b')$	$C - (c+c')$	$D - (d+d')....$
Total	n	A	B	C	D,....

The determination of error and error + variety variance-covariance matrix were calculated by pivotal condensation method of using 'V' statistics which, in turn, utilizes Wilk's criteria. A simultaneous test of differences between mean values of characters from all the genotypes in the present study was performed, as per the details given below:

The Wilk's test is:

$$V = -m \log e \lambda$$

Where,

$$\lambda = \frac{W}{W + Q}$$

$$= \frac{\text{Determinant of error matrix}}{\text{Determinant of error + variety matrix}}$$

and,

$$m = n - \frac{q + k + 1}{2}$$

Where,

- n = Total number of observations minus one,
- q = Number of variable minus one, and
- K = Number of characters under study

'V' Statistics so obtained was compared with the tabulated value of χ^2 for 2qk degrees of freedom.

3.12.4.2 Transformation of correlated variables

Plot means of the varieties corresponding to the characters studied were transformed to uncorrelated variables by Pivotal Condensation Method, which rendered the computation of D^2 values between any combinations of two varieties to simple summation of squares of differences in transformed values for various

characters. The skeleton procedure of obtaining transformed variables by Pivotal Condensation Method is described below:

Let dispersion matrix of original variables $x_1, x_2, \dots, x_p$ be

$$\begin{array}{cccc} \lambda_{11} & \lambda_{12} & \dots & \lambda_{1p} \\ \lambda_{21} & \lambda_{22} & \dots & \lambda_{2p} \\ \cdot & \cdot & \dots & \cdot \\ \cdot & \cdot & \dots & \cdot \\ \cdot & \cdot & \dots & \cdot \\ \cdot & \cdot & \dots & \cdot \\ \cdot & \cdot & \dots & \cdot \\ \lambda_{p1} & \lambda_{p2} & \dots & \lambda_{pp} \end{array}$$

and consider the extended matrix

$$\begin{array}{cccc} \lambda_{11} & \lambda_{12} & \dots & \lambda_{1px-1} \\ \lambda_{21} & \lambda_{22} & \dots & \lambda_{2px-2} \\ \cdot & \cdot & \dots & \cdot \\ \cdot & \cdot & \dots & \cdot \\ \cdot & \cdot & \dots & \cdot \\ \cdot & \cdot & \dots & \cdot \\ \cdot & \cdot & \dots & \cdot \\ \lambda_{p1} & \lambda_{p2} & \dots & \lambda_{pp \times p} \end{array}$$

taking λ_{11} as the first pivotal element, the first row is replaced by

$$1 \quad \frac{\lambda_{12}}{\lambda_{11}} \quad \dots \quad \frac{\lambda_{1p}}{\lambda_{11}} \quad \frac{x_1}{\lambda_{11}}$$

Sweeping out first column and using the first pivotal row, following reduced matrix is obtained

$$\begin{pmatrix} \lambda_{22'} & \dots\dots\dots & \lambda_{2p'} \\ \cdot & & \cdot \\ \cdot & & \cdot \\ \cdot & & \cdot \\ \cdot & & \cdot \\ \lambda_{p2'} & \dots\dots\dots & \lambda_{pp'} \end{pmatrix} \begin{bmatrix} X_{2'} \\ \cdot \\ \cdot \\ \cdot \\ \cdot \\ X_{p'} \end{bmatrix}$$

Where,

$$\lambda_{ij} = - \frac{\lambda_{ij}}{\lambda_{11}} \lambda_{ij} X_i$$

$$x_i = - \frac{\lambda_{i1}}{\lambda_{11}} X_1$$

$$\text{Now, } V_{(xi)} = V_{(xi)} - \frac{2\lambda_{i1}}{\lambda_{11}} \text{Cov. } (x_i x_1) + \frac{2\lambda_{i1}}{\lambda_{11}} V(X_1)$$

$$= \lambda_{ii} - \frac{\lambda_{i1}^2}{\lambda_{11}} X_{1i}$$

$$\text{Now, } V_{(xi')} = + \frac{\lambda_{i1}}{\lambda_{ii}} V(x_1)$$

$$\text{Similarly, Cov. } (x'_{i1} x'_j) = \lambda_{ij}'$$

$$\text{Similarly, Cov. } (x'_i x'_j) = \lambda_{ij}'$$

$$\begin{aligned} \text{also, cov. } (x_1 x'_i) &= \text{cov. } (x_1 x_i) - \frac{\lambda_{i1}}{\lambda_{11}} v(x_i) \\ &= \lambda_{1i} - \lambda_{i1} = 0 \end{aligned}$$

So the new variables are uncorrelated.

Considering the second pivotal row

$$\frac{\lambda_{23}}{\lambda_{22'}} \quad \frac{\lambda_{2p'}}{\lambda_{22'}} \quad \frac{x_{2'}}{22'}$$

the further reduced matrix is

$$\left| \begin{array}{ccc|c|c} \lambda_{33}'' & \dots & \lambda_{3p}'' & \lambda_{x3}'' & \\ \cdot & & \cdot & \cdot & \\ \cdot & & \cdot & \cdot & \\ \cdot & & \cdot & \cdot & \\ \lambda_{p3}'' & & \lambda_{pp}'' & x_{p''} & \end{array} \right|$$

Resulting into variables

$x_1' \times x_2' \times x_3'' \dots$ with variance

$x_1' \times \lambda_{22'} \lambda_{33}'' \dots$

They are all mutually uncorrelated as shown above and further x_2' depends on x_1' and x_2' , and x_3 on x_1' , x_2 and x_3 only.

3.12.4.3 Computation of D^2 values

For each pair-wise combination of the varieties the differences in transformed values for various characters were computed and D^2 -values were calculated according to the following formula:

$$D^2 = \sum_{i=1}^p (\bar{Y}_{ij} - Y_{ik})^2$$

Where,

P = number of characters studied, and

Y_{ij} and Y_{ik} = are two transformed variables of the i^{th} character for two genotypes

3.12.4.4 Relative contribution of individual characters towards total divergences

The ranking of differences in uncorrelated means between all the characters for all pair-wise combinations of varieties was carried out, with first rank being assigned to the highest differences. Finally relative contribution of a character towards total divergence was estimated by calculating the percentage of first rank in that character.

3.12.4.5 Group constellation

Tocher's method was used for assigning various varieties to different clusters. The two varieties having smallest distance from each other were considered first to which a third variety having smallest average D^2 value from the first two varieties was added. Next the nearest fourth variety was added and the process continued till the average D^2 value increased. The remaining varieties were then considered for the next cluster and the process was continued till all varieties were included in various clusters.

The spatial distances between clusters were arrived at by taking square root of average intra and inter cluster D^2 values.

For each combination (pair of genotypes) the mean deviation (d^2_i) i.e. $Y_1 - Y_i$ with $i = 1, 2, 3, \dots, p$ was computed and D^2 values were calculated as sum of these deviations i.e. $(y_i^1 - y_i^2)$, where, y_i is the transformed variable from the original variable x_i . Accordingly D^2 values for all combinations were calculated. The D^2 values so obtained for each pair of population were treated as x^2 and were tested against the tabulated values of λ^2 for p degrees of freedom, where p is the number of traits considered.

In all combinations each character was ranked on the basis of $d_i = y_{ij} - y_{ik}$ values. Rank I was given to the highest mean difference and rank p to the lowest mean difference, where p is the total number of characters. In this manner contribution of each character to the total divergence was computed.

Tocher method for grouping of varieties into various clusters was adopted. This method is detailed in a simplified way by Rao (1952) and Singh and Choudhary (1985).

All the above computations were carried out using the software Indostat at Bio-informatics Laboratory of the Division of Plant Breeding and Genetics, SKUAST-Kashmir, Shalimar.

Chapter -4

EXPERIMENTAL FINDINGS

The present investigation entitled “Identification of Resistant Sources against Wilt Disease of Chilli (*Capsicum annuum* L.)” was undertaken at Experimental Field, Division of Vegetable Science and Mycology and Forest Pathology Laboratory, Division of Plant Pathology, Sher-e-Kashmir University of Agricultural Science & Technology of Kashmir, Shalimar, Srinagar. The experiment was laid out in RCBD with three replications. The experimental material consisted of 107 genotypes of chilli. The data collected was analyzed as per standard statistical procedures. The experimental results thus obtained are presented under following headings:

- 4.1 Isolation and purification of causal fungus.
- 4.2 Morphology based identification of the pathogen.
- 4.3 DNA extraction.
- 4.4 PCR validation of DNA.
- 4.5 Sequencing and Bioinformatics analysis.
- 4.6 Pathogenicity of the associated fungus.
- 4.7 Germplasm screening under field conditions.
- 4.8 Germplasm screening under artificially inoculated controlled conditions.
- 4.9 DUS Characterisation.
- 4.10 Mean performance and Analysis of Variance.
- 4.11 Variability and genetic components of variation.
- 4.12 Correlation.
- 4.13 Genetic divergence.

4.1 Isolation and purification of causal fungi

The causal fungus of the disease was isolated from the stem portion of the affected plants by tissue bit technique. Similar type of fungus was yielded from all the isolations attempted. The cultures so obtained were purified by single spore method and maintained on PDA by repeated sub-culturing at monthly intervals.

4.2 Morphology based identification of the pathogen

The cultural and morphological characters of the fungus were studied on potato dextrose agar (PDA) medium. The purified culture of the fungus initially produced, submerged, profuse fluffy, fussy white cottony colonies which gradually turned creamy white with yellowish pigmentation and developed brownish colour at backside of the petriplate. The fungus attained a growth of 90 mm in 7 days of incubation at $25\pm 1^{\circ}\text{C}$. Microscopic observations revealed that mycelium was smooth, branched, septate and slendrical and measured $1.2\text{-}3.6\text{ }\mu\text{m}$ in width (Plate 2a). Microconidia and macroconidia were abundantly present. Microconidia were cylindrical to oval shaped, 0-1 septate and measured $4.8\text{-}9.6 \times 1.8\text{-}2.4\text{ }\mu\text{m}$ (Plate 2b). Macroconidia were sickle-shaped, slightly curved at apex with foot shaped basal cell, 3-5 septate and $17.3\text{-}23.1 \times 2.4\text{-}4.8\text{ }\mu\text{m}$ in size (Plate 2c). Chlamydospores were intercalary, produced singly or in chains, nearly spherical, hyaline and measured $8.4\text{-}12\text{ }\mu\text{m}$ in width (Plate 2d).

4.3 DNA Extraction

The genomic DNA was isolated as described in material and methods (section 3.3) and loaded on 0.7% agarose in 1X TAE for 30 minutes. The DNA isolation procedure was found effective for all fungal species. The gel showed intact DNA bands near wells without any smearing and degradation.

Table 7: Cultural and morphological characteristics of *Fusarium solani*

Fungal propagule	Colour	Shape	Size*	Septation
Colony	Initially white gradually turning creamish with yellowish pigmentation	Floccose, sparse aerial mycelium	90 mm dia. in 7 days	-
Mycelium	Hyaline	Smooth, slendrical, branched	1.2-3.6 μm (wide)	Septate
Microconidia	Hyaline	Cylindrical to oval shaped	4.8-9.6 x 1.8-2.4 μm	0-1 septate
Macroconidia	Hyaline	Sickle-shaped, slightly curved at apex and foot-shaped at basal end	17.3-23.1 x 2.4-4.8 μm	3-5 septate
Chlamydospore	Hyaline	Spherical, smooth, intercalary, single or in chains	8.4-12 μm (wide)	-

*Mean of 100 microscopic observations



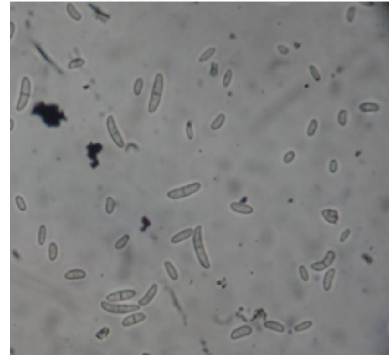
Plate 1: View of experimental field



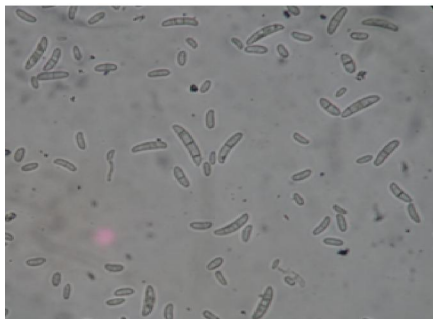
a. 7 Days Old Culture



b. Mycelium



c. Microconidia



d. Macroconidia



e. Chlamydospore

Plate 2: Cultural and Morphological characteristics of *Fusarium solani*

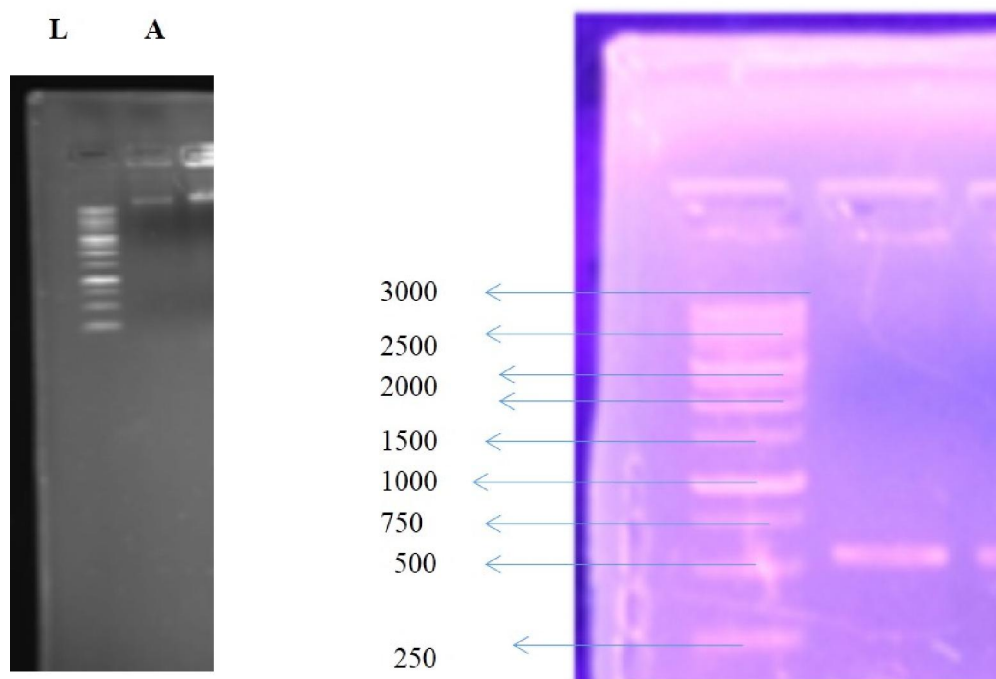


Plate3 (a): Band showing presence of quality DNA
Plate 3(b): PCR amplification of target sequences

NCBI Resources How To

Nucleotide Nucleotide Advanced

The Nucleotide database will include EST and GSS sequences in early 2019. [Read more.](#)

GenBank Send to

Fusarium solani isolate Farwa-2 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence

GenBank: MK990041.1

[FASTA](#) [Graphics](#)

Go to: ☺

LOCUS MK990041 523 bp DNA linear PLN 04-JUN-2019

DEFINITION Fusarium solani isolate Farwa-2 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence.

ACCESSION MK990041

VERSION MK990041.1

KEYWORDS .

SOURCE Fusarium solani

ORGANISM [Fusarium solani](#)

Eukaryota; Fungi; Dikarya; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; Fusarium; Fusarium solani species complex.

REFERENCE 1 (bases 1 to 523)

AUTHORS Farwah,S., Hussain,K., Hami,A., Bhat,Z.A., Bhat,K.A., Seerat,R., Mazahir,S.H., Rashid,M. and Masoodi,K.Z.

TITLE DNA Barcoding of Chili Wilt causing Pathogen

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 523)

AUTHORS Farwah,S., Hussain,K., Hami,A., Bhat,Z.A., Bhat,K.A., Seerat,R., Mazahir,S.H., Rashid,M. and Masoodi,K.Z.

TITLE Direct Submission

JOURNAL Submitted (30-MAY-2019) Plant Biotechnology, SKUAST-Kashmir, Shalimar, Srinagar, J&K 190025, India

COMMENT ##Assembly-Data-START##

Sequencing Technology :: Sanger dideoxy sequencing

##Assembly-Data-END##

FEATURES Location/Qualifiers

source 1..523

/organism="Fusarium solani"

/mol_type="genomic DNA"

/isolate="Farwa-2"

/db_xref="taxon:169388"

misc_RNA <1..>523

/note="contains internal transcribed spacer 1, 5.8S ribosomal RNA, internal transcribed spacer 2, and large subunit ribosomal RNA"

ORIGIN

1 gggtgatca gccgtgact acctaaact tcttcggcg ggaacagacg gccctgtaac

61 aacggccgc cccgcocaga ggaaccctaa ctctgtttt ataattgttt tctagtaaa

121 caagcaata aattaaaact ttaacnacc gatctcttg ctcggcate catgaaaaac

181 gccgcgaat ggcataagta atggcaatg cagaattcg tgaatcac aatcttgaa

241 cccacattgg gccgcagat atttcggcg ccatgcctg tggagctca ttacaacct

301 cagcccccg gccctggcgt tggcgatcg cgaagcccc ctgtggcac acgccgtccc

361 tcaaatcac tggcggtccc gccgcagctt ccattcgta gtactaaac ctcgcaact

421 ggagagcgc gcgcacatc cgtaaaacac ccaacttcg atgttgacc tgaatcagg

481 taggaatacc gctgaactt aagcatatca ataacggag gaa

//

Plate 4: Sequence of *Fusarium solani* isolate Farwa-2 submitted to NCBI

4.4 PCR validation of DNA

After PCR amplification was carried out under standard condition, the amplified product were run on 1% agarose gel. Plate 3 shows the amplified product of ITS1 and ITS 2 (620 bp). 100 bp ladder was used to access size of amplicon.

4.5 Sequencing and Bioinformatic analysis

The PCR product was sequenced, the pathogen was collected from Srinagar (Shalimar) and identified through DNA sequencing. The pathogen identified was *Fusarium solani*.

4.5.1 BLAST (Basic Local Alignment Search Tool)

BLAST was used to find regions of similarity between the query sequence and the sequence present in the NCBI (www.ncbi.nlm.in) database.

4.5.2 Sequence submitted to GenBank

The sequence designated as Farwa-2 with accession No. MK990041.1 and 523 base pairs was successfully published in GenBank (Plate 4).

4.6 Pathogenicity

The pathogenicity of isolated fungi was established by confirming postulates of Koch on potted chilli plants cv. Kashmir Long-1. The initial disease symptoms of *Fusarium solani* inoculated seedlings developed after 7-10 days of inoculation. The re-isolation of *Fusarium solani* from the inoculated chilli plants was also carried and compared with their original inoculated culture. The reisolated pathogen completely resembled the original inoculated fungi in their morphological, cultural and pathogenic characteristics, so satisfied Koch's postulates.



Plate 5: Preparation of inoculum (*Fusarium solani*)



Control /Uninoculated (Healthy)

Inoculated (Susceptible)

Plate 6: Pathogenicity test of isolated organism (*Fusarium solani*) on potted chilli plants (cv. Kashmir Long-1)

4.7 Germplasm screening under field condition

One hundred and seven genotypes were screened under field conditions against wilt disease. The results revealed that only one chilli genotype *viz.*, SKAU-193 showed immune reaction against wilt disease and twenty two genotypes *viz.*, SKAU-221, SKAU-96, SKAU-177, SKAU-80, SKAU-84, SKAU-89, SKAU-91, SKAU-132, SKAU-173, SKAU-211, SKAU-227, SKAU-216, SKAU-148, SKAU-208, SKAU-231, SKAU-237, Arka Lohit, SKAU-191, SKAU-68, SKAU-77, SKAU-128 and SKAU-106 showed resistant reaction with disease incidence ranging from 11.0 to 27.70 per cent (Table-8). The rest of the genotypes were moderately resistant, susceptible or highly susceptible.

4.8 Germplasm screening under artificially inoculated controlled conditions

In order to validate the field resistance of fifty one genotypes of chilli they were further screened under artificially inoculated controlled conditions. The results confirmed the immune reaction of one genotype *viz.*, SKAU-193, resistant reaction of twenty one genotypes *viz.*, SKAU-208, SKAU-224, SKAU-218, IC-505242, SKAU-198, SKAU-177, SKAU-211, SKAU-80, SKAU-43, SKAU-191, SKAU-68, Arka Lohit, SKAU-153, SKAU-188, SKAU-173, SKAU-128, KL-1, SKAU-216, SKAU-221, SKAU-96, SKAU-89; moderately resistant reaction of seventeen genotypes *viz.*, SKAU-58, SKAU-40, SKAU-73, SKAU-160, SKAU-118, SKAU-84, SKAU-91, SKAU-106, SKAU-45, SKAU-62, SKAU-32, SKAU-36, SKAU-148, SKAU-132, SKAU-38, SC-1019, SKAU-195; and while susceptible reaction of twelve genotypes *viz.*, SKAU-77, SKAU-231, SKAU-247, SKAU-52, SC-104, SKAU-227, SKAU-237, SKAU-111, IC-561617, SKAU-139, IC-391082, SKAU-243 (Table-9).

Table 8: Field reaction of chilli genotypes to *Fusarium solani*.

Genotypes	Disease Incidence (%)	Disease Reaction
SKAU-193	0.0	I
SKAU-221	11.0	R
SKAU-96	11.0	R
SKAU-177	11.0	R
SKAU-80	11.0	R
SKAU-84	13.8	R
SKAU-89	13.8	R
SKAU-91	13.8	R
SKAU-132	13.8	R
SKAU-211	13.8	R
SKAU-227	13.8	R
SKAU-173	16.6	R
SKAU-216	16.6	R
SKAU-148	16.6	R
SKAU-208	16.6	R
SKAU-231	22.2	R
SKAU-237	22.1	R
Arka Lohit	22.2	R
SKAU-191	22.2	R
SKAU-68	24.9	R
SKAU-77	24.9	R
SKAU-128	24.9	R
SKAU-106	27.7	R
SKAU-43	30.5	MR
SKAU-58	30.5	MR
SKAU-111	30.5	MR
KL-1	30.5	MR

SKAU-218	33.3	MR
SKAU-224	33.3	MR
SC-104	33.3	MR
SKAU-45	36.0	MR
SKAU-40	36.0	MR
SKAU-160	36.0	MR
IC-561617	36.0	MR
SKAU-38	36.0	MR
SKAU-62	36.0	MR
SKAU-153	38.8	MR
SC-1019	38.8	MR
SKAU-32	41.6	MR
SKAU-188	41.6	MR
SKAU-195	41.6	MR
SKAU-36	44.4	MR
SKAU-73	44.4	MR
SKAU-198	44.4	MR
SKAU-247	44.4	MR
IC-505242	44.4	MR
SKAU-52	47.1	MR
SKAU-139	47.1	MR
SKAU-118	47.1	MR
IC-391082	47.1	MR
SKAU-243	49.9	MR
SKAU-181	55.5	S
Local Kashmiri Chilli-1	58.2	S
SKAU-163	63.8	S
KAU-233	63.8	S
SKAU-122	66.6	S
SKAU-109	72.2	S
SKAU-141	74.96	S

SKAU-157	74.96	S
SKAU-167	80.4	HS
SKAU-249	100	HS
SKAU-251	100	HS
SKAU-257	100	HS
SKAU-259	100	HS
SKAU-261	100	HS
SKAU-263	100	HS
SKAU-265	100	HS
SKAU-267	100	HS
IC-413048	100	HS
IC-362021	100	HS
IC-302026	100	HS
SKAU-269	100	HS
IC-565072	100	HS
IC-505203	100	HS
SKAU-271	100	HS
SKAU-273	100	HS
SKAU-275	100	HS
SKAU-277	100	HS
IC-561622	100	HS
IC-278298	100	HS
IC-284648	100	HS
SKAU-285	100	HS
SKAU-287	100	HS
SKAU-289	100	HS
SKAU-291	100	HS
SKAU-293	100	HS
SKAU-295	100	HS
SKAU-297	100	HS

IC-572480	100	HS
IC-343448	100	HS
IC-3446540	100	HS
IC-362010	100	HS
IC-347044	100	HS
IC-561701	100	HS
IC-561721	100	HS
SKAU-299	100	HS
SKAU-302	100	HS
SKAU-305	100	HS
SKAU-310	100	HS
IC-561634	100	HS
IC-505276	100	HS
IC-276117	100	HS
IC-390033	100	HS
SKAU-253	100	HS
SKAU-255	100	HS
IC-344727	100	HS
IC-561615	100	HS



SKAU-193

Plate 7: Chilli genotype Immune to wilt under natural field conditions (*Kharif* 2018)



SKAU-227



SKAU-128



SKAU-132



SKAU-148



SKAU-80



SKAU-68



SKAU-89



SKAU-91

**Plate 8: Chilli genotypes Resistant to wilt under natural field conditions
(Kharif 2018)**



SKAU-173



SKAU-177



SKAU-106



SKAU-191

Plate 9: Chilli genotypes Resistant to wilt under natural field



SKAU-38



SKAU-43



SKAU-45



SKAU-73



SKAU-62



SKAU-198



SC-243



SKAU-218

Plate 10: Chilli genotypes Moderately Resistant to wilt under natural field conditions (*Kharif* 2018)



SKAU-195



SKAU-111



SKAU-188



KL-1

Plate 11: Chilli genotypes Moderately Resistant to wilt under natural field conditions (*Kharif* 2018)



SKAU-122



SKAU-141



SKAU-157



Local Kashmiri Chilli-1



SKAU-109



SKAU-157



SKAU-157

Plate 12: Chilli genotypes Susceptible to wilt under natural field conditions (*Kharif*2018)

Table 9: Reaction of chilli genotypes to *Fusarium solani* under artificially inoculated conditions

Genotypes	Disease Incidence (%)	Disease Reaction
SKAU-193	0	I
SKAU-208	13.3	R
SKAU-224	13.3	R
SKAU-218	13.3	R
IC-505242	13.3	R
SKAU-198	13.3	R
SKAU-177	13.3	R
SKAU-211	13.3	R
SKAU-80	13.3	R
SKAU-43	13.3	R
SKAU-191	13.3	R
SKAU-68	13.3	R
Arka Lohit	13.3	R
SKAU-153	13.3	R
SKAU-188	20	R
SKAU-173	20	R
SKAU-128	20	R
KL-1	20	R
SKAU-216	20	R
SKAU-221	20	R
SKAU-96	20	R
SKAU-89	20	R

SKAU-58	33.3	MR
SKAU-40	33.3	MR
SKAU-73	33.3	MR
SKAU-160	33.3	MR
SKAU-118	33.3	MR
SKAU-84	33.3	MR
SKAU-91	33.3	MR
SKAU-106	33.3	MR
SKAU-45	46.6	MR
SKAU-62	46.6	MR
SKAU-32	46.6	MR
SKAU-36	46.6	MR
SKAU-148	46.6	MR
SKAU-132	46.6	MR
SKAU-38	46.6	MR
SC-1019	46.6	MR
SKAU-195	46.6	MR
SKAU-77	60.0	S
SKAU-231	60.0	S
SKAU-247	66.6	S
SKAU-52	66.6	S
SC-104	73.3	S
SKAU-227	73.3	S
SKAU-237	73.3	S
SKAU-111	73.3	S
IC-561617	80.0	S
SKAU-139	80.0	S
IC-391082	80.0	S
SKAU-243	80.0	S



Plate 13: Germplasm screening under artificially inoculated (*Fusarium solani*) controlled conditions



SKAU-193

Plate 14: Chilli genotype Immune to wilt under artificially inoculated (*Fusarium solani*) controlled conditions



Plate 15: Chilli genotypes Resistant to wilt under artificially inoculated (*Fusarium solani*) controlled conditions.



SKAU-198



SKAU-43



SKAU-208



SKAU-218



SKAU-211



SKAU-191



IC-505242



SKAU-177



SKAU-80



SKAU-216

Plate 16: Chilli genotypes Resistant to wilt under artificially inoculated (*Fusarium solani*) controlled conditions



SKAU-38



SKAU-73



SKAU-36



SKAU-106



SKAU-132



SKAU-160



SKAU-139



SKAU-148



SKAU-118



SKAU-40

Plate 17: Chilli genotypes Resistant to wilt under artificially inoculated (*Fusarium solani*) controlled conditions

4.9 DUS characterization

DUS traits were recorded in all genotypes of chilli and are presented in Appendix-I.

4.9.1 Plant habit

Out of the sixty genotypes, forty-three genotypes viz., SKAU-32, SKAU-36, SKAU-58, SKAU-45, SKAU-43, SKAU-68, SKAU-73, SKAU-77, SKAU-84, SKAU-91, SKAU-106, SKAU-109, SKAU-132, SKAU-139, SKAU-153, SKAU-157, SKAU-160, SKAU-163, SKAU-233, KL-1, SKAU-173, SKAU-177, SKAU-181, SKAU-188, SKAU-191, SKAU-193, SKAU-195, SKAU-198, SKAU-216, SKAU-218, SKAU-221, SKAU-224, SC-104, IC-561617, SKAU-231, SKAU-167, SKAU-38, SKAU-237, Arka Lohit, SKAU-243, SKAU-247, IC-391082 and IC-505242 exhibited semi-upright plant habit, fourteen genotypes viz., SKAU-208, SKAU-211, SKAU-227, SKAU-40, SKAU-52, SKAU-89, Local Kashmiri Chilli-1, SKAU-96, SKAU-111, SKAU-118, SKAU-122, SKAU-128, SKAU-141 and SKAU-148 exhibited spreading plant habit, three genotypes viz., SKAU-62, SKAU-80 and SC-1019 exhibited upright plant habit.

4.9.2 Length of main stem (cm)

Twenty-two genotypes viz., SKAU-32, SKAU-62, SKAU-77, SKAU-84, SKAU-89, SKAU-111, SKAU-141, SKAU-177, SKAU-181, SKAU-188, SKAU-191, SKAU-193, SKAU-195, SKAU-218, SKAU-221, SKAU-224, SC-104, SC-1019, IC-561617, SKAU-237, Arka Lohit and SKAU-243 showed long length of main stem, twenty genotypes viz., SKAU-36, SKAU-38, SKAU-40, SKAU-43, SKAU-45, SKAU-52, SKAU-58, SKAU-148, SKAU-153, SKAU-163, SKAU-198, SKAU-208, SKAU-211, SKAU-216, SKAU-227, SKAU-231, SKAU-233, SKAU-247, IC-391082, IC-505242 showed medium length of main stem and eighteen genotypes viz., SKAU-68, SKAU-73, SKAU-80, Local Kashmiri Chilli-1, SKAU-91, SKAU-96, SKAU-106, SKAU-109, SKAU-118, SKAU-122,

SKAU-128, SKAU-132, SKAU-139, SKAU-157, SKAU-160, SKAU-167, KL-1 and SKAU-173 showed small length of main stem.

4.9.3 Length of first internode

Twenty-seven genotypes viz., SKAU-36, SKAU-38, SKAU-52, SKAU-68, SKAU-73, SKAU-77, SKAU-118, SKAU-128, SKAU-132, SKAU-139, SKAU-141, SKAU-148, SKAU-153, KL-1, SKAU-173, SKAU-181, SKAU-191, SKAU-193, SKAU-208, SKAU-211, SKAU-218, SKAU-224, SKAU-227, SKAU-231, SKAU-237, Arka Lohit, SKAU-243 exhibited medium length of first internode, seventeen genotypes viz., SKAU-80, Local Kashmiri Chilli-1, SKAU-91, SKAU-96, SKAU-106, SKAU-109, SKAU-111, SKAU-122, SKAU-157, SKAU-160, SKAU-167, SKAU-188, SKAU-216, SKAU-233, SKAU-247, IC-391082, IC-505242 exhibited short length of first internode, thirteen genotypes viz., SKAU-32, SKAU-40, SKAU-43, SKAU-45, SKAU-58, SKAU-62, SKAU-84, SKAU-89, SKAU-163, SKAU-221, SC-104, SC-1019 and IC-561617 exhibited long length of first internode, and three genotypes viz., SKAU-195, SKAU-198 and SKAU-177 exhibited very short length of first internode.

4.9.4 Anthocyanin colouration of nodes

Anthocyanin colouration of nodes was present in fifty six genotypes viz., SKAU-32, SKAU-36, SKAU-38, SKAU-40, SKAU-43, SKAU-45, SKAU-52, SKAU-58, SKAU-62, SKAU-68, SKAU-77, SKAU-80, SKAU-84, SKAU-89, Local Kashmiri Chilli-1, SKAU-91, SKAU-96, SKAU-106, SKAU-109, SKAU-111, SKAU-118, SKAU-122, SKAU-132, SKAU-139, SKAU-141, SKAU-148, SKAU-153, SKAU-157, SKAU-160, SKAU-163, SKAU-167, KL-1, SKAU-177, SKAU-181, SKAU-188, SKAU-191, SKAU-193, SKAU-195, SKAU-198, SKAU-208, SKAU-216, SKAU-218, SKAU-221, SKAU-224, SC-104, SC-1019, SKAU-227, IC-561617, SKAU-231, SKAU-233, Arka Lohit, SKAU-243, SKAU-237, SKAU-247, IC-391082 and IC-505242 and absent in four genotypes viz., SKAU-73, SKAU-128, SKAU-173 and SKAU-211.

4.9.5 Intensity of anthocyanin colouration of nodes

Intensity of anthocyanin colouration of nodes was weak in twenty-seven genotypes viz., SKAU-52, SKAU-58, SKAU-62, SKAU-68, SKAU-73, SKAU-77, Local Kashmiri Chilli-1, SKAU-111, SKAU-118, SKAU-128, SKAU-132, SKAU-141, SKAU-177, SKAU-181, SKAU-188, SKAU-211, SKAU-216, SKAU-224, IC-561617, SKAU-231, SKAU-233, SKAU-237, Arka Lohit, SKAU-243, SKAU-247, IC-391082 and IC-505242, medium in twenty-one genotypes viz., SKAU-32, SKAU-40, SKAU-43, SKAU-45, SKAU-80, SKAU-96, SKAU-106, SKAU-109, SKAU-122, SKAU-139, SKAU-148, SKAU-153, SKAU-157, SKAU-160, SKAU-167, SKAU-173, SKAU-191, SKAU-193, SKAU-195, SKAU-208 and SC-104 and strong in twelve genotypes viz., SKAU-36, SKAU-38, SKAU-84, SKAU-89, SKAU-91, SKAU-163, KL-1, SKAU-198, SKAU-218, SKAU-221, SC-1019 and SKAU-227.

4.9.6 Plant height (cm)

Sixty genotypes viz., SKAU-32, SKAU-36, SKAU-38, SKAU-40, SKAU-43, SKAU-45, SKAU-52, SKAU-58, SKAU-62, SKAU-68, SKAU-73, SKAU-77, SKAU-80, SKAU-84, SKAU-89, Local Kashmiri Chilli-1, SKAU-91, SKAU-96, SKAU-106, SKAU-109, SKAU-111, SKAU-118, SKAU-122, SKAU-132, SKAU-139, SKAU-141, SKAU-148, SKAU-153, SKAU-157, SKAU-160, SKAU-163, SKAU-167, KL-1, SKAU-177, SKAU-181, SKAU-188, SKAU-191, SKAU-193, SKAU-195, SKAU-198, SKAU-208, SKAU-216, SKAU-218, SKAU-221, SKAU-224, SC-104, SC-1019, SKAU-227, IC-561617, SKAU-231, SKAU-233, Arka Lohit, SKAU-243, SKAU-237, SKAU-247, IC-391082, IC-505242, SKAU-128, SKAU-173 and SKAU-211 exhibited medium plant habit.

4.9.7 Plant spread (cm)

Fifty six genotypes viz., SKAU-32, SKAU-36, SKAU-38, SKAU-40, SKAU-43, SKAU-45, SKAU-52, SKAU-58, SKAU-62, SKAU-68, SKAU-73,

SKAU-77, SKAU-80, SKAU-84, SKAU-89, Local Kashmiri Chilli-1, SKAU-91, SKAU-96, SKAU-106, SKAU-109, SKAU-111, SKAU-118, SKAU-132, SKAU-139, SKAU-141, SKAU-148, SKAU-153, SKAU-157, SKAU-163, KL-1, SKAU-177, SKAU-181, SKAU-188, SKAU-191, SKAU-193, SKAU-195, SKAU-198, SKAU-208, SKAU-216, SKAU-218, SKAU-221, SKAU-224, SC-104, SC-1019, SKAU-227, IC-561617, SKAU-231, SKAU-233, Arka Lohit, SKAU-237, SKAU-247, IC-391082, IC-505242, SKAU-128, SKAU-173 and SKAU-211 exhibited medium plant spread and four genotypes SKAU-122, SKAU-160, SKAU-243 and SKAU-167 exhibited narrow plant spread.

4.9.8 Stem pubescence

Stem pubescence was present in fifty six genotypes viz., SKAU-32, SKAU-36, SKAU-38, SKAU-40, SKAU-43, SKAU-45, SKAU-52, SKAU-58, SKAU-62, SKAU-68, SKAU-73, SKAU-77, SKAU-80, SKAU-84, SKAU-89, Local Kashmiri Chilli-1, SKAU-91, SKAU-96, SKAU-106, SKAU-109, SKAU-111, SKAU-118, SKAU-122, SKAU-132, SKAU-139, SKAU-141, SKAU-148, SKAU-153, SKAU-157, SKAU-160, SKAU-163, SKAU-167, SKAU-191, SKAU-193, SKAU-195, SKAU-198, SKAU-208, SKAU-216, SKAU-218, SKAU-221, SKAU-224, SC-104, SC-1019, SKAU-227, IC-561617, SKAU-231, SKAU-233, Arka Lohit, SKAU-243, SKAU-237, SKAU-247, IC-391082, IC-505242, SKAU-128, SKAU-173 and SKAU-211, while it was absent in four genotypes KL-1, SKAU-177, SKAU-181 and SKAU-188.

4.9.9 Intensity of Stem pubescence

Sixty genotypes showed sparse intensity of stem pubescence viz., SKAU-32, SKAU-36, SKAU-38, SKAU-40, SKAU-43, SKAU-45, SKAU-52, SKAU-58, SKAU-62, SKAU-68, SKAU-73, SKAU-77, SKAU-80, SKAU-84, SKAU-89, Local Kashmiri Chilli-1, SKAU-91, SKAU-96, SKAU-106, SKAU-109, SKAU-111, SKAU-118, SKAU-122, SKAU-132, SKAU-139, SKAU-141, SKAU-148, SKAU-153, SKAU-157, SKAU-160, SKAU-163,

SKAU-167, KL-1, SKAU-177, SKAU-181, SKAU-188, SKAU-191, SKAU-193, SKAU-195, SKAU-198, SKAU-208, SKAU-216, SKAU-218, SKAU-221, SKAU-224, SC-104, SC-1019, SKAU-227, IC-561617, SKAU-231, SKAU-233, Arka Lohit, SKAU-243, SKAU-237, SKAU-247, IC-391082, IC-505242, SKAU-128, SKAU-173 and SKAU-211.

4.9.10 Stem shape

Sixty genotypes viz., SKAU-32, SKAU-36, SKAU-38, SKAU-40, SKAU-43, SKAU-45, SKAU-52, SKAU-58, SKAU-62, SKAU-68, SKAU-73, SKAU-77, SKAU-80, SKAU-84, SKAU-89, Local Kashmiri Chilli-1, SKAU-91, SKAU-96, SKAU-106, SKAU-109, SKAU-111, SKAU-118, SKAU-122, SKAU-132, SKAU-139, SKAU-141, SKAU-148, SKAU-153, SKAU-157, SKAU-160, SKAU-163, SKAU-167, KL-1, SKAU-177, SKAU-181, SKAU-188, SKAU-191, SKAU-193, SKAU-195, SKAU-198, SKAU-208, SKAU-216, SKAU-218, SKAU-221, SKAU-224, SC-104, SC-1019, SKAU-227, IC-561617, SKAU-231, SKAU-233, Arka Lohit, SKAU-243, SKAU-237, SKAU-247, IC-391082, IC-505242, SKAU-128, SKAU-173 and SKAU-211 showed round stem shape.

4.9.1 Length of leaf blade

Sixty genotypes viz., SKAU-32, SKAU-36, SKAU-38, SKAU-40, SKAU-43, SKAU-45, SKAU-52, SKAU-58, SKAU-62, SKAU-68, SKAU-73, SKAU-77, SKAU-80, SKAU-84, SKAU-89, Local Kashmiri Chilli-1, SKAU-91, SKAU-96, SKAU-106, SKAU-109, SKAU-111, SKAU-118, SKAU-122, SKAU-132, SKAU-139, SKAU-141, SKAU-148, SKAU-153, SKAU-157, SKAU-160, SKAU-163, SKAU-167, KL-1, SKAU-177, SKAU-181, SKAU-188, SKAU-191, SKAU-193, SKAU-195, SKAU-198, SKAU-208, SKAU-216, SKAU-218, SKAU-221, SKAU-224, SC-104, SC-1019, SKAU-227, IC-561617, SKAU-231, SKAU-233, Arka Lohit, SKAU-243, SKAU-237, SKAU-247,

IC-391082, IC-505242, SKAU-128, SKAU-173 and SKAU-211 exhibited long leaf blade.

4.9.12 Width of leaf blade

Sixty genotypes viz., SKAU-32, SKAU-36, SKAU-38, SKAU-40, SKAU-43, SKAU-45, SKAU-52, SKAU-58, SKAU-62, SKAU-68, SKAU-73, SKAU-77, SKAU-80, SKAU-84, SKAU-89, Local Kashmiri Chilli-1, SKAU-91, SKAU-96, SKAU-106, SKAU-109, SKAU-111, SKAU-118, SKAU-122, SKAU-132, SKAU-139, SKAU-141, SKAU-148, SKAU-153, SKAU-157, SKAU-160, SKAU-163, SKAU-167, KL-1, SKAU-177, SKAU-181, SKAU-188, SKAU-191, SKAU-193, SKAU-195, SKAU-198, SKAU-208, SKAU-216, SKAU-218, SKAU-221, SKAU-224, SC-104, SC-1019, SKAU-227, IC-561617, SKAU-231, SKAU-233, Arka Lohit, SKAU-243, SKAU-237, SKAU-247, IC-391082, IC-505242, SKAU-128, SKAU-173 and SKAU-211 exhibited broad leaf blade.

4.9.13 Leaf colour

Fifty four genotypes viz., SKAU-32, SKAU-38, SKAU-43, SKAU-52, SKAU-58, SKAU-62, SKAU-68, SKAU-73, SKAU-77, SKAU-89, Local Kashmiri Chilli-1, SKAU-91, SKAU-96, SKAU-106, SKAU-109, SKAU-111, SKAU-118, SKAU-122, SKAU-132, SKAU-139, SKAU-141, SKAU-153, SKAU-157, SKAU-160, SKAU-163, SKAU-167, KL-1, SKAU-177, SKAU-181, SKAU-188, SKAU-191, SKAU-193, SKAU-195, SKAU-198, SKAU-208, SKAU-216, SKAU-218, SKAU-221, SKAU-224, SC-104, SC-1019, SKAU-227, IC-561617, SKAU-231, SKAU-233, Arka Lohit, SKAU-243, SKAU-237, SKAU-247, IC-391082, IC-505242, SKAU-128, SKAU-173 and SKAU-211 exhibited green leaf colour while six genotypes viz., SKAU-36, SKAU-40, SKAU-45, SKAU-80, SKAU-84 and SKAU-148 showed green colour with purple tinge.

4.9.14 Intensity of green colour

Intensity of green colour was medium in thirty five genotypes viz., SKAU-32, SKAU-62, SKAU-77, SKAU-109, SKAU-118, SKAU-122, SKAU-128, SKAU-132, SKAU-139, SKAU-141, SKAU-153, SKAU-157, KL-1, SKAU-181, SKAU-188, SKAU-191, SKAU-193, SKAU-195, SKAU-211, SKAU-216, SKAU-218, SKAU-221, SKAU-224, SC-104, SC-1019, SKAU-227, IC-561617, SKAU-231, SKAU-233, SKAU-237, Arka Lohit, SKAU-243, SKAU-247, IC-391082 and IC-505242, light in seventeen genotypes viz., SKAU-36, SKAU-38, SKAU-40, SKAU-45, SKAU-52, SKAU-73, SKAU-80, SKAU-84, Local Kashmiri Chilli-1, SKAU-106, SKAU-111, SKAU-148, SKAU-160, SKAU-163, SKAU-167, SKAU-177 and SKAU-198 and dark in eight genotypes viz., SKAU-43, SKAU-58, SKAU-68, SKAU-89, SKAU-91, SKAU-96, SKAU-173 and SKAU-208.

4.9.15 Intensity of purple colour

Intensity of purple colour was light in fifty four genotypes viz., SKAU-32, SKAU-38, SKAU-43, SKAU-52, SKAU-58, SKAU-62, SKAU-68, SKAU-73, SKAU-77, SKAU-89, Local Kashmiri Chilli-1, SKAU-91, SKAU-96, SKAU-106, SKAU-109, SKAU-111, SKAU-118, SKAU-122, SKAU-132, SKAU-139, SKAU-141, SKAU-153, SKAU-157, SKAU-160, SKAU-163, SKAU-67, KL-1, SKAU-177, SKAU-181, SKAU-188, SKAU-191, SKAU-193, SKAU-195, SKAU-198, SKAU-208, SKAU-216, SKAU-218, SKAU-221, SKAU-224, SC-104, SC-1019, SKAU-227, IC-561617, SKAU-231, SKAU-233, Arka Lohit, SKAU-243, SKAU-237, SKAU-247, IC-391082, IC-505242, SKAU-128, SKAU-173 and SKAU-211 and medium in six genotypes SKAU-36, SKAU-40, SKAU-45, SKAU-80, SKAU-84 and SKAU-148.

4.9.16 Leaf shape

Leaf shape was lanceolate in forty seven genotypes viz., SKAU-32, SKAU-36, SKAU-40, SKAU-43, SKAU-45, SKAU-52, SKAU-58, SKAU-73,

SKAU-77, Local Kashmiri Chilli-1, SKAU-91, SKAU-96, SKAU-106, SKAU-111, SKAU-118, SKAU-122, SKAU-132, SKAU-153, SKAU-157, SKAU-32, SKAU-36, SKAU-160, SKAU-163, SKAU-167, KL-1, SKAU-177, SKAU-188, SKAU-191, SKAU-193, SKAU-195, SKAU-198, SKAU-216, SKAU-218, SKAU-221, SKAU-224, SC-104, SC-1019, SKAU-227, IC-561617, SKAU-231, SKAU-233, Arka Lohit, SKAU-243, SKAU-237, SKAU-247, IC-391082, IC-505242, SKAU-128 and SKAU-173, nine genotypes viz., SKAU-38, SKAU-62, SKAU-89, SKAU-109, SKAU-139, SKAU-141, SKAU-181, SKAU-208 and SKAU-211 had ovate and four genotypes viz., SKAU-68, SKAU-80, SKAU-84 and SKAU-148 had broad elliptic leaf shape.

4.9.17 Leaf undulation of margin

Forty five genotypes viz., SKAU-32, SKAU-45, SKAU-62, SKAU-73, SKAU-77, SKAU-80, SKAU-84, SKAU-89, Local Kashmiri Chilli-1, SKAU-91, SKAU-96, SKAU-106, SKAU-109, SKAU-111, SKAU-118, SKAU-122, SKAU-132, SKAU-139, SKAU-141, SKAU-148, SKAU-153, SKAU-157, SKAU-160, SKAU-163, SKAU-167, SKAU-188, SKAU-191, SKAU-198, SKAU-208, SKAU-221, SKAU-224, SC-104, SC-1019, SKAU-227, IC-561617, SKAU-231, SKAU-233, Arka Lohit, SKAU-243, SKAU-237, SKAU-247, IC-391082, IC-505242, SKAU-128 and SKAU-211 had weak undulation of margin, thirteen genotypes viz., SKAU-36, SKAU-38, SKAU-40, SKAU-43, SKAU-52, KL-1, SKAU-173, SKAU-177, SKAU-181, SKAU-193, SKAU-195, SKAU-216, SKAU-218 had medium undulation of margin and two genotypes viz., SKAU-58 and SKAU-68 had strong undulation of margin.

4.9.18 Leaf pubescence

Leaf pubescence was present in fifty five genotypes viz., SKAU-36, SKAU-40, SKAU-43, SKAU-45, SKAU-52, SKAU-58, SKAU-62, SKAU-68, SKAU-73, SKAU-77, SKAU-80, SKAU-84, SKAU-89, Local Kashmiri Chilli-1, SKAU-91, SKAU-96, SKAU-106, SKAU-109, SKAU-111, SKAU-118,

SKAU-122, SKAU-132, SKAU-139, SKAU-141, SKAU-148, SKAU-153, SKAU-157, SKAU-160, SKAU-163, SKAU-167, KL-1, SKAU-177, SKAU-181, SKAU-188, SKAU-195, SKAU-198, SKAU-208, SKAU-216, SKAU-218, SKAU-221, SKAU-224, SC-104, SC-1019, SKAU-227, IC-561617, SKAU-231, SKAU-233, Arka Lohit, SKAU-243, SKAU-237, SKAU-247, IC-391082, IC-505242, SKAU-128 and SKAU-211 and absent in five genotypes viz., SKAU-32, SKAU-38, SKAU-173, SKAU-191 and SKAU-193.

4.9.19 Leaf: Intensity of pubescence

It was sparse in sixty genotypes viz., SKAU-32, SKAU-36, SKAU-38, SKAU-40, SKAU-43, SKAU-45, SKAU-52, SKAU-58, SKAU-62, SKAU-68, SKAU-73, SKAU-77, SKAU-80, SKAU-84, SKAU-89, Local Kashmiri Chilli-1, SKAU-91, SKAU-96, SKAU-106, SKAU-109, SKAU-111, SKAU-118, SKAU-122, SKAU-132, SKAU-139, SKAU-141, SKAU-148, SKAU-153, SKAU-157, SKAU-160, SKAU-163, SKAU-167, KL-1, SKAU-177, SKAU-181, SKAU-188, SKAU-191, SKAU-193, SKAU-195, SKAU-198, SKAU-208, SKAU-216, SKAU-218, SKAU-221, SKAU-224, SC-104, SC-1019, SKAU-227, IC-561617, SKAU-231, SKAU-233, Arka Lohit, SKAU-243, SKAU-237, SKAU-247, IC-391082, IC-505242, SKAU-128, SKAU-173 and SKAU-211.

4.9.20 Petal colour

Petal colour was white in sixty genotypes viz., SKAU-32, SKAU-36, SKAU-38, SKAU-40, SKAU-43, SKAU-45, SKAU-52, SKAU-58, SKAU-62, SKAU-68, SKAU-73, SKAU-77, SKAU-80, SKAU-84, SKAU-89, Local Kashmiri Chilli-1, SKAU-91, SKAU-96, SKAU-106, SKAU-109, SKAU-111, SKAU-118, SKAU-122, SKAU-132, SKAU-139, SKAU-141, SKAU-148, SKAU-153, SKAU-157, SKAU-160, SKAU-163, SKAU-167, KL-1, SKAU-177, SKAU-181, SKAU-188, SKAU-191, SKAU-193, SKAU-195, SKAU-198, SKAU-208, SKAU-216, SKAU-218, SKAU-221, SKAU-224, SC-104, SC-1019, SKAU-227, IC-561617, SKAU-231, SKAU-233, Arka Lohit, SKAU-243,

SKAU-237, SKAU-247, IC-391082, IC-505242, SKAU-128, SKAU-173 and SKAU-211.

4.9.21 Anther colour

Anther colour was pale blue in sixty genotypes viz., SKAU-32, SKAU-36, SKAU-38, SKAU-40, SKAU-43, SKAU-45, SKAU-52, SKAU-58, SKAU-62, SKAU-68, SKAU-73, SKAU-77, SKAU-80, SKAU-84, SKAU-89, Local Kashmiri Chilli-1, SKAU-91, SKAU-96, SKAU-106, SKAU-109, SKAU-111, SKAU-118, SKAU-122, SKAU-132, SKAU-139, SKAU-141, SKAU-148, SKAU-153, SKAU-157, SKAU-160, SKAU-163, SKAU-167, KL-1, SKAU-177, SKAU-181, SKAU-188, SKAU-191, SKAU-193, SKAU-195, SKAU-198, SKAU-208, SKAU-216, SKAU-218, SKAU-221, SKAU-224, SC-104, SC-1019, SKAU-227, IC-561617, SKAU-231, SKAU-233, Arka Lohit, SKAU-243, SKAU-237, SKAU-247, IC-391082, IC-505242, SKAU-128, SKAU-173 and SKAU-211.

4.9.22 Days to 50% flowering

It was medium in thirty four genotypes viz., SKAU-32, SKAU-36, SKAU-38, SKAU-40, SKAU-43, SKAU-45, SKAU-52, SKAU-58, SKAU-62, SKAU-68, SKAU-73, SKAU-77, SKAU-80, SKAU-84, SKAU-89, Local Kashmiri Chilli-1, SKAU-91, SKAU-96, SKAU-106, SKAU-109, SKAU-111, SKAU-118, SKAU-122, SKAU-128, SKAU-132, SKAU-139, SKAU-141, SKAU-148, SKAU-153, SKAU-157, SKAU-160, SKAU-163, SKAU-167, Arka Lohit, and late in twenty six genotypes viz., KL-1, SKAU-177, SKAU-181, SKAU-188, SKAU-191, SKAU-193, SKAU-195, SKAU-198, SKAU-208, SKAU-216, SKAU-218, SKAU-221, SKAU-224, SC-104, SC-1019, SKAU-227, IC-561617, SKAU-231, SKAU-233, SKAU-243, SKAU-237, SKAU-247, IC-391082, IC-505242, SKAU-173 and SKAU-211.

4.9.23 Fruit orientation

Fruit orientation was drooping in fifty eight genotypes viz., SKAU-32, SKAU-36, SKAU-38, SKAU-40, SKAU-43, SKAU-45, SKAU-52, SKAU-58, SKAU-62, SKAU-73, SKAU-77, SKAU-80, SKAU-84, SKAU-89, Local Kashmiri Chilli-1, SKAU-91, SKAU-96, SKAU-109, SKAU-111, SKAU-118, SKAU-122, SKAU-132, SKAU-139, SKAU-141, SKAU-148, SKAU-153, SKAU-157, SKAU-160, SKAU-163, SKAU-167, KL-1, SKAU-177, SKAU-181, SKAU-188, SKAU-191, SKAU-193, SKAU-195, SKAU-198, SKAU-208, SKAU-216, SKAU-218, SKAU-221, SKAU-224, SC-104, SC-1019, SKAU-227, IC-561617, SKAU-231, SKAU-233, Arka Lohit, SKAU-243, SKAU-237, SKAU-247, IC-391082, IC-505242, SKAU-128, SKAU-173 and SKAU-211 and semi-drooping in two genotypes viz., SKAU-68 and SKAU-106.

4.9.24 Fruit bearing habit

It was solitary in sixty genotypes viz., SKAU-32, SKAU-36, SKAU-38, SKAU-40, SKAU-43, SKAU-45, SKAU-52, SKAU-58, SKAU-62, SKAU-68, SKAU-73, SKAU-77, SKAU-80, SKAU-84, SKAU-89, Local Kashmiri Chilli-1, SKAU-91, SKAU-96, SKAU-106, SKAU-109, SKAU-111, SKAU-118, SKAU-122, SKAU-132, SKAU-139, SKAU-141, SKAU-148, SKAU-153, SKAU-157, SKAU-160, SKAU-163, SKAU-167, KL-1, SKAU-177, SKAU-181, SKAU-188, SKAU-191, SKAU-193, SKAU-195, SKAU-198, SKAU-208, SKAU-216, SKAU-218, SKAU-221, SKAU-224, SC-104, SC-1019, SKAU-227, IC-561617, SKAU-231, SKAU-233, Arka Lohit, SKAU-243, SKAU-237, SKAU-247, IC-391082, IC-505242, SKAU-128, SKAU-173 and SKAU-211.

4.9.25 Fruit colour (at mature unripe stage)

Fruit colour was green in sixty genotypes viz., SKAU-32, SKAU-36, SKAU-38, SKAU-40, SKAU-43, SKAU-45, SKAU-52, SKAU-58, SKAU-62, SKAU-68, SKAU-73, SKAU-77, SKAU-80, SKAU-84, SKAU-89, Local Kashmiri Chilli-1, SKAU-91, SKAU-96, SKAU-106, SKAU-109, SKAU-111,

SKAU-118, SKAU-122, SKAU-132, SKAU-139, SKAU-141, SKAU-148, SKAU-153, SKAU-157, SKAU-160, SKAU-163, SKAU-167, KL-1, SKAU-177, SKAU-181, SKAU-188, SKAU-191, SKAU-193, SKAU-195, SKAU-198, SKAU-208, SKAU-216, SKAU-218, SKAU-221, SKAU-224, SC-104, SC-1019, SKAU-227, IC-561617, SKAU-231, SKAU-233, Arka Lohit, SKAU-243, SKAU-237, SKAU-247, IC-391082, IC-505242, SKAU-128, SKAU-173 and SKAU-211.

4.9.26 Fruit intensity of colour (at mature unripe stage)

It was dark in twenty two genotypes viz., SKAU-36, SKAU-40, SKAU-45, SKAU-52, SKAU-62, SKAU-80, SKAU-84, SKAU-89, SKAU-96, SKAU-106, SKAU-109, SKAU-111, SKAU-118, SKAU-128, SKAU-132, SKAU-139, SKAU-148, SKAU-153, SKAU-173, SKAU-195, SKAU-211 and SKAU-231, twenty genotypes have light intensity viz., SKAU-43, SKAU-58, SKAU-68, SKAU-77, Local Kashmiri Chilli-1, SKAU-91, SKAU-157, SKAU-160, SKAU-163, KL-1, SKAU-177, SKAU-181, SKAU-188, SKAU-191, SKAU-193, SKAU-221, SKAU-224, SC-1019, SKAU-227, SKAU-237 and medium in eighteen genotypes viz., SKAU-32, SKAU-38, SKAU-73, SKAU-122, SKAU-141, SKAU-167, SKAU-198, SKAU-208, SKAU-216, SKAU-218, SC-104, IC-561617, SKAU-233, Arka Lohit, SKAU-243, SKAU-247, IC-391082 and IC-505242.

4.9.27 Fruit length

Fruit length was long in sixty genotypes viz., SKAU-32, SKAU-36, SKAU-38, SKAU-40, SKAU-43, SKAU-45, SKAU-52, SKAU-58, SKAU-62, SKAU-68, SKAU-73, SKAU-77, SKAU-80, SKAU-84, SKAU-89, Local Kashmiri Chilli-1, SKAU-91, SKAU-96, SKAU-106, SKAU-109, SKAU-111, SKAU-118, SKAU-122, SKAU-132, SKAU-139, SKAU-141, SKAU-148, SKAU-153, SKAU-157, SKAU-160, SKAU-163, SKAU-167, KL-1, SKAU-177, SKAU-181, SKAU-188, SKAU-191, SKAU-193, SKAU-195, SKAU-198,

SKAU-208, SKAU-216, SKAU-218, SKAU-221, SKAU-224, SC-104, SC-1019, SKAU-227, IC-561617, SKAU-231, SKAU-233, Arka Lohit, SKAU-243, SKAU-237, SKAU-247, IC-391082, IC-505242, SKAU-128, SKAU-173 and SKAU-211.

4.9.28 Fruit diameter

Fruit diameter was medium in fifty eight genotypes viz., SKAU-32, SKAU-36, SKAU-40, SKAU-43, SKAU-45, SKAU-52, SKAU-58, SKAU-62, SKAU-68, SKAU-73, SKAU-77, SKAU-80, SKAU-84, SKAU-89, Local Kashmiri Chilli-1, SKAU-91, SKAU-96, SKAU-106, SKAU-109, SKAU-111, SKAU-118, SKAU-122, SKAU-132, SKAU-139, SKAU-141, SKAU-148, SKAU-153, SKAU-157, SKAU-160, SKAU-163, SKAU-167, KL-1, SKAU-177, SKAU-181, SKAU-188, SKAU-191, SKAU-193, SKAU-195, SKAU-198, SKAU-208, SKAU-216, SKAU-218, SKAU-224, SC-104, SC-1019, SKAU-227, IC-561617, SKAU-231, SKAU-233, Arka Lohit, SKAU-243, SKAU-237, SKAU-247, IC-391082, IC-505242, SKAU-128, SKAU-173 and SKAU-211 and broad in two genotypes viz., SKAU-38 and SKAU-221.

4.9.29 Fruit curvature

Fruit curvature was present in fifty four genotypes viz., SKAU-36, SKAU-38, SKAU-40, SKAU-43, SKAU-45, SKAU-52, SKAU-58, SKAU-73, SKAU-77, SKAU-84, SKAU-89, Local Kashmiri Chilli-1, SKAU-91, SKAU-96, SKAU-109, SKAU-111, SKAU-118, SKAU-122, SKAU-132, SKAU-139, SKAU-141, SKAU-148, SKAU-153, SKAU-157, SKAU-160, SKAU-163, SKAU-167, KL-1, SKAU-177, SKAU-181, SKAU-188, SKAU-191, SKAU-193, SKAU-195, SKAU-198, SKAU-208, SKAU-216, SKAU-218, SKAU-221, SKAU-224, SC-104, SC-1019, SKAU-227, IC-561617, SKAU-231, SKAU-233, Arka Lohit, SKAU-243, SKAU-237, SKAU-247, IC-391082, IC-505242, SKAU-128, SKAU-173 and SKAU-211 and absent in six genotypes viz., SKAU-32, SKAU-62, SKAU-68, SKAU-80, SKAU-89 and SKAU-106.

4.9.30 Fruit curvature intensity

It was low in fifty four genotypes viz., SKAU-32, SKAU-36, SKAU-38, SKAU-40, SKAU-43, SKAU-45, SKAU-52, SKAU-58, SKAU-62, SKAU-68, SKAU-73, SKAU-77, SKAU-80, SKAU-84, SKAU-89, Local Kashmiri Chilli-1, SKAU-91, SKAU-96, SKAU-106, SKAU-109, SKAU-111, SKAU-118, SKAU-122, SKAU-132, SKAU-139, SKAU-141, SKAU-148, SKAU-153, SKAU-157, SKAU-160, SKAU-163, SKAU-167, SKAU-177, SKAU-188, SKAU-195, SKAU-198, SKAU-208, SKAU-216, SKAU-218, SKAU-221, SKAU-224, SC-104, SKAU-227, IC-561617, SKAU-231, SKAU-233, Arka Lohit, SKAU-243, SKAU-237, SKAU-247, IC-391082, IC-505242, SKAU-128 and SKAU-173 and medium in six genotypes KL-1, SKAU-181, SKAU-191, SKAU-193, SKAU-211 and SC-1019.

4.9.31 Fruit neck at basal end

It was absent in forty genotypes viz., SKAU-36, SKAU-40, SKAU-43, SKAU-45, SKAU-52, SKAU-58, SKAU-62, SKAU-68, SKAU-73, SKAU-80, SKAU-84, SKAU-89, Local Kashmiri Chilli-1, SKAU-91, SKAU-96, SKAU-106, SKAU-109, SKAU-111, SKAU-118, SKAU-122, SKAU-132, SKAU-139, SKAU-141, SKAU-148, SKAU-153, SKAU-157, SKAU-160, SKAU-163, SKAU-167, SC-1019, IC-561617, SKAU-231, SKAU-233, Arka Lohit, SKAU-243, SKAU-237, SKAU-247, IC-391082, IC-505242 and SKAU-128 and present in twenty genotypes viz., SKAU-32, SKAU-38, SKAU-77, KL-1, SKAU-177, SKAU-181, SKAU-188, SKAU-191, SKAU-193, SKAU-195, SKAU-198, SKAU-208, SKAU-216, SKAU-218, SKAU-221, SKAU-224, SC-104, SKAU-173, SKAU-211 and SKAU-227.

4.9.32 Fruit sinuation of pericarp

It was medium in thirty four genotypes viz., SKAU-32, SKAU-38, SKAU-40, SKAU-43, SKAU-45, SKAU-68, SKAU-73, SKAU-77, SKAU-80, SKAU-84, SKAU-89, Local Kashmiri Chilli-1, SKAU-91, SKAU-96,

SKAU-106, SKAU-109, SKAU-132, SKAU-139, SKAU-141, SKAU-148, SKAU-157, SKAU-160, SKAU-163, SKAU-167, SKAU-181, SKAU-188, SKAU-191, SKAU-193, SKAU-195, SKAU-198, SKAU-231, SKAU-233, Arka Lohit, SKAU-247, weak in twenty five genotypes viz., SKAU-36, SKAU-52, SKAU-58, SKAU-62, SKAU-111, SKAU-118, SKAU-122, SKAU-128, SKAU-153, KL-1, SKAU-177, SKAU-173, SKAU-208, SKAU-216, SKAU-218, SKAU-221, SKAU-224, SC-104, SC-1019, IC-561617, SKAU-237, SKAU-243, IC-391082, IC-505242, and SKAU-211 and strong in SKAU-227.

4.9.33 Fruit texture of surface

Fruit texture of surface was smooth in thirty five genotypes viz., SKAU-36, SKAU-43, SKAU-45, SKAU-52, SKAU-58, SKAU-62, SKAU-80, SKAU-109, SKAU-111, SKAU-118, SKAU-122, SKAU-139, SKAU-141, SKAU-148, SKAU-153, SKAU-177, SKAU-181, SKAU-198, SKAU-208, SKAU-218, SKAU-221, SKAU-224, SC-1019, SKAU-227, IC-561617, SKAU-231, SKAU-233, Arka Lohit, SKAU-243, SKAU-237, SKAU-247, IC-391082, IC-505242, SKAU-173 and SKAU-211, slightly rough in twenty three genotypes viz., SKAU-32, SKAU-38, SKAU-40, SKAU-68, SKAU-73, SKAU-77, SKAU-84, SKAU-89, Local Kashmiri Chilli-1, SKAU-91, SKAU-96, SKAU-106, SKAU-132, SKAU-128, SKAU-157, SKAU-160, SKAU-163, SKAU-167, KL-1, SKAU-188, SKAU-191, SKAU-216, SC-104 and rough in SKAU-193 and SKAU-195.

4.9.34 Fruit colour

Fruit colour was red in sixty genotypes viz., SKAU-32, SKAU-36, SKAU-38, SKAU-40, SKAU-43, SKAU-45, SKAU-52, SKAU-58, SKAU-62, SKAU-68, SKAU-73, SKAU-77, SKAU-80, SKAU-84, SKAU-89, Local Kashmiri Chilli-1, SKAU-91, SKAU-96, SKAU-106, SKAU-109, SKAU-111, SKAU-118, SKAU-122, SKAU-132, SKAU-1139, SKAU-141, SKAU-148, SKAU-153, SKAU-157, SKAU-160, SKAU-163, SKAU-167, KL-1, SKAU-177,

SKAU-181, SKAU-188, SKAU-191, SKAU-193, SKAU-195, SKAU-198, SKAU-208, SKAU-216, SKAU-218, SKAU-221, SKAU-224, SC-104, SC-1019, SKAU-227, IC-561617, SKAU-231, SKAU-233, Arka Lohit, SKAU-243, SKAU-237, SKAU-247, IC-391082, IC-505242, SKAU-128, SKAU-173 and SKAU-211.

4.9.35 Fruit intensity of colour

Intensity of colour was medium in sixty genotypes viz., SKAU-32, SKAU-36, SKAU-38, SKAU-40, SKAU-43, SKAU-45, SKAU-52, SKAU-58, SKAU-62, SKAU-68, SKAU-73, SKAU-77, SKAU-80, SKAU-84, SKAU-89, Local Kashmiri Chilli-1, SKAU-91, SKAU-96, SKAU-106, SKAU-109, SKAU-111, SKAU-118, SKAU-122, SKAU-132, SKAU-139, SKAU-141, SKAU-148, SKAU-153, SKAU-157, SKAU-160, SKAU-163, SKAU-167, KL-1, SKAU-177, SKAU-181, SKAU-188, SKAU-191, SKAU-193, SKAU-195, SKAU-198, SKAU-208, SKAU-216, SKAU-218, SKAU-221, SKAU-224, SC-104, SC-1019, SKAU-227, IC-561617, SKAU-231, SKAU-233, Arka Lohit, SKAU-243, SKAU-237, SKAU-247, IC-391082, IC-505242, SKAU-128, SKAU-173 and SKAU-211.

4.9.36 Fruit shape at base

Shape at base was acute in fifty two genotypes viz., SKAU-36, SKAU-40, SKAU-43, SKAU-45, SKAU-52, SKAU-58, SKAU-62, SKAU-68, SKAU-77, SKAU-80, SKAU-84, SKAU-89, Local Kashmiri Chilli-1, SKAU-91, SKAU-96, SKAU-106, SKAU-109, SKAU-111, SKAU-118, SKAU-122, SKAU-132, SKAU-139, SKAU-141, SKAU-148, SKAU-153, SKAU-157, SKAU-160, SKAU-163, SKAU-167, KL-1, SKAU-177, SKAU-181, SKAU-188, SKAU-191, SKAU-193, SKAU-195, SKAU-198, SKAU-208, SKAU-216, SKAU-218, SKAU-221, SKAU-224, SKAU-227, SKAU-231, SKAU-233, SKAU-237, SKAU-247, IC-391082, IC-505242, SKAU-128, SKAU-173 and SKAU-211 and

round in eight genotypes viz., SKAU-32, SKAU-38, SKAU-73, SC-104, SC-1019, IC-561617, Arka Lohit and SKAU-243.

4.9.37 Fruit shape at apex

It was acute in fifty nine genotypes viz., SKAU-36, SKAU-38, SKAU-40, SKAU-43, SKAU-45, SKAU-52, SKAU-58, SKAU-62, SKAU-68, SKAU-73, SKAU-77, SKAU-80, SKAU-84, SKAU-89, Local Kashmiri Chilli-1, SKAU-91, SKAU-96, SKAU-106, SKAU-109, SKAU-111, SKAU-118, SKAU-122, SKAU-132, SKAU-139, SKAU-141, SKAU-148, SKAU-153, SKAU-157, SKAU-160, SKAU-163, SKAU-167, KL-1, SKAU-177, SKAU-181, SKAU-188, SKAU-191, SKAU-193, SKAU-195, SKAU-198, SKAU-208, SKAU-216, SKAU-218, SKAU-221, SKAU-224, SC-104, SC-1019, SKAU-227, IC-561617, SKAU-231, SKAU-233, Arka Lohit, SKAU-243, SKAU-237, SKAU-247, IC-391082, IC-505242, SKAU-128, SKAU-173 and SKAU-211 and blunt in SKAU-32.

4.9.38 Fruit calyx cover

It was enveloping in fifty five genotypes viz., SKAU-36, SKAU-43, SKAU-45, SKAU-52, SKAU-58, SKAU-62, SKAU-68, SKAU-73, SKAU-77, SKAU-80, SKAU-84, SKAU-89, Local Kashmiri Chilli-1, SKAU-91, SKAU-96, SKAU-106, SKAU-109, SKAU-111, SKAU-118, SKAU-122, SKAU-132, SKAU-139, SKAU-141, SKAU-148, SKAU-153, SKAU-157, SKAU-160, SKAU-163, SKAU-167, KL-1, SKAU-177, SKAU-181, SKAU-188, SKAU-191, SKAU-193, SKAU-195, SKAU-198, SKAU-208, SKAU-216, SKAU-218, SKAU-221, SKAU-224, SC-104, SKAU-227, SKAU-231, SKAU-233, Arka Lohit, SKAU-243, SKAU-237, SKAU-247, IC-391082, IC-505242, SKAU-128, SKAU-173 and SKAU-211 and non-enveloping in five genotypes SKAU-32, SKAU-38, SKAU-40, SC-1019 and IC-561617.

4.9.39 Fruit calyx margin

It was dented in fifty seven genotypes viz., SKAU-32, SKAU-36, SKAU-38, SKAU-40, SKAU-43, SKAU-45, SKAU-52, SKAU-58, SKAU-62, SKAU-68, SKAU-73, SKAU-77, SKAU-89, Local Kashmiri Chilli-1, SKAU-91, SKAU-106, SKAU-109, SKAU-111, SKAU-118, SKAU-122, SKAU-132, SKAU-139, SKAU-141, SKAU-148, SKAU-153, SKAU-157, SKAU-160, SKAU-163, SKAU-167, KL-1, SKAU-177, SKAU-181, SKAU-188, SKAU-191, SKAU-193, SKAU-195, SKAU-198, SKAU-208, SKAU-216, SKAU-218, SKAU-221, SKAU-224, SC-104, SC-1019, SKAU-227, IC-561617, SKAU-231, SKAU-233, Arka Lohit, SKAU-243, SKAU-237, SKAU-247, IC-391082, IC-505242, SKAU-128, SKAU-173 and SKAU-211 and smooth in three genotypes SKAU-80, SKAU-84 and SKAU-96.

4.9.40 Fruit calyx constriction

It was absent in forty nine genotypes viz., SKAU-36, SKAU-43, SKAU-45, SKAU-52, SKAU-58, SKAU-62, SKAU-80, SKAU-84, SKAU-89, Local Kashmiri Chilli-1, SKAU-91, SKAU-96, SKAU-111, SKAU-118, SKAU-122, SKAU-132, SKAU-139, SKAU-141, SKAU-148, SKAU-153, SKAU-157, SKAU-160, SKAU-163, SKAU-167, KL-1, SKAU-177, SKAU-181, SKAU-188, SKAU-191, SKAU-193, SKAU-195, SKAU-198, SKAU-208, SKAU-216, SKAU-218, SKAU-221, SKAU-224, SKAU-227, SKAU-231, SKAU-233, Arka Lohit, SKAU-243, SKAU-237, SKAU-247, IC-391082, IC-505242, SKAU-128, SKAU-173 and SKAU-211 and present in eleven genotypes SKAU-32, SKAU-38, SKAU-40, SKAU-68, SKAU-73, SKAU-77, SKAU-106, SKAU-109, SC-104, SC-1019 and IC-561617.

4.9.41 Fruit pedicel attachment

It was weak in thirty three genotypes viz., SKAU-36, SKAU-40, SKAU-43, SKAU-45, SKAU-52, SKAU-58, SKAU-80, SKAU-84, SKAU-89, Local Kashmiri Chilli-1, SKAU-111, SKAU-118, SKAU-122, KL-1, SKAU-177,

SKAU-188, SKAU-191, SKAU-193, SKAU-198, SKAU-208, SKAU-216, SKAU-218, SKAU-221, SKAU-224, IC-561617, SKAU-231, SKAU-233, Arka Lohit, SKAU-243, SKAU-237, SKAU-247, IC-391082, IC-505242 and strong in twenty six genotypes viz., SKAU-32, SKAU-38, SKAU-62, SKAU-68, SKAU-73, SKAU-77, SKAU-91, SKAU-96,SKAU-106, SKAU-109, SKAU-128, SKAU-132, SKAU-139, SKAU-141, SKAU-148, SKAU-153, SKAU-157, SKAU-160, SKAU-163, SKAU-167, SKAU-173, SKAU-181, SKAU-195, SKAU-211, SC-104, SC-1019 and SKAU-227.

4.9.42 Fruit blossom end appendage

It was present in thirty genotypes viz., SKAU-36, SKAU-43, SKAU-58, SKAU-62, SKAU-80, SKAU-84, SKAU-118, SKAU-122, KL-1, SKAU-181, SKAU-191, SKAU-193, SKAU-195, SKAU-198, SKAU-216, SKAU-218, SKAU-221, SKAU-224, SC-104, SKAU-227, IC-561617, SKAU-231, SKAU-233, Arka Lohit, SKAU-243, SKAU-237, SKAU-247, IC-391082, IC-505242 and SKAU-173 and absent in thirty genotypes viz., SKAU-32, SKAU-38, SKAU-40, SKAU-45, SKAU-52, SKAU-68, SKAU-73, SKAU-77, SKAU-89, Local Kashmiri Chilli-1,SKAU-91, SKAU-96,SKAU-106, SKAU-109, SKAU-111, SKAU-128, SKAU-132, SKAU-139, SKAU-141, SKAU-148, SKAU-153, SKAU-157, SKAU-160, SKAU-163, SKAU-167, SKAU-177, SKAU-188, SKAU-208, SKAU-211 and SC-1019.

4.10 Mean performance and analysis of variance

The mean values of different growth and quality characters for all the genotypes of chilli are presented in Appendix-II. Analysis of variance for all the traits under study is presented in Table 10. Perusal of the tables revealed significant mean sum of squares due to yield and attributing characters suggesting existence of considerable variability in material studied.

4.11 Variability and genetic components of variation

The genetic variability estimates including genotypic mean, range, genotypic variance (GV), phenotypic variance (PV), genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (bs) and genetic gain as a per cent of mean were estimated for the quality and quantitative and characters studied are presented in Table 11. A comparative performance of all the genotypes under study is described as under:

4.11.1 Plant height (cm)

Plant height ranged from 49.16-86.00 cm with an overall mean of 63.83 cm. The maximum plant height was attained by SKAU-77 (86.00 cm) followed by SKAU-38 (81.33 cm) and SKAU-231 (80.73 cm) and minimum height was attained by SKAU-181 (49.16 cm) followed by Local Kashmiri Chilli-1 (49.24 cm) and SKAU-153 (50.00 cm). The phenotypic and genotypic variance for this trait were 78.53 and 77.49 respectively. The phenotypic and genotypic coefficient of variation for this trait were 13.88 and 13.79 respectively. High heritability (98%) along with high genetic gain as a per cent of mean (28.21) was observed for this trait.

4.11.2 Plant spread (cm)

Plant spread ranged from 44.33-86.64 cm with an average value of 64.22 cm. The maximum plant spread was attained by SKAU-106 (86.64cm) followed by SKAU-62 (85.58 cm) and SKAU-128 (85.18 cm). The minimum spread was attained by SKAU-167(44.33 cm) followed by SKAU-160 (49.46 cm) and SKAU-243 (49.56 cm). The phenotypic and genotypic variances were 102.3 and 101.33 respectively. Phenotypic coefficient of variation (15.73) and genotypic coefficient of variation (15.67) were observed for the trait. High heritability (99%) along with genetic gain as a per cent of mean (32.15) were observed for this trait.

4.11.3 Number of branches plant⁻¹

Number of branches ranged from 14.26-48.93 with an overall mean of 34.08. The minimum number of branches were recorded in SKAU- 167 (14.26)

followed by Local Kashmiri Chilli-1 (17.66) and SKAU-163 (20.73). The maximum number of branches plant⁻¹ were recorded in SKAU-173 (48.93) followed by SKAU-181 (47.73) and SKAU-191 (46.40). The phenotypic and genotypic variance for this trait were 74.68 and 74.46 respectively. Phenotypic coefficient of variation (25.35) and genotypic coefficient of variation (25.32) were observed. High heritability (99%) with high genetic gain as a per cent of mean (52.08) were recorded for the trait.

4.11.4 Days to flower initiation

Days to flower initiation ranged from 24.40-38.60 with an average of 34.78. The minimum number of days to flower initiation were taken by SKAU-38 (24.40) followed by SKAU-106 (24.60) and SKAU-96, SKAU-32 (24.66 each). The maximum number of days to flower initiation were taken by SKAU-237 and SKAU-247 (38.60 each) followed by SKAU-231, SKAU-233, Arka Lohit (38.46 each), SKAU-243 (38.40). The phenotypic and genotypic for the trait was found to be 15.22 and 15.18 respectively. Phenotypic coefficient of variation (11.21) and genotypic coefficient of variation (11.20) were found for the trait. High heritability (99%) along with moderate genetic gain as a per cent of mean (23.04) were observed.

4.11.5 Days to fruit initiation

Days to fruit initiation ranged from 31.40-46.53 with an average of 43.77. The minimum number of days to fruit initiation were observed in SKAU-96 (31.40) followed by SKAU-32 and SKAU-38 (31.53 each). The maximum number of days to fruit initiation were taken by SKAU-198 and SKAU-208 (46.53 each) followed by SKAU-173 (46.40) and SKAU-160 (45.53). The phenotypic and genotypic variance was observed to be 9.96 and 9.92 respectively. Moderate phenotypic coefficient of variation (7.28) and genotypic coefficient of variation (7.27) were observed. High heritability (99%) along with high genetic gain as a per cent of mean (14.95) was observed.

4.11.6 Days to harvesting

Days to harvesting ranged from 102.40-134.66 with an overall mean of 117.26. The minimum number of days to harvest were observed in SKAU-32 (102.40) followed by SKAU-96, SKAU-106 (102.53 each) and SKAU-62, SKAU-153 (102.60). The maximum number of days to harvest was observed in SKAU-188, SKAU-195, SKAU-208, SKAU-216 (134.66) each, followed by SKAU-198 (134.60) and SKAU-231 (131.46). The phenotypic and genotypic variance were found to be 131.27 and 131.212 respectively. Phenotypic coefficient of variation (9.77) and genotypic coefficient of variation (9.76) were observed for the trait. High heritability (100%) along with high genetic gain as a per cent of mean (20.11) was observed.

4.11.7 Fruit length (cm)

Fruit length of genotypes ranged from 7.00-16.07 with an average of 12.27. The maximum value was recorded for SKAU-198 (16.07) followed by SKAU-195 (16.03) and SKAU-148 (15.97). The minimum value was recorded in SKAU-160 (7.00) followed by Local Kashmiri Chilli-1 (7.10) and SKAU-32 (8.18). The phenotypic and genotypic variance was found to be 6.32 and 6.12 respectively. High phenotypic coefficient of variation (20.49) and genotypic coefficient of variation (20.16) was observed. High heritability (96%) coupled with high genetic gain as a per cent of mean (40.89) was observed for this trait.

4.11.8 Fruit diameter (cm)

Fruit diameter ranged 0.78-1.92 cm with an overall mean of 1.08 cm. SKAU-141 recorded the maximum fruits diameter (1.92 cm) followed by SKAU-221 (1.59 cm) and SKAU-38 (1.52 cm). SKAU-36 recorded the minimum fruit diameter (0.78 cm) followed by IC-561617 (0.82 cm) and SKAU-109 (0.84 cm). The phenotypic and genotypic variance was found to be 0.04 and 0.03 respectively. Moderate phenotypic coefficient of variation (20.37) and genotypic coefficient of variation (16.82) was observed. Moderate heritability (68%)

coupled with high genetic gain as a per cent of mean (28.61) was recorded for this trait.

4.11.9 Fruit weight (g)

Fruit weight ranged from 1.38-9.28 g with an overall mean of 5.13g. Maximum weight was recorded in SKAU-141 (9.28 g) followed by Arka Lohit (9.09 g), SKAU-216 (8.51 g) and SKAU-193 (8.26 g). SKAU-153 recorded minimum fruit weight (1.38 g) followed by SKAU-36 (1.69 g) and SKAU-91 (2.35 g). The phenotypic and genotypic variance was found to be 3.95 and 3.94 respectively. The phenotypic coefficient of variation (38.73) and genotypic coefficient of variation (38.67) were observed to be high. High heritability (99%) along with high genetic gain as a per cent of mean (79.53) was observed for this trait.

4.11.10 Fruit pedicel length (cm)

Fruit pedicel length ranged from 2.10-6.01 cm with an average of 4.75 cm. SKAU-141 recorded maximum value of 6.01 cm followed by SKAU-211 (5.89 cm), and SKAU-38 (5.88 cm). The lowest value was observed in Local Kashmiri Chilli-1 (2.10 cm) followed by SKAU-181 (3.10 cm) and SKAU-247 (3.62 cm). The phenotypic and genotypic variance was found to be 0.50 and 0.40 (respectively). High phenotypic coefficient of variation (14.87) and genotypic coefficient of variation (13.38) were observed for this trait. High heritability (80%) coupled with high genetic gain as a per cent of mean (24.79) was observed for this trait.

4.11.11 Fruit pedicel diameter (cm)

It ranged from 0.21-0.44 with an average of 0.28. The maximum value was recorded in Arka Lohit (0.44) followed by SKAU- 148 (0.40) and SKAU-224 (0.35). The minimum value was recorded in SKAU-181 (0.21) followed by SKAU-122 (0.22) and Local Kashmiri Chilli-1 (0.24). The phenotypic and genotypic variance was observed to be 0.00 and 0.000, respectively. High

phenotypic coefficient of variation (15.03) and genotypic coefficient of variation (13.40) were observed for the trait. High heritability (79%) along with high genetic gain as a per cent of mean (24.60) was observed for fruit pedicel diameter in chilli.

4.11.12 Number of fruits plant⁻¹

Average number of fruits per plant ranged from 29.66-99.86 with an overall mean of 54.31. Maximum number was recorded in SKAU-188 (99.86) followed by SKAU-193 (91.86), KL-1 (89.26) and SKAU-224 (87.13). Minimum number of fruits were recorded in Local Kashmiri Chilli-1 (29.66) followed by IC-505242 (29.86) and SKAU-118 (30.40). High phenotypic and genotypic variance was observed to be 291.69 and 291.13 respectively. High phenotypic coefficient of variation (31.44) and genotypic coefficient of variation (31.41) was observed for the trait. High heritability (99%) along with high genetic gain as a per cent of mean (64.64).

4.11.13 Fruit yield hectare⁻¹ (g)

Average red ripe fruit yield per gram ranged from 59.10-759.52 g with an overall mean of 276.14 g. The maximum red ripe fruit yield was recorded in SKAU-193 (759.52 g) followed by SKAU-173 (649.20 g), KL-1 (581.80 g), SKAU-195 (558.35 g) SKAU-188 (539.83 g), and SKAU-198 (526.12 g). The lowest red ripe fruit yield was recorded in SKAU-163 (59.10 g) followed SKAU-153 (75.59 g) and Local Kashmiri Chilli-1 (76.40 g). The phenotypic and genotypic variance were found to be 25578.97 and 25319.47 respectively. The phenotypic coefficient of variation (57.91) and genotypic coefficient of variation (57.62) was high. High heritability (99%) coupled with high genetic gain as a per cent of mean (118.09) was observed.

4.11.14 Fruit yield hectare⁻¹ (q)

Average red ripe fruit yield per hectare ranged from 23.90-239.43 q with an overall mean of 90.64 q. The maximum red ripe fruit yield was recorded in

SKAU-193 (239.43 q) followed by SKAU-173 (206.02 q), KL-1(184.54 q), SKAU-195 (117.14 q) SKAU-188 (171.21 q) and SKAU-198 (166.87 q). The lowest red ripe fruit yield was recorded in SKAU-153 (23.90 q) followed Local Kashmiri Chilli-1 (24.13 q) and SKAU-118 (26.02 q). The phenotypic and genotypic variance were found to be 2608.53 and 2606.95 respectively. The phenotypic coefficient of variation (56.34) and genotypic coefficient of variation (56.32) was high. High heritability (99%) coupled with high genetic gain as a per cent of mean (115.99) was observed.

4.11.15 Dry matter content (%)

Dry matter content of the genotypes ranged from 61.54-86.07% with an overall mean of 79.58%. Maximum dry matter content was recorded in SKAU-237 (86.07%) followed by SKAU-52 (85.92%) and SKAU-167 (85.84%). The minimum dry matter content was recorded in SKAU-84 (61.54%) followed by SKAU-89 (62.86%) and SKAU-32 (69.42%). The phenotypic and genotypic variance was observed to be 25.52 and 25.44 respectively. Phenotypic coefficient of variation (6.34) and genotypic coefficient of variation (6.33) were observed for the trait. High heritability (99%) along with high genetic gain as a per cent of mean (13.03) was observed for this trait.

4.11.16 Vitamin C content at green stage (mg100g⁻¹)

Vitamin C content at green stage ranged from 43.86-201.16 (mg100g⁻¹) with an overall mean of 133 mg100g⁻¹. The maximum vitamin C content at green stage was recorded in SKAU-58 (201.16 mg100g⁻¹) followed by SKAU-73 (199.76 mg100g⁻¹), SKAU-173 (196.28 mg100g⁻¹) and SKAU-141 (195.01 mg100g⁻¹). The lowest vitamin C content at green stage was recorded in Local Kashmiri Chilli-1 (43.86 mg100g⁻¹) followed by SKAU-84 (57 mg100g⁻¹) and SKAU-45 (62.62 mg100g⁻¹). The phenotypic and genotypic variance was found to be 2150.34 and 2149.88 respectively. The phenotypic coefficient of variation (34.86) and genotypic coefficient of variation (34.86) were high. High heritability

(100%) coupled with high genetic gain as a per cent of mean (71.80) was observed.

4.11.17 Capsaicin content (mg g^{-1})

Capsaicin content of the genotypes ranged from 0.29-0.75 mg/g with an overall mean of 0.53 mg g^{-1} . Highest Capsaicin content was recorded in SKAU-62 (0.75 mg g^{-1}) followed by SKAU-52 (0.73 mg g^{-1}), SKAU-68, SKAU-96 (0.71 mg g^{-1} each), and SKAU-89 (0.70 mg g^{-1}). Lowest Capsaicin content was recorded in SKAU-157 (0.29 mg g^{-1}) followed by SKAU-167 (0.31 mg g^{-1}), SKAU-38 (0.33 mg g^{-1}) and SKAU-160 (0.35 mg g^{-1}). The phenotypic and genotypic variance was found to be 0.01 and 0.01 respectively. The phenotypic coefficient of variation (20.21) and genotypic coefficient of variation (20.04) was found to be high. High heritability (98%) along with high genetic gain as a per cent of mean (40.95) was observed for the trait.

4.11.18 Capsanthin content ASTA units

Capsanthin content of the genotypes ranged from 66.24-125.83 units with an overall mean of 96.03 ASTA units. Highest Capsanthin content was recorded in SKAU-198 (125.83 units) followed by SKAU-227 (125.05 units), SKAU-193 (123.63 units) and SKAU-106 (122.20 units). Lowest Capsanthin content was recorded in SKAU-58 (66.24 units) followed by SKAU-163 (67.28 units), SKAU-38 (70.14 units), SKAU-211 (70.71 units) and SKAU-40 (72.67 units). The phenotypic and genotypic variance were found to be 275.82 and 251.19 respectively. Phenotypic coefficient of variation (17.29) and genotypic coefficient of variation (16.50) was observed for the trait. High heritability (91%) along with high genetic gain as a per cent of mean (32.44) was observed for the trait.

4.11.19 Total Phenol (mg100g^{-1})

Total Phenol of the genotypes ranged from 4.90-7.70 (mg100g^{-1}) with an overall mean of 6.41 (mg100g^{-1}). Highest Phenol content was recorded in SKAU-193 (7.70 mg100g^{-1}) followed by SKAU-177(7.46 mg100g^{-1}), SKAU-191(7.43

mg100g⁻¹) and SKAU-173, IC-561617 (7.20 mg100g⁻¹). Lowest Phenol content was recorded in Local Kashmiri Chilli-1 (4.90 mg100g⁻¹) followed by SKAU-109 (4.93 mg100g⁻¹), SKAU-157 (5.10 mg100g⁻¹), SKAU-122 (5.13 mg100g⁻¹) and SKAU-167 (5.30 mg100g⁻¹). The phenotypic and genotypic variance were found to be 0.46 and 0.45 respectively. Phenotypic coefficient of variation (10.63) and genotypic coefficient of variation (10.56) was observed for the trait. High heritability (98%) along with high genetic gain as a per cent of mean (21.59) was observed for the trait.

4.11.20 Instrumental colour L*

Instrumental colour L* of the genotypes ranged from 35.22-50.11 with an overall mean of 41.18. Highest L* value was recorded in SKAU-118 (50.11) followed by SC-1019 (49.25), SKAU-122 (48.25) and SKAU-45(47.26). Lowest L* content was recorded in SKAU-40 (35.22) followed by IC-391082 (35.57), SKAU-91(35.87), SKAU-62(35.97) and SKAU-181 (36.20). The phenotypic and genotypic variance were found to be 12.53 and 12.05 respectively. Phenotypic coefficient of variation (8.59) and genotypic coefficient of variation (8.43) was observed for the trait. High heritability (96%) along with high genetic gain as a per cent of mean (17.03) was observed for the trait.

4.11.21 Instrumental colour a

Instrumental colour 'a' of the genotypes ranged from 30.78-45.26 with an overall mean of 36.82. Highest 'a' value was recorded in SKAU-118 (45.26) followed by IC-505242 (43.66), SKAU-122 (43.32) and SKAU-45 (42.25). Lowest 'a' value was recorded in SKAU-40 (30.78) followed by IC-391082 (30.87), SKAU-181 (31.11), SKAU-91 (31.43) and SKAU-62 (31.78). The phenotypic and genotypic variance were found to be 13.38 and 8.82 respectively. Phenotypic coefficient of variation (9.93) and genotypic coefficient of variation (8.06) was observed for the trait. High heritability (65%) along with high genetic gain as a per cent of mean (13.49) was observed for the trait.

Tocher Method

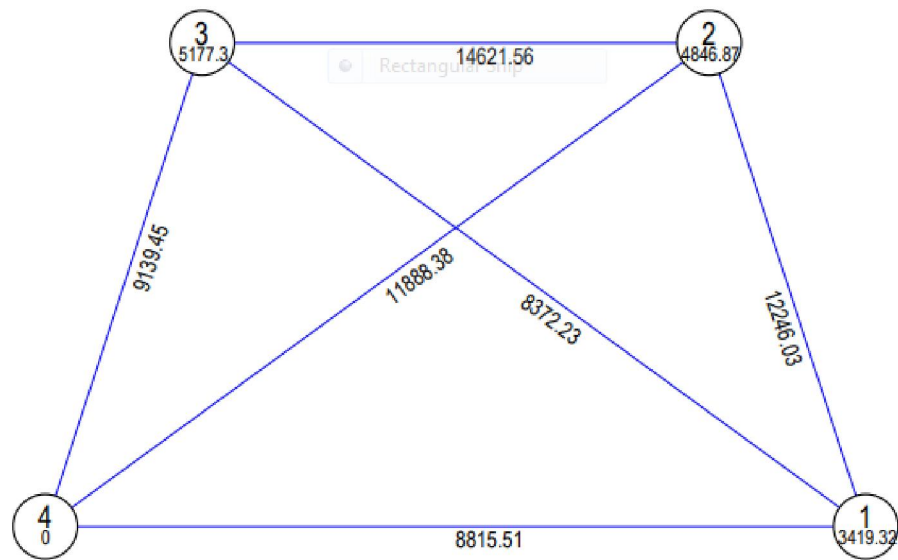


Fig. 1: Mahalanobis Euclidean Distance (Not to the Scale)

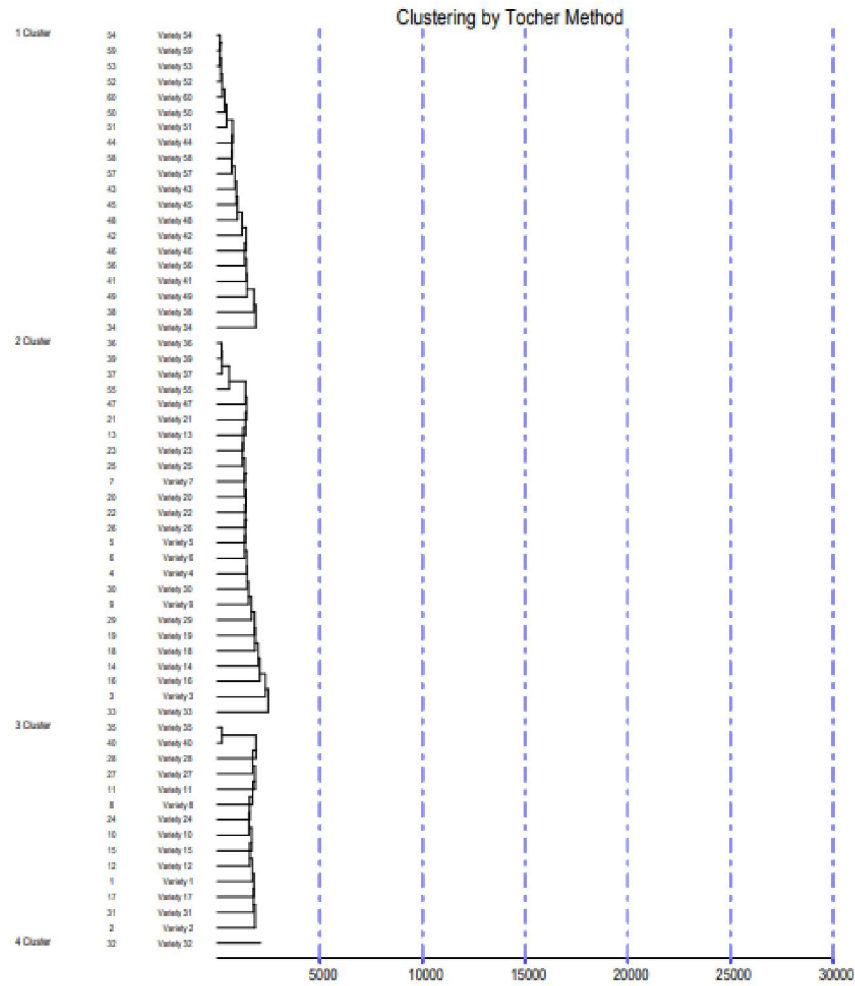


Fig. 2: Clustering by Tocher method (Dendrogram)

1 = SKAU-32; 2= SKAU-36; 3= SKAU-38; 4= SKAU-40; 5= SKAU-43; 6= SKAU-45; 7= SKAU-52; 8= SKAU-58; 9= SKAU-62; 10= SKAU-68; 11= SKAU-73; 12= SKAU-77; 13= SKAU-80; 14= SKAU-84; 15= SKAU-89; 16= Local Kashmiri Chilli-1; 17= SKAU-91; 18= SKAU-96; 19= SKAU-106; 20= SKAU-109; 21= SKAU-111; 22= SKAU-118; 23= SKAU-122; 24= SKAU-128; 25= SKAU-132; 26= SKAU-139; 27= SKAU-141; 28= SKAU-148; 29= SKAU-153; 30= SKAU-157; 31= SKAU-160; 32= SKAU-163; 33= SKAU-167; 34= KL-1; 35= SKAU-173; 36= SKAU-177; 37= SKAU-181; 38= SKAU-188; 39= SKAU-191; 40= SKAU-193; 41= SKAU-195; 42= SKAU-198; 43= SKAU-208; 44= SKAU-211; 45= SKAU-216; 46= SKAU-218; 47= SKAU- 221; 48= SKAU-224; 49= SC-104; 50= SC-1019; 51= SKAU-227; 52= IC-561617; 53= SKAU-231; 54= SKAU-233; 55= SKAU-237; 56= Arka Lohit; 57= SKAU-243; 58= SKAU-247; 59= IC-391082; 60= IC-505242.

4.11.22 Instrumental colour b

Instrumental colour 'b' of the genotypes ranged from 14.34-18.58 with an overall mean of 15.84. Highest 'b' value was recorded in SKAU-193 (18.58) followed by SKAU-132 (17.89), SKAU-43 (17.77) and SKAU-38 (17.45). Lowest 'a' value was recorded in SKAU-237 (14.34) followed by SKAU-231, IC-561617 (14.43 each), SKAU-247 (14.47), SKAU-243 (14.53) and SKAU-216 (14.63). The phenotypic and genotypic variance were found to be 1.03 and 0.85 respectively. Phenotypic coefficient of variation (6.41) and genotypic coefficient of variation (5.83) was observed for the trait. High heritability (82%) along with high genetic gain as a per cent of mean (10.93) was observed for the trait. The genotypes appearing to be best on the basis of their *per se* performance are indicated in Table-12.

4.12 Correlation coefficient

The correlation coefficients were determined using variances and co variances to obtain relationship among various characters and their relationship with economically desirable trait i.e., fruit yield plant⁻¹, both at genotypic and phenotypic levels.

The correlation coefficients both genotypic (r_g) and phenotypic (r_p) among the various growth characters of chilli genotypes are presented in Table 13 and Table 14. Correlation coefficients revealed that the economically important trait i.e. fruit yield plant⁻¹ exhibited significant positive association with fruit length ($r_g = 0.646$, $r_p = 0.635$), number of fruits plant⁻¹ ($r_g = 0.849$, $r_p = 0.848$), number of branches plant⁻¹ ($r_g = 0.588$, $r_p = 0.587$), fruit diameter ($r_g = 0.496$, $r_p = 0.407$) both at genotypic and phenotypic levels.

Plant spread exhibited negative and non-significant association ($r_g = -0.174$, $r_p = -0.174$) with fruit yield plant⁻¹. Plant height ($r_g = 0.104$, $r_p = 0.103$), Days to fruit initiation ($r_g = 0.151$, $r_p = 0.151$) and fruit weight ($r_g = 0.189$, $r_p = 0.170$) showed positive but non-significant association with fruit yield plant⁻¹.

Fruit pedicel length and diameter showed positive and significant association with fruit length and fruit diameter.

It was noticed that fruit weight was positively and significantly associated with fruit length, fruit diameter, days to harvesting and number of branches plant⁻¹ but negatively associated with plant spread.

Number of fruits plant⁻¹ showed positive and significant association with number of branches plant⁻¹, days to flower initiation, days to harvesting and fruit length but negative and non-significant association with plant spread. Days to harvesting showed positive and significant association with number of branches plant⁻¹, days to flower initiation and days to fruit initiation. Fruit weight showed positive and significant association with number of branches, days to harvesting, fruit length and fruit diameter. Days to fruit initiation showed positive and significant association with days to flower initiation but days to flower initiation showed positive and significant association with number of branches plant⁻¹. Fruit diameter showed positive and significant association with number of branches and fruit length. Fruit length showed positive and significant association with number of branches, plant height and days to harvesting. Plant spread showed positive and significant association with plant height. Association between other traits were found to be either positive or negative but non-significant.

Table-10: Analysis of Variance for various traits in chilli (*Capsicum annum* L.)

S. No.	Source of variation	d.f	Plant height (cm)	Plant spread (cm)	No. of branches plant ⁻¹	Days to flower initiation	Days to fruit initiation	Days to harvesting	Fruit length (cm)	Fruit diameter (cm)	Fruit weight (g)	Fruit pedicel length (cm)
1.	Replication	2	8.23	1.94	2.46	0.31	0.05	0.43	0.50	0.01	0.05	0.23
2.	Genotype	59	233.53**	304.79**	223.61**	45.58**	29.81**	393.69**	18.57**	0.11**	11.83**	1.31**
3.	Error	118	1.04	0.80	0.21	0.04	0.03	0.05	0.19	0.01	0.01	0.09

*Significant at 0.05 probability level

**Significant at 0.01 probability level

Table-10 contd...

S. No.	Source of variation	d.f	Fruit pedicel diameter (cm)	No. of fruits plant ⁻¹	Fruit yield plant ⁻¹ (g)	Fruit yield ha ⁻¹ (q)	Dry matter content (%)	Vitamin C (green) (mg100g ⁻¹)	Capsaicin content (mg g ⁻¹)	Capsanthin content (ASTA units)	Total phenol (mg100 ⁻¹ g)	Instrumental Colour L*	Instrumental colour a	Instrumental colour b
1.	Replication	2	0.00	3.27	155.46	1.92	1.34	2.06	0.00	42.81	0.02	2.89	3.20	3.42
2.	Genotype	59	0.00**	11.83**	76217.91**	7822.44**	76.41**	6450.12**	0.03**	778.20**	1.38**	36.64**	31.03**	2.74**
3.	Error	118	0.00	0.01	259.49	1.58	0.07	0.46	0.00	24.62	0.00	0.47	4.55	0.17

*Significant at 0.05 probability level

**Significant at 0.01 probability level

Table-11: Estimates of mean, range, phenotypic variance, genotypic variance, phenotypic and genotypic coefficients of variation for various quantitative and qualitative characters in chilli (*Capsicum annuum* L.)

S. No.	Parameters	Mean	Range	Phenotypic variance (PV)	Genotypic variance (GV)	Phenotypic coefficient of variation (PCV)	Genotypic coefficient of variation (GCV)	H ² (broad sense)	Genetic gain (Genetic advance as% of mean)
1.	Plant height (cm)	63.83	49.16-86.00	78.53	77.49	13.88	13.79	0.98	28.21
2.	Plant spread (cm)	64.22	44.33-86.64	102.13	101.33	15.73	15.67	0.99	32.15
3.	No. of branches plant ⁻¹	34.08	14.26-48.93	74.68	74.46	25.35	25.32	0.99	52.08
4.	Days to flower initiation	34.78	24.40-38.60	15.22	15.18	11.21	11.20	0.99	23.04
5.	Days to fruit initiation	46.05	31.40-46.53	9.96	9.92	7.28	7.27	0.99	14.95
6.	Days to harvesting	117.26	102.40-134.66	131.27	131.212	9.77	9.76	0.99	20.11
7.	Fruit length (g)	12.27	7.00-16.07	6.32	6.12	20.49	20.16	0.96	40.89
8.	Fruit diameter (cm)	1.08	0.78-1.92	0.04	0.03	20.37	16.82	0.68	28.61
9.	Fruit weight (g)	5.13	1.38-9.28	3.95	3.94	38.73	38.67	0.99	79.53
10.	Fruit pedicel length (cm)	4.75	2.10-6.01	0.50	0.40	14.87	13.38	0.80	24.79
11.	Fruit pedicel diameter (cm)	0.28	0.21-0.44	0.00	0.00	15.03	13.40	0.79	24.60
12.	No. of fruits plant ⁻¹	54.31	29.66-99.86	291.69	291.13	31.44	31.41	0.99	64.64
13.	Fruit yield/ plant(g)	276.14	59.10-759.52	25578.97	25319.47	57.91	57.62	0.99	118.09
14.	Fruit yield (q hec ⁻¹)	90.64	23.90-239.43	2608.53	2606.95	56.34	56.32	0.99	115.99
15.	Dry matter content (%)	79.58	61.54-86.07	25.52	25.44	6.34	6.33	0.99	13.03
16.	Vitamin C content at green stage (mg/100g)	133.00	43.86-201.16	2150.34	2149.88	34.86	34.86	0.99	71.80
17.	Capsaicin content (mg/g)	0.53	0.29-0.75	0.01	0.01	20.21	20.04	0.98	40.95
18.	Capsanthin content (ASTA units)	96.03	66.24-125.83	275.821	251.19	17.29	16.50	0.91	32.44
19.	Total phenol(mg/100g)	6.41	4.90-7.70	0.46	0.45	10.63	10.56	0.98	21.59
20.	Instrumental colour L*	41.18	35.22-50.11	12.53	12.05	8.59	8.43	0.96	17.03
21.	Instrumental colour a	36.82	30.78-45.26	13.38	8.82	9.93	8.06	0.65	13.49
22.	Instrumental colour b	15.84	14.34-18.58	1.03	0.85	6.41	5.83	0.82	10.93

Table-12: Genotypes with respect to yield and quality traits in chilli (*Capsicum annuum* L.) based on *per se* performance

S. No.	Traits	Best genotypes
1.	Plant height (cm)	SKAU-77 (86.00), SKAU-38 (81.33), SKAU-231 (80.73), SKAU-227 (79.73), SKAU-106 (79.46), SKAU-84 (79.20), SKAU-218 (74.20), SKAU-208 (73.20), SKAU-211 (72.73), SKAU-221 (72.06).
2.	Plant spread (cm)	SKAU-106 (86.64), SKAU-62 (85.58), SKAU-128 (85.18), SKAU-45 (84.04), SKAU-40 (82.93), SKAU-43 (82.91), SKAU-73 (81.96), SKAU-52 (81.10), SKAU-139 (78.49), SKAU-109 (74.59).
3.	Number of branches plant ⁻¹	SKAU-173 (48.93), SKAU-181 (47.53), SKAU-191 (46.40), SKAU-188 (46.00), SKAU-40 (45.93), KL-1 (45.53), SKAU-208 (45.06), SKAU-177 (44.86), SKAU-38 (44.66), SKAU-198 (42.06)
4.	Days to flower initiation	SKAU-237 (38.60), SKAU-247 (38.60), Arka Lohit (38.46), SKAU-233 (38.46), SKAU-231 (38.46), SKAU-243 (38.40), IC-561617 (38.00), KL-1 (37.93), IC-505242 (37.93), SKAU-62 (37.80)
5.	Days to fruit initiation	SKAU-198 (46.53), SKAU-173 (46.40), SKAU-208 (46.33), SKAU-211 (45.86), IC-391082 (45.73), SKAU-193 (45.73), SKAU-218 (45.66), SKAU-188 (45.66), SKAU-216 (45.60), SC-104 (45.60).
6.	Days to harvesting	SKAU-195 (134.66), SKAU-208 (134.66), SKAU-216 (134.66), SKAU-188 (134.66), SKAU-198 (134.60), SKAU-231 (131.46), SKAU-177 (130.80), KL-1 (130.53), IC-505242 (129.93), SKAU-193 (129.66)
7.	Fruit length (cm)	SKAU-198 (16.07), SKAU-195 (16.03), SKAU-148 (15.97), SKAU-221 (15.96), SKAU-216 (15.73), SKAU-77 (15.63), SKAU-38 (15.58), SKAU-208 (15.46), SKAU-43 (15.10), SKAU-191 (15.08).
8.	Fruit diameter (cm)	SKAU-141 (1.92), SKAU-221 (1.59), SKAU-38 (1.52), SKAU-193 (1.40), SKAU-233 (1.40), SKAU-148 (1.38), SKAU-32 (1.32), Arka Lohit (1.32), SKAU-216 (1.26), SKAU-73 (1.24).
9.	Fruit weight (g)	SKAU-141 (9.28), Arka Lohit (9.09), SKAU-216 (8.51), SKAU-193 (8.26), SKAU-148 (8.15), SKAU-38 (8.15), SKAU-198 (7.66), SKAU-73 (7.46), SKAU-208 (7.34), SKAU-43 (7.18).
10.	Fruit pedicel length (cm)	SKAU-141 (6.01), SKAU-211 (5.89), SKAU-38 (5.88), SKAU-148 (5.80), SKAU-52 (5.70), SKAU-233 (5.39), SKAU-111 (5.34), SKAU-96 (5.32), IC-561617 (5.31), SKAU-221 (5.25).
11.	Fruit pedicel diameter (cm)	Arka Lohit (0.44), SKAU-148 (0.40), SKAU-193 (0.35), SKAU-224 (0.35), SKAU-227 (0.34), SKAU-247 (0.33), SKAU-38 (0.33), SKAU-221 (0.33), SKAU-243 (0.33), SKAU-141 (0.33).
12.	No. of fruits plant ⁻¹	SKAU-188 (99.86), SKAU-193 (91.86), KL-1 (89.26), SKAU-224 (87.13), SKAU-221 (84.00), SKAU-195 (80.80), SKAU-173 (78.73), SKAU-191 (73.80), SKAU-198 (70.53), SKAU-148 (69.13).

13.	Fruit yield plant ⁻¹ (g)	SKAU-193(759.52), SKAU-173 (649.20), KL-1 (581.80), SKAU-195 (558.35), SKAU-188 (539.83), SKAU-198 (526.12), SKAU-221 (506.22), SKAU-216 (476.86), SKAU-208 (466.87), SKAU-247 (450.74).
14.	Fruit yield hectare ⁻¹ (q)	SKAU-193 (239.43), SKAU-173 (206.02), SKAU-163 (186.24), KL-1 (184.54), SKAU-195 (177.14), SKAU-188 (171.21), SKAU-198 (166.87), SKAU-221 (160.09), SKAU-216 (151.21), SKAU-208 (148.10).
15.	Dry matter content (%)	SKAU-237 (86.07), SKAU-52 (85.92), SKAU-167 (85.84), SKAU-160 (85.74), Local Kashmiri Chilli-1 (8.50), SKAU-163 (84.60), SC-104 (83.96), SKAU-233 (83.91), SKAU-132 (83.19), SKAU-141 (83.10).
16.	Vitamin C content at green stage (mg/100g)	SKAU-58 (201.16), SKAU-73 (199.76), SKAU-173 (196.28), SC-104 (196.10), SKAU-141 (195.01), SKAU-68 (193.44), SKAU-218 (193.44), Arka Lohit (192.59), SKAU-193 (192.28), SKAU-89 (191.98).
17.	Capsaicin content (mg/g)	SKAU-62 (0.75), SKAU-106 (0.75), SKAU-52 (0.73), SKAU-68 (0.71), SKAU-96 (0.71), SKAU-89 (0.70), SKAU-84 (0.64), SKAU-77 (0.63), SKAU-193 (0.63), SKAU-221 (0.63)
18.	Capsanthin content (ASTA) units	SKAU-198 (125.83), SKAU-227 (125.05), SKAU-193 (123.63), SKAU-106 (122.20), SC-1019 (120.49), SKAU-208 (119.29), SKAU-224 (118.76), SKAU-191 (117.30), SKAU-153 (116.52), SC-104 (115.60).
19.	Total phenol l(mg/100g)	SKAU-193 (7.70), SKAU-221 (7.46), SKAU-177 (7.46), SKAU-191 (7.43), SKAU-173 (7.20), IC-561617 (7.20), SKAU-188 (7.16), SKAU-181 (7.10), SKAU-96 (7.10).
20.	Instumental colour L*	SKAU-118 (50.11), SC-1019 (49.25), SKAU-122 (48.28), SKAU-45 (47.26), SC-104 (46.20), SKAU-195 (46.11), SKAU-111 (46.06), SKAU-58 (45.92), SKAU-52 (45.91), SKAU-32 (45.83).
21.	Instumental colour a	SKAU-118 (45.26), IC-505242 (43.66), SKAU-122 (43.32), SKAU-45 (42.25), SKAU-52 (41.26), SC-104 (41.20), SKAU-195 (41.10), SKAU-58 (40.79), SKAU-32 (40.78), SKAU-111 (40.66).
22.	Instumental colour b	SKAU-193 (18.58), SKAU-132 (17.89), SKAU-43 (17.77), SKAU-195 (17.70), SKAU-38 (17.45), Local Kashmiri Chilli-1 (17.12), SKAU-128 (17.06), SKAU-89 (17.00), SKAU-118 (16.83), SKAU-73 (16.79).

Table-13: Estimates of genotypic (above diagonal) correlation coefficients among different characters in chilli (*Capsicum annuum* L.)

S. No.	Parameters	Plant height (cm)	Plant spread (cm)	No. of branches per plant	Days to flower initiation	Days to fruit initiation	Days to harvesting	Fruit length (cm)	Fruit diameter (cm)	Fruit weight(g)	Fruit pedicel length (cm)	Fruit pedicel diameter (cm)	No. of fruits per plant	Fruit yield per plant(g)
1.	Plant height	1.00	0.292*	0.106	-0.084	-0.098	0.010	0.281*	0.139	0.212	0.209	0.263*	0.115	0.104
2.	Plant spread(cm)		1.00	0.035	-0.413**	-0.199	0.397**	-0.037	-0.147	-0.060	0.128	-0.092	-0.177	-0.174
3.	No. of branches per plant			1.00	0.279*	0.092	0.656**	0.338**	0.268*	0.402**	0.114	0.156	0.565**	0.588**
4.	Days to flower initiation				1.00	0.683**	0.571**	-0.028	-0.134	-0.065	-0.135	-0.013	0.367**	0.282*
5.	Days to fruit initiation					1.00	0.384**	-0.005	-0.142	-0.025	0.093	0.049	0.237	0.151
6.	Days to harvesting						1.00	0.354**	0.171	0.410**	-0.021	-0.016	0.486**	0.585**
7.	Fruit length(cm)							1.00	0.478**	0.757**	0.525**	0.341**	0.441**	0.646**
8.	Fruit diameter (cm)								1.00	0.767**	0.369*	0.570**	0.222	0.496**
9.	Fruit weight(g)									1.00	0.405**	0.277*	0.102	0.189
10.	Fruit pedicel length(cm)										1.00	0.001	0.197	0.336**
11.	Fruit pedicel diameter (cm)											1.00	0.352**	0.692**
12.	No. of fruits per plant												1.00	0.849**
13	Fruit yield per plant(g)													1.00

Table-14: Estimates of phenotypic (above diagonal) correlation coefficients among different characters in chilli (*Capsicum annuum* L.)

S. No.	Parameters	Plant height (cm)	Plant spread (cm)	No. of branches per plant	Days to flower initiation	Days to fruit initiation	Days to harvesting	Fruit length (cm)	Fruit diameter (cm)	Fruit weight(g)	Fruit pedicel length (cm)	Fruit pedicel diameter (cm)	No. of fruits per plant	Fruit yield per plant(g)
1.	Plant height	1.00	0.291*	0.107	-0.084	-0.098	0.009	0.277*	0.108	0.209	0.186	0.223	0.114	0.103
2.	Plant spread (cm)		1.00	0.035	-0.410**	-0.197	-0.396**	-0.035	-0.129	-0.060	0.109	-0.083	-0.177	-0.174
3.	No. of branches per plant			1.00	0.277*	0.091	0.655**	0.331**	0.219	0.400**	0.105	0.140	0.563**	0.587**
4.	Days to flower initiation				1.00	0.681**	0.570**	-0.026	-0.108	-0.064	-0.126	-0.008	0.366**	0.281*
5.	Days to fruit initiation					1.00	0.383**	-0.005	-0.124	-0.025	-0.082	0.051	0.237	0.151
6.	Days to harvesting						1.00	0.348**	0.140	0.409**	-0.019	-0.014	0.486**	0.584**
7.	Fruit length(cm)							1.00	0.419**	0.744**	0.460**	0.301*	0.434**	0.635**
8.	Fruit diameter (cm)								1.00	0.635**	0.286*	0.378**	0.182	0.407**
9.	Fruit weight(g)									1.00	0.501**	0.233	0.092	0.170
10.	Fruit pedicel length(cm)										1.00	0.001	0.173	0.300*
11.	Fruit pedicel diameter (cm)											1.00	0.351**	0.691**
12.	No. of fruits per plant												1.00	0.848**
13	Fruit yield per plant(g)													1.00

*, **=Significant at 5% and 1% respectively.

4.13 Genetic divergence

Analysis of variance for dispersion revealed that the genotypes expressed significant variability for various traits under study. Genetic divergence was estimated for sixty genotypes of chilli.

Based upon the performance of genotypes, 60 chilli genotypes were grouped into four clusters (Table 15) as per Mahalanobis D^2 analysis employing Tochers method (Rao, 1952). The cluster diagram and dendrogram indicated that the maximum number of genotypes fall in cluster II (25) followed by cluster I (20), cluster III (14) and cluster IV (1). Cluster I consisted of SKAU-233, IC-391082, SKAU-231, IC-561617, IC-505242, SC-1019, SKAU-227, SKAU-211, SKAU-247, SKAU-243, SKAU-208, SKAU-216, SKAU-224, SKAU-198, SKAU-218, Arka Lohit, SKAU-195, SC-104, SKAU-188, and KL-1 genotypes. The genotypes SKAU-177, SKAU-191, SKAU-181, SKAU-237, SKAU-221, SKAU-111, SKAU-80, SKAU-122, SKAU-132, SKAU-52, SKAU-109, SKAU-118, SKAU-139, SKAU-43, SKAU-45, SKAU-40, SKAU-157, SKAU-62, SKAU-153, SKAU-106, SKAU-96, SKAU-84, Local Kashmiri Chilli-1, SKAU-38 and SKAU-167 fell in cluster II. In cluster III, the genotypes were SKAU-173, SKAU-193, SKAU-148, SKAU-141, SKAU-58, SKAU-73, SKAU-128, SKAU-68, SKAU-89, SKAU-77, SKAU-32, SKAU-91, SKAU-160, SKAU-32 while SKAU-163 was included in Cluster IV.

The average intra and inter cluster distance (D^2) values (Table 16) revealed that cluster III had the highest intra cluster distance (D^2) value of 5177.30 followed by cluster II (4846.87) and cluster I (3419.32). The inter cluster distance D^2 values was highest between cluster II and cluster III (14621.56) followed by cluster I and II (12246), cluster II and cluster IV (11888.38), cluster III and cluster IV (9139.45), cluster I and cluster IV (8815.51), and cluster I and cluster III (8372.23).

Cluster means for different characters (Table 17) revealed that cluster I having genotypes (20), the average plant height and plant spread was 66.03cm and 60.67 cm respectively. The average number of branches plant⁻¹ were 39.65. It took 37.48 days to flower initiation, 52.28 days to fruit initiation and 129.92 days to harvesting. The average fruit length was 12.80 cm average fruit diameter was 1.10 cm average fruit weight was 5.78 g, average fruit pedicel length was 4.74 cm, average fruit pedicel diameter of 0.29 cm, number of fruits plant⁻¹ was 62.61 with an average fruit yield plant⁻¹ was 358.16 g. The mean of the traits in cluster II having maximum genotypes (25) were 61.23cm for plant height, 67.16 cm for plant spread, 32.19 for number of branches plant⁻¹, 33.47 for days to flower initiation, 42.84 for days to fruit initiation, 111.09 for days to harvesting, 11.84 cm for fruit length, 1.04 cm for fruit diameter, 4.40 g for average fruit weight, 4.73 cm for fruit pedicel length, 0.28 cm for fruit pedicel diameter, 49.18 for number of fruits plant⁻¹ and 211.83 g for fruit yield plant⁻¹.

Cluster III consisting of 14 genotypes possessed an average of 65.02cm for plant height, 64.95cm for plant spread, 30.45 for number of branches, 33.10 for days to flower initiation, 42.95 for days to fruit initiation, 42.95 for days to harvesting, 12.39 cm for fruit length, 1.15 cm for fruit diameter. The genotypes possessed an average fruit weight of 5.66 g, 4.89 fruit pedicel length, 0.30 fruit pedicel diameter, 53.35 number of fruits plant⁻¹ with an average fruit yield plant⁻¹ of 289.34 g.

Cluster IV constituted of only one genotype with a mean of traits as 68.67 cm for plant height, 52.07 cm for plant spread, 20.73 for number of branches plant⁻¹, 37.13 for days to flower initiation, 45.47 for days to fruit initiation, 109.47 for days to harvesting, 11.01 cm for fruit length, 1.05cm for fruit diameter, 3.19 g for average fruit weight, 4.03 for fruit pedicel length, 0.28 for fruit pedicel diameter, 30.53 for number of fruits plant⁻¹ and 59.11g for fruit yield plant⁻¹.

The per cent contributions of the traits towards total genetic divergence (Table 18) revealed that fruit yield (q ha^{-1}) was the main factor contributing to divergence accounting for 51.64% followed by number of fruits plant^{-1} (26.67%), vitamin C (12.43%), dry matter (2.49%), days to flower initiation (1.92%), days to harvesting (1.64%), number of branches plant^{-1} (1.41%) and fruit weight (1.24%). The minimum contribution towards divergence was from Capsaicin (0.06%) followed by total phenol (0.06%), plant height (0.17%) and plant spread (0.28%).

Table-15: Distribution of chilli (*Capsicum annuum* L.) genotypes into different clusters based on D² statistics

Cluster number	No. of genotypes	Genotypes
I	20	SKAU-233, IC-391082, SKAU-231, IC-561617, IC-505242, SC-1019, SKAU-227, SKAU-211, SKAU-247, SKAU-243, SKAU-208, SKAU-216, SKAU-224, SKAU-198, SKAU-218, Arka Lohit, SKAU-195, SC-104, SKAU-188, KL-1.
II	25	SKAU-177, SKAU-191, SKAU-181, SKAU-237, SKAU-221, SKAU-111, SKAU-80, SKAU-122, SKAU-132, SKAU-52, SKAU-109, SKAU-118, SC SKAU-139, SKAU-43, SKAU-45, SKAU-40, SKAU-157, SKAU-62, SKAU-153, SKAU-106, SKAU-96, SKAU-84, Local Kashmiri Chilli-1, SKAU-38, SKAU-167.
III	14	SKAU-173, SKAU-193, SKAU-148, SKAU-141, SKAU-58, SKAU-73, SKAU-128, SKAU-68, SKAU-89, SKAU-77, SKAU-32, SKAU-91, SKAU-160, SKAU-36.
IV	1	SKAU-163.

Table -16: Average intra-cluster (Diagonal) and inter-cluster (Above Diagonal) distance values in chilli (*Capsicum annuum* L.)

S. No.	Cluster	I	II	III	IV
1	I	3419.32	12246	8372.23	8815.51
2	II		4846.87	14621.56	11888.38
3	III			5177.30	9139.45
4	IV				0.00

Table -17: Clusters means for various characters in chilli (*Capsicum annum* L.) genotypes

Clusters	Plant height (cm)	Plant spread (cm)	No. of branches plant ⁻¹	Days to flower initiation	Days to fruit initiation	Days to harvesting	Fruit length (cm)	Fruit diameter (cm)	Fruit weight (g)	Fruit pedicel length (cm)	Fruit pedicel diameter (cm)	No. of fruits plant ⁻¹	Fruit yield plant ⁻¹ (g)
I	66.03	60.67	39.65	37.48	52.28	129.92	12.80	1.10	5.78	4.74	0.29	62.61	358.16
II	61.23	67.16	32.19	33.47	42.84	111.09	11.84	1.04	4.40	4.73	0.28	49.18	211.83
III	65.02	64.95	30.45	33.10	42.95	110.76	12.39	1.15	5.66	4.89	0.30	53.35	289.34
IV	68.67	52.07	20.73	37.13	45.47	109.47	11.01	1.05	3.19	4.03	0.28	30.53	59.11

Table-18: Per cent contribution of individual traits towards total genetic divergence in chilli (*Capsicum annuum* L.).

S. No.	Characters	Per cent contribution
1.	Plant height(cm)	0.17%
2.	Fruit weight(g)	1.24%
3.	No. of fruits/plant	26.67%
4.	Plant spread(cm)	0.28%
5.	Days to flower initiation	1.92%
6.	Fruit yield(q/hac)	51.64%
7.	Days to harvesting	1.64%
8.	No. of branches/plant	1.41%
9.	Dry matter(%)	2.49%
10.	Vitamin C(mg/100g)	12.43%
11.	Capsaicin(mg/g)	0.06%
12.	Total phenol(mg/100g)	0.06%
Total		100.00

Chapter – 5

DISCUSSION

Wilt is one of the important disease of chilli crop, occurring in both temperate and warmer regions of the world. The disease has been reported to cause 10-50 per cent losses around the world and 10-80 per cent in India (Thoyajashi *et al.*, 2018). The occurrence of the disease has been reported from different parts of the world (Fernandez, 1983; Sarhan and Sharif, 1986; Camino *et al.*, 1987; Khan *et al.*, 1979; Vidhyasakaran and Thiagarajan, 1981; Srivastava and Diwakar, 1987; Moens and Benaicha, 1990; Jyothi *et al.*, 1993; Kaur, 1993; Dar and Mir, 1995; Chatterjee *et al.*, 1997; Singh and Singh, 1998; Najar, 2001). Host plant resistance has been a choice in all crop improvement programmes and is perhaps the best method available to tackle the soil borne diseases in particular. *Fusarium* wilt is a typical soil borne disease which can be mitigated appropriately by the use of disease resistant cultivars. Further the use of resistant variety will go a long way not only in reducing loss due to disease but also in avoiding fungicidal toxicity likely to occur due to their application (Tembhurne *et al.*, 2017).

The fungi associated with chilli wilt was isolated from diseased plants by tissue bit technique and further purified by single spore technique. Isolation from the stem portion of chilli plants with typical symptoms of wilt disease revealed the presence of *Fusarium solani* as the pathogen of the disease. On PDA medium, *Fusarium solani* formed white fluffy or cottony colonies which later turned creamy white with yellowish pigmentation. The colonies attained a growth of 90 mm within 7 days of incubation at 25±1°C. The microscope observations of the fungus revealed the presence of septate, smooth, branched and slendrical mycelium. Microconidia were cylindrical to oval shaped and macroconidia were sickle-shaped, slightly curved at apex. Chlamydospores were intercalary, produced singly or in chains, globose and hyaline. On the basis of morphological and pathological characteristics and comparison with authentic descriptions the pathogen was identified as *Fusarium solani*. The *F. solani* as causal organism of

wilt disease has also been reported earlier by various workers (Hafizi *et al.*, 2014, Patil *et al.*, 2014. Gogoi *et al.*, 2017).

The fungal pathogen isolated from wilted chilli plants, when artificially inoculated through rhizosphere inoculation technique on potted chilli plants produced typical disease symptoms. Re-isolation of pathogen from the artificially inoculated and infected plants confirmed postulates of Koch. The initial disease symptoms of *F. solani* inoculated seedlings as yellowing and wilting in younger leaflets, epinasty, stunting and yellowing of older leaves, clinging to the plant of dried leaves, brown vascular discoloration of collar portion. The present observations on symptomatological development of chilli plants due to *F. solani* infection are more or less in agreement with those reported by Tembhurne *et al.* 2017 and Thoyajakshi Bai *et al.* 2018.

One hundred seven genotypes were screened under field conditions against wilt disease followed by screening of immune, resistant, moderately resistant genotypes under artificially inoculated controlled conditions. Among the genotypes screened under field conditions, one was categorized as immune, twenty two as resistant, twenty eight as moderately resistant totalling fifty one genotypes and fifty six as susceptible and highly susceptible based on the scale given by Kesavan and Chaudary (1977). Of these fifty one immune, resistant and moderately resistant genotypes screened under controlled conditions only one genotype was found immune, twenty one were found resistant, seventeen were found moderately resistant and twelve showed susceptible reaction. Similar efforts have been made earlier to identify chilli germplasm with varied levels of resistance by (Jabeena *et al.*, 2009, Tembhurne *et al.*, 2017, Singh *et al.*, 2017, Shoba *et al.*, 2018).

In the present study the ITS amplification with genera and species specific ITS primers, clearly identified *Fusarium solani*, based on amplification and size of amplicons which were identified with ITS primer combination viz., K-Lab-FusOxy-ITS1F2 and K-Lab-FusOxy-ITS4R2. The primers directed the

amplification of 523bp ITS rRNA uniform amplicons in *Fusarium solani*. The present result was also in conformity with other workers (Larena *et al.*, 1999, Arif *et al.*, 2013, Datta and Lal., 2013).

The immediate and long term objective of plant breeding is to increase the productivity or yield to the requirements of consumer. Crop improvement largely depends on the existence of variability and its exploitation by the plant breeder. For this plant breeder needs to identify sources of favourable genes, incorporate them into breeding populations/lines and select for a combination of desirable traits that might result in the isolation of productive genotypes. To achieve these goals, plant breeder needs to know the extent of variability of different traits present in a population. Effective evaluation and identification of potentially useful germplasm forms the first and foremost step in a crop improvement programme. The high yielding genotypes with good adaptation and desirable attributes could be directly utilized for general massive hybridization programme. This improvement in any crop is based on the extent of genetic variation and magnitude of available beneficial genetic variability. The proportion of genotypic, environmental variance and their interaction ($G \times E$), can be determined by employing useful biometrical and genetical methods. Some of these parameters include genotypic (GCV) and phenotypic (PCV) coefficients of variation. High value of these coefficients indicates wider diversity. Similarly narrow differences between GCV and PCV reveals low sensitivity to the environmental effects. Another indicator of variability is heritability, which is the ratio of genetic variance to total variance. Broad sense heritability gives an idea about that portion of observed variability which is attributable to genetic differences. Heritability is a component in the computation of expected progress which is most meaningful when accompanied by genetic gain. Genetic gain would be less in cases where the non-additive genetic variance is more than additive genetic variance (Lush, 1949). Genotypic, phenotypic and environmental correlations reveal the degree of association between different characters.

5.1 DUS characterization of chilli genotypes

DUS characterization of chilli genotypes was attempted as per DUS test guidelines of PPV & FR Authority. The genotypes were characterized for forty two scorable traits. Plant habit exhibited a wide range that varied from semi-upright, spreading, upright and erect and forty three genotypes semi-upright, fourteen genotypes spreading and three genotypes exhibited upright growth habit. Length of main stem exhibited a wide range from long, medium and small and twenty two genotypes long, twenty genotypes medium and eighteen genotypes exhibited small length of main stem. Length of first internode exhibited a wide range from medium, short, long and very short and twenty seven genotypes medium, seventeen genotypes short, thirteen genotypes long and three genotypes exhibited very short length of first internode. Anthocyanin colouration of nodes was present in fifty six genotypes and absent in four genotypes. Intensity of anthocyanin colouration exhibited a wide range from weak, medium and strong and twenty seven genotypes weak, twenty one genotypes medium and twelve genotypes exhibited strong intensity of anthocyanin colouration of nodes. Plant height was medium in sixty genotypes. Plant spread was medium in fifty six genotypes and four genotypes exhibited narrow plant spread. Stem pubescence was present in fifty six genotypes and absent in four genotypes. Intensity of stem pubescence was sparse in sixty genotypes. Stem shape was round in sixty genotypes. Length and width of leaf blade was long and broad respectively in sixty genotypes. Leaf colour ranged from green to green with purple tinge and fifty four genotypes showed green and six genotypes showed green with purple tinge. Intensity of green colour was medium in thirty five genotypes, light in seventeen genotypes and dark in eight genotypes. Intensity of purple colour was light in fifty four genotypes and medium in six genotypes. Leaf shape was lanceolate in forty seven genotypes, ovate in nine genotypes and broad elliptic in four genotypes. Leaf undulation of margin exhibited a wide range from weak, medium and strong and forty five genotypes showed weak, thirteen genotypes

medium, and two genotypes showed strong undulations of margins. Leaf pubescence was present in fifty five genotypes, absent in five genotypes and intensity of leaf pubescence was sparse in sixty genotypes. Flower petal colour was white and anther colour was pale blue in sixty genotypes. Days to 50% flowering ranged from medium to late and thirty four genotypes medium and twenty six genotypes exhibited late days to 50% flowering. Fruit orientation was drooping in fifty eight with semi-drooping in two. Fruit bearing habit was solitary in sixty genotypes. Fruit colour (at mature unripe stage) was green in sixty genotypes and fruit intensity of colour (at mature unripe stage) was dark in twenty two and medium in eighteen genotypes. Fruit length was long in sixty genotypes and fruit diameter was medium in fifty eight genotypes and two genotypes had broad fruit length. Fruit curvature was present in fifty four genotypes and absent in six genotypes and fruit curvature intensity was low in fifty four genotypes and medium in six genotypes. Fruit neck at basal end was absent in forty genotypes and present in twenty genotypes.

Fruit situation of pericarp was medium in thirty four genotypes, weak in twenty five genotypes and strong in one genotype. Fruit texture of surface was smooth in thirty five genotypes, slightly rough in twenty three genotypes and rough in two genotypes. Fruit colour was red and intensity of colour was medium in sixty genotypes. Fruit shape at base was acute in fifty two genotypes, round in eight genotypes and fruit shape at apex was acute in fifty nine genotypes and blunt in one genotype. Fifty five genotypes showed enveloping calyx cover and five genotypes had non-enveloping. Fifty seven genotypes had dented calyx margin and three had smooth calyx margin. Calyx constriction was absent in forty nine genotypes and was present in eleven genotypes. Pedicel attachment was weak in thirty three genotypes and strong attachment in twenty six genotypes. Fruit blossom end appendage was present in thirty genotypes and was absent in thirty genotypes. These findings are in conformity with those obtained by Datta and Das (2013), Hasan *et al.* (2014), Zhani *et al.* (2015), Padma *et al.* (2017), Ain (2018).

5.2 Mean performance of genotypes

In this study, chilli genotypes showed wide range of variability for most of the morphological, growth and fruit characters. The estimates of mean values from Table 5 revealed that no genotype was superior for all the characters under study. However SKAU-77 (86.00), SKAU-38 (81.33), SKAU-231 (80.73), SKAU-227 (79.73) were superior for plant height, SKAU-106 (86.64), followed by SKAU-62 (85.58) and SKAU-128 (85.18) for plant spread; SKAU-173 (48.93) followed by SKAU-181 (47.53) and SKAU-191 (46.40) for number of branches plant⁻¹; SKAU-237 (38.60) followed by SKAU-247 (38.60) and Arka Lohit (38.46) for days to flower initiation; SKAU-198 (46.53) followed by SKAU-173 (46.40) and SKAU-208 (46.33) for days to fruit initiation; SKAU-195 (134.66) followed by SKAU-208 (134.66) and SKAU-216 (134.66) for days to harvesting. For fruit length; SKAU-198 (16.07) recorded maximum fruit length followed by SKAU-195 (16.03) and SKAU-148 (15.97). For fruit diameter; SKAU-141 (1.92) recorded maximum fruit diameter followed by SKAU-221 (1.59) and SKAU-38 (1.52). For fruit weight; SKAU-141 (9.28) recorded maximum fruit weight followed by Arka Lohit (9.09) and SKAU-216 (8.51). For fruit pedicel length; SKAU-141 (6.01) recorded maximum fruit pedicel length followed by SKAU-211(5.89) and SKAU-38 (5.88), for fruit pedicel diameter; Arka Lohit (0.44) followed by SKAU-148 (0.40) and SKAU-193 (0.35), for number of fruits plant⁻¹; SKAU-188 (99.86) followed by SKAU-193 (91.86) and KL-1 (89.26). For fruit yield per hectare; SKAU-193 (239.43) followed by SKAU-173 (206.02) and SKAU-163 (186.24), for dry matter content; SKAU-237(86.07) followed by SKAU-52 (85.92) and SKAU-167 (85.84) were found superior. In case of quality parameters the highest vitamin C content was recorded in SKAU-58 (201.16 mg100g⁻¹) followed by SKAU-73(199.76 mg100g⁻¹) and SKAU-173 (196.28 mg100g⁻¹). Highest capsaicin content was recorded in SKAU-62 (0.75 mg g⁻¹) followed by SKAU-106 (0.75 mg g⁻¹) and SKAU-52 (0.73 mg g⁻¹). Highest capsanthin content was recorded in SKAU-198 (125.83 units) followed by

SKAU-227 (125.05 units) and SKAU-193(123.63 units) for capsanthin content. Highest phenol content was recorded in SKAU-193(7.70) followed by SKAU-221 (7.46) and SKAU-177 (7.46). Highest instrumental colour L* was recorded in SKAU-118 (50.11) followed by SC-1019(49.25) and SKAU-122 (48.28), SKAU-118(45.26) followed by IC-505242 (43.66) and SKAU-122 (43.32) for instrumental colour a, SKAU-193 (18.58), SKAU-132 (17.89), SKAU-43 (17.77) for instrumental colour b.

An overall perusal of Table 5 on performance of genotypes revealed that none of the genotypes exhibited superior performance for all the traits however, certain genotypes exhibited superior performance for some economically important traits viz., SKAU-193 was superior for fruit weight, fruit pedicel diameter, number of fruits plant⁻¹, fruit yield plant⁻¹, capsanthin content, total phenol and instrumental colour b, SKAU-38 for plant height, fruit diameter, fruit pedicel length and fruit pedicel diameter while SKAU-141 for fruit diameter, fruit weight, fruit pedicel length and fruit pedicel diameter.

Since no genotype could be identified to have superior performance for all the characters, the genotype with maximum good characteristics could be used in a well planned hybridization programme to select superior performing lines in the successive segregating lines.

5.3 Genetic variability, heritability and genetic gain (as per cent of mean)

The range in the values reflect the amount of phenotypic variability, which is not very reliable since it includes genotypic, environmental and genotype × environmental interaction components and does not reveal as to which character is showing higher degree of genetic variability. The phenotype of crop is influenced by additive gene effect (heritable), dominance (non-heritable), epistasis (no allelic interaction) and genotype x environment interaction. Hence, it becomes necessary to split the observed variability into phenotypic coefficient of variation and

genotypic coefficient of variation, which ultimately indicates the extent of genetic variability existing for various traits.

The analysis of variance revealed that all the twenty two quantitative and quality characters exhibited highly significant differences among the genotypes (Table 6). The estimates of phenotypic and genotypic coefficients of variation of all the characters studied are presented in (Table 9 & Table 10). In general the phenotypic and genotypic coefficients of variation were almost similar with slightly higher phenotypic coefficients of variation than the corresponding genotypic coefficient of variation, which indicates the role of environment in the expression of traits under observation. This was in agreement with the study of Farhad *et al.* (2008), Jyothi *et al.* (2008), Patel *et al.* (2009), Gupta *et al.* (2009), Chattopadhyay *et al.* (2011), Zehra (2014), Janaki *et al.* (2015), Pandiyaraj *et al.* (2017) Jogi *et al.* (2017), Ain (2018).

It is evident from the data presented in Table 7 that average fruit yield hectare⁻¹ (56.34, 56.32), number of fruits plant⁻¹ (31.44, 31.41), fruit length (20.49 and 20.16), fruit diameter (20.37, 16.82), fruit weight (38.73, 38.67), number of branches plant⁻¹ (25.35, 25.32), recorded high phenotypic and genotypic coefficients of variation, indicating that genotypes had broad genetic base for these characters. Similar results were obtained by Singh *et al.* (2009), Sarkar *et al.* (2009) for fruit length, Patel *et al.* (2009), Singh *et al.* (2009), Sarkar *et al.* (2009), Padhar and zaveri (2010), Basavaraja *et al.* (2012) and Zehra (2014), Janaki *et al.* (2015), Ain (2018) for number of fruits plant⁻¹ and fruit yield per plant and Sarkar *et al.* (2009) for plant height. Rest of the traits such as days to flower initiation (11.21 and 11.20%), days to fruit initiation (7.28, 7.27), days to harvesting (9.77, 9.76), fruit pedicel length (14.87, 13.38), fruit pedicel diameter (15.03, 13.40), dry matter content (17.34, 17.35), plant height (13.88, 13.79), plant spread (15.73, 15.67) exhibited low phenotypic and genotypic coefficients of variation. Thus these characters were less amenable for improvement through selection. This was in conformity with findings of Singh *et al.* (2009), Diwakar *et al.* (2012) and

Zehra (2014). Among quality parameters Vitamin C content (34.89, 34.86), capsanthin content (17.29, 16.50), capsaicin content (20.21, 20.04) recorded high phenotypic and genotypic coefficients of variation, indicating that genotypes under study have broad genetic base for these characters as well. Similar results were obtained by Datta and Jana (2010), Zehra (2014), Pandiyaraj *et al.* (2017) and Ain (2018) while total phenol (10.63, 10.56), Instrumental colour L*(8.59, 8.43), Instrumental colour a (9.93, 8.06) and Instrumental colour b (6.41, 5.83) low phenotypic and genotypic coefficient of variation, thus less amenable for improvement through selection.

The characters which possessed moderate to high coefficients of variation suggested that there is better potential for improvement through selection. A wide range of variability, high estimates of phenotypic and genotypic coefficients of variation further, along with high GCV and PCV ratio indicate that these attributes would respond to selection.

Even phenotypic and genotypic coefficients of variation does not give a true picture about the extent of inheritance of the character. Therefore, the heritability of a character can be relied upon, as it enables the breeder to decide the extent of selection pressure to be applied under a particular environment, which separates out the environmental influence from the total variability. The estimation of heritability has a greater role to play in determining the effectiveness of selection of a character provided it is considered in conjunction with the predicated genetic gain as suggested by Panse and Sukhatme (1957) and Johnson *et al.* (1955) as the heritability is influenced by bio-metrical method, generation of hybrid, sample size of experimental material and environment. Furthermore the progress in selection is also directly proportional to the amount of genetic gain. Therefore, the effect of selection is realized more quickly in those characters which have high heritability as well as high genetic gain. The relative amount of heritable portion of variation was, therefore, estimated with the help of heritability estimates and genetic gain.

When high heritability is accompanied by high GAM, it indicates additive gene effects and selection may be effective. High heritability with low GAM indicates predominance of non-additive gene action where high heritability is exhibited due to favourable influence of environment rather than genotype and the selection for such traits may not be rewarding. Low heritability with high GAM is governed by additive gene effects in which low heritability is exhibited due to favourable environmental effects and the selection may be effective in such cases. Low heritability coupled with low GAM indicates that character is highly influenced by environmental effects and selection would be ineffective.

Heritability (b.s.) estimates were high for almost all the characters and ranged from 65 to 100 per cent indicating that the characters were less influenced by environmental effects and the characters are effectively transmitted to the progeny, suggesting major role of genetic constitution in the expression of a character and thus selection based on phenotypic expression could be relied upon. Similar results were observed by Ain (2018). High heritability was observed for number of fruits plant⁻¹, fruit length, fruit diameter, fruit weight, number of fruits plant, and fruit yield plant⁻¹. This is in accordance with the findings of Smitha and Basavaraja (2006), Johari and Kumar (2007); Sarkar *et al.* (2009) for number of fruits plant⁻¹, number of branches plant⁻¹, plant height, length of fruit and fruit yield plant⁻¹, Ibrahim *et al.* (2001); Rathod *et al.* (2002), Smitha and Basavaraja (2006), Krishna *et al.* (2007), Janaki *et al.* (2015), Chakarbarty *et al.* (2017) for number of fruits plant⁻¹ and plant height and Zehra (2014), Ain (2018) for number of fruits plant⁻¹, fruit length, fruit diameter, fruit weight, number of fruits plant, and fruit yield plant⁻¹; Jogi *et al.* (2017) for plant spread. High heritability values for these traits indicates that variation observed was mainly under genetic control and was less influenced by environment.

Among quality characters, high heritability estimates were recorded for vitamin C content, capsaicin content, capsanthin content and total phenol while

moderate heritability estimate recorded for fruit diameter. This is consistent with the reports of Ain (2018).

High estimate of heritability along with genetic gain (per cent of mean) is more reliable than heritability alone for predicting the effect of selection (Johnson *et al.*, 1955). The characters *viz.*, plant height, plant spread, number of branches plant⁻¹, fruit length, fruit weight, number of fruits plant⁻¹, fruit yield plant⁻¹, vitamin C content at green stage, capsaicin content, capsanthin content, days to flower initiation, showed high estimates of heritability coupled with high genetic gain as per cent of mean (GAM), indicating the preponderance of additive gene action in control of these traits. This suggests that real progress in improvement of such traits through selection could be realized. These results are in conformity with several workers *viz.*, Smitha and Basavaraja (2006) for days to flower initiation; Johnson *et al.* (1955) and Arya and Saini (1977); Berjees (2012); Jogi *et al.* (2017) for number of fruits plant⁻¹, fruit weight, fruit length and fruit yield plant⁻¹; Munshi and Behera (2000); Manju and Sreelathkumary (2004) for vitamin C and capsaicin content; Chattopadhyay *et al.* (2011) for vitamin C.

Fruit yield is an important character, which decides the commercial viability of the hybrid/variety. Thus the trait deserves the highest priority in any breeding programme. High heritability along with high genetic gain as per cent of mean for this trait suggested the possibility of selecting high yielding cultivars from the present collection. This was supported by Patel *et al.* 2009; Sharma *et al.* 2010; Singh and and Surya *et al.* 2014.

5.4 Correlation coefficients

Yield is an ultimate criterion which a plant breeder has always to keep in view for evolving improved cultivars of any crop. However, yield is a polygenic character and highly influenced by environment. Knowledge of the association of quantitative characters specifically for yield and its attributes is of immense practical value during selection. Variability studies provide information on the

extent of improvement possible in different characters, but they do not throw light on the extent and nature of relationship existing between various contributing characters and economically important characters. Hence, a knowledge regarding association of various characters among themselves and with economic character is necessary for making indirect selection for improvement of economical characters. Correlation studies pave way to know the association prevailing between highly heritable characters with most economic characters and gives better understanding of the contribution of each trait in building up the genetic make up of the crop. The phenotypic correlations indicate the extent of the observed relationship between two characters. This does not give true genetic picture of the relationship because it indicates both heritability as well as environmental influences. Genotypic correlations provide an estimate of inherent association between genes controlling any two characters. Hence, it is of greater significance and could be effectively utilized in formulating an effective selection scheme. Perusal of Table-9 and Table-10 indicated that in the present investigation, the estimates of genotypic correlation were in general slightly higher than phenotypic correlation showing that masking effects of the environment was little indicating the presence of inherent association between various characters. In all instances, however, more reliance may be placed on the genotypic correlations. The nature of genotypic correlation was more or less similar to phenotypic correlation under study. Similar results were reported by Mathew *et al.* (2004), Patel *et al.* (2015), Jogi *et al.* (2017).

The economically important trait i.e., fruit yield plant⁻¹ exhibited significant and positive association with plant height, number of branches plant⁻¹, days to flower initiation, days to fruit initiation, days to harvesting, fruit diameter, fruit weight, fruit length, fruit pedicel length, fruit pedicel diameter, number of fruits plant⁻¹, at both phenotypic and genotypic levels, which suggested that rational improvement in yield is possible through simultaneous selection for these component characters. Moreover this trait showed positive and non-significant

association with plant height, days to fruit initiation and fruit weight and negative non-significant association with plant spread, which clearly indicated the independent nature of these characters and selection for fruit yield based on these is not reliable. These results are in confirmation with findings of Tembhurne *et al.* (2008) and Kumari *et al.* (2011). Fruit length showed significant and positive correlation with plant height, number of branches plant⁻¹, days to harvesting at both phenotypic and genotypic levels indicating that simultaneous improvement of these traits is possible. These results are in conformity with earlier observations of Farhad *et al.* (2008), Gupta *et al.* (2009), Jabeen *et al.* (2009), Patel *et al.* (2009), Singh *et al.* (2009), Padhar and Zaveri (2010), Singh and Singh (2011), Lahbib *et al.* (2012), Bijalwan *et al.* (2014). Similarly, fruit weight showed significant positive correlation with fruit length, fruit diameter, number of branches plant⁻¹ and days to harvesting, however, it showed non-significant negative association with plant spread, days to flower initiation and days to fruit initiation. The number of fruits plant⁻¹ exhibited positive significant correlation with number of branches plant, days to flower initiation, fruit length and fruit pedicel diameter. This was in agreement with the study of Zehra (2014), Patel *et al.*, (2015).

5.5 Genetic diversity

As an initial step to develop high yielding and superior quality chilli varieties for cultivation under temperate conditions of Kashmir valley, it is imperative to evaluate a large number of existing genotypes. These genotypes must have been selected on the basis of their *per se* performance from diverse sources. Superior genotypes are selected and used as parents in hybridization programmes. However, the selection of superior parents from a large number of genotypes is a difficult task to perform. Genetic divergence analysis among genotypes is helpful to screen the genetically diverse parents that are likely to produce high heterotic effects among crosses and also generate large spectrum of variability during segregation and recombination of genes at heterozygous

polygenic blocks. Multivariate technique using D^2 statistics (Mahalanobis, 1928) is a powerful tool in quantifying the degree of divergence among the genotypes. This would help to identify putative parents for executing an effective breeding strategy to obtain high heterotic response and transgressive segregants. Estimation of genetic divergence helps in reducing the large data of genotypes to manageable proportions. It is assumed that the parents showing wide genetic divergence are best suited for being used in the hybridization programme. In the process of formulating the chilli improvement programme through hybridization and creating variability for the improvement of yield and other desirable traits, it is essential to understand the nature and degree of genetic divergence present in the available germplasm.

The utility of multivariate analysis in quantifying the degree of divergence between populations so as to understand the trend of their evolutionary pattern and assess the relative contribution of different components to the total divergence together with the nature of forces operating at intra and inter cluster levels had greatly been emphasized (Murty and Qadri, 1966; Anand and Murty, 1968; Mishra *et al.*, 1994).

In the present study, 60 genotypes of chilli were evaluated to estimate the genetic divergence for identification of potential parents using Mahalanobis D^2 statistics. Analysis of variance for divergence revealed that the value of V-statistic were significant indicating substantial genetic diversity in the material.

The genotypes were grouped in to four clusters. Cluster II had the highest number of genotypes (25) followed by cluster I (20), cluster III (14) and cluster IV (1) (Table 11).

In chilli, utility of multivariate analysis in selecting genetically divergent parents for successful hybridization has been discussed by Karad *et al.* (2002), Manju and Sreelathakumary (2004), Hasanuzzaman and Golam (2011), Pujar *et al.* (2017). Intracluster distance (D^2) was maximum in cluster III (5177.30),

followed by the cluster II (4846.87) and cluster I (3419.32). The intercluster distance (D^2) was maximum between the cluster II and III (14621.56) followed by cluster I and II (12246), cluster II and IV (11888.38), cluster III and IV (9139.45), cluster I and IV (8815.51) and cluster I and cluster III (8372.23) (Table 12). The maximum intra cluster distance (D^2) (cluster III) indicated high heterogeneity in genetic constitution of genotypes in that cluster while minimum intra cluster distance (D^2) (cluster I) indicated homogeneity in genetic constitution of genotypes in that cluster. Similarly the high value of intercluster distance (cluster II and III) indicated also more heterogeneous genetic constitution of genotypes included in both clusters. In contrast, minimum intercluster distance (cluster I and III) indicated closer relationship among the genotypes included (Farhad *et al.*, 2010; Pujar *et al.*, 2017).

The per cent contribution (Table-14) of traits towards the total genetic divergence revealed that the fruit yield (q ha^{-1}) was the main factor contributing to divergence in the present study, accounting for about 51.64 per cent contribution, followed by number of fruits plant^{-1} (26.67 %), vitamin C (12.43 %), dry matter content (2.49 %), days to flower initiation (1.92 %), days to harvesting (1.64 %), number of branches plant^{-1} (1.41%), fruit weight (1.24%), plant spread (0.28 %), plant height (0.17 %), capsaicin and total phenol (0.06 %).

The traits contributing maximum towards the divergence should be given great emphasis for deciding the clusters to be chosen for hybridisation and the subsequent selection of the parents from the clusters be based on their *per se* performance. In chilli, maximum contribution from traits towards divergence has been reported to be different for different sets of materials used in experimentation depending upon the genotypes under study (Karad *et al.*, 2002; Misra *et al.*, 2011; Lahbib *et al.*, 2013; Zehra (2014). Similarly Karad *et al.* (2002) concluded that the most potent factors for divergence were number of fruits plant^{-1} , fruit length, fruit girth, fruit weight, while Zehra (2014) concluded that plant spread, seed yield plant^{-1} , average fruit weight were the highest contributors to D^2 values.

Persual of the results representing cluster means (Table-13) for different growth characters revealed that lowest cluster mean for plant spread (52.07), number of branches plant⁻¹ (20.73), days to harvesting (109.47), fruit length (11.01), fruit weight (3.19), fruit pedicel length (4.03), fruit pedicel diameter (0.28), number of fruits plant⁻¹ (30.53), fruit yield plant⁻¹ (59.11) and highest cluster mean plant height (68.67) were recorded in cluster IV ; highest cluster mean for number of branches plant⁻¹ (39.65) ,days to flower initiation (37.48) , days to fruit initiation (52.28), days to harvesting (129.92), fruit length (12.80), fruit weight (5.78), number of fruits plant⁻¹(62.61) and fruit yield plant⁻¹(358.16) were recorded in cluster I ;highest cluster mean for plant spread (67.16) and lowest for plant height (61.23), days to fruit initiation (42.84) and fruit diameter (1.04) were recorded in cluster II ; highest cluster mean for fruit diameter (1.15), fruit pedicel length (4.89), fruit pedicel diameter (0.30) and lowest for days to flower initiation (33.10) were recorded in cluster III. Thus the traits showing high contribution towards genetic divergence can be improved upon by selecting the genotypes from those clusters having maximum cluster means for the respective traits, which inturn depends upon the objective of the breeding programme.

It is clear from the above discussion that tremendous potential exists for converging the elite allelic resources present in the present set of chilli genotypes through a systematic breeding and selection approach so as to recover high yielding recombinants, with good quality characteristics. Selection of the parents for hybridization should be done from different clusters having wide inter-cluster distance and those selected parents should have high *per se* performance for the traits contributing maximum towards divergence.

Clusters consisting of only one genotype with specific traits could be used in hybridisation programme for the exploitation of heterosis mainly as testers for expression of maximum heterosis.

Thus from present study, crosses between the genotype of cluster IV with those of I, II and III are likely to exhibit high heterosis and produce recombinants with desired traits.

Chapter – 6

SUMMARY AND CONCLUSION

The present study on the “**Identification of Resistant Sources against Wilt Disease of Chilli (*Capsicum annum* L.)**” was carried out during *kharif* 2018 in the Division of Vegetable Science and Mycology and Forest Pathology Laboratory, Division of Plant Pathology, Faculty of Horticulture, Sher-e-Kashmir University of Agricultural Sciences and Technology of Kashmir, Shalimar, Srinagar. The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications. The experimental material consisted of 107 chilli genotypes. The plot size was kept 2.7x1.4m (3.78m²). Each plot consisted of 2 rows of each genotype in each replication at spacing of 45 x 45 cm. The causal agent of the disease was isolated from wilted chilli plant in pure culture on potato dextrose agar medium. On the basis of morphological and pathological characteristics it was concluded that the fungi inciting the disease was identified as *Fusarium solani*.

The pathogenicity of isolated fungi (*Fusarium solani*) was established by proving Koch's postulates on susceptible potted chilli plants (cv. Kashmir Long-1). The initial disease symptoms in case of *Fusarium solani* inoculated seedlings were noticed 7-10 days after inoculation. Molecular identification also confirmed that the isolate was *Fusarium solani*.

Among one hundred and seven genotypes, evaluated for their resistance to wilt disease under field conditions, it was concluded that only one genotype i.e., SKAU-193 was found immune, twenty two were found resistant, twenty eight as moderately resistant (totalling fifty one genotypes) and fifty six as susceptible and highly susceptible.

After field screening the fifty one chilli genotypes were further screened under controlled condition, it was concluded one genotype SKAU-193 was found immune, twenty one genotypes were found resistant while seventeen genotypes

showed moderately resistant reaction and remaining twelve genotypes showed susceptible reaction.

Taking into consideration the DUS characteristics assessed, it was concluded that the chilli accessions present great variation. It was concluded that forty three genotypes showed semi-upright, fourteen genotypes spreading plant habit and three genotypes exhibited upright plant habit. Twenty two genotypes showed long, twenty genotypes medium and eighteen genotypes small length of main stem. Twenty seven genotypes showed medium, seventeen genotypes showed short, thirteen genotypes long and three genotypes showed very short length of first internode. Anthocyanin colouration of nodes was present in fifty six genotypes and absent in four genotypes. Intensity of anthocyanin colouration was weak in twenty seven genotypes, medium in twenty one genotypes and strong in twelve genotypes. Plant height was medium in sixty genotypes. Plant spread was medium in fifty six genotypes and four genotypes exhibited narrow plant spread. Stem pubescence was present in fifty six genotypes and absent in four genotypes. Intensity of stem pubescence was sparse in sixty genotypes. Stem shape was round in sixty genotypes. Length and width of leaf blade was long and broad respectively in sixty genotypes. Fifty four genotypes showed green leaf colour and six genotypes showed green with purple tinge. Intensity of green colour was medium in thirty five genotypes, light in seventeen genotypes and dark in eight genotypes. Intensity of purple colour was light in fifty four genotypes and medium in six genotypes. Leaf shape was lanceolate in forty seven genotypes, ovate in nine genotypes and broad elliptic in four genotypes. Leaf undulation of margin was weak in forty five genotypes, medium in thirteen genotypes and strong in two genotypes. Leaf pubescence was present in almost fifty five genotypes, absent in five genotypes and intensity of leaf pubescence was sparse in sixty genotypes. Flower petal colour was white and anther colour was pale blue in sixty genotypes. Days to 50% flowering was medium in thirty four genotypes and late in twenty six genotypes. Fruit orientation was drooping in fifty eight and

semi-drooping in two genotypes. Fruit bearing habit was solitary in sixty genotypes. Fruit colour (at mature unripe stage) was green in sixty genotypes and fruit intensity of colour (at mature unripe stage) was dark in twenty two genotypes and medium in eighteen genotypes. Fruit length was long in sixty genotypes and fruit diameter was medium in fifty eight genotypes and broad in two genotypes. Fruit curvature was present in fifty four genotypes, absent in six genotypes and fruit curvature intensity was low in fifty four genotypes and medium in six genotypes. Fruit neck at basal end was absent in forty genotypes and present in twenty genotypes.

Fruit situation of pericarp was medium in thirty four genotypes, weak in twenty five genotypes and strong in one genotype. Fruit texture of surface was smooth in thirty five genotypes, slightly rough in twenty three genotypes and rough in two genotypes. Fruit colour was red and intensity of colour was medium in sixty genotypes. Fruit shape at base was acute in fifty two genotypes and round in eight genotypes. Fruit shape at apex was acute in fifty nine genotypes and blunt in one genotype. Fifty five genotypes showed enveloping calyx cover while five genotypes had non-enveloping. Fifty seven genotypes had dented calyx margin while three had smooth. Calyx constriction was absent in forty nine genotypes and was present in eleven genotypes. Pedicel attachment was weak in thirty three genotypes and strong in twenty six genotypes. Fruit blossom end appendage was present in thirty genotypes and absent in thirty genotypes.

Observations were recorded on twenty quantitative and qualitative parameters viz., plant height (cm), plant spread (cm), number of branches plant⁻¹, days to flower initiation, days to fruit initiation, days to harvesting, fruit length (cm), fruit diameter (cm), fruit weight plant⁻¹ (g), fruit pedicel length (cm), fruit pedicel diameter (cm), number of fruits plant⁻¹, fruit yield plant⁻¹, fruit yield hectare⁻¹, dry matter content (%), vitamin C content (mg/100g), capsaicin content (mg/g), capsanthin content (ASTA units), total phenols (mg/100g) and instrumental colour (L*,a*,b*).

The data collected on various quantitative characters was subjected to statistical analysis and the results obtained from the investigation is summarized as follows:

- Analysis of variance revealed significant differences among genotypes for all the traits studied. The maximum range was recorded for fruit yield hectare⁻¹, followed by Vitamin C content, days to harvesting, plant height (cm), no. of fruits plant⁻¹, capsanthin content, while the lowest range was observed for fruit diameter, fruit pedicel diameter, capsaicin content, fruit weight. On the basis of mean performance of the genotypes the maximum fruit yield hectare⁻¹ was recorded in SKAU-193 (239.43) followed SKAU-173 (206.02), SKAU-163 (186.24), KL-1 (184.54) and SKAU-195 (177.14). The lowest fruit yield was recorded in SKAU-153 (23.90q) followed by Local Kashmiri chilli-1 (24.13q) and SKAU-118 (26.02q).
- As indicated by the results on variability and heritability, the estimates of phenotypic variance were higher than the corresponding genotypic variance for all the characters studied indicating the influence of environment in the expression of these traits. Since these estimates alone do not provide means to assess the nature of genetic variability, the phenotypic and genotypic coefficients of variation are also estimated to draw conclusions. In the present study, the PCV was slightly higher than GCV for almost all the traits. It is obvious because PCV includes variability due to genotype and genotype x environment interaction. The phenotypic and genotypic coefficients of variation ranged from 6.34-57.91 and 5.83-57.62, respectively. The highest phenotypic and genotypic coefficients of variability were observed for average fruit yield plant⁻¹ (57.91, 57.61) followed by number of fruits plant⁻¹ (31.44, 31.41), fruit length (20.49 and 20.16), fruit diameter (20.37, 16.82), fruit weight (38.73, 38.67) and number of branches plant⁻¹ (25.35, 25.32). The difference between the phenotypic coefficient of variation (PCV) and genotypic

coefficient of variation (GCV) was found to be narrow for days to flower initiation, days to fruit initiation, days to harvesting, fruit pedicel length, fruit pedicel diameter, dry matter content, plant height, plant spread suggesting that these traits were least affected by the environment and selection for these traits based on phenotypic would be rewarding.

- High heritability coupled with high genetic gain as per cent of mean was recorded for all the characters, indicating the genetic factors strongly influence the amount of variation.
- In the present investigation, the estimates of genotypic correlation coefficients were in general slightly higher than phenotypic correlation coefficients showing that masking effects of the environment was little indicating the presence of inherent association between various characters. Correlation coefficients revealed that the economically important trait i.e. fruit yield plant⁻¹ exhibited significant and positive association with plant height, no. of branches plant⁻¹, days to flower initiation, days to fruit initiation, days to harvesting, fruit diameter, fruit weight, fruit length, fruit pedicel length, fruit pedicel diameter, number of fruits plant⁻¹ positive but non-significant association with plant height, days to fruit initiation and fruit weight, negative non-significant association with plant spread.
- Traits like plant height, no. of branches plant⁻¹, days to flower initiation, days to fruit initiation, days to harvesting, fruit weight, fruit diameter, fruit length, fruit pedicel length, fruit pedicel diameter, number of fruits plant⁻¹ which had significant positive association with fruit yield plant⁻¹, were positively and significantly associated with each other. Moreover this trait showed positive and non-significant association with plant height, days to fruit initiation and fruit weight and negative non-significant association with plant spread. Fruit weight showed significant positive correlation with fruit length, fruit diameter, no. of branches and days to harvesting but it showed non-significant negative association with plant spread, days to

flower initiation and days to fruit initiation. Fruit length showed significant and positive correlation with plant height, no. of branches plant⁻¹, days to harvesting. Number of fruits plant⁻¹ exhibited positive significant correlation with no. of branches plant, days to flower initiation, fruit length and fruit pedicel diameter.

- Estimates of divergence among 60 chilli genotypes revealed that significant divergence existed among them. The chilli genotypes got grouped into 4 clusters with maximum number of genotypes in cluster II (25) followed by cluster I (20), cluster III (14) and cluster IV (1). Intra cluster distance (D^2) was maximum in cluster III (5177.30), followed by the cluster II (4846.87) and cluster I (3419.32). The inter cluster distance (D^2) was maximum between the cluster II and III (14621.56) followed by cluster I and II (12246), cluster II and IV (11888.38), cluster III and IV (9139.45) , cluster I and IV (8815.51) and cluster I and cluster III (8372.23)
- Cluster means for different growth characters revealed substantial genetic variability for all the traits. The mean values were maximum mostly in those clusters containing genotypes having high values for the traits contributing maximum towards divergence i.e. plant spread, average fruit weight, number of fruits plant⁻¹, plant height, number of branches⁻¹, days to flower initiation and days to harvesting. Thus these characters viz., plant spread, average fruit weight, number of fruits plant⁻¹, plant height, number of branches⁻¹, days to flower initiation and days to harvesting should be given priority over other traits for selecting high yielding genotypes.

Based on the findings of the present investigation, the following conclusions could be drawn:

- The pathogen associated with chilli wilt disease under Kashmir condition is *Fusarium solani*.
- The resistant sources with varied levels of resistance exist against the chilli disease. The determination of genetic basis of these sources and incorporation of their resistant genes into susceptible commercial cultivars may help in the development of high yielding wilt resistant chilli cultivars.
- Analysis of variance indicated significant variation existed among genotypes for various characters under study.
- Correlation studies indicated that characters like plant height, no. of branches plant⁻¹, days to flower initiation, days to fruit initiation, days to harvesting, fruit diameter, fruit weight, fruit length, fruit pedicel length, fruit pedicel diameter and number of fruits plant⁻¹ should be considered for improving quantitative traits in chilli.
- Selection of parents from most divergent clusters, having high cluster means and showing high performance can be used in hybridization programme for development of high yielding varieties.

LITERATURE CITED

- Anand, I. J. and Murty, M. B. R. 1968. Genetic divergence and hybrid performance in linseed. *The Indian Journal of Genetics and Plant Breeding* **28**: 178-185.
- Ain, Q.U. 2018. Msc. thesis submitted to Division of Vegetable Science, SKUAST-Kashmir, Shalimar, Srinagar.
- Ajjapplavara, P. S. and Channagoudra, R. F. 2009. Studies on variability, heritability and genetic gain in chilli (*Capsicum annuum* L.). *Asian Journal of Horticulture* **4**(1): 99-101.
- Arriel, N. H. C., Mauro, A. O., Arriel, E. F., Costa, M. M., Bárbaro, I. M. and Muniz, F. R. S. 2007. Genetic divergence in sesame based on morphological and agronomic characters. *Crop Breeding and Applied Biotechnology* **7**: 253-261.
- Amit, K., Ahad, I., Kumar, V. and Takur, S. 2014. Genetic variability and correlation studies for growth and yield characters in chilli (*Capsicum annuum* L.). *Journal of Spices and Aromatic Crops* **23**(2): 170-177.
- Arya, P. S. and Saini, S. S. 1977. Variability studies in salad type peppers. *Prog. Horticulture* **9**(1): 37-42.
- Arif, M., Zaidi, N.W., Haq, Q. M. R., Singh, Y. P., Khan, S., and Singh, U. S. 2013. Molecular phylogeny and pathotyping of *Fusarium solani*: A causal agent of Dalbergia sisso decline. *Forest pathology* **43**: 478-487.
- AOAC, 1984. Official Methods of Analysis. Association of official Analytical Chemists 13th edition, Washington D.C., p. 497.
- Alavi, A., Saber, M. and Akhavizadegan, M. D. 1986. Rhizoctonia crown and root rot of pepper in Iran. *Iranian Journal of Plant Pathology* **22**: 9-12.

- Bharadwaj, D. N., Singh, S. K. and Singh, H. L. 2007. Genetic variability and association of component characters for yield in chilli. *International Journal of Plant Sciences* **2**(2): 93-96.
- Bray, H. G. and Thorpe, W. V. 1954. Methods of Biochemical Analysis **1**: 27-52.
- Belwansi, R. 2012. Studies on cultural and morphological character of *Fusarium oxysporum f.sp.circi* M.Sc. thesis, RVSKVV, Gwalior (India).
- Bosland, P.W. and Votava, E. J. 2000. Pepper Vegetables and Spice Capsicum CABI Publishing CAB International Wallingford UK.
- Bhattacharya, A., Chattopadhyay, A. and Mazumdar. 2010. Antioxidant constituents and enzyme Activities in chilli peppers. *International Journal of Vegetable Science* **16**: 201-211.
- Bijalwan, P., Mishra, A. C. 2014. Correlation and Path analysis in chilli capsicum annuum for yield and yield attributing traits. *International Journal of Science and Research* **5**(3):1589-1592.
- Burton, G.W. and Devane, C. H. 1953. Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. *Agronomy Journal* **45**: 478-481.
- Burton, G.W. 1952. Quantitative inheritance in grasses. *Proceedings of 6th International Grassland congress* **11**: 277-283.
- Booth, C. 1977. *Fusarium*; laboratory guide to identification of major species. Commonwealth Mycological Institute, Kew Survey, England pp. 58.
- Booth, C. and Sutton, B. C. 1984. *Fusarium pallidoroseum*, the correct name for *F. semitectum*. Transactions of the British Mycological Society **83**: 702-704.
- Benlloch, M. and Dominguez, F. 1934. La enfermedad de Los Pimentales en Aldeanueva del Camino. *Agriculture Research* **7**: 1-20.

- Brown, J. G. and Gibson, F. 1926. Plant Pathology. **In:** 34th Annual Report, Arizona Agriculture Experimentation Station for the year ending June 30th 1923, p 448-506.
- Chatterjee, S., Mukherjee, N. and Katua, D. C. 1997. Status of bacterial wilt disease in West Bengal. *Journal of Interacademica* **1**: 97-99.
- Crawford, R. F. 1934. The etiology and control of chilli wilt produced by *Fusarium annuum*. *Technical Bulletin, New Mexico Agriculture Experimental Station* **223**: 1-20.
- Chaves, B.A. 1947. Principals doencas das plantas en nordeste. *Brazil Bollettino Agriculture Pernambuco* **14**: 5-46.
- Chakrabarty, S. and Islam, A. K. M. A. 2017. Selection criteria for improving yield in chilli (*Capsicum annum* L.). *Advances in Agriculture Article* ID 5437870, 9 pp.
- Ciferri, R. 1926. Primer Informe, Annual de la Estacion Agron. U. Col. De. Agric. De Haina. *Republica Dominicana* **1**: 27-36.
- Cenis, J. 1992. Rapid extraction of fungal DNA for PCR amplification. *Nucleic acids Research* **20**: 2380.
- Copcu, M. and Saydam, C. 1974. A preliminary study on the cross-inoculation of isolates of *Verticillium dahliae* obtained from various hosts. *Journal of Turkish Phytopathology* **3**: 39-49.
- Camino, V., Despestre, T. and Espinosa, J. 1987. Search for *Capsicum annum* susceptibility to *Fusarium*. *Capsicum Newsletter* **6**: 70.
- Chatterjee, S., Mukherjee, N. and Katua, D. C. 1997. Status of bacterial wilt disease in West Bengal. *Journal of Interacademica* **1**: 97-99.
- Chattopadhyay, A., Sharangi, A. B., Dai, N. S. and Dutta, S. 2011. Diversity of genetic resources and genetic association analysis of green and dry chillies of eastern India. *Chilean Journal of Agricultural Research* **71**(3): 350-356.

- Datta, S. and Jana, J. C. 2010. Genetic Variability, heritability and correlation in chilli genotypes under Terai zone of West Bengal. *SAARC Journal of Agriculture* **8**(1): 33-45.
- Dos Anjos, I.V., De Melo, S. S., Gilio, T. A. S., Kreitlow, J. P., Da S Neves, S. M. A., Araujo, K. L., Serafim, M. E. and Neves, L. G. 2019. Molecular characterization of isolates of *Fusarium* spp. Associated with wilt in *Capsicum* spp. *Journal of Agricultural Sciences* **11**(6): 1916-9760.
- Datta, J., and Lal, N. 2013. Genetic diversity of *Fusarium* wilt races of pigeon pea in major regions of India. *African Crop Science Journal* **21**: 201-212.
- Datta, S. and Jana, J. C. 2011. Studies on genetic divergence in chilli (*Capsicum* spp.) under sub Himalayan tracts of West Bengal. *Journal of Crop and Weed* **7**(1): 44-48.
- Datta, S. and Das, L. 2013. Characterization and Genetic Variability Analysis in *Capsicum annuum* L. germplasm, *SAARC Journal of Agriculture* **11**(1): 91-103.
- Diwaker, K., Vijay, B., Rangare, S. B. and Devi, S. 2012. Genetic variability, heritability and correlation studies in chilli (*Capsicum annuum* L.). *HortFlora Research Spectrum* **1**(3): 248-252.
- Dar, G. M. and Mir, N. A. 1995. Pepper wilt causes and prevalence in Kashmir. **In:** *Proceedings of National Symposium on Recent Trends in the Management of Biotic and Abiotic Stresses in Plants*. HPKVV, Palampur (India), 2-3, November.
- El-Ghoraba, A. H., Javed, Q., Anjum, F. M., Hamed, S. F. and Shaabana, H. A. 2013. Pakistani bell pepper (*Capsicum annuum* L.): Chemical compositions and its antioxidant activity. *International Journal of Food Properties* **16**(1): 18-32.

- FOASTAT. 2018. <http://www.faostat.org/food> and agriculture organisation, United Nations, Rome.
- Foaster, R. E. and Walker, J. C. 1947. Predisposition of tomato to *Fusarium* wilt. *Journal of Agricultural Research* **74**:165-168.
- Fisher, R. A. 1918. The correlation among relatives on the supposition of Mendelian inheritance. *Transactions of the Royal Society of Edinberg* **52**: 399-433.
- Fernandez, M. C. 1983. *Phytophthora capsici*, causal agent of wilt of *Capsicum annum* in Chile. *Agricultura Technics* **43**: 91-93.
- Faisal, H., Shahid, S., Abid, M., Farzana, U. and Akbar, M. 2013. Pathogenicity of some important root rot fungi to the chilli crop and their biological control. *International Journal of Biology and Biotechnology* **10**: 101-108.
- Farhad M., Hasanuzzaman M., Biswas B. K., Azad A. K. and Arifuzzaman M. 2008. *Reliability of Yield Contributing Characters for Improving Yield Potential in Chilli (Capsicum annum)*. *Int. J. Sustain. Crop Prod.* **3**(3):30-38.
- Farhad, M., Hasanuzzaman, M., Biswas, B. K., Arifuzzaman, M. and Islam, M.M. 2010. Genetic divergence in chilli (*Capsicum annum* L.). *Bangladesh Research Publications Journal* **3**(3): 1045-1051.
- Ferniah, R. S., Daryono, B. S., Kasiamdari, R. S., and Priyatmojo, A. 2014. Characterization and pathogenicity of *Fusarium oxysporum* as causal agent of *Fusarium* wilt in chilli (*Capsicum annum* L.). *Microbiology Indonesia* **8**(3): 121-126.
- Gogate, S. M., Patel, R. K., Patel, M. J. and Patel, J. A. 2006. Genetic divergence in chilli (*Capsicum annum* var. *longum* (D.C.) Sendt.). *Vegetable Science* **33**(1): 21-25.

- Garofalo, F. 1957. Preliminary experiments on soil sterilization with steam and vapam in plantings of eggplant and capsicum. *Fitopathologia* **20**: 59-78.
- Gonzalez, S. M. M. and Bosland, P. W. 1993. Enhanced capsicum germplasm resistant to Verticillium wilt. *Capsicum and Eggplant Newsletter* **12**: 85-87.
- Goigoi, M., Sarmah, D. K. and Ali, S. 2017. Cultural and morphological Variations of *Fusarium solani* (Mart.) Sacc. Causing root rot of Patchouli in Assam, India. *International Journal of current microbiology and applied sciences* **6**: 1889-1901.
- Gupta, M. A., Singh, D. and Kumar, A. 2009. Genetic variability, genetic gain and correlation in chilli (*Capsicum annuum* L.). *Indian J. Agric. Sci.*, **79**(3): 221-223.
- Hasanuzzaman, M. and Golam, F. 2011. Selection of parents in chilli (*Capsicum annuum* L.). *International Journal of Sustainable Crop Production* **6**(1): 63-75.
- Hafizi, R., Salleh, B. and Lattifah, Z. 2014. Morphological and molecular characterization of *Fusarium solani* and *Fusarium oxysporum* associated with crown disease of oil palm. *Brazilian journal of microbiology* **44**(3): 959-968.
- Hansford, C. G. 1940. Report of the Senior Plant Pathologist, Department of Agriculture, Uganda, 1938-39, p 28-29.
- Herison, C., Handaayaningsih, N., Fahrurrozi, F. And Rustikawati, R. 2014. Evaluation of growth and yield performance on inoculated chilli pepper hybrids by CMV (cucumber mosaic virus). *Journal of Agriculture Science* **36**(1):14-18.
- Huber, D. M. and Watson, R. D. 1974. Nitrogen form and plant disease. *Annual Review of Phytopathology* **12**: 139-165.

- Harland, S. C., 1939. The genetics of cotton jonathan cope London.
- Hartman, G. L. and Huang, Y. H. 1993. Pathogenecity and virulence of *Phytophthora capsici* isolates from Taiwan on tomatoes and other selected hosts. *Plant Disease* **77**(6): 581-591.
- Hashmi, M. H. 1989. Seed-borne mycoflora of *Capsicum annum* L. *Pakistan Journal of Botany* **21**: 302-308.
- Hwang, B. K. and Kim, C. H. 1995. Phytophthora blight of pepper and its control in Korea. *Plant Disease* **3**: 221-227.
- Hanson, C. H., Robinson, H. F. and Comstock, R. E. 1956. Biometrical studies of yield in segregating populations of Korean Lespedeza. *Agronomy Journal* **48**(6): 268-272.
- Hasan, M. J., Kulsum, M. U., Ullah, M. Z., Hossain, M. M., and Mahmud, M.E. 2014. Genetic diversity of some chilli (*Capsicum annum* L.) genotypes. *Int. J. Agril. Res. Innov. & Tech.* **4**(1): 32-35.
- Hasan, R., Huque, A. K. M. M., Hossain, M. K., and Alam, N. 2015. Assessment of genetic divergence in chilli (*Capsicum annum* L.) genotypes. *Plant gene and trait* **6**(3):1-5.
- Ibrahim, M., Ganigar, V.M. and Yenjerappa, S.T. 2001. Genetic variability, heritability, genetic gain and correlation studies in chilli. *Karnataka Journal of Agricultural Sciences* **14**: 784-878.
- Jyothi, A. R., Koshy, A., Mathew, J. and Abraham, K. 1993. Bacterial wilt of chillies in Kerala and reaction of certain chilli accessions to *Pseudomonas solanacearum*. *Bacterial Wilt Newsletter* **9**: 6.
- Janaki, M. and Naidu, N. 2015. Assessment of genetic variability, heritability and genetic gain for quantitative traits in chilli (*Capsicum annum* L.). *The Bioscan* **10**(2): 729-733.

- Janaki, M., Ramana, C. V, Naidu, L. N. and Rao, M. P. 2015. Performance of chilli (*Capsicum annum* L.) genotypes for yield and yield attributing traits. *Plant Archives* **15**(2):661-666.
- Johnson, H. W., Robinson, H. F. and Comstock, R. E. 1955. Estimation of genetic and environmental variability in soybean. *Agronomy Journal* **47**: 477-483.
- Jabeen, N., Sofi, P. A. and Wani, S. A. 2009. Character Association in Chilli (*Capsicum annum* L.). *Revista-Cientifica UDO Agricola* **9**(3): 487-490.
- Jabeen, N., Ahmed, N., Khan, S. H., Chattoo, M. A. and Sofi, P. A., 2007, Inheritance of resistance to *Fusarium* wilt (*Fusarium pallidorozeum* (Cooke) Sacc.) in chilli (*Capsicum annum* L.). *Indian Journal of Genetics* **67**(4): 334-336.
- Jaisankar, I., Shrawan, S., Goutham, R. K., Velmurugan, A., Singh, A.K., Dam Roy, S., Divya, P. and Sajan, S. 2015. Performance of chilli genotypes for green fruit yield in Andaman and Nicobar Islands. *J. Andaman Sci. Assoc.*, **20**(1): 39-42.
- Johnston, A. and Booth, C. 1983. *Plant Pathologist's Pocket Book*. Commonwealth Agricultural Bureaux, England pp. 439.
- Johari, S. and Kumar, V. 2007. Studies of combining ability, variability, heritability and genetic gain for yield and its attributes in bell pepper (*capsicum annum* L.). *Vegetable Science* **34**(1): 103-105.
- Jogi, M. Y., Madalageri, M. B., Mallimar, M., Bawoor, S., Mangi, V. And Porika, H. 2017. Genetic variability studies in chilli (*Capsicum annum* L.) for growth and early yield. *International Journal of Pure Applied Bioscience* **5**(5): 858-862.
- Jabeen, N. 2006. Phd. thesis submitted to Division of Vegetable Science, SKUAST-Kashmir, Shalimar, Srinagar.

- Jia, J. S. 1992. Studies on the chilli pepper Phytophthora blight and its control in Xingjiang. *Acta-Phytopathologica Sinica* **22**: 257-263.
- Kaur, S. 1993. *Fusarium* wilt a cause of chilli crop failure in Punjab. *Plant Disease Research* **8**: 181-183.
- Kumar, D.; Bahadur, V., Rangare, S. B. A. and Singh, D. 2012. Genetic variability, heritability and correlation studies in chilli (*Capsicum annuum* L.). *Hort. Flora Research Spectrum* **1**(3): 248-252.
- Kaur, S., Dhunna, O. S. and Khurana, D. S. 2004. Identification of resistance for wilt disease of chilli and its practical utility. *Environment and Ecology* **22**: 52-53.
- Khan, A. N. A., Shetty, K. S. and Patil, R. B. 1979. Occurrence of bacterial wilt of chilli in Karnataka and its relationship to the wilts of other Solanaceous crops. *Indian Phytopathology* **32**: 507-512.
- Koleva, K. and Vitanov, M. 1990. *Fusarium* species related to root rot of pepper. *Rasteniyev dni Nauki* **27**: 61-63.
- Karungi, J., Obua, T., Kyamanywa, S., Mortensen, C.N. and Erbaugh, M. 2013. Seedling protection and field practices for management of insect vectors and viral diseases of hot pepper (*Capsicum chinense* Jacq.) in Uganda. *International Journal of Pest Management* **59**(2): 103-110.
- Kumar, H., Patil, H. B., Ajjappalavara, P. S., KC, M., D, S. and Revawnawpa. 2018. Performance of chilli (*Capsicum annum* L.) genotypes for green chilli yield and quality. *International Journal of Chemical Studies* **6**(5):150-153.
- Karad, S. R., Raikar, G. R. and Navale, P. A. 2002. Genetic divergence in chilli. *Journal of Maharashtra Agricultural Universities* **27**(2): 143-145.

- Khurana, D. S., Singh, P. and Hundal, J. S. 2003. Studies on genetic diversity for growth, yield and quality traits in chilli (*Capsicum annuum* L.). *Indian Journal of Horticulture* **60** (3): 277-282.
- Kerketta, A., Collis, J. P., Tirkey, M., Lal, R. and Singh, N. V. 2018. Evaluation of chilli (*Capsicum annuum* L.) Genotypes for Growth, Yield and Quality Characters under Allahabad Agro Climatic Conditions. *International Journal Pure Applied Biosciences* **6**(4): 451-455
- Krishna, C., Madalageri, M. B., Patil, M. P. and Kotlkal, Y. K. 2007. Variability Studies in Green Chilli (*Capsicum annuum* L.). *Karnataka Journal of Agricultural Sciences* **20**(1): 102-104.
- Kumar, B. M. D., Kantti, A. and Mallikarjunaiah, H. 2010. Genetic divergence in chilli accessions. *Electronic Journal of Plant Breeding* **1**(5): 1363-1366.
- Kumari, S. S., Jyothi, K. U., Reddy, V. C., Srihari, D., Sankar, A. S. and Sankar, C.V. 2011. Character association in paprika (*Capsicum annuum* L.). *Journal of Spices and Aromatic Crops* **20**(1): 43-47.
- Kaur, S. 1993. *Fusarium* wilt a cause of chilli crop failure in Punjab. *Plant Disease Research* **8**: 181-183.
- Khan, A. N. A., Shetty, K. S. and Patil, R. B. 1979. Occurrence of bacterial wilt of chilli in Karnataka and its relationship to the wilts of other solanaceous crops. *Indian Phytopathology* **32**: 507-512.
- Kelaiya, D. S. and Parakhia, A. M. 2000. Screening of chilli varieties against wilt. *Gujarat Agricultural University Research Journal* **25**:101-102.
- Kesavan, G. and chowdhary, B. 1977. Screening for resistance to *Fusarium* wilt of tomato. *SABRAO Journal* **9**:57-65.
- Larena, I., Salazar, O., Gonzalez, V. Z., Gulian, M. Z. and Rubio, V. 1999. Design of a primer for rDNA Internal Transcribed Spacer with enhanced specificity for ascomycetes. *Journal of Biotechnology* **75**: 187-194.

- Lannes, S. D., Finger, F. L., Schuelter, A. R. and Casali, V. W. D. 2007. Growth and quality of Brazilian accessions of *Capsicum chinense* fruits. *Science Horticulture* **112**: 266-270.
- Lush, J. L. 1940. Intra-sire correlation and regression of offspring on Rams as a method of estimating heritability of characters. *Proceedings of American Society Animal Production* **33**: 293-301.
- Lu, J. Y., Yu, C. F. and Ju, L. H. 1984. Studies on differentiation of the virulence of *Verticillium dahliae* on pepper. *Acta Phytopathologica Sinica* **14**: 213-218.
- Lush, J. L. 1949. Heritability of quantitative characters in farm animals. *Proceedings of the Eight International Congress on Genetics*. Genetics Supplement volume. *Heredity*, pp. 356-395.
- Lahbib, K., Bnejdi, F. and El-Gazzah, M. 2012. Genetic diversity evaluation of pepper (*Capsicum annuum* L.) in Tunisia based on morphological characters. *African Journal of Agricultural Research* **7**(23): 3413-3417.
- Lahbib, K., Bnejdi, F. and Gazzah, M. E. 2013. Selection of pepper parent from a collection of *Capsicum annuum* landraces based on genetic diversity. *Journal of Plant Breeding and Crop Science* **5**(5): 68-72.
- Leonian, L.H. 1919. *Fusarium* wilt of chilli pepper. *Technical Bulletin* No. 121. New Mexico Agricultural Experiment Station, Las Cruces, USA.
- Mankar, S. K., Sakhare, S. B., Akhare, A. A. and Kharkar, A. P. 2007. Genetic divergence studies in chilli. *Annals of Plant Physiology* **21**(2): 225-228.
- Mathur, K. and Gurjar, R. B. S. 2001. *Sclerotium rolfsii*-a new threat to chilli in Rajasthan. *Journal of Mycology and Plant Pathology* **31**: 261.
- Mekonnen, A., Woubit, D., Alemu, L. and Tariku, H. 2015. Assessment of wilt intensity and identification of causal fungal and bacterial pathogens on hot

- pepper (*Capsicum annum* L.) in bakotibbe and nonno districts of west shewa zone, Ethiopia. *International Journal of Phytopathology* **4**: 21-28.
- Mohammed Ibrahim, Ganiger, V. M. and Yenjerappa, S. T. 2001. Genetic variability, heritability, genetic gain and correlation studies in chilli. *Karnataka J. Agril. Sci.* **14**(3): 784-787; 5 ref.
- Manju, P. R. and Sreelathakumary, I. 2002. Genetic variability, heritability and genetic gain in hot chilli (*Capsicum chinense* jacq.). *Journal of Tropical Agriculture* **40**: 4-6.
- Mahalanobis, P. C. 1928. A Statistical study of Chinese head measurement. *Man in India* **8**: 32-64.
- Misra, S., Lal, R. K., Darokar, M. P. and Khanuja, S. P. S. 2011. Genetic variability in germplasm accessions of *Capsicum annum* L. *American Journal of Plant Sciences* **2**: 629-635.
- Mishra, S.B., Singh, U.K. and Sahu, P.K. 1994. Studies on genetic divergence in five land race races of rice in northern Bihar. *Annals of Agricultural Research* **15**(2): 217-221.
- Murty, B. R. and Qadri, M. I. 1966. Analysis of divergence in some self compatible forms of *Brassica campestris* var. Brown sarson. *The Indian Journal of Genetics and Plant Breeding* **26**: 45-55.
- Madi, A. I., Abdel-Aal, H. M., Amal, M. I. E., Ali, H. E. and Hassan, A. G. 2017. Virulence of wilt pathogens against pepper cultivars in Egypt. *International Journal of Technical Research and Science* **1**: 304-314.
- Mushtaq, M. and Hashmi, M. H. 1997. Fungi associated with wilt disease of Capsicum in Sindh Pakistan. *Pakistan Journal of Botany* **29**: 217-222.
- Matta, A. and Garibaldi, A. 1972. Effect of different moisture conditions on certain plant diseases caused by soil fungi. *Agricoltura Italiana* **74**: 237-253.

- McRae, N. 1932. Science Report for 1930-31 Imperial Institution of Agriculture, Research, Pusa, p. 84.
- Marchionatto, J. B. 1935. Species of *Fusarium* existing in Argentina. *International Bulletin of Plant Protection* **9**: 125-138.
- Manju, P. R. and Sreelathakumary, I. 2002. Genetic Variability, heritability and genetic gain in hot chilli (*Capsicum chinense* jacq.). *Journal of Tropical Agriculture* **40**: 4-6.
- Munshi, A. D. and Behera, T. K. 2000. Genetic variability, heritability and genetic gain for some traits in chillies (*Capsicum annuum* L.). *Vegetable Science* **27**(1): 39-41.
- Mahantesh, Y. J. and Madalageri, M. B. 2017. Genetic variability studies in chilli (*Capsicum annuum* L.) for growth and early yield. *International Journal of Pure Applied Bioscience* **5**(5): 858-862.
- Manju, P. R. and Sreelathakumary, I. 2004. Genetic divergence in hot chilli (*Capsicumchinense* Jacq.). *Capsicum and EggplantNewsl.* pp. 69-72.
- Madhukar, H. M., Naik, M. K. and Patil, M. G. 2002, Evaluation of chilli genotypes and bioagents against *Fusarium* wilt of chilli. **In**: *Proceedings of National Symposium on Crop Protection and WTO an Indian Scenario*, Feb. 2002. CPCRI, Kasaragod. Kerala, India.
- Meena, M. L., Kumar, N., Meena, J. K. and Rai, T. 2016. Genetic variability, heritability and genetic gains in chilli (*Capsicum annum* L.). *Bioscience Biotechnology Research Communication* **9**(2): 258-262.
- Maruti, T. B., Tembhurne, B. V., Chavan, R. L. and Amaresh, Y. S. 2014. Reaction of chilli (*Capsicum annum* L.) genotypes and hybrids against *Fusarium* wilt (*Fusarium solani*). *Journal of Spices and Aromatic Crops* **23**(2):186-191.

- Maurya, A. K., Kushwaha, M. L., Jain, S. K., Maurya, M. K. and Jain, V. K. 2015. Assessment of genetic variability, heritability and genetic gain in chilli (*Capsicum annum* L.). *International Journal of Plant Science* **30**(2):365-368
- Mathew, D., Doijode, S. D. and Reddy, K. M. 2004. Correlation and path coefficient analysis in five species of capsicum. *Capsicum and Eggplant Newsletter* **23**(1): 57-60.
- Moens, M. and Benaicha, B. 1990. Control of pepper wilt in Tunisia. *Parasitica* **46**: 103-109.
- Naik, M. K., Madhukar, H. M. and Devika Rani, G. S. 2007. Evaluation of fungicides against *Fusarium solani*, the causal agent of wilt of chilli. *Vegetable Science* **34**: 173-176.
- Naik, M. K. 2006. Wilt of chilli with special reference to cultural, morphological, molecular characterization and pathogenic variability of *Fusarium* isolates of India. **In**: Proceedings of Midterm Review Meeting of the Project (23rd July, 2006), *Indian Institute of Vegetable Research*, Varanasi.
- Nahak, S. C., Nandi, A., Sahu, G. S., Tripathy, P., Dash, S. K., Patnaik, A. and Pradhan, S.R. 2018. Studies on variability, heritability and genetic gain for yield and yield contributing characters in chilli (*Capsicum annum* L.). *Journal of Pharmacognosy and Phytochemistry* **7**(1):2506-2510.
- Naqvi, S. A. M. H. 2004. Diseases of fruits and vegetables. **In**: *Diseases of pepper and their management* (Eds. P. D. Roberts, S. Adkins, K. Pernezny and J. B. Jones). *Kluwer Academic Publishers, The Netherlands* **2**: 333-387.
- Naik, M. K., Madhukar, H. M. and Devika Rani, G. S. 2007. Evaluation of fungicides against *Fusarium solani*, the causal agent of wilt of chilli. *Vegetable Science* **34**: 173-176.

- Naik, M. K., Devika Rani, G. S. and Madhukar, H. M. 2008. Identification of resistant sources against wilt of chilli (*Capsicum annuum* L.) caused by *Fusarium solani* (Mart) Sacc. *Journal of Mycopathological Research* **46**(1):93-96.
- National Horticulture Board, 2017. Data Base of Horticultural crops. Gurgaon, New Delhi.
- Najar, A. G. 2001. Cause and management of chilli wilt in Kashmir. Ph. D. Thesis submitted to Sher-e-Kashmir University of Agricultural Sciences and Technology of Kashmir, Shalimar pp. 143.
- Oka, H. 1958. International variation and classification of cultivated rice. *Indian J. Genet. Plant Breed* **18**:79-89.
- Pickersgill, B. 1997. Genetic resources and breeding of *Capsicum* spp. *Euphytica* **96**: 129-133.
- Palloix, A. 1986. The resistance of pepper (*Capsicum annum*) to *Phytophthora capsici*. Thesis submitted to the University Lyoni, France pp. 131.
- Padhar, P. R. and Zaveri, P. P. 2010. Genetic studies in relation to selection criteria in chilli. *Research on Crops* **11**(3): 722-727.
- Pandiyaraj, P. 2017. Genetic variability, heritability and genetic gain for quantitative and qualitative traits in chilli (*Capsicum annuum* L.). *International Journal of Agriculture Sciences* **9**(14): 4081-4083.
- Pandit, M. K., Muthukumar, P. and Mukhopadhyay, T. P. 2010. Study of Genetic divergence through Multivariate analysis in chilli (*Capsicum annuum* L.) germplasms. *Journal of Interacademia* **14**(3): 298-301.
- Prasath, D., Ponnuswami, V. and Muralidharan, V. 2007. Evaluation of chilli (*Capsicum* spp.) germplasm for extractable colour and pungency. *Indian Journal of Genetics and Plant Breeding* **67**(1): 97-98.

- Panse, V. G. 1957. Genetics of quantitative characters in relation to plant breeding. *Indian Journal of Genetics* **17**: 318-328.
- Patel, P. N., Fougat, R. S. and Sasidharan, N. 2009. Studies on genetic variability, correlation and path analysis in chillies (*Capsicum annuum* L.). *Research on Crops* **10**(3): 626-631.
- Panse, V.G. and Sukhatme, P.V. 1985. Statistical methods for agricultural workers. Indian Council of Agricultural Research, New Delhi, pp. 152-156.
- Panse, V. G. and Sukhatme, P. V. 1957. Statistical methods for agricultural workers. Indian Council of Agricultural Research, New Delhi, pp. 157-165.
- Prasath, D., Ponnuswami, V. and Muralidharan, V. 2007. Evaluation of chilli (*Capsicum spp.*) germplasm for extractable colour and pungency. *Indian Journal of Genetics and Plant Breeding* **67**(1): 97-98.
- Pandit, M. K., Muthukumar, P. and Mukhopadhyay, T. P. 2009. Genetic variability, character association and path analysis in chilli (*Capsicum annuum* L.) genotypes. ICH.pp41.
- Padma., Anbu, S. And Sivasubramaniam, K. 2017. Efficacy of morphological characters for varietal identification of chilli. *International Journal of Current Microbiology and Applied Sciences* **6**(2):690-700.
- Panse, V. G. and Sukhatme, P. V. 1967. Statistical methods for Agricultural Workers 2nd Edn. ICAR, New Delhi. pp 361.
- Patel, D. K., Patel, B. R., Patel, J. R. and Kuchhadiya, G. V. 2015. Genetic variability and character association studies for green fruit yield and quality component traits in chilli (*Capsicum annum* var. *longum* (dc.) sendt.). *Electronic journal of plant breeding* **6**(2):472-478.

- Pawaskar, J. R., Kadam, S. N. and Kadam, J. S. 2014. Response of chilli varieties and genotypes to bacterial wilt caused by *Ralstonia solanacearum* and its management. *Indian Journal of Science* **11**(29):66-72.
- Pujar, U. U., Tirakannanavar, S., Jagadeesha, R. C., Gasti, V. D. and Sandhyarani, N 2017. Analysis of genetic divergence in Chilli (*Capsicum annum* L.) genotypes. *International journal pure applied biosciences* **5**(5): 503-508.
- Patil, M. J., Lambat, A., Gadewar, R. and Charjan, S. 2014. Morphological and cultural variability of *Fusarium solani* isolates from chilli (*capsicum annum* L.). *International Journal of Researches In: Biosciences, Agriculture & Technology* **2**(2): 2347-517.
- PPV and FR. 2001. Protection of Plant Varieties and Farmer's Right Act (No.53 of 2001). Department of Agriculture and Cooperation, Ministry of Agriculture, Government of India and Krishi Bhavan, New Delhi.
- Rego, E. R. 2011. Morphological and chemical characterization of fruits of *Capsicum spp.* accessions *Horticultura Brasileira* **29**(2): 364-371.
- Rahman, S., Hossain, M. A. and Afroz, R. 2017. Morphological characterization of chilli germplasm in Bangladesh. *Bangladesh Journal of Agricultural Research* **42**(2): 207-219.
- Rao, C. R. 1952. Advanced statistical Methods in Biometrical Research. Wiley and Sons, New York.
- Rathod, R. P., Deshmukh, D. T., Ghode, P. B. and Gonge, V. S. 2002. Correlation and path analysis studies in chilli (*Capsicum annum* L.). *Haryana Journal of Horticulture Science* **31**(1/2): 141- 143.
- Raghu, S., Benagi, V. I., Nargund, V. B. and Jayalakshmi, K. 2016. Seed borne nature and infectivity of *Fusarium solani* causing chilli wilt: Its early detection from seeds and soil using conventional and molecular methods. *An International Quarterly Journal of Life Science* **11**(4): 2939-2945

- Robinson, H.F., Comstock, R.E. and Harvey, P.H. 1949. Estimates of heritability and degree of dominance in Corn. *Agronomy Journal* **41**: 353-359.
- Senapati, B. K., Sahu, P. K. and Sarkar, G. 2003. Genetic divergence in chilli. *Crop Research Hisar* **26** (2) 314-317.
- Singh, A. and Singh, H. N. 1976. Genetic divergence in chilli. *Indian Journal of Genetics and Plant Breeding* **36**: 425-430.
- Sarhan, A. R. T. and Sharif, F. M. 1986. Integrated control of *Fusarium* wilt of pepper. *Acta Phytopathologica et Entomologica Hungarica* **21**: 123-126.
- Singh, A. and Singh, A. K. 1998. Screening of chilli germplasm against *Fusarium* wilt. *Crop Research* **15**: 132-133.
- Singh, J. K., Manoj, K., Sanjeev, K., Anil, K. and Naresh, M. 2017. Effect of botanicals on growth and sporulation of *Fusarium oxysporum* inciting wilt of Chilli (*Capsicum annum* L.). *Journal of Pharmacognosy and Phytochemistry* **6**: 2199-2204.
- Srivastava, V. K. and Diwakar, M. C. 1987. Note on stem rot and wilt of chillies in Haryana. *Plant Protection Bulletin* **39**: 35.
- Sarkar, S., Murmu, D., Chattopadhyay, A. and Hazra, P. 2009. Genetic variability, correlation and path analysis of some morphological characters in chilli. *Journal of Crop and Weed* **5**(1): 162-166.
- Singh, A. K. and Chaudhary, B. R. 2011. Genetic architecture in the improvement of chilli (*Capsicum annum* L.) crops. *Vegetable Science* **24**(1): 132-136.
- Singh, Y., Sharma, M. and Sharma, A. 2009. Genetic variation, association of characters, and their direct and indirect contributions for improvement in chilli peppers. *International Journal of Vegetable Science* **15**(4): 340-368.
- Sreelathakumary, I. and Rajamony, L. 2004. Variability, heritability and genetic gain in chilli (*Capsicum annum* L.). *Journal of Tropical Agriculture* **42**(1-2): 35-37.

- Sudre, C. P., Rodrigues, R., Riva, E. M., Karasawa, M. and Amaraljunior, A.T. 2005. Genetic divergence between chilli and sweet pepper accessions using Multivariate techniques. *Horticultura Brasileira* **23**(1): 22-27.
- Smitha, R. P. and Basavaraja, N. 2006b. Variability and correlation studies in chilli (*Capsicum annuum* L.). *Karnataka Journal of Agricultural Sciences* **19**(4): 888-891.
- Surya, S. K., Srihari, D., Shankar, C. R., Reddy, V. C., and Sanker, A.S. 2014. Genetic divergence and combining ability studies for exploitation of heterosis in paprika (*Capsicum annum* L.). *International Journal of Agricultural Science and Research* **4**(2): 59-66.
- Savolainen, V., Cowan, R. S., Vogler, A. P., Roderick, G. K. and Lane, R. 2005. Towards writing the encyclopedia of life: an introduction to DNA barcoding. *Philosophical Transactions of the Royal Society* **360**: 1805-1811.
- Sreelathakumari, I. and Rajamony, L. 2002. Variability, heritability and correlation studies in chilli (*Capsicum* spp.) under shade. *Indian Journal of Horticulture* **59**: 493-494.
- Sharma, V. K., Semwal, C. S. and Uniyal, S. P. 2010. Genetic variability and character association analysis in bell pepper (*Capsicum annuum* L.). *Journal of Horticulture and Forestry* **2**(3): 58-65.
- Smitha, R. P. and Basavaraja, N. 2006a. Genetic divergence studies in chilli (*Capsicum annuum* L.). *Karnataka Journal of Agricultural Sciences* **19**(4): 975-977.
- Smitha, R. P. and Basavaraja, N. 2006b. Variability and Correlation Studies in Chilli (*Capsicum annuum* L.). *Karnataka Journal of Agricultural Sciences* **19** (4): 888-891.

- Srivastava, U., Mahajan, R. K. and Gangpadhyay, K. K., 2001. *Minimal Descriptors of Agri-Horticultural Crops* (part II). NBPGR, New Delhi/India.
- Singh, R. K. and Singh, D. B. 2010. Genetic divergence and selection of genotypes in chilli (*Capsicum annuum* L.). *Green Farming* **3**(2): 116-118.
- Shweta, Basavarajappa, H. R. and Satish, D. 2018. Genetic correlation and path coefficient analysis in chilli (*Capsicum annum* L.) genotypes for growth and yield contributing traits. *Journal of Pharmacognosy and Phytochemistry* **7**(2): 1312-1315.
- Simmonds, N. W. and Shepherd, K. 1955 .The taxonomy and origins of the cultivated Bananas. *The Botanical Journal of Linnean Society of London* **55**:302-312.
- Singh, R. K. and Choudhary, B. D. 1985. Biometrical Methods in Quantitative Genetic Analysis. Kalyani Publishers, Ludhiana/NewDelhi.
- Shoba., Tembhurne, B. V., Naik, M. K., Khan, H. And Patil, B. V. 2018. Screening of M₄ mutants of chilli (*Capsicum annum* L.) against *Fusarium* wilt (*Fusarium solani*) resistance. *International Journal of Current Microbiology and Applied Sciences* **7**:879-884.
- Tariq, R. R. 2005. Studies on the wilt complex disease of chilli (*Capsicum annum* L.). Ph. D. Thesis submitted to Sher-e-Kashmir University of Agricultural Sciences and Technology of Jammu.
- Tayyaba, S., Farah-Naz., Muhammad, I. U. H., Shahid, B. and Muhammad, F. A. 2014. Characterization and relative contribution of fungal and bacterial pathogens involved in sudden death syndrome of chillies. *Pakistan Journal of Phytopatology* **26**: 51-59.

- Toshi, L., Buonauro, R. and Guiderdone, S. M. 2000. Pepper wilt caused by *Fusarium solani* in Central Italy. *Atti Giornate fitopatologiche Perugia* **2**: 305-306.
- Thul, S.T., Lal, R. K., Shasany, A. K., Darokar, M. P., Gupta, A. K., Gupta, M. M., Verma R. K. and Khanuja, S. P. S. 2009. Estimation of phenotypic divergence in a collection of *Capsicum* species for yield-related traits. *Euphytica* **168**(2):189-196.
- Tembhurne, B.V., Belabadevi, B., Kisan, B., Tilak, I.S., Ashwathanarayana, D. S., Survana., Nidagundi. and Naik, M. K. 2017. Molecular characterization and screening for *Fusarium* (*Fusarium solani*) resistance in chilli (*Capsicum annum* L.) genotypes. *International Journal of current microbiology and applied sciences* **9**:1585-1597.
- Thoyajakshi Bai, A., Ruth, Ch., Gopal, K., Arunodhayam, K., Tanuja priya, B. and Ramakrishna, M. 2018. Survey and identification of *Fusarium* wilt disease in chilli (*Capsicum annum* L.). *International Journal of Current Microbiology and Applied Sciences* **7**: 06.
- Tembhurne, B. V., Revanappa and Kuchanur, P. H. 2008. Varietal Performance, Genetic Variability and Correlation Studies in Chilli (*Capsicum annum* L.). *Karnataka Journal of Agricultural Sciences* **21**(4) 541-543.
- Thind, T. S. and Jhooty, J. S. 1985. Relative prevalence of fungal diseases of chilli fruits in Punjab. *Indian Journal of Mycology and Plant Pathology* **15**: 305-307.
- Verma, S. K., Singh, R. K. and Arya, R. R. 2004. Genetic variability and correlation studies in chillies. *Progressive Horticulture* **36**(1): 113-117.
- Varalakshmi, B. and Haribabu, K. 1991. Genetic divergence, heritability and genetic gain in chilli (*Capsicum annum* L.). *Indian Journal of Genetics and Plant Breeding* **51**: 174-178.

- Viana, A. P., Pereira, T. N. S., Pereira, M. G., Souza, M. M. and Maldonado, J. F. M. 2006. Genetic diversity in yellow passion fruit populations. *Crop Breeding and Applied Biotechnology* **6**: 87-94.
- Vani, S. K., Sridevi, O. and Salimath, P. M. 2007. Genetic divergence in chilli (*Capsicum annuum* L.). *Annals of Biology* **23**(2): 123-128.
- Vidya, C., Jagtap, V. S., Santhosh, N. 2018. Correlation and Path Coefficient Analysis for Yield and Yield Attributing Characters in Chilli (*Capsicum annuum* L.) genotypes. *International Journal of Current Microbiology Applied Science* **7**(1): 3265-3268.
- Verma, B. R. and Sharma, B. K. 1995. Management of chilli wilt. **In: Proceedings of the National Symposium on Recent Trends in the Management of Biotic and Abiotic Stresses in Plants**, Palampur, India, 2-3, November.
- Vidhyasakaran, P. and Thiagarajan, C. P. 1981. Seed-borne transmission of *Fusarium oxysporum* in chilli. *Indian Phytopathology* **34**: 211-213.
- Wani, M. A. 1994. Studies on fungal wilt of chilli (*Capsicum annuum* L.). M.Sc. (Agri.) thesis submitted to Sher-e-Kashmir University of Agricultural Sciences and Technology of Kashmir, Shalimar, p. 1-74.
- Woolliams, G. E., Denby, L. G. and Hansen, A. S. F. 1962. Screening sweet and hot peppers for Verticillium wilt resistance. *Canadian Journal of Plant Science* **42**: 515-520.
- Williams, P. H. 1979. Vegetable crop protection in the Peoples' Republic of China. *Annual Review of Phytopathology* **17**: 311-324.
- Wangiliar, P. D., Somani, R. B. and Bobade, K. P. 1988. Sclerotium collar rot-a new menace to chilli in Vidharbha. *PKV Research Journal* **12**: 88-89.
- Wahyuni, Y., Ballester, A. R. and Sodarmonowati, E. 2013. Secondary metabolites of *Capsicum* species and their importance in human diet. *Journal of National Production* (online first).

- Wilson, D. and Philip. 2009. Genetic variability and genetic divergence in paprika (*capsicum annum*L.). ICH.pp16.
- Xie, J. H., Cardenas, E. S., Sammis, T. W. and Lindsay, D. L. 1999. Effect of irrigation method on chilli pepper yield and Phytophthora root rot incidence. *Agricultural Water Management* **42**: 127-142.
- Zhani, K. and Hamdi, W. 2015. A comparative study of morphological characterization of Tunisian accessions of Chili pepper (*Capsicum frutescens* L.). *International Research Journal of Engineering and Technology (IRJET)* **2**: 4.
- Zehra, S. B. 2014. Msc. thesis submitted to Division of Vegetable Science, SKUAST-Kashmir, Shalimar, Srinagar.

APPENDIX- I

DUS Characterization of chilli genotypes (*Capsicum annuum* L.)

S. No.	Genotypes	Plant habit	Length of main stem(cm)	Length of first internode	Anthocyanin colouration of nodes	Intensity of anthocyanin colouration of nodes	Plant height(cm)	Plant spread(cm)
1.	SKAU-32	Semi-upright	Long	Long	Present	Medium	Medium	Medium
2.	SKAU-36	Semi-upright	Medium	Medium	Present	Strong	Medium	Medium
3.	SKAU-38	Semi-upright	Medium	Medium	Present	Strong	Medium	Medium
4.	SKAU-40	Spreading	Medium	Long	Present	Medium	Medium	Medium
5.	SKAU-43	Semi-upright	Medium	Long	Present	Medium	Medium	Medium
6.	SKAU-45	Semi-upright	Medium	Long	Present	Medium	Medium	Medium
7.	SKAU-52	Spreading	Medium	Medium	Present	Weak	Medium	Medium
8.	SKAU-58	Semi-upright	Medium	Long	Present	Weak	Medium	Medium
9.	SKAU-62	Upright	Long	Long	Present	Weak	Medium	Medium
10.	SKAU-68	Semi-upright	Small	Medium	Present	Weak	Medium	Medium
11.	SKAU-73	Semi-upright	Small	Medium	Absent	Weak	Medium	Medium
12.	SKAU-77	Semi-upright	Long	Medium	Present	Weak	Medium	Medium
13.	SKAU-80	Upright	Small	Short	Present	Medium	Medium	Medium

14.	SKAU-84	Semi-upright	Long	Long	Present	Strong	Medium	Medium
15.	SKAU-89	Spreading	Long	Long	Present	Strong	Medium	Medium
16.	SKAU-91	Semi-upright	Small	Short	Present	Strong	Medium	Medium
17.	SKAU-96	Spreading	Small	Short	Present	Medium	Medium	Medium
18.	SKAU-106	Semi-upright	Small	Short	Present	Medium	Medium	Medium
19.	SKAU-109	Semi-upright	Small	Short	Present	Medium	Medium	Medium
20.	SKAU-111	Spreading	Long	Short	Present	Weak	Medium	Medium
21.	SKAU-118	Spreading	Small	Medium	Present	Weak	Medium	Medium
22.	SKAU-122	Spreading	Small	Short	Present	Medium	Medium	Narrow
23.	SKAU-128	Spreading	Small	Medium	Absent	Weak	Medium	Medium
24.	SKAU-132	Semi-upright	Small	Medium	Present	Weak	Medium	Medium
25.	SKAU-139	Semi-upright	Small	Medium	Present	Medium	Medium	Medium
26.	SKAU-141	Spreading	Long	Medium	Present	Weak	Medium	Medium
27.	SKAU-148	Spreading	Medium	Medium	Present	Medium	Medium	Medium
28.	SKAU-153	Semi-upright	Medium	Medium	Present	Medium	Medium	Medium
29.	SKAU-157	Semi-upright	Small	Short	Present	Medium	Medium	Medium
30.	SKAU-160	Semi-upright	Small	Short	Present	Medium	Medium	Narrow

S. No.	Traits	Plant habit	Length of main stem(cm)	Length of first internode	Anthocyanin colouration of nodes	Intensity of anthocyanin colouration of nodes	Plant height(cm)	Plant spread(cm)
31	SKAU-163	Semi-upright	Medium	Long	Present	Strong	Medium	Medium
32	SKAU-167	Semi-upright	Small	Short	Present	Medium	Medium	Narrow
33	SKAU-173	Semi-upright	Small	Medium	Absent	Medium	Medium	Medium
34	SKAU-177	Semi-upright	Long	Very short	Present	Weak	Medium	Medium
35	SKAU-181	Semi-upright	Long	Medium	Present	Weak	Medium	Medium
36	SKAU-188	Semi-upright	Long	Short	Present	Weak	Medium	Medium
37	SKAU-191	Semi-upright	Long	Medium	Present	Medium	Medium	Medium
38	SKAU-193	Semi-upright	Long	Medium	Present	Medium	Medium	Medium
39	SKAU-195	Semi-upright	Long	Very short	Present	Medium	Medium	Medium
40	SKAU-198	Semi-upright	Medium	Very Short	Present	Strong	Medium	Medium
41	SKAU-208	Spreading	Medium	Medium	Present	Medium	Medium	Medium
42	SKAU-211	Spreading	Medium	Medium	Absent	Weak	Medium	Medium
43	SKAU-216	Semi-upright	Medium	Short	Present	Weak	Medium	Medium

44	SKAU-218	Semi-upright	Long	Medium	Present	Strong	Medium	Medium
45	SKAU-221	Semi-upright	Long	Long	Present	Strong	Medium	Medium
46	SKAU-224	Semi-upright	Long	Medium	Present	Weak	Medium	Medium
47	SKAU-227	Spreading	Medium	Medium	Present	Strong	Medium	Medium
48	SKAU-231	Semi-upright	Medium	Medium	Present	Weak	Medium	Medium
49	SKAU-233	Semi-upright	Medium	Short	Present	Weak	Medium	Medium
50	SKAU-237	Semi-upright	Long	Medium	Present	Weak	Medium	Medium
51	SKAU-243	Semi-upright	Long	Medium	Present	Weak	Medium	Narrow
52	SKAU-247	Semi-upright	Medium	Short	Present	Weak	Medium	Medium
53	SC-104	Semi-upright	Long	Long	Present	Medium	Medium	Medium
54	SC-1019	Upright	Long	Long	Present	Strong	Medium	Medium
55	IC-391082	Semi-upright	Medium	Short	Present	Weak	Medium	Medium
56	IC-505242	Semi-upright	Medium	Short	Present	Weak	Medium	Medium
57	IC-561617	Semi-upright	Long	Long	Present	Weak	Medium	Medium
58	Local Kashmiri Chilli-1	Spreading	Small	Short	Present	Weak	Medium	Medium
59	Arka Lohit	Semi-upright	Long	Medium	Present	Weak	Medium	Medium
60	KL-1	Semi-upright	Small	Medium	Present	Strong	Medium	Medium

S. No.	Genotypes	Stem pubescence	Intensity of pubescence	Stem shape	Length of leaf blade	Width of leaf blade	Leaf colour	Intensity of green colour
1.	SKAU-32	Present	Sparse	Round	Long	Broad	Green	Medium
2.	SKAU-36	Present	Sparse	Round	Long	Broad	Greenwithpurple tinge	Light
3.	SKAU-38	Present	Sparse	Round	Long	Broad	Green	Light
4.	SKAU-40	Present	Sparse	Round	Long	Broad	Greenwith purple tinge	Light
5.	SKAU-43	Present	Sparse	Round	Long	Broad	Green	Dark
6.	SKAU-45	Present	Sparse	Round	Long	Broad	Greenwith purple tinge	Light
7.	SKAU-52	Present	Sparse	Round	Long	Broad	Green	Light
8.	SKAU-58	Present	Sparse	Round	Long	Broad	Green	Dark
9.	SKAU-62	Present	Sparse	Round	Long	Broad	Green	Medium
10.	SKAU-68	Present	Sparse	Round	Long	Broad	Green	Dark
11.	SKAU-73	Present	Sparse	Round	Long	Broad	Green	Light
12.	SKAU-77	Present	Sparse	Round	Long	Broad	Green	Medium
13.	SKAU-80	Present	Sparse	Round	Long	Broad	Greenwith purple tinge	Light
14.	SKAU-84	Present	Sparse	Round	Long	Broad	Greenwith purple tinge	Light
15.	SKAU-89	Present	Sparse	Round	Long	Broad	Green	Dark
16.	SKAU-91	Present	Sparse	Round	Long	Broad	Green	Dark

17.	SKAU-96	Present	Sparse	Round	Long	Broad	Green	Dark
18.	SKAU-106	Present	Sparse	Round	Long	Broad	Green	Light
19.	SKAU-109	Present	Sparse	Round	Long	Broad	Green	Medium
20.	SKAU-111	Present	Sparse	Round	Long	Broad	Green	Light
21.	SKAU-118	Present	Sparse	Round	Long	Broad	Green	Medium
22.	SKAU-122	Present	Sparse	Round	Long	Broad	Green	Medium
23.	SKAU-128	Present	Sparse	Round	Long	Broad	Green	Medium
24.	SKAU-132	Present	Sparse	Round	Long	Broad	Green	Medium
25.	SKAU-139	Present	Sparse	Round	Long	Broad	Green	Medium
26.	SKAU-141	Present	Sparse	Round	Long	Broad	Green	Medium
27.	SKAU-148	Present	Sparse	Round	Long	Broad	Green with purple tinge	Light
28.	SKAU-153	Present	Sparse	Round	Long	Broad	Green	Medium
29.	SKAU-157	Present	Sparse	Round	Long	Broad	Green	Medium
30.	SKAU-160	Present	Sparse	Round	Long	Broad	Green	Light
S. No.	Traits	Stem pubescence	Intensity of pubescence	Stem shape	Length of leaf blade	Width of leaf blade	Leaf colour	Intensity of green colour
31	SKAU-163	Present	Sparse	Round	Long	Broad	Green	Light
32	SKAU-167	Present	Sparse	Round	Long	Broad	Green	Light

33	SKAU-173	Present	Sparse	Round	Long	Broad	Green	Dark
34	SKAU-177	Absent	Sparse	Round	Long	Broad	Green	Light
35	SKAU-181	Absent	Sparse	Round	Long	Broad	Green	Medium
36	SKAU-188	Absent	Sparse	Round	Long	Broad	Green	Medium
37	SKAU-191	Present	Sparse	Round	Long	Broad	Green	Medium
38	SKAU-193	Present	Sparse	Round	Long	Broad	Green	Medium
39	SKAU-195	Present	Sparse	Round	Long	Broad	Green	Medium
40	SKAU-198	Present	Sparse	Round	Long	Broad	Green	Light
41	SKAU-208	Present	Sparse	Round	Long	Broad	Green	Dark
42	SKAU-211	Present	Sparse	Round	Long	Broad	Green	Medium
43	SKAU-216	Present	Sparse	Round	Long	Broad	Green	Medium
44	SKAU-218	Present	Sparse	Round	Long	Broad	Green	Medium
45	SKAU-221	Present	Sparse	Round	Long	Broad	Green	Medium
46	SKAU-224	Present	Sparse	Round	Long	Broad	Green	Medium
47	SKAU-227	Present	Sparse	Round	Long	Broad	Green	Medium
48	SKAU-231	Present	Sparse	Round	Long	Broad	Green	Medium
49	SKAU-233	Present	Sparse	Round	Long	Broad	Green	Medium

50	SKAU-237	Present	Sparse	Round	Long	Broad	Green	Medium
51	SKAU-243	Present	Sparse	Round	Long	Broad	Green	Medium
52	SKAU-247	Present	Sparse	Round	Long	Broad	Green	Medium
53	SC-104	Present	Sparse	Round	Long	Broad	Green	Medium
54	SC-1019	Present	Sparse	Round	Long	Broad	Green	Medium
55	IC-391082	Present	Sparse	Round	Long	Broad	Green	Medium
56	IC-505242	Present	Sparse	Round	Long	Broad	Green	Medium
57	IC-561617	Present	Sparse	Round	Long	Broad	Green	Medium
58	Local Kashmiri Chilli-1	Present	Sparse	Round	Long	Broad	Green	Medium
59	Arka Lohit	Present	Sparse	Round	Long	Broad	Green	Medium
60	KL-1	Absent	Sparse	Round	Long	Broad	Green	Medium

S. No.	Genotypes	Intensity of purple colour	Leaf shape	Undulation of margin	Leaf pubescence	Intensity of pubescence	Petal colour	Anther colour
1.	SKAU-32	Light	Lanceolate	Weak	Absent	Sparse	White	Pale blue
2.	SKAU-36	Medium	Lanceolate	Medium	Present	Sparse	White	Pale blue
3.	SKAU-38	Light	Ovate	Medium	Absent	Sparse	White	Pale blue
4.	SKAU-40	Medium	Lanceolate	Medium	Present	Sparse	White	Pale blue
5.	SKAU-43	Light	Lanceolate	Medium	Present	Sparse	White	Pale blue
6.	SKAU-45	Medium	Lanceolate	Weak	Present	Sparse	White	Pale blue
7.	SKAU-52	Light	Lanceolate	Medium	Present	Sparse	White	Pale blue
8.	SKAU-58	Light	Lanceolate	Strong	Present	Sparse	White	Pale blue
9.	SKAU-62	Light	Ovate	Weak	Present	Sparse	White	Pale blue
10.	SKAU-68	Light	Broad elliptic	Strong	Present	Sparse	White	Pale blue
11.	SKAU-73	Light	Lanceolate	Weak	Present	Sparse	White	Pale blue
12.	SKAU-77	Light	Lanceolate	Weak	Present	Sparse	White	Pale blue
13.	SKAU-80	Medium	Broad elliptic	Weak	Present	Sparse	White	Pale blue
14.	SKAU-84	Medium	Broad elliptic	Weak	Present	Sparse	White	Pale blue
15.	SKAU-89	Light	Ovate	Weak	Present	Sparse	White	Pale blue

16.	SKAU-91	Light	Lanceolate	Weak	Present	Sparse	White	Pale blue
17.	SKAU-96	Light	Lanceolate	Weak	Present	Sparse	White	Pale blue
18.	SKAU-106	Light	Lanceolate	Weak	Present	Sparse	White	Pale blue
19.	SKAU-109	Light	Ovate	Weak	Present	Sparse	White	Pale blue
20.	SKAU-111	Light	Lanceolate	Weak	Present	Sparse	White	Pale blue
21.	SKAU-118	Light	Lanceolate	Weak	Present	Sparse	White	Pale blue
22.	SKAU-122	Light	Lanceolate	Weak	Present	Sparse	White	Pale blue
23.	SKAU-128	Light	Lanceolate	Weak	Present	Sparse	White	Pale blue
24.	SKAU-132	Light	Lanceolate	Weak	Present	Sparse	White	Pale blue
25.	SKAU-139	Light	Ovate	Weak	Present	Sparse	White	Pale blue
26.	SKAU-141	Light	Ovate	Weak	Present	Sparse	White	Pale blue
27.	SKAU-148	Medium	Broad elliptic	Weak	Present	Sparse	White	Pale blue
28.	SKAU-153	Light	Lanceolate	Weak	Present	Sparse	White	Pale blue
29.	SKAU-157	Light	Lanceolate	Weak	Present	Sparse	White	Pale blue
30.	SKAU-160	Light	Lanceolate	Weak	Present	Sparse	White	Pale blue

S. No.	Traits	Intensity of purple colour	Leaf shape	Undulation of margin	Leaf pubescence	Intensity of pubescence	Petal colour	Anther colour
31	SKAU-163	Light	Lanceolate	Weak	Present	Sparse	White	Pale blue
32	SKAU-167	Light	Lanceolate	Weak	Present	Sparse	White	Pale blue
33	SKAU-173	Light	Lanceolate	Medium	Absent	Sparse	White	Pale blue
34	SKAU-177	Light	Lanceolate	Medium	Present	Sparse	White	Pale blue
35	SKAU-181	Light	Ovate	Medium	Present	Sparse	White	Pale blue
36	SKAU-188	Light	Lanceolate	Weak	Present	Sparse	White	Pale blue
37	SKAU-191	Light	Lanceolate	Weak	Absent	Sparse	White	Pale blue
38	SKAU-193	Light	Lanceolate	Medium	Absent	Sparse	White	Pale blue
39	SKAU-195	Light	Lanceolate	Medium	Present	Sparse	White	Pale blue
40	SKAU-198	Light	Lanceolate	Weak	Present	Sparse	White	Pale blue
41	SKAU-208	Light	Ovate	Weak	Present	Sparse	White	Pale blue
42	SKAU-211	Light	Ovate	Weak	Present	Sparse	White	Pale blue
43	SKAU-216	Light	Lanceolate	Medium	Present	Sparse	White	Pale blue
44	SKAU-218	Light	Lanceolate	Medium	Present	Sparse	White	Pale blue
45	SKAU-221	Light	Lanceolate	Weak	Present	Sparse	White	Pale blue
46	SKAU-224	Light	Lanceolate	Weak	Present	Sparse	White	Pale blue

47	SKAU-227	Light	Lanceolate	Weak	Present	Sparse	White	Pale blue
48	SKAU-231	Light	Lanceolate	Weak	Present	Sparse	White	Pale blue
49	SKAU-233	Light	Lanceolate	Weak	Present	Sparse	White	Pale blue
50	SKAU-237	Light	Lanceolate	Weak	Present	Sparse	White	Pale blue
51	SKAU-243	Light	Lanceolate	Weak	Present	Sparse	White	Pale blue
52	SKAU-247	Light	Lanceolate	Weak	Present	Sparse	White	Pale blue
53	SC-104	Light	Lanceolate	Weak	Present	Sparse	White	Pale blue
54	SC-1019	Light	Lanceolate	Weak	Present	Sparse	White	Pale blue
55	IC-391082	Light	Lanceolate	Weak	Present	Sparse	White	Pale blue
56	IC-505242	Light	Lanceolate	Weak	Present	Sparse	White	Pale blue
57	IC-561617	Light	Lanceolate	Weak	Present	Sparse	White	Pale blue
58	Local Kashmiri Chilli-1	Light	Lanceolate	Weak	Present	Sparse	White	Pale blue
59	Arka Lohit	Light	Lanceolate	Weak	Present	Sparse	White	Pale blue
60	KL-1	Light	Lanceolate	Medium	Present	Sparse	White	Pale blue

S. No.	Genotypes	Days to 50% flowering	Fruit orientation	Fruit bearing habit	Fruit colour (mature unripe)	Intensity of colour	Fruit length	Fruit diameter
1.	SKAU-32	Medium	Drooping	Solitary	Green	Medium	Long	Medium
2.	SKAU-36	Medium	Drooping	Solitary	Green	Dark	Long	Medium
3.	SKAU-38	Medium	Drooping	Solitary	Green	Medium	Long	Broad
4.	SKAU-40	Medium	Drooping	Solitary	Green	Dark	Long	Medium
5.	SKAU-43	Medium	Drooping	Solitary	Green	Light	Long	Medium
6.	SKAU-45	Medium	Drooping	Solitary	Green	Dark	Long	Medium
7.	SKAU-52	Medium	Drooping	Solitary	Green	Dark	Long	Medium
8.	SKAU-58	Medium	Drooping	Solitary	Green	Light	Long	Medium
9.	SKAU-62	Medium	Drooping	Solitary	Green	Dark	Long	Medium
10.	SKAU-68	Medium	Semi drooping	Solitary	Green	Light	Long	Medium
11.	SKAU-73	Medium	Drooping	Solitary	Green	Medium	Long	Medium
12.	SKAU-77	Medium	Drooping	Solitary	Green	Light	Long	Medium
13.	SKAU-80	Medium	Drooping	Solitary	Green	Dark	Long	Medium
14.	SKAU-84	Medium	Drooping	Solitary	Green	Dark	Long	Medium
15.	SKAU-89	Medium	Drooping	Solitary	Green	Dark	Long	Medium
16.	SKAU-91	Medium	Drooping	Solitary	Green	Light	Long	Medium

17.	SKAU-96	Medium	Drooping	Solitary	Green	Dark	Long	Medium
18.	SKAU-106	Medium	Semi drooping	Solitary	Green	Dark	Long	Medium
19.	SKAU-109	Medium	Drooping	Solitary	Green	Dark	Long	Medium
20.	SKAU-111	Medium	Drooping	Solitary	Green	Dark	Long	Medium
21.	SKAU-118	Medium	Drooping	Solitary	Green	Dark	Long	Medium
22.	SKAU-122	Medium	Drooping	Solitary	Green	Medium	Long	Medium
23.	SKAU-128	Medium	Drooping	Solitary	Green	Dark	Long	Medium
24.	SKAU-132	Medium	Drooping	Solitary	Green	Dark	Long	Medium
25.	SKAU-139	Medium	Drooping	Solitary	Green	Dark	Long	Medium
26.	SKAU-141	Medium	Drooping	Solitary	Green	Medium	Long	Medium
27.	SKAU-148	Medium	Drooping	Solitary	Green	Dark	Long	Medium
28.	SKAU-153	Medium	Drooping	Solitary	Green	Dark	Long	Medium
29.	SKAU-157	Medium	Drooping	Solitary	Green	Light	Long	Medium
30.	SKAU-160	Medium	Drooping	Solitary	Green	Light	Long	Medium

. No.	Traits	Days to 50% flowering	Fruit orientation	Fruit bearing habit	Fruit colour (mature unripe)	Intensity of colour	Fruit length	Fruit diameter
31	SKAU-163	Medium	Drooping	Solitary	Green	Light	Long	Medium
32	SKAU-167	Medium	Drooping	Solitary	Green	Medium	Long	Medium
33	SKAU-173	Late	Drooping	Solitary	Green	Dark	Long	Medium
34	SKAU-177	Late	Drooping	Solitary	Green	Light	Long	Medium
35	SKAU-181	Late	Drooping	Solitary	Green	Light	Long	Medium
36	SKAU-188	Late	Drooping	Solitary	Green	Light	Long	Medium
37	SKAU-191	Late	Drooping	Solitary	Green	Light	Long	Medium
38	SKAU-193	Late	Drooping	Solitary	Green	Light	Long	Medium
39	SKAU-195	Late	Drooping	Solitary	Green	Dark	Long	Medium
40	SKAU-198	Late	Drooping	Solitary	Green	Medium	Long	Medium
41	SKAU-208	Late	Drooping	Solitary	Green	Medium	Long	Medium
42	SKAU-211	Late	Drooping	Solitary	Green	Dark	Long	Medium
43	SKAU-216	Late	Drooping	Solitary	Green	Medium	Long	Medium
44	SKAU-218	Late	Drooping	Solitary	Green	Medium	Long	Medium
45	SKAU-221	Late	Drooping	Solitary	Green	Light	Long	Broad

46	SKAU-224	Late	Drooping	Solitary	Green	Light	Long	Medium
47	SKAU-227	Late	Drooping	Solitary	Green	Light	Long	Medium
48	SKAU-231	Late	Drooping	Solitary	Green	Dark	Long	Medium
49	SKAU-233	Late	Drooping	Solitary	Green	Medium	Long	Medium
50	SKAU-237	Late	Drooping	Solitary	Green	Light	Long	Medium
51	SKAU-243	Late	Drooping	Solitary	Green	Medium	Long	Medium
52	SKAU-247	Late	Drooping	Solitary	Green	Light	Long	Medium
53	SC-104	Late	Drooping	Solitary	Green	Medium	Long	Medium
54	SC-1019	Late	Drooping	Solitary	Green	Medium	Long	Medium
55	IC-391082	Late	Drooping	Solitary	Green	Light	Long	Medium
56	IC-505242	Medium	Drooping	Solitary	Green	Medium	Long	Medium
57	IC-561617	Late	Drooping	Solitary	Green	Medium	Long	Medium
58	Local Kashmiri Chilli-1	Medium	Drooping	Solitary	Green	Light	Long	Medium
59	Arka Lohit	Medium	Drooping	Solitary	Green	Medium	Long	Medium
60	KL-1	Late	Drooping	Solitary	Green	Light	Long	Medium

S. No.	Genotypes	Fruit curvature	Fruit curvature intensity	Fruit neck at basal end	Fruit sinuation of pericarp	Fruit texture of surface	Fruit colour	Intensity of colour
1.	SKAU-32	Absent	Low	Present	Medium	Slightly rough	Red	Medium
2.	SKAU-36	Present	Low	Absent	Weak	Smooth	Red	Medium
3.	SKAU-38	Present	Low	Present	Medium	Slightly rough	Red	Medium
4.	SKAU-40	Present	Low	Absent	Medium	Slightly rough	Red	Medium
5.	SKAU-43	Present	Low	Absent	Medium	Smooth	Red	Medium
6.	SKAU-45	Present	Low	Absent	Medium	Smooth	Red	Medium
7.	SKAU-52	Present	Low	Absent	Weak	Smooth	Red	Medium
8.	SKAU-58	Present	Low	Absent	Weak	Smooth	Red	Medium
9.	SKAU-62	Absent	Low	Absent	Weak	Smooth	Red	Medium
10.	SKAU-68	Absent	Low	Absent	Medium	Slightly rough	Red	Medium
11.	SKAU-73	Present	Low	Absent	Medium	Slightly rough	Red	Medium
12.	SKAU-77	Present	Low	Present	Medium	Slightly rough	Red	Medium
13.	SKAU-80	Absent	Low	Absent	Medium	Smooth	Red	Medium
14.	SKAU-84	Present	Low	Absent	Medium	Slightly rough	Red	Medium
15.	SKAU-89	Absent	Low	Absent	Medium	Slightly rough	Red	Medium
16.	SKAU-91	Present	Low	Absent	Medium	Slightly rough	Red	Medium

17.	SKAU-96	Present	Low	Absent	Medium	Slightly rough	Red	Medium
18.	SKAU-106	Absent	Low	Absent	Medium	Slightly rough	Red	Medium
19.	SKAU-109	Present	Low	Absent	Medium	Smooth	Red	Medium
20.	SKAU-111	Present	Low	Absent	Weak	Smooth	Red	Medium
21.	SKAU-118	Present	Low	Absent	Weak	Smooth	Red	Medium
22.	SKAU-122	Present	Low	Absent	Weak	Smooth	Red	Medium
23.	SKAU-128	Present	Low	Absent	Weak	Slightly rough	Red	Medium
24.	SKAU-132	Present	Low	Absent	Medium	Slightly rough	Red	Medium
25.	SKAU-139	Present	Low	Absent	Medium	Smooth	Red	Medium
26.	SKAU-141	Present	Low	Absent	Medium	Smooth	Red	Medium
27.	SKAU-148	Present	Low	Absent	Medium	Smooth	Red	Medium
28.	SKAU-153	Present	Low	Absent	Weak	Smooth	Red	Medium
29.	SKAU-157	Present	Low	Absent	Medium	Slightly rough	Red	Medium
30.	SKAU-160	Present	Low	Absent	Medium	Slightly rough	Red	Medium

S. No.	Traits	Fruit curvature	Fruit curvature intensity	Fruit neck at basal end	Fruit sinuation of pericarp	Fruit texture of surface	Fruit colour	Intensity of colour
31	SKAU-163	Present	Low	Absent	Medium	Slightly rough	Red	Medium
32	SKAU-167	Present	Low	Absent	Medium	Slightly rough	Red	Medium
33	SKAU-173	Present	Low	Present	Weak	Smooth	Red	Medium
34	SKAU-177	Present	Low	Present	Weak	Smooth	Red	Medium
35	SKAU-181	Present	Medium	Present	Medium	smooth	Red	Medium
36	SKAU-188	Present	Low	Present	Medium	Slightly rough	Red	Medium
37	SKAU-191	Present	Medium	Present	Medium	Slightly rough	Red	Medium
38	SKAU-193	Present	Medium	Present	Medium	Rough	Red	Medium
39	SKAU-195	Present	Low	Present	Medium	Rough	Red	Medium
40	SKAU-198	Present	Low	Present	Medium	Smooth	Red	Medium
41	SKAU-208	Present	Low	Present	Weak	Smooth	Red	Medium
42	SKAU-211	Present	Medium	Present	Weak	Smooth	Red	Medium
43	SKAU-216	Present	Low	Present	Weak	Slightly rough	Red	Medium
44	SKAU-218	Present	Low	Present	Weak	Smooth	Red	Medium
45	SKAU-221	Present	Low	Present	Weak	Smooth	Red	Medium
46	SKAU-224	Present	Low	Present	Weak	Smooth	Red	Medium

47	SKAU-227	Present	Low	Present	Strong	Smooth	Red	Medium
48	SKAU-231	Present	Low	Absent	Weak	Smooth	Red	Medium
49	SKAU-233	Present	Low	Absent	Medium	Smooth	Red	Medium
50	SKAU-237	Present	Low	Absent	Medium	Smooth	Red	Medium
51	SKAU-243	Present	Low	Absent	Weak	Smooth	Red	Medium
52	SKAU-247	Present	Low	Absent	Medium	Smooth	Red	Medium
53	SC-104	Present	Low	Present	Weak	Slightly rough	Red	Medium
54	SC-1019	Present	Medium	Absent	Weak	Smooth	Red	Medium
55	IC-391082	Present	Low	Absent	Weak	Smooth	Red	Medium
56	IC-505242	Present	Low	Absent	Weak	Smooth	Red	Medium
57	IC-561617	Present	Low	Absent	Weak	Smooth	Red	Medium
58	Local Kashmiri Chilli-1	Present	Low	Absent	Medium	Slightly rough	Red	Medium
59	Arka Lohit	Present	Low	Absent	Medium	Smooth	Red	Medium
60	KL-1	Present	Medium	Present	Weak	Slightly rough	Red	Medium

S. No.	Genotypes	Fruit shape at base	Fruit shape of apex	Calyx cover	Calyx margin	Calyx constriction	Pedicel attachment	Blossom end appendage
1.	SKAU-32	Round	Blunt	Non-enveloping	Dented	Present	Strong	Absent
2.	SKAU-36	Acute	Acute	Enveloping	Dented	Absent	Weak	Present
3.	SKAU-38	Round	Acute	Non-enveloping	Dented	Present	Strong	Absent
4.	SKAU-40	Acute	Acute	Non-enveloping	Dented	Present	Weak	Absent
5.	SKAU-43	Acute	Acute	Enveloping	Dented	Absent	Weak	Present
6.	SKAU-45	Acute	Acute	Enveloping	Dented	Absent	Weak	Absent
7.	SKAU-52	Acute	Acute	Enveloping	Dented	Absent	Weak	Absent
8.	SKAU-58	Acute	Acute	Enveloping	Dented	Absent	Weak	Present
9.	SKAU-62	Acute	Acute	Enveloping	Dented	Absent	Strong	Present
10.	SKAU-68	Acute	Acute	Enveloping	Dented	Present	Strong	Absent
11.	SKAU-73	Round	Acute	Enveloping	Dented	Present	Strong	Absent
12.	SKAU-77	Acute	Acute	Enveloping	Dented	Present	Strong	Absent
13.	SKAU-80	Acute	Acute	Enveloping	Smooth	Absent	Weak	Present
14.	SKAU-84	Acute	Acute	Enveloping	Smooth	Absent	Weak	Present
15.	SKAU-89	Acute	Acute	Enveloping	Dented	Absent	Weak	Absent
16.	SKAU-91	Acute	Acute	Enveloping	Dented	Absent	Strong	Absent

17.	SKAU-96	Acute	Acute	Enveloping	Smooth	Absent	Strong	Absent
18.	SKAU-106	Acute	Acute	Enveloping	Dented	Present	Strong	Absent
19.	SKAU-109	Acute	Acute	Enveloping	Dented	Present	Strong	Absent
20.	SKAU-111	Acute	Acute	Enveloping	Dented	Absent	Weak	Absent
21.	SKAU-118	Acute	Acute	Enveloping	Dented	Absent	Weak	Present
22.	SKAU-122	Acute	Acute	Enveloping	Dented	Absent	Weak	Present
23.	SKAU-128	Acute	Acute	Enveloping	Dented	Absent	Strong	Absent
24.	SKAU-132	Acute	Acute	Enveloping	Dented	Absent	Strong	Absent
25.	SKAU-139	Acute	Acute	Enveloping	Dented	Absent	Strong	Absent
26.	SKAU-141	Acute	Acute	Enveloping	Dented	Absent	Strong	Absent
27.	SKAU-148	Acute	Acute	Enveloping	Dented	Absent	Strong	Absent
28.	SKAU-153	Acute	Acute	Enveloping	Dented	Absent	Strong	Absent
29.	SKAU-157	Acute	Acute	Enveloping	Dented	Absent	Strong	Absent
30.	SKAU-160	Acute	Acute	Enveloping	Dented	Absent	Strong	Absent

S. No.	Traits	Fruit shape at base	Fruit shape of apex	Calyx cover	Calyx margin	Calyx constriction	Pedicel attachment	Bolossom end appendage
31	SKAU-163	Acute	Acute	Enveloping	Dented	Absent	Strong	Absent
32	SKAU-167	Acute	Acute	Enveloping	Dented	Absent	Strong	Absent
33	SKAU-173	Acute	Acute	Enveloping	Dented	Absent	Strong	Present
34	SKAU-177	Acute	Acute	Enveloping	Dented	Absent	Weak	Absent
35	SKAU-181	Acute	Acute	Enveloping	Dented	Absent	Strong	Present
36	SKAU-188	Acute	Acute	Enveloping	Dented	Absent	Weak	Absent
37	SKAU-191	Acute	Acute	Enveloping	Dented	Absent	Weak	Present
38	SKAU-193	Acute	Acute	Enveloping	Dented	Absent	Weak	Present
39	SKAU-195	Acute	Acute	Enveloping	Dented	Absent	Strong	Present
40	SKAU-198	Acute	Acute	Enveloping	Dented	Absent	Weak	Present
41	SKAU-208	Acute	Acute	Enveloping	Dented	Absent	Weak	Absent
42	SKAU-211	Acute	Acute	Enveloping	Dented	Absent	Strong	Absent
43	SKAU-216	Acute	Acute	Enveloping	Dented	Absent	Weak	Present
44	SKAU-218	Acute	Acute	Enveloping	Dented	Absent	Weak	Present
45	SKAU-221	Acute	Acute	Enveloping	Dented	Absent	Weak	Present
46	SKAU-224	Acute	Acute	Enveloping	Dented	Absent	Weak	Present

47	SKAU-227	Acute	Acute	Enveloping	Dented	Absent	Strong	Present
48	SKAU-231	Acute	Acute	Enveloping	Dented	Absent	Weak	Present
49	SKAU-233	Acute	Acute	Enveloping	Dented	Absent	Weak	Present
50	SKAU-237	Acute	Acute	Enveloping	Dented	Absent	Weak	Present
51	SKAU-243	Round	Acute	Enveloping	Dented	Absent	Weak	Present
52	SKAU-247	Acute	Acute	Enveloping	Dented	Absent	Weak	Present
53	SC-104	Round	Acute	Enveloping	Dented	Present	Strong	Present
54	SC-1019	Round	Acute	Non-Enveloping	Dented	Present	Strong	Absent
55	IC-391082	Acute	Acute	Enveloping	Dented	Absent	Weak	Present
56	IC-505242	Acute	Acute	Enveloping	Dented	Absent	Weak	Present
57	IC-561617	Round	Acute	Non-Enveloping	Dented	Present	Weak	Present
58	Local Kashmiri Chilli-1	Acute	Acute	Enveloping	Dented	Absent	Weak	Absent
59	Arka Lohit	Round	Acute	Enveloping	Dented	Absent	Weak	Present
60	KL-1	Acute	Acute	Enveloping	Dented	Absent	Weak	Present

Appendix -II

Mean performance of chilli (*Capsicum annuum* L.) genotypes for various quantitative traits

S. No.	Genotypes	Plant height (cm)	Plant spread (cm)	No. of branches plant-1	Days to flower initiation	Days to fruit initiation	Days to harvestin g	Fruit length (cm)	Fruit diameter (cm)	Fruit Weight (g)	Fruit pedicel length (cm)	Fruit pedicel diameter (cm)
1.	SKAU-32	63.26	65.16	30.93	24.66	31.53	102.40	8.18	1.32	4.50	3.92	0.31
2.	SKAU-36	61.73	69.39	38.73	35.40	42.66	102.80	9.02	0.78	1.69	5.02	0.28
3.	SKAU-38	81.33	68.74	44.66	24.40	31.53	109.60	15.58	1.52	8.15	5.88	0.33
4	SKAU-40	64.80	82.93	45.93	30.86	42.66	108.40	12.22	1.02	6.28	4.92	0.31
5.	SKAU-43	62.93	82.91	40.80	31.80	42.73	108.86	15.10	1.08	7.18	4.35	0.29
6.	SKAU-45	62.53	84.04	34.46	31.73	42.66	107.26	12.22	1.01	3.25	5.09	0.28
7.	SKAU-52	54.86	81.10	33.80	31.80	42.60	110.46	12.00	0.96	4.19	5.70	0.26
8.	SKAU-58	57.26	62.25	26.93	31.80	42.46	108.93	15.00	1.05	6.28	5.12	0.28
9.	SKAU-62	67.26	85.58	34.26	37.80	44.73	102.60	10.17	0.88	2.36	4.52	0.28
10.	SKAU-68	69.93	73.81	27.53	37.66	44.53	103.66	11.18	0.98	4.40	4.35	0.30
11.	SKAU-73	70.20	81.96	23.73	31.33	42.60	108.06	13.06	1.24	7.46	5.07	0.30
12.	SKAU-77	86.00	68.10	23.20	31.40	42.73	108.93	15.63	1.14	8.28	4.85	0.30
13	SKAU-80	67.06	55.59	22.80	37.66	44.80	109.66	12.90	0.96	3.31	4.92	0.32

14.	SKAU-84	79.20	69.54	31.00	37.60	44.46	102.73	9.95	0.94	3.25	4.16	0.27
15.	SKAU-89	65.93	69.86	23.33	31.60	42.66	107.73	12.14	0.98	4.24	4.95	0.25
16.	SKAU-91	52.40	52.66	31.80	31.40	42.73	109.73	10.11	0.92	2.35	4.58	0.30
17.	SKAU-96	65.33	64.88	22.73	24.66	31.40	102.53	14.90	1.03	4.34	5.32	0.25
18.	SKAU-106	79.46	86.64	31.73	24.60	42.66	102.53	10.12	0.99	3.63	4.76	0.28
19.	SKAU-109	65.13	74.29	29.86	31.40	42.60	109.46	8.54	0.84	3.06	4.44	0.28
20.	SKAU-111	51.93	73.72	31.00	31.40	43.26	109.93	12.75	1.12	6.59	5.34	0.27
21.	SKAU-118	50.53	59.80	25.33	31.46	43.00	108.80	11.57	1.02	4.14	4.53	0.26
22.	SKAU-122	51.73	49.16	26.20	31.60	43.73	109.60	10.21	0.90	4.21	4.76	0.22
23.	SKAU-128	70.00	85.18	25.86	31.60	43.66	110.80	12.79	0.94	4.64	4.97	0.27
24.	SKAU-132	62.33	70.53	24.33	31.73	43.66	110.40	11.87	1.02	4.45	5.04	0.28
25.	SKAU-139	63.53	78.49	29.60	37.66	44.80	102.73	8.98	0.98	2.67	4.79	0.25
26.	SKAU-141	60.20	61.67	36.00	31.73	42.66	109.46	13.21	1.92	9.28	6.01	0.33
27.	SKAU-148	59.60	54.89	26.53	31.73	45.33	110.26	15.97	1.38	8.15	5.80	0.40
28.	SKAU-153	50.00	59.81	22.86	37.66	42.80	102.60	8.46	0.98	1.38	5.04	0.26
29.	SKAU-157	51.73	56.85	23.20	37.66	44.73	109.80	13.16	0.98	3.44	4.67	0.28
30.	SKAU-160	69.00	49.46	21.13	37.66	45.53	108.53	7.00	0.89	2.52	3.91	0.27
31.	SKAU-163	68.66	52.06	20.73	37.13	45.46	109.46	11.00	1.05	3.18	4.03	0.28

32.	SKAU-167	53.53	44.33	14.26	37.40	45.46	110.20	11.42	0.94	3.30	5.08	0.27
33.	SKAU-173	58.66	61.76	48.93	37.66	46.40	129.60	15.08	1.18	7.16	4.69	0.28
34.	SKAU-177	58.26	51.37	44.86	37.46	45.40	130.80	14.90	1.12	6.28	4.88	0.32
35.	SKAU-181	49.16	60.02	47.53	36.13	44.73	125.20	9.16	0.98	4.13	3.10	0.21
36.	SKAU-188	63.00	63.20	46.00	36.66	45.66	134.66	13.75	1.06	5.32	4.72	0.27
37.	SKAU-191	63.73	60.35	46.40	34.80	44.80	129.60	15.08	1.05	5.47	4.96	0.31
38.	SKAU-193	66.06	53.02	41.60	37.73	45.73	129.66	15.08	1.40	8.26	5.12	0.35
39.	SKAU-195	61.33	62.79	41.60	37.53	45.46	134.66	16.03	1.09	6.52	4.96	0.26
40.	SKAU-198	62.26	61.15	42.06	37.53	46.53	134.60	16.07	1.16	7.66	5.05	0.26
41.	SKAU-208	73.20	61.41	45.06	37.60	46.33	134.66	15.46	1.12	7.34	4.96	0.25
42.	SKAU-211	72.73	60.31	41.13	36.93	45.86	129.73	13.41	0.99	5.32	5.89	0.25
43.	SKAU-216	65.00	60.46	33.00	35.86	45.60	134.66	15.73	1.26	8.51	4.75	0.26
44.	SKAU-218	74.20	60.82	36.20	35.60	45.66	129.46	15.05	1.01	5.46	4.64	0.26
45.	SKAU-221	72.06	58.43	39.60	37.66	45.40	114.40	15.96	1.59	6.02	5.25	0.33
46.	SKAU-224	70.26	59.02	43.73	37.60	45.53	121.06	13.36	1.00	4.64	5.14	0.35
47.	SKAU-227	79.73	66.38	36.33	36.80	45.40	128.66	13.50	1.21	7.08	4.04	0.34
48.	SKAU-231	80.73	62.17	35.93	38.46	45.40	131.46	10.69	0.97	3.41	5.18	0.27

49.	SKAU-233	62.13	60.29	39.80	38.46	45.30	128.53	10.31	1.40	4.19	5.39	0.24
50.	SKAU-237	53.06	62.16	39.93	38.60	44.06	129.26	11.50	1.12	5.54	4.59	0.26
51.	SKAU-243	60.40	49.56	39.80	38.40	44.33	124.73	11.78	1.10	6.85	4.30	0.33
52.	SKAU-247	55.46	57.46	40.20	38.60	45.00	129.40	10.66	1.14	6.38	3.62	0.34
53.	SC-104	71.73	61.65	37.33	36.00	45.60	124.80	13.66	1.10	6.26	4.40	0.27
54.	SC-1019	66.86	62.38	39.86	37.66	45.46	129.66	9.94	0.97	4.16	3.92	0.26
55.	IC-391082	52.66	61.33	35.73	37.46	45.73	129.13	8.98	1.10	3.52	4.03	0.25
56.	IC-505242	55.06	58.60	32.73	37.93	45.46	129.93	10.53	1.00	4.37	5.04	0.25
57.	IC-561617	66.46	62.43	39.86	38.00	45.26	128.60	10.42	0.82	2.90	5.31	0.26
58.	Local Kashmiri Chilli-1	49.24	57.70	17.66	31.20	42.20	109.66	7.10	0.95	3.24	2.10	0.24
59.	Arka Lohit	65.80	58.83	41.06	38.46	43.73	129.46	13.00	1.32	9.09	5.17	0.44
60.	KL-1	61.46	63.02	45.53	37.93	45.46	130.53	13.60	1.02	6.49	4.23	0.26
	CD at 5%	1.64	1.45	0.75	0.33	0.11	0.38	0.71	0.20	0.18	0.50	0.03
	SE(d)	0.58	0.51	0.26	0.11	0.32	0.31	0.25	0.07	0.06	0.17	0.01

S. No.	Genotypes	No. of fruits plant-1	Fruit yield plant-1(g)	Fruit yield ha-1 (q)	Dry matter content (%)	Vitamin C (green) (mg100-1g)	Capsaicin content (mg g-1)	Capsanthin content (ASTA units)	Total phenol (mg100-1g)	Instrumental colour L*	Instrument al colour a	Instrumental colour b
1.	SKAU-32	50.46	226.83	71.32	69.42	180.94	0.41	86.46	6.20	45.83	40.78	14.72
2.	SKAU-36	55.06	106.07	33.49	79.51	162.95	0.37	84.68	5.80	42.04	37.24	15.86
3.	SKAU-38	40.60	247.15	78.41	72.12	140.24	0.33	70.14	6.40	38.67	35.25	17.45
4	SKAU-40	49.26	259.62	82.41	82.30	129.50	0.46	72.67	6.56	35.22	30.78	15.78
5.	SKAU-43	39.40	229.75	72.77	79.76	65.52	0.53	82.76	5.73	38.18	34.30	17.77
6.	SKAU-45	42.86	152.91	48.53	74.89	62.62	0.61	94.90	6.16	47.26	42.25	15.90
7.	SKAU-52	41.80	200.38	63.48	85.92	71.06	0.73	94.81	6.56	45.91	41.26	16.13
8.	SKAU-58	35.73	163.42	74.06	75.94	201.16	0.60	66.24	6.43	45.92	40.79	16.11
9.	SKAU-62	50.53	114.19	36.14	76.80	71.00	0.75	107.30	6.26	35.97	31.78	14.90
10.	SKAU-68	53.60	244.36	77.45	77.77	193.44	0.71	109.09	5.83	37.85	34.98	16.12
11.	SKAU-73	50.73	353.57	112.06	70.08	199.76	0.61	85.40	6.13	40.79	35.83	16.79
12.	SKAU-77	48.66	172.01	54.49	75.87	178.69	0.63	96.35	6.43	38.49	33.45	15.85
13	SKAU-80	60.13	251.54	79.78	74.94	88.62	0.57	99.32	6.23	41.45	38.12	15.97
14	SKAU-84	62.66	206.77	66.02	61.54	57.00	0.64	84.13	6.76	43.22	39.33	15.77
15.	SKAU-89	49.86	216.16	68.46	62.86	191.98	0.70	82.19	7.00	45.30	40.19	17.00
16.	SKAU-91	33.73	86.20	27.19	80.66	163.98	0.52	80.80	6.26	35.87	31.43	15.10

17.	SKAU-96	42.73	167.52	53.11	81.30	64.39	0.71	76.00	7.10	38.70	35.15	15.83
18.	SKAU-106	32.13	128.13	40.52	78.10	124.74	0.75	122.20	6.43	41.22	36.91	14.79
19.	SKAU-109	40.86	105.83	33.43	75.02	83.12	0.56	97.81	4.93	41.00	37.10	15.81
20.	SKAU-111	44.93	301.36	95.44	75.02	108.56	0.51	93.72	6.20	46.06	40.66	16.05
21.	SKAU-118	30.40	82.62	26.02	81.94	96.72	0.60	98.20	6.03	50.11	45.26	16.83
22.	SKAU-122	63.73	241.98	76.60	79.93	73.78	0.47	96.59	5.13	48.28	43.32	15.35
23.	SKAU-128	43.60	207.22	65.71	81.92	190.84	0.51	103.33	6.06	39.47	36.53	17.06
24.	SKAU-132	60.13	261.42	82.74	83.19	111.86	0.62	97.74	6.76	37.98	34.96	17.89
25.	SKAU-139	60.00	260.12	82.42	73.90	80.20	0.62	102.72	6.26	40.88	36.13	16.64
26.	SKAU-141	51.00	348.90	110.57	83.10	195.01	0.51	83.96	5.23	38.88	34.98	15.88
27.	SKAU-148	69.13	410.12	130.19	81.54	183.74	0.43	95.36	6.13	41.11	37.88	14.77
28.	SKAU-153	41.40	75.59	23.90	74.00	102.57	0.39	116.52	6.76	36.35	38.26	15.89
29.	SKAU-157	44.93	169.43	53.54	74.18	114.26	0.29	83.39	5.10	41.54	38.34	15.00
30.	SKAU-160	34.66	107.10	33.85	85.74	183.00	0.35	73.27	5.70	36.97	32.01	16.63
31.	SKAU-163	30.53	59.10	186.24	84.80	142.20	0.37	67.28	5.20	42.15	37.43	14.88
32.	SKAU-167	32.40	117.01	36.92	85.84	130.94	0.31	74.67	5.30	41.26	35.83	16.58

33.	SKAU-173	78.73	649.20	206.02	81.72	196.28	0.55	106.69	7.20	41.00	36.13	15.21
34.	SKAU-177	65.26	295.72	93.75	82.84	74.37	0.62	99.68	7.46	41.71	36.98	16.00
35.	SKAU-181	65.06	280.14	88.67	81.30	64.18	0.40	85.02	7.10	36.20	31.11	14.87
36.	SKAU-188	99.86	539.83	171.21	80.00	179.81	0.43	112.06	7.16	41.03	36.03	14.91
37.	SKAU-191	73.80	408.68	129.62	81.41	78.92	0.46	117.30	7.43	38.84	34.51	14.77
38.	SKAU-193	91.86	759.52	239.43	83.49	192.28	0.63	123.63	7.70	45.34	40.15	18.58
39.	SKAU-195	80.80	558.35	177.14	80.06	173.98	0.53	100.33	7.06	46.11	41.10	17.70
40.	SKAU-198	70.53	526.12	166.87	80.20	114.80	0.61	125.83	7.00	44.17	38.66	16.66
41.	SKAU-208	64.40	466.87	148.03	79.44	133.84	0.57	119.29	7.00	42.95	38.22	16.32
42.	SKAU-211	67.73	391.44	124.01	79.98	163.67	0.54	70.71	7.06	41.19	36.36	15.88
43.	SKAU-216	63.93	476.86	151.21	82.85	122.70	0.51	106.69	7.00	39.89	35.00	14.63
44.	SKAU-218	56.20	326.29	103.38	81.53	193.44	0.53	96.18	6.83	41.69	36.74	15.73
45.	SKAU-221	84.00	506.22	160.09	82.90	104.46	0.63	108.20	7.46	41.26	36.34	15.66
46.	SKAU-224	87.13	428.15	135.76	82.90	155.02	0.57	118.76	6.83	39.09	35.87	16.54
47.	SKAU-227	58.40	342.11	108.46	81.84	143.70	0.62	125.05	6.86	37.86	36.09	15.62
48.	SKAU-231	38.66	148.48	46.87	81.65	142.54	0.51	84.30	6.70	39.45	36.13	14.43
49.	SKAU-233	43.53	182.35	57.77	83.91	154.89	0.46	83.33	6.26	40.67	35.81	15.73
50.	SKAU-237	30.80	155.20	49.09	86.07	80.94	0.51	92.72	6.66	40.99	35.78	14.34

51.	SKAU-243	62.20	399.90	126.76	82.82	164.20	0.53	85.26	6.13	40.88	36.47	14.53
52.	SKAU-247	68.80	450.74	142.95	80.06	134.42	0.56	105.43	5.86	41.25	35.91	14.47
53.	SC-104	56.26	261.80	82.95	83.96	196.10	0.47	115.60	6.76	46.20	41.20	15.80
54.	SC-1019	47.86	195.98	62.00	80.11	115.40	0.51	120.49	7.00	49.25	33.88	15.54
55.	IC-391082	57.46	191.07	60.52	80.95	145.21	0.53	113.24	5.83	35.57	30.87	14.91
56.	IC-505242	29.86	119.88	37.98	82.06	135.94	0.51	113.91	5.83	38.95	43.66	15.91
57.	IC-561617	63.60	174.05	55.02	82.20	131.15	0.57	97.39	7.20	41.10	35.65	14.43
58.	Local Kashmiri Chilli-1	29.66	76.40	24.13	85.20	43.86	0.43	80.07	4.90	41.22	38.91	17.12
59.	Arka Lohit	45.66	401.03	127.08	82.92	192.59	0.49	96.05	6.36	37.02	31.79	15.59
60.	KL-1	89.26	581.80	184.54	80.84	106.77	0.52	78.93	7.00	40.30	35.19	15.77
	CD at 5%	1.21	2.15	2.03	0.45	1.09	0.02	8.02	0.13	1.11	3.45	0.68
	SE(d)	0.43	9.3	0.72	0.16	0.39	0.00	2.86	0.04	0.39	1.23	0.24

Sher-e-Kashmir
University of Agricultural Sciences & Technology of Kashmir
Faculty of Horticulture, Division of Vegetable Science

C E R T I F I C A T E

Certified that all the corrections/amendments as suggested by External Examiner **Dr. Shri Dhar** (Principal Scientist) Division of Vegetable Science IARI, Pusa New Delhi during Viva-Voce examination held on **10-01-2020** have been incorporated in the manuscript entitled “**Identification of Resistant Sources against Wilt Disease of Chilli (*Capsicum annuum* L.)** submitted by **Ms. Syeda Farwah** (Regd. No. 2017-H-191-M).

(Dr. Khursheed Hussain)
Chairman
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