EVALUATION OF CAULIFLOWER GENOTYPES FOR HORTICULTURAL TRAITS AND RESISTANCE TO SOME DISEASES AND INSECT PESTS

THESIS

by

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(Vegetable Crops)

COLLEGE OF HORTICULTURE
Dr Yashwant Singh Parmar University of Horticulture and Forestry
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Dedicated to

My Grandmother

&

Parents

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CERTIFICATE-I

This is to certify that the thesis entitled **"Evaluation of Cauliflower Genotypes for Horticultural Traits and Resistance to some Diseases and Insect Pests"** submitted in partial fulfilment of the requirements for the award of degree of **MASTER OF SCIENCE** in **HORTICULTURE (Vegetable Crops)** to Dr Yashwant Singh Parmar University of Horticulture & Forestry, Solan (H.P.) is a record of bonafide research work carried out by **Mr Alaksh Pathania** under my guidance and supervision and that no part of this thesis has been submitted for any other degree or diploma.

The assistance and help received during the course of research work have been fully acknowledged.

Place: Nauni-Solan

Dated: 31-07-, 2003

(H.S. Kanwar)
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CERTIFICATE-II

This is to certify that the thesis entitled **"Evaluation of Cauliflower Genotypes for Horticultural Traits and Resistance to some Diseases and Insect Pests"** submitted by **Mr Alaksh Pathania** to Dr.Y.S. Parmar University of Horticulture and Forestry, Solan (H.P.), in partial fulfilment of the requirements for the award of degree of **MASTER OF SCIENCE** in **HORTICULTURE (Vegetable Crops)** has been approved by the Student's Advisory Committee after an oral examination of the same in collaboration with the External Examiner.

30.8.03

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INTRODUCTION

INTRODUCTION

Cauliflower (*Brassica oleracea* var. *botrytis* L.), is one of the important member of cole crops and belongs to family cruciferae. It attained important place because of its delicious taste, flavour and nutritive value. It is grown throughout the country for its white tender curd which is used as vegetable, soup and for pickling (Choudhary, 1996). The popularity of the crop has been constantly increasing and now it occupies more area than other vegetables in certain parts of the world.

At global level it is grown in an area of 833,090 ha with annual production of 14,421,146 MT whereas in India cauliflower occupies an area of 3,50,000 ha with a production of 65,00000 MT (Anonymous, 2003). In Himachal Pradesh it is also grown as an off season crop due to its favourable climatic conditions in an area of 1340 hectares with annual production of 24,300 MT (Anonymous, 2000). The snowball group has attained special significance in the state because it is grown for producing seeds and is meeting almost the whole seed requirement of the country.

Though, it is an important crop but no such work has been initiated to increase the yield per unit area. Very less work has been done to screen the varieties showing some resistance to various diseases like stalk rot and black rot and insect pests like Diamondback moth and cabbage white butterfly which causes considerable damage to the crop in terms of yield. Yield being the complex character depends on many attributes of the plant, therefore, the assessment of genotypic and phenotypic variability and correlation between various qualitative and quantitative traits are important prerequisites to formulate any effective breeding programme.

In Himachal Pradesh, cauliflower production has also suffered because of extensive cultivation of Pusa Snowball-1 for curd and seed as well. This practice has resulted in the appearance of many diseases like black rot [*Xanthomonas campestris* pv. *campestris* (Pam.) Dowson] and stalk rot [*Sclerotinia sclerotiorum* (lib) de Bary]. These two diseases have created a havoc on the cauliflower curd and seed industry. Variability is expected to be immense as curd vary greatly in size, shape, colour, maturity and resistance to various insect pest and diseases. A lot of work has been done on cauliflower for improvement of horticultural traits. But breeding for diseases and insect pests resistance is in its infancy. Before commencing upon a breeding programme it would be beneficial to start with vast germplasm and select elite types.

Therefore, in view of the importance of the crop, the present investigations were undertaken with the following objectives:

1. To estimate the extent of variability
2. To evaluate the genotypes for horticultural and yield traits
3. To study the association among different traits
4. To evaluate the genotypes for resistance against stalk rot (*Sclerotinia sclerotiorum*) and black rot (*Xanthomonas campestris*)
5. To evaluate the genotypes for resistance against Diamondback moth *Plutella xylostella* L.) and cabbage white butterfly *(Pieris brassicae L.)*.

Chapter-2

REVIEW OF LITERATURE

REVIEW OF LITERATURE

The available information on cauliflower is reviewed and reported under the following headings:

2.1 Means and genetic variability

2.2 Heritability and genetic advance

2.3 Correlation studies

2.4 Quality character

2.5 Stalk rot

2.6 Black rot

2.7 Pest incidence – Diamondback moth (*Plutella xylostella* L.) and cabbage white butterfly (*Pieris brassicae* L.)

2.1 Means and genetic variability

Fisher (1918) partitioned the continuous variation exhibited by quantitative characters into heritable and non-heritable components. The heritable are attributed to genotype and non-heritable to environmental factors.

Vavilov (1951) was probably the first to realize that a wide range of variability in any crop provides a better chance of selecting the desirable types.

Nieuwhof and Garretsen (1961) reported that in Snowball group the inheritance of the solidity of the curd is controlled by polygenes. Visual scoring for curd compactness has also been reported by Singh *et al.* (1978).

Pal and Swarup (1966) in a study of 14 intervarietal crosses involving nine parents reported variability for total number of leaves, marketable curds and net yield per plot. They concluded that the variation ranged from 34.14 to 155.55 per cent.

Crisp and Kesavan (1978) observed the highest mean curd weight in Autumn Glory (328 g) while studying genotypic x environmental effects. Thamburaj *et al.* (1980) in a performance trial of cauliflower at Coimbatore reported three high yielding cultivars viz., 'Patna mid season' (31.78 t/ha), 'Mid season marvel' (31.52 t/ha) and 'Second early' (31.24 t/ha)

Sharma *et al.* (1988) in a study involving six varieties of cauliflower (three summer and three winter types) found that 'Pyramis' (winter type) gave the highest mean value for gross weight (1.390 kg), curd weight (1.096 kg), days to fifty per cent curd formation (18.86), curd size index (222.03 cm^2) and leaf size index (1071.26 cm^2).

Aditya *et al.* (1989) studied genetic variability in eight cultivars of cauliflower for nine yield related characters and obtained highly significant differences with Kartika being earliest and Snowball, late in curd maturity. Early Snowball produced the highest curd weight (895 g) and yield (38.8 t/ha).

Aalbersberg (1990) evaluated 7 cauliflower varieties for days to maturity and observed that Planca and Siria were early maturing varieties and took 118 and 123 days whereas Sernio, Linex, Jura and Orco were late maturing varieties and took 140-150 days from sowing to maturity

Pandey and Naik (1991) observed significant differences for days to curd initiation, curd maturity, total plant weight and curd weight, while studying the variability and correlation coefficients in biparental, F_2 and F_3 progenies of cauliflower.

Jamwal *et al.* (1992) recorded data on yield and its related traits in 16 varieties of cauliflower and found substantial variability for most of the traits with PCV predominant over GCV in all the cases

Khar *et al.* (1997) observed that in Pusa Snowball-2 and White Rock, net curd yield per plant exhibited high phenotypic and genotypic variation, heritability and genetic advance whereas gross weight per plant, curd size index and leaves per plant had moderate values.

Thakur (1998) while studying 21 genotypes in cauliflower observed significant differences for different characters. The mean performance of the characters showed large variation for gross weight of the plant, marketable yield of curd and leaf size index, while it was moderate to narrow for number of leaves per plant, stalk length, curd depth and days to marketable maturity.

Dharminder (1999) concluded that the phenotypic and genotypic coefficient of variability were moderate for net curd weight and gross curd weight.

Anshul (2002) while working on 22 divergent genotypes reported that PCV and GCV were moderate for number of leaves per plant and net curd weight while high for gross curd weight.

2.2 Heritability and genetic advance

Variation was first partitioned into heritable and non-heritable components by Fisher (1918). Detailed division of genotypic variation into additive and non-additive was given by Wright (1921, 1934) and suggested that additive components of genetic variance contributes towards the genetic improvement through selection.

Lush (1940) defined heritability in two ways, that is broad and narrow sense. In broad sense heritability refers to the ratio of genetic variance to the total variance whereas in narrow sense it is the ratio of additive genetic variance to the total variance.

Buiatti *et al.* (1974) reported that heritability was high for days to flowering in cauliflower. Crisp (1977) found low heritability for maturity period whereas Sandhu and Singh (1977) found high heritability (in broad sense) and expected genetic advance for maturity period and curd weight.

Dhiman (1979) reported heritability estimates (broad sense) of medium order for marketable yield, number of leaves per plant, curd size index and gross weight per plant.

Sabita Jyoti and Vashistha (1986) revealed that the heritability (broad sense) ranged from 26.3 to 67.0 per cent in five crosses in cauliflower curd weight.

Lal *et al* (1990) estimated low heritability for curd weight, curd diameter, curd depth and curd maturity. Dutta (1991) found that estimates of heritability were high for days to curd initiation, number of leaves per plant, stalk length and gross curd weight but low for days to marketable maturity from curd initiation and curd diameter.

Radhakrishna and Korla (1994) found that heritability and genetic advance as a percentage of mean were high for gross plant weight, net curd weight, harvest index and stalk length.

Baswana *et al* (1995) reported that earliness was partially dominant over late maturity. Sanjeev (1998) observed comparatively high genetic advance as percentage of mean for characters like stalk length, plant frame, leaf size index, gross curd weight and net curd weight.

Dharminder (1999) obtained maximum genetic advance as percentage of mean for net curd weight and gross curd weight indicating that this is controlled by additive gene action and could be improved by direct selection.

Anshul (2002) observed high heritability estimates for days taken to marketable maturity, number of leaves, leaf shape index, net curd weight, curd width and curd compactness indicate that there is an ample scope for bringing desirable improvement in these traits.

2.3 Correlation studies

The correlation studies between different characters is very much essential. The phenotypic correlation indicate the relationship between two characters which include both hereditary and environmental influences, whereas genotypic correlation coefficient

provides a real association between the two characters and this may be useful for a plant breeder in improving the efficiency of selection (Johnson *et al.*, 1955a).

Jensma (1957) found a positive correlation between earliness and leaf number in cauliflower. An association between early curding with low leaf number and late curding with high leaf number may be of value in breeding for earliness (Watts, 1966).

Lal (1973) studied the correlation coefficient and concluded that curd weight was significantly associated with curd size index, leaf size and plant spread. The environmental correlation between curd weight and curd size index were significant and positive.

Baroncelli *et al.* (1974) observed positive correlation between curd diameter and leaf width and negative correlation between days to flowering and curd diameter.

Thamburaj *et al.* (1982) found that plant height and weight were related to curd yield. A highly significant positive or negative correlation coefficient of curd yield with curd diameter, dry matter production, leaf number and leaf area index was recorded by Sharma *et al.* (1982).

Dhiman *et al.* (1983) found that marketable yield per plant was positively correlated with number of leaves, curd size index and gross weight per plant.

Singh (1984) revealed that the leaf number per plant, curd diameter, plant height and leaf weight per plant were positively and significantly correlated with yield. In Snowball group (late type) the correlation being the strongest for leaf weight.

Pandey and Naik (1985) reported that yield was affected by characters like days taken to curd initiation, curd weight, weight of leaves and plant height. In 1986 they concluded that number of leaves was directly correlated with net curd weight.

Dadlani *et al.* (1986) found that the curd weight was significantly positive or negative correlated with curd depth, diameter and angle in BIPs in two intervarietal crosses of Indian cauliflower.

Aditya *et al* (1989) observed that curd weight was positively correlated with plant height, number of leaves per plant, plant spread and gross weight per plant. Booij (1990) recorded non-significant association between curd weight and number of days from curd initiation to maturity

Dutta and Korla (1991) studied positive and significant correlation of curd weight with days to marketable maturity, curd depth, curd diameter, gross weight and harvest index While positive and significant association of net curd weight with weight of leaves per plant was observed by Pandey and Naik (1991).

Radhakrishna and Korla (1995) found that net curd weight was positively and significantly correlated with gross plant weight, curd diameter and curd depth while curd diameter was positively correlated with curd depth and negatively with days to marketable maturity

Zhang *et al* (1995) reported a closest positive correlation between curd weight and leaf weight and stem diameter (r = 0.7703 and 0.8023, respectively).

Sanjeev (1998) found that net curd weight was positively and significantly associated with gross curd weight, plant frame, leaf size index and curd depth. Similarly, Dharminder (1999) showed significant correlation with plant frame, leaf size index, gross curd weight and harvest index

Anshul (2002) indicated that net curd weight had positive and significant association with number of leaves, gross curd weight, curd depth and curd compactness.

2.4 Quality character

2.4.1 Curd compactness

It is the character which means how much the curd is solid.

Singh *et al* (1978) reported that curd compactness is governed by two dominant major genes Co-1 and Co-2 while studying the F_1's, F_2's and BC's of four Indian cauliflower varieties

Jamwal (1984) found that gross weight per plant and marketable maturity had positive and significant association with curd compactness. Curd compactness was reported under the control of additive gene action by Vashistha *et al.* (1984).

Butt *et al.* (1988) reported that curd compactness was significantly affected both by cultivar and planting dates.

Radhakrishna (1992) reported that most of the progenies including checks in general, produced compact curds ranging from 70-100 per cent, while three progenies exhibited 12-17 per cent semi-compact curds. Additive gene action was reported to control the compactness (Li *et al.*, 1996).

Baswana *et al.* (1993) reported that inheritance of curd compactness was mainly governed by additive or dominance gene effects.

Sepehia (1996) showed that maximum solid curds were obtained in PSBK-1, $KJBC_3$ F_2-2-65 and KTF_4-4-11 out of 15 advanced generations when transplanted on 5th October in comparison to 20th October.

Sanjeev (1998) reported that 14 progenies out of 40; gave completely compact curds and percentage of compact curds was comparatively more in mix pollinated progenies.

Dharminder (1999) observed completely compact curds in White rock, EC-103576, Grodan, ACC-320 and KM-1.

2.5 Stalk rot

In cauliflower, the fungus was recorded for the first time in California by Snyder and Baker (1945).

Fuller *et al.* (1984) were the first to report recessive gene control of stalk rot resistance in *Phaseolus vulgaris*. Additive gene action was primarily responsible for controlling the resistance.

Kapoor (1986) tested 79 line of cauliflower at seedling stage. Out of these, four heading broccolis viz , EC-103576, EC-131592, Janavon and French line KN-81 were found to be resistant

Dohroo and Korla (1988) reported EC-191203 as resistant and EC-191030, EC-191177 and EC-191021 as moderately resistant to stalk rot among 40 collections of cauliflower when 40 days old seedlings were inoculated artificially with inoculum developed in corn sand meal

Baswana *et al* (1990) reported Janavon as resistant to *Sclerotinia sclerotiorum*, while Early Winter Adams White (EWAW) as moderately resistant and PSB-1 and PSBK-1 as highly susceptible

Baswana *et al* (1991) reported polygenic recessive gene control of resistance to stalk rot in cauliflower These genes were reported to have additive effects.

Dutta (1991) found that the selfed progenies of Janavon (S_3) and F_4 progenies of Pusa Snowball K-1 x Janavon showed minimum incidence of stalk rot disease than commercial cultivar Pusa Snowball K-1 (Check) at the time of curd maturity.

Harinder Singh *et al* (1995) evaluated 69 lines of cauliflower for resistance to stalk rot and found that four lines viz , Janavon, EC-103576, EWAW and EC-177283 were resistant

Dickson *et al* (1996) reported resistance to be controlled by one major recessive gene with modifiers when they evaluated F_1, F_2 and backcross population of the crosses of resistant PI 206942 x cabbage and cauliflower. All the F_1 and susceptible plants died after inoculating with pathogen

Thakur (1998) reported that recessive genes with additive effects result in resistance to stalk rot

Thakur (1998) screened 21 genotypes of mid, late and late group and reported that Janavon, RSK-1301 and EC-162587 were resistant while Sharma *et al* (2000) reported

that besides RSK-1301, SN-445, BR-2 and KM-1 were also resistant out of 34 lines screened under Solan conditions.

Sharma *et al.* (2000) found that the resistance to the disease is inherited polygenically and under the control of recessive genes and primary to additive gene action.

2.6 Black rot

In India, Black rot (*Xanthomonas campestris* pv. *campestris*) was first reported by Patwardhan (1928) on cabbage.

Bain (1954) selected some black rot tolerant species from a cross of Snowball and an Indian cauliflower. Camargo (1956) in Brazil also reported a few black rot resistant plants of cauliflower from a variety 'Campinas' and an Indian cauliflower 'Early Banaras'.

Sydorenko (1961) reported a varying degree of field tolerance in cauliflower with infection varying from 3.5 to 5.1 per cent.

Mazzucchi (1970) classified 35 varieties of cauliflower as mildly, moderately or highly susceptible.

Chatterjee and Swarup (1972) reported that resistance is polygenic and dominant in expression. Dominant gene for resistance has been reported in varieties MGS-2-3, Puakea and Sn-445 by Swarup and Chatterjee (1974).

Swarup and Chatterjee (1974) reported MGS, Puakea, S-1 and Sn-445 as highly resistant to black rot. Sharma *et al.* (1977) also observed MGS-2-3, Puakea, Sn-445 and Sn-401 as highly resistant to black rot. 'Avans' and 'Iglory' were reported to be resistant while Snowball as susceptible by Dua *et al.* (1978).

Sharma *et al.* (1979) observed that in cauliflower resistance is polygenically controlled and concluded that resistance to black rot is dominant over susceptibility with additive effects of genes.

Ohata *et al* (1982) gave the technique of clip inoculation to screen the germplasm for black rot resistance

Dickson and Hunter (1985) concluded that resistance to black rot is controlled by one recessive gene with a modifier as a line PI 436606 exhibited erratic juvenile resistance to stalk rot

Jamwal and Sharma (1986) reported that the resistance in Sn-445 is under control of one dominant gene as F_1 and backcross with Sn-445 gave immune reaction to black rot.

Singh *et al* (1987) found that in Puakea, Sn-445 and MGS-2-3 resistance to black rot was governed by dominant polygenes They concluded that Pusa Snowball K-1, a selection from EC-12012 was field resistant to black rot

Monakhos *et al* (1990) reported as many as 25 genes to control resistance to black rot with dominance effects

Sharma *et al* (1991) reported KT-9 to be the best performer for resistance while evaluating five temperate cauliflower varieties i.e. KT-9, KT-16, PSB-1, PSBK-1 and KPS-1 against black rot Singh *et al* (1991) developed Pusa Shubhra as black rot resistance for early maturity group

Swarup *et al* (1993) developed cultivar 'Pusa Synthetic' out of 7 best combiner homozygous lines of 'Dania-96', having resistance to black rot and good curd quality as well

Hansen and Earle (1995) indicated resistance to be governed by a single dominant gene and they transferred this gene to *Brassica oleracea* by protoplast fusion technique under controlled conditions from *Brassica napus* (PI-199947), highly resistant to black rot

Sharma *et al* (1995) showed that RBS-1, EC-162587, Sn-445 and Lawyna were resistant to black rot while studying 75 lines of cauliflower

Zhou-Zhi Jiang *et al.* (1997) reported single recessive gene for black rot immune reaction while using protoplast fusion of *Brassica napus* x *Brassica oleracea*.

Thakur (1998) observed that the resistance to black rot to be polygenic and under the control of dominant genes.

Sharma *et al.* (2000) also screened 34 genotypes and reported that Kn-81 and BR-2 were resistant to this disease.

Sharma *et al.* (2000) while evaluating the genotypes of cauliflower found that the resistance to black rot is inherited polygenically and governed by dominant genes.

Sanjeev (2002) while evaluating 51 genotypes of cauliflower found that Winter cauliflower (Armel) was resistant to black rot whereas six genotypes viz., White Heart, Polar Ice, Early March, April, KJ38-6 and Monopreeco showed moderate resistance to the disease.

2.7 Pest incidence

2.7.1 Effect of genotype on the biology of Diamondback moth (*Plutella xylostella L.*)

Lin *et al.* (1983) reported that larvae of *P. xylostella* completed development on all the genotypes included in tests but the survival rate and feeding injury differed. In greenhouse the females preferred to oviposit on lines with dark green leaves such as PI-234599 (cauliflower) and G-8329 (cabbage). All genotypes on which oviposition was high were heavily damaged. However, under field conditions, G-8329 and PI-234599 were only lightly damaged by small number of larvae. Laboratory tests indicated that heavy mortality of early 1st instar larvae occurred on G-8329. Khaire *et al.* (1986) found that out of 4 cultivars included in the study, Nasik-1 had the lowest incidence of *P. xylostella* (1.19/plant) and Katki with highest incidence of the pest. According to Peterka *et al.* (1986) in cabbage tolerant cultivars to 4th instar larvae of *P. xylostella* had 50 per cent lower sinigrin content than the susceptible ones. It was also reported that spraying leaf discs with sinigrin attracted the adults of *P. xylostella*.

Sastrosiswojo *et al* (1987) evaluated nineteen *brassica* cultivars and a radish cultivar Lobak in a screenhouse for resistance to *P. xylostella*. The cultivar Rotan F_1 of white cabbage, Marner Rocco of Red cabbage and Cerateun of cauliflower were found to be resistant. The most susceptible cultivars were Michil 70 of white cabbage and Talaud of Chinese cabbage.

Asyakin *et al* (1988) in a laboratory study with resistant and tolerant cabbage varieties showed that the former exerted a depressive effect on the development of *P. xylostella* resulting in deterioration of their physiological state, expressed as preimaginal weight and mortality, fecundity, duration of generation and length of adult life.

In a study of behavioural changes on resistant and susceptible cultivars of cabbage, Eigenbrode *et al* (1988) reported that *P. xylostella* larvae moved more rapidly on glossy resistant plant descended from PI-234599 than on the non-glossy resistant types or the susceptible controls. Increased movement lead to reduced feeding activity by the larvae and after 24 hours, 500 resistant plants had about 120 lesions/plant compared with 990 lesions/plant on susceptible plant.

Eigenbrode *et al* (1990) reported that in cabbage polar fractions of ethanol extracts of partially resistant lines 2535 and 2503, when incorporated into diet reduced the survival of *P. xylostella* larvae by 14.9 and 19.0 per cent, respectively. However, it could not be determined whether this effect was due to reduced feeding or posingestive toxicity. Resistance to the pest in the lines investigated was therefore, due to at least two mechanisms, antibiosis or non-preference. Non-preference was due to extractable compounds present in normal bloom of resistant cabbage genotypes, 2503 and 2535, and possible non-preference for glossleated 2518 by neonate larvae, as suggested by the greater dispersal rates of neonates on these plants.

Dickson *et al* (1990) in cabbage reported three distinct classes of susceptibility against *P. xylostella* viz., highly susceptible controls, highly resistant glossy leaved lines and intermediate selections with normal leaf bloom. It was found that selection for higher

specific combining ability for higher resistance level at maturity was effective and glossy leaved hybrids did not require any sprays for marketable crops.

Eigenbrode and Shelton (1990) reported that the cabbage line NY-2518 (glossy leaved inbred line) was highly resistant to *P. xylostella* due to reduced larval survival, not higher than 10.3 per cent from two weeks after transplanting in comparison to 77.2 per cent larval survival on hybrid 'Round up'.

Eigenbrode *et al.* (1991a) observed that neonate larvae of *P. xylostella* moved more rapidly for most of the time in searching rather than feeding on leaves of NY-8329, a resistant cabbage variety with glossy leaves than on Round up hybrid, a susceptible hybrid with normal wax bloom. Various compounds such as Triterphenols, α and β-amyrin found in waxes of NY-8329 lead to reduced acceptance by *P. xylostella*. The percentage of the major wax constituents differed in the wax extracts of the two cabbage genotypes which resulted in differential resistance to *P. xylostella*.

Eigenbrode *et al.* (1991b) concluded that incorporation of genes that cause the greatest reduction in amount of leaf wax and crystallite density will permit development of the most resistant cultivars.

Studies on temperate cultivars of cabbage by Verkerk and Wright (1994) revealed longer mean larval duration and lesser survival percentage on older plants in comparison to younger plants, however, the plant age did not effect pupal weight. The fecundity of *P. xylostella* reared on outdoor grown cabbage cultivar varied tenfold between the poorest and the best cultivar however, plant age had least effect on *P. xylostella* reared on Chinese cabbage. Under glass house conditions, survival of pest was significantly more in comparison to field grown glossy leaved, normal bloom green cabbage and red cabbage

Eigenbrode and Pillai (1998) revealed that some primary wax components, including specific long chain alkyl components, had allelochemical activity influencing host acceptance behaviour by *P. xylostella* larvae.

Ganesan and Narayanasamy (1998) in virulence studies of three strains of *P. xylostella*, from Tamil Nadu, India found B mutlur strain as the most virulent to cauliflower followed by the Annamalainagar strain and the Dharampuri strain as least virulent, whereas the Indian Early cauliflower accession was found highly susceptible to Annamalainagar strain while it was resistant to Dharampuri strain. However, Katki and Poosi were susceptible to B mutlur and Dharampuri strains, respectively.

Ramchandran *et al* (1998) described significant differences among normal and glossy leaved of *Brassica napus* cultivars. These studies revealed *B. napus* entry PI-470055 with low level of feeding damage in the restrictive feeding test and some level of antibiosis against *P. xylostella*. Non-preference for larval feeding and oviposition were exhibited by PI-171538. However, in oviposition tests, PI-171538 received 0.9 per cent of eggs as compared with normal leaved *B. napus* plants (2.1-4.4%).

2.7.2 Effect of genotypes on the biology of cabbage white butterfly (*Pieris brassicae* L.)

Dickson and Eckenrode (1975) in cauliflower observed PI-234599 as resistant to feeding by larvae of *Pieris rapae* L. under field conditions. However, the least resistance was found under greenhouse conditions. The degree of maturity and environment influenced the resistance which was apparently associated with antibiosis. Red cabbage was less preferred host of *P. rapae* in field and greenhouse conditions. Feasibility of transferring resistance characters from PI-234599 into desirable cabbage and cauliflower line was detected

Mitchell (1977) reported preference of *P. brassicae* for food plants. In his opinion alyl nitrile present in certain cruciferous plants served as a specific attractant for *P. brassicae* females for egg laying. However, the larvae did not show selective choice of food plants

Dickson (1978) performed screening of cabbage, broccoli and cauliflower introductions for resistance to *P. rapae* and found PI-234599, a glossy leaved late cauliflower from Australia as highly tolerant.

According to Dickson and Eckenrode (1980) resistance to *P. rapae*, *P. xylostella* and *Trichoplusia ni* (Hubner) was quantitatively inherited without undesirable linkages. Heritability range of 22-47 per cent was obtained for resistance these pests when PI-234599 was used as parent. The resistance was maintained irrespective of plant age or the presence or absence of alternate hosts for oviposition with moderate tolerance only expressed at maturity.

Rangappa and Benepal (1983) reported that cabbage cultivars, viz., Copenhagen Market 86, Copenhagen Market Late, Houston, Evergreen, Gormet, Superette and Yoshin Summer early were resistant to *P. rapae*.

Asyakin *et al.* (1988) reported that resistant varieties in cabbage exerted depressive effect on the development of *P. brassicae* which lead to deterioration of physiological state as expressed by indices like preimaginal weight, mortality, reduced fecundity, longer duration of generation and reduced adult longevity.

In a study of 23 crosses of cabbage in Kullu valley of Himachal Pradesh, Lal (1991) found that Red Pickling, Red Drum and Red Rock Mammoth were resistant to *P. brassicae*, while 6 hybrids were found moderately resistant and none immune to pest attack. However, Red Rock Mammoth x September was the best hybrid but had lower market value due to the presence of purple leaf veins. Most of the agronomically acceptable cultivars were highly susceptible.

Vail *et al.* (1991) studied the level of *P. rapae* infestation corresponding to maturity dates in some broccoli cultivars and reported that more larvae were found on late maturing cultivars than on early maturing ones. Symphony, an early maturing cultivar, had the lowest number of larvae whereas, Green Defender, a late maturing cultivar, had the highest.

Renwick and Huang (1995) reported that in Nasturtium, a member of Brassicae family, the presence of a compound chlorogenic acid which acted as a strong antifeedant for *P. brassicae*. The results demonstrated that dietary experience can affect the response of an insect to a potentially antifeedant compound in a plant.

Aslam *et al* (2000) in a study focused on the preference of *P. brassicae* to different genotypes of brassica found that pest showed maximum preference to the genotype Cyclone and lowest to CON-11.

Chapter-3

MATERIAL & METHODS

Renwick and Huang (1995) reported that in Nasturtium, a member of Brassicae family, the presence of a compound chlorogenic acid which acted as a strong antifeedant for *P. brassicae*. The results demonstrated that dietary experience can affect the response of an insect to a potentially antifeedant compound in a plant.

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Chapter-3

MATERIAL & METHODS

MATERIAL AND METHODS

The present investigations were carried out at the experimental farm as well as laboratory conditions of the Department of Vegetable Crops, Dr. Y.S. Parmar University of Horticulture and Forestry, Nauni-Solan (H.P.) from September 2002 to March 2003.

3.1 Location and climate

Experimental farm of Department of Vegetable Crops is situated at an elevation of 1200 m above mean sea level and is in 30°50' N latitude and 77°11'30" E longitude. The area being in the mid hill zone of Himachal Pradesh, the texture of the soil is gravelly loam to gravelly clay loam with pH ranging from 6.85-7.04.

The climate of area is sub-temperate. The region has January-February as the coldest months while May-June the hottest months in the year. The annual rainfall ranges from 1000-1300 mm of which maximum rainfall occurs from June to September. The mean monthly meteorological data with regard to temperature, relative humidity and rainfall during the season is given in Appendix-I.

3.2 Experimental Material

The experimental material comprised of 20 diverse genotypes of cauliflower out of which one is commercially grown cultivar viz., PSBK-1 (Check). These were obtained from different sources for undertaking the study. These genotypes were transplanted on 10.10.2002 during 2002-2003 in a Randomized Block Design with three replications at a

spacing of 60x45 cm. Recommended package of practices were followed during growth period of the crop. The list of genotypes along with source is as under.

Sr No	Genotype	Source
1	Grodan	NBPGR
2	White Impress	HRI, Wellesbourne, UK
3	Autumn Giant	NBPGR
4	EC-103576	NBPGR
5	Dochligan	NBPGR
6	ACC-328	IARI, Katrain
7	KI-47	UHF, Solan
8	All the year round	HRI, Wellesbourne, UK
9	Lawyna	UHF, Solan
10	ACC-330	IARI, Katrain
11	KJ-38	UHF, Solan
12	Champion	HRI, Wellesbourne, UK
13	ACC-320	IARI, Katrain
14	Holland Special	Holland
15	ACC-331	IARI, Katrain
16	ACC-329	IARI, Katrain
17	KT-25	IARI, Katrain
18	RS-199	IARI, Katrain
19	Poonam	NBPGR
20	PSBK-1 (Check)	IARI, Katrain

A separate experiment was conducted in PG Laboratory of Department of Vegetable Crops, UHF, Nauni during 2002-2003 against the Diamondback moth (*Plutella xylostella* L.) and cabbage white butterfly (*Pieris brassicae* L.).

For Diamondback moth (*Plutella xylostella* L.) two pairs of newly emerged moths were released in a glass chimney (20x13 cm) containing fresh leaves of a particular genotype in a plastic vial for egg laying. In each chimney cotton swabs soaked in 10 per cent sugar solution were placed which serve as a food for the moths. Leaves bearing eggs were daily observed by using hand lens and the number of eggs were counted daily till the adults died. The eggs were reared on the same genotype upto adult stage and observations of various developmental stages were recorded and analysed. Whereas for cabbage white butterfly (*Pieris brassicae* L.), the freshly laid egg masses were collected from the field on the original leaves and brought to the laboratory for rearing. The leaves with egg masses were placed in petri dishes over a moist filter paper and allowed to hatch. On hatching, the larvae were provided with fresh bits of leaves of different genotypes and different parameters were recorded. The experiment was laid in Completely Randomized Design with three replications for both the pests, at room temperature.

3.3 Observations recorded

3.3.1 Horticultural traits

Observations on five randomly selected plants were recorded in each plot.

3.3.1.1 Days taken to marketable curds: The number of days taken from the date of transplanting to the date when curds attained marketable maturity.

3.3.1.2 Stalk length (cm): Length of the stalk was measured in centimeter from the first secondary root level to the position of the first leaf.

3.3.1.3 Number of leaves per plant: Total number of leaves at the time of maturity were counted.

3.3.1.4 Gross curd weight (kg): Gross curd weight including curd, leaves and stalk was recorded in kilograms.

3.3.1.5 Net curd weight (g) Net curd weight excluding all the leaves and stalk was weighed to record the net curd weight in grams

3.3.1.6 Curd depth (cm) The length from surface to the first flower segment of vertically cut curd was measured in centimeter

3.3.1.7 Curd width (cm) Equitorial length in centimeter was measured after cutting the curd into two equal halves, longitudinally

3.3.1.8 Curd compactness (g/cm) Curd compactness was obtained by dividing net curd weight to the curd depth

3.3.2 Stalk rot incidence (%)

The stalk rot incidence was recorded on leaves under natural epiphytotic conditions The observations were recorded on number of leaves showing disease symptoms and total number of leaves on each plant in a plot, at weekly intervals. Finally the data were cumulated and expressed as per cent stalk rot incidence as per the method given by Dohroo (1988)

$$\text{Disease incidence (\%)} = \frac{\text{Number of diseased leaves}}{\text{Total number of leaves per plant}} \times 100$$

Based on the per cent disease incidence, the ratings were made as follows:

Disease incidence (%)	Rating
0-10	Resistant
11-20	Moderately resistant
21-40	Susceptible
>40	Highly susceptible

3.3.3 Black rot severity (%)

For evaluating resistance against black rot [*Xanthomonas campestris* pv. *campestris* (Pam.) Dowson] the severity was recorded on leaves showing the disease symptoms under natural epiphytotic conditions. The individual plants were scored 0-9 IP scale as suggested by William *et al.* (1972).

Disease rating	Description
0	No external symptoms
1	Marginal necrosis of the leaf
3	Small V-shaped lesions on the leaf
5	V-shaped lesions extending upto half of the leaf area
7	V-shaped lesions extending often upto mid rib
9	Seedling death, severe chlorosis and necrosis of the leaf

The disease was recorded at weekly interval and the data obtained was converted to per cent disease severity. The genotypes were classified into resistant (0-10%), moderately resistant (11-20%) and susceptible (>20%).

$$\text{Disease severity (\%)} = \frac{\text{Sum of all disease rating}}{\text{Total number of rating x maximum disease grade}} \times 100$$

3.3.4 Effect of genotype on the biology of Diamondback moth (*Plutella xylostella* L.)

3.3.4.1 Oviposition preference: The total number of eggs laid on leaves of particular genotype were counted daily with the help of a hand lens.

3.3.4.2 Egg incubation period: The time interval in days between egg laying and emergence of larvae was taken as the incubation period. The freshly laid eggs were picked up along with the leaf bits on which the eggs were laid and kept in petridish containing a wet blotting paper at the bottom, in batches of 10 eggs/dish. The average incubation period was worked out by observing the time taken for hatching.

3.3.4.3 Per cent hatching

$$\frac{\text{Total number of eggs hatched}}{\text{Total number of eggs laid}} \times 100$$

3.3.4.4 Larval duration It is the time interval between hatching of larva and pupa formation To work out larval duration 10 randomly selected larvae were placed in petridish containing fresh piece of leaf and wet blotting paper at the bottom. They were observed daily and larval duration was worked out.

3.3.4.5 Per cent larval survival

$$\frac{\text{Total number of larvae transformed into pupae}}{\text{Total number of larvae emerged}} \times 100$$

3.3.4.6 Pupal duration On the day of pupation of the larvae, 10 pupae were transferred to the plastic vials (6 5x2 0 cm) These were observed daily for emergence of adult moths. The time period between date of pupation and date of moth emergence gives the pupal duration

3.3.4.7 Per cent pupal survival

$$\frac{\text{Total number of adults emerged}}{\text{Total number of pupae formed}} \times 100$$

3.3.4.8 Per cent generation survival

$$\frac{\text{Total number of adults formed}}{\text{Total number of eggs laid}} \times 100$$

3.3.5 Effect of genotype on the biology of cabbage white butterfly (*Pieris brassicae* L.)

3.3.5.1 Larval duration: The duration of larvae was recorded for 10 randomly selected caterpillars.

3.3.5.2 Per cent larval survival

$$\frac{\text{Total number of pupae formed}}{\text{Total number of larvae emerged from eggs}} \times 100$$

3.3.5.3 Pupal duration: The period from pupa formation to adult emergence was recorded as the pupal period. Pupae formed on particular day were marked and observations were recorded on 10 pupae to record the duration of pupal period.

3.3.5.4 Per cent pupal survival

$$\frac{\text{Total number of adults emerged from pupae}}{\text{Total number of pupae formed}} \times 100$$

3.3.5.5 Number of adults formed: Number of adults emerged from pupae were counted.

3.3.5.6 Per cent generation survival

$$\frac{\text{Total number of adults formed}}{\text{Total number of eggs kept}} \times 100$$

3.4 Statistical Analysis

3.4.1 Horticultural traits

The average value of all the 5 plants for various characters were subjected to statistical analysis.

Randomized Block Design

The estimates of different parameters of variability (genotypic and phenotypic), heritability, genetic advance, genetic gain and correlation coefficients were worked out to facilitate selection for various characters

To estimate these parameters different genotypes were treated as independent treatments and the data was analysed as per randomized block design. The analysis of variance was carried out as suggested by Gomez and Gomez (1976).

Analysis of variance

Source of variation	d.f.	Mean sum of square	Variance
Replications	r-1	Mr	Mr/Me
Treatments	t-1	Mt	Mt/Me=F
Error	(r-1)(t-1)	Me=Ve	

where,

r = number of replications
t = number of treatments
Ve = error variance

The data on character, that showed significant F-test for the genotypes, were further utilized for the estimation of following genetic constant and parameters.

1 Coefficients of variability (phenotypic and genotypic)
2 Heritability
3 Genetic advance
4 Genetic gain
5 Correlation coefficients

3.4.1.1 Coefficients of variability: The genotypic and phenotypic coefficients of variability were calculated as per the method suggested by Burton and DeVane (1953).

Genotypic coefficient of variability:

$$GCV = (VVg/\bar{X}) \times 100$$

Phenotypic coefficient of variability:

$$PCV = (VVp/\bar{X}) \times 100$$

where,

Vg = Genotypic variance (Mt-Me)/r
Vp = Phenotypic variance (Vg+Ve)
$\bar{X}$ = Population mean

3.4.1.2 Heritability: Heritability (in broad sense) was calculated as per formula given by Allard (1960).

$$H = (Vg/Vp) \times 100$$

where,

H = Heritability (%)
Vg = Genotypic variance (Mt-Me)/r
Vp = Phenotypic variance (Vg+Ve)

3.4.1.3 Genetic advance: The expected genetic advance (GA) resulting from selection of five per cent superior individuals was calculated as per Allard (1960).

$$GA = H \times rp \times K$$

where,

H = Heritability
rp = Phenotypic standard deviation
K = Selection differential at 5% selection intensity K = 2.06

3.4.1.4 Genetic gain: Genetic advance expressed as per cent of population mean was calculated by the formula suggested by Johnson *et al.* (1955b).

$$GG = (GA/\bar{X}) \times 100$$

where,

GG = Genetic gain
$\bar{X}$ = Population mean

For categorizing the magnitude of different parameter, Sharma (1994) suggested the following limits

PCV and GCV	> 30%	High
	15-30%	Moderate
	<15%	Low
Heritability (H)	>80%	High
	50-80%	Moderate
	<50%	Low
Genetic gain	>50%	High
	25-50%	Moderate
	<25%	Low

3.4.1.5 Correlation The correlation coefficients (genotypic and phenotypic) were calculated as per Al-Jibouri *et al.* (1958) by variance-covariance matrix in which total variability had been split into replications, genotypes and errors. All the components of variance were estimated from the analysis of co-variance given below:

Analysis of variance and co-variance

Source of variation	d.f.	Mean sum of squares		Mean sum of production
		X	Y	
Replication	(r-1)	Mrx	Mry	Mrxy
Genotypes	(t-1)	Mtx	Mty	Mtxy
Error	(r-1)(t-1)	Mex	Mey	Mexy

where,

Genotypic variance (Vg) = (Mt-Me)/r
Phenotypic variance (Vp) = (Vg+Ve)

Phenotypic coefficient of correlation

$$rp = \frac{Vpxy}{\sqrt{Vpx.\ Vpy}}$$

where,

Vpxy = Phenotypic co-variance between character x and y
Vpx = Phenotypic variance of character x
Vpy = Phenotypic variance of character y

Genotypic coefficient of correlation

$$rg = \frac{Vgxy}{\sqrt{Vgx.\ Vgy}}$$

where,

Vgxy = Genotypic co-variance between character x and y
Vgx = Genotypic variance of character x
Vgy = Genotypic variance of character y

The correlation coefficients (rg and rp) were compared with tabulated 'r' value at (n-2) degree of freedom (Fisher and Yates, 1963). If the calculated value of correlation coefficients was greater than tabulated value at 5 per cent level of significance the correlation was said to be significant.

3.4.2 Susceptibility to pests

Data obtained for all three replication for various characters was subjected to completely randomized design analysis and analysis of variance as under:

ANOVA

Source of variation	d.f.	Mean sum of square	Variance ratio
Treatment	t-1	Mt	Mt/Me=F
Error	t(r-1)	Me	

For judging the significance, the observed F value was compared with tabulated value If tabulated F-value was less than calculated F-value the difference was considered to be significant

Chapter-4

EXPERIMENTAL RESULTS

EXPERIMENTAL RESULTS

The present investigations were undertaken to evaluate twenty genotypes of cauliflower (*Brassica oleracea* var. *botrytis* L.) for horticultural traits and resistance against diseases and pests. The parameters of variability and correlation analysis were worked out in order to facilitate selection for various traits in cauliflower. The results obtained are presented under the following sub-heads:

4.1 Variability studies

- 4.1.1 General evaluation of genotypes
- 4.1.2 Parameters of variability

4.2 Correlation studies

- 4.2.1 Phenotypic correlation
- 4.2.2 Genotypic correlation

4.3 Disease reactions

- 4.3.1 Stalk rot incidence
- 4.3.2 Black rot severity

4.4 Effect of genotype on the biology of insect pests

- 4.4.1 Diamondback moth (*Plutella xylostella* L.)
- 4.4.2 Cabbage white butterfly (*Pieris brassicae* L.)

4.1 Variability studies

4.1.1 General evaluation of genotypes

The analysis of variance for different characters indicated significant variation among the genotypes under study (Appendix-II). The 'F' values revealed significant differences among genotypes for different traits viz., days to marketable curds, stalk

length, number of leaves, gross curd weight, net curd weight, curd depth, curd width and curd compactness Regarding pest incidence in case of Diamondback moth (*Plutella xylostella*) parameters viz , effect on oviposition preference, effect on incubation period, egg hatchability, larval duration, larval survival, pupal duration, pupal survival and overall generation survival had shown significant differences whereas, significant variation for larval duration, larval survival, pupal duration, adult emergence and overall generation survival in cabbage white butterfly (*Pieris brassicae*) were observed.

4.1.1.1 Days taken to marketable curds: Among the genotypes under study significant variations for days to marketable maturity were observed. The differences between the genotypes for this trait ranged from 102.7 to 132.1 days (Table 1a). Lawyna (102.7) took minimum days whereas maximum days to reach marketable maturity were taken by Poonam (132.1) On an average all the genotypes took 117.55 days to reach marketable maturity (Table 3). The standard cultivar PSBK-1 (Check) took 128.9 days for marketable maturity Seven genotypes including check viz., Autumn Giant (127.0), Dochligan (126.3), KJ-47 (131.3), KJ-38 (126.1), Holland Special (130.8), KT-25 (129.3) and PSBK-1 (128.9) were found to be at par with Poonam (132.1). However, seven genotypes were found to be at par with Lawyna (102.7) which took minimum number of days for marketable maturity. Eleven genotypes took significantly less number of days to reach marketable maturity, than the check i.e. PSBK-1. None of the genotype took significantly more number of days than PSBK-1 (Check) to reach marketable maturity.

4.1.1.2 Stalk length: Genotypes exhibited significant differences for stalk length (Table 1a) It ranged from 3.20 cm in Autumn Giant to 5.10 cm in KJ-47. The general population mean was 3.63 cm and none of the genotypes had significantly less stalk length than the population mean The commercially grown cultivar PSBK-1 had the stalk length of 4.53 cm and only KJ-47 recorded stalk length significantly higher than the PSBK-1 (Check). Twelve genotypes gave stalk length at par with Autumn Giant (3.20 cm). Eighteen genotypes had significantly less stalk length than the PSBK-1 (Check).

Table 1a: Mean performance of days taken to marketable curds, stalk length and number of leaves in cauliflower

Name of Genotype	Days taken to marketable curds (days)	Stalk length (cm)	Number of leaves
Grodan	105.5	3.50	17.27
White Impress	107.2	3.37	16.07
Autumn Giant	127.0	3.20	20.27
EC-103576	110.4	3.34	18.00
Dochligan	126.3	3.81	19.33
ACC-328	121.9	3.75	19.20
KJ-47	131.3	5.10	21.47
All the year round	104.3	3.43	16.93
Lawyna	102.7	3.23	14.27
ACC-330	123.3	3.31	19.73
KJ-38	126.1	4.05	21.00
Champion	113.7	3.41	17.13
ACC-320	108.4	3.32	15.20
Holland Special	130.8	3.90	18.93
ACC-331	105.7	3.23	14.67
ACC-329	107.8	3.75	16.00
KT-25	129.3	3.45	18.00
RS-199	108.4	3.57	16.20
Poonam	132.1	3.33	17.47
PSBK-1 (Check)	128.9	4.53	18.73
CD at 5%	6.47	0.43	2.38

4.1.1.3 Number of leaves per plant: Number of leaves per plant revealed significant differences among the various genotypes studied (Table 1a). It ranged from 14.27 (Lawyna) to 21.47 (KJ-47) with general population mean of 17.79. Three genotypes viz., Lawyna (14.27), ACC-320 (15.20) and ACC-331 (14.67) had significantly less number of leaves than the population mean whereas Autumn Giant (20.27),KJ-47 (21.47) and KJ-38 (21.00) produced significantly more number of leaves per plant than the general population mean. The commercial grown cultivar (PSBK-1) produced 18.73 leaves per plant. Six genotypes viz., White Impress (16.07), Lawyna (14.27), ACC-320 (15.20), ACC-331 (14.67), ACC-329 (16.00) and RS-199 (16.20) produced significantly less number of leaves than PSBK-1. Only one genotype KJ-47 (21.47) was found to possess significantly higher number of leaves than the PSBK-1 (Check). The number of leaves were at par with PSBK-1 (Check) in genotypes viz., Autumn Giant (20.27), Dochligan (19.33), ACC-328 (19.20), ACC-330 (19.73), KJ-38 (21.00) and Holland Special (18.93).

4.1.1.4 Gross curd weight: A wide range of variability was recorded for gross curd weight among the twenty genotypes (Table 1b). It was maximum in KJ-47 (2.40 kg) and minimum in Lawyna (0.72 kg). The gross curd weight recorded for the standard cultivar PSBK-1 was 1.81 kg. In three genotypes viz., Autumn Giant (2.28 kg), KJ-47 (2.40 kg) and Holland Special (2.20 kg) the gross curd weight was significantly higher than the PSBK-1 (Check) while it was recorded significantly less in ten genotypes. Four genotypes were at par with the PSBK-1 (Check) viz., EC-103576 (1.92 kg), ACC-328 (1.89 kg), KT-25 (2.04 kg) and Poonam (1.82 kg). The general population mean for gross curd weight was 1.57 kg. Six genotypes viz., Autumn Giant, EC-103576, ACC-328, KJ-47, Holland Special and KT-25 produced significantly higher gross curd weight than the population mean. Two genotypes viz., Autumn Giant (2.28 kg) and Holland Special (2.20 kg) were at par with KJ-47 whereas ACC-331 (0.82 kg) and ACC-329 (0.77 kg) were found to be statistically at par with Lawyna (0.72 kg).

4.1.1.5 Net curd weight: Among the various genotypes evaluated the net curd weight varied from 236.7 g (Lawyna) to 808.3 g (EC-103576) (Table 1b). General population mean was found to be 560.83 g. Eight genotypes possess significantly higher net curd

weight than the general population mean. Net curd weight of PSBK-1 (Check) was found to be 660.0 g. Four genotypes viz., Autumn Giant (790.0 g), EC-103576 (808.3 g), ACC-328 (750.0 g) and Holland Special (796.7 g) had significantly higher net curd weight than the standard cultivar PSBK-1 (Check). Net curd weight of genotypes viz., Autumn Giant (790.0 g), ACC-328 (750.0 g) and Holland Special (796.7 g) were at par with highest curd weight genotype EC-103576 whereas, two genotypes i.e. ACC-331 (276.7 g) and ACC-329 (293.3 g) exhibited statistically at par net weight with Lawyna. The genotypes found to be at par with PSBK-1 were Grodan (653.3 g), KJ-47 (633.3 g), KT-25 (703.3 g) and Poonam (658.3 g).

4.1.1.6 Curd depth: Data pertaining to this trait revealed significant variations among the genotypes (Table 1b). Curd depth ranged from 7.18 cm in RS-199 to 11.60 cm in KT-25. The PSBK-1 (Check) exhibited curd depth of 10.43 cm. Nine genotypes including PSBK-1 were found to be at par with KT-25. The general population mean of all the genotypes was found to be 9.74 cm. Significantly higher curd depth than the population mean was found in three genotypes viz., EC-103576 (11.50 cm), KJ-47 (11.35 cm) and KT-25 (11.60 cm). Three genotypes i.e. Champion (8.35 gm), ACC-320 (8.33 cm) and ACC-331 (8.00 cm) were at par with RS-199.

4.1.1.7 Curd width: The range of curd width varied from 8.83 cm to 17.29 cm in Lawyna and Autumn Giant, respectively (Table 1c), however, it was found to be 15.38 cm in PSBK-1 (Check). Four genotypes viz., Autumn Giant (17.29 cm), KJ-38 (16.68 cm), Holland Special (16.74 cm) and KT-25 (16.72 cm) exhibited significantly more curd width than the Check (PSBK-1), whereas genotypes EC-103576 (15.53 cm), Dochligan (15.49 cm) and ACC-328 (16.60 cm) were found to be at par with PSBK-1 (Check).

The general population mean was 14.72 cm and only three genotypes viz., White Impress (13.38 cm), Lawyna (8.83 cm) and ACC-331 (12.19 cm) had significantly less curd width than the general population mean.

4.1.1.8 Curd compactness: A wide range of variation was observed for curd compactness (Table 1c). It ranged from 24.87 g/cm in Lawyna to 77.33 g/cm in Holland

Table 1b: Mean performance of gross curd weight, net curd weight and curd depth in cauliflower

Name of Genotype	Gross curd weight (kg)	Net curd weight (g)	Curd depth (cm)
Grodan	1.45	653.3	10.27
White Impress	1.09	398.3	8.73
Autumn Giant	2.28	790.0	11.13
EC-103576	1.92	808.3	11.50
Dochligan	1.65	570.0	9.53
ACC-328	1.89	750.0	10.60
KJ-47	2.40	633.3	11.35
All the year round	1.11	446.7	9.53
Lawyna	0.72	236.7	9.48
ACC-330	1.63	596.7	8.93
KJ-38	1.45	575.0	10.13
Champion	1.58	543.3	8.35
ACC-320	1.19	415.0	8.33
Holland Special	2.20	796.7	10.50
ACC-331	0.82	276.7	8.00
ACC-329	0.77	293.3	8.87
KT-25	2.04	703.3	11.60
RS-199	1.54	411.7	7.18
Poonam	1.82	658.3	10.37
PSBK-1 (Check)	1.81	660.0	10.43
CD at 5%	0.25	85.60	1.48

Table 1c: Mean performance of curd width and curd compactness in cauliflower

Name of Genotype	Curd width (cm)	Curd compactness (g/cm)
Grodan	15.25	63.60
White Impress	13.38	45.54
Autumn Giant	17.29	71.06
EC-103576	15.53	70.36
Dochligan	15.49	59.95
ACC-328	16.60	70.87
KJ-47	14.27	55.90
All the year round	13.67	46.74
Lawyna	8.83	24.87
ACC-330	13.92	66.78
KJ-38	16.68	56.91
Champion	14.87	65.15
ACC-320	13.67	49.84
Holland Special	16.74	77.33
ACC-331	12.19	34.68
ACC-329	14.65	33.05
KT-25	16.72	60.72
RS-199	14.73	57.29
Poonam	14.52	63.58
PSBK-1 (Check)	15.38	63.44
CD at 5%	1.28	7.09

Special, respectively. The general population mean for curd compactness was found to be 56.88 g/cm. Three genotypes viz., Autumn Giant (71.06 g/cm), EC-103576 (70.36 g/cm) and ACC-328 (70.87 g/cm) were at par with Holland Special.

The curds were found to be fairly compact in PSBK-1 (63.44 g/cm). These genotypes viz., Autumn Giant (71.06 g/cm), ACC-328 (70.87 g/cm) and Holland Special (77.33 g/cm) were found significantly superior to PSBK-1. Six genotypes had significantly higher curd compactness than the general population mean. Semi compact curds (50-60 g/cm) were observed in four genotypes viz., Dochligan (59.95 g/cm), KJ-47 (55.90 g/cm),KJ-38 (56.91 g/cm) and RS-199 (57.29 g/cm), whereas, White Impress (45.54 g/cm), All the year round (46.74 g/cm), Lawyna (24.87 g/cm), ACC-320 (49.84 g/cm), ACC-331 (34.68 g/cm) and ACC-329 (33.05 g/cm) produced loose curds (<50 g/cm). Five genotypes were found to be at par with PSBK-1 (Check).

4.1.2 Parameters of variability

The estimates of variability like coefficients of variability (phenotypic and genotypic), heritability (broad sense) and genetic advance as per cent of mean (genetic gain) were worked out to facilitate selection for various characters. The results are presented in Table 3.

4.1.2.1 Coefficients of variability: The given data indicated that phenotypic coefficients of variability (PCV) were higher in magnitude than the genotypic coefficients of variability (GCV) for all the characters studied (Table 3). The phenotypic and genotypic coefficients of variability were comparatively high for stalk rot incidence (92.42 and 45.44%), gross curd weight (32.69 and 31.20%) and net curd weight (32.59 and 31.26%), moderate for black rot severity (27.03 and 12.96%) and curd compactness (25.25 and 24.10%), whereas, low for days taken to marketable curds (9.64 and 9.05%), number of leaves (13.26 and 10.50%), curd width (13.73 and 12.68%), stalk length (14.45 and 12.55%) and curd depth (14.89 and 11.70%).

4.1.2.2 Heritability: The heritability estimates (broadsense) varied from 23.00 per cent in black rot severity to 92.00 per cent in net curd weight (Table 3). It was high for five traits viz., net curd weight (92.00%), gross curd weight (91.10%), curd compactness (91.10%), days taken to marketable curds (88.10%) and curd width (85.40%). Heritability estimates were moderate for stalk length (75.40%), number of leaves (62.80%) and curd depth (61.80%), while it was low for two characters i.e., stalk rot incidence (24.20%) and black rot severity (23.00%)

4.1.2.3 Genetic advance as per cent of mean: The magnitude of genetic advance as per cent of mean ranged from 12.80 per cent (black rot) to 61.75 per cent (net curd weight) (Table 3). It was high for only two characters viz., net curd weight (61.75%) and gross curd weight (61.15%), while it was moderate for curd compactness (47.38%) and stalk rot incidence (46.09%) and low for curd width (24.11%), stalk length (22.31%), curd depth (18.99%), days taken to marketable curds (17.50%), number of leaves (17.14%) and black rot severity (12.80%)

4.2 Correlation studies

The correlation coefficients among various characters were worked out at phenotypic and genotypic levels (Table 4). In general the results showed that the genotypic correlations were higher in magnitude than phenotypic correlations.

4.2.1 Phenotypic correlation

The phenotypic correlation coefficients among eight horticultural traits showed that the most important trait i.e., net curd weight had positive and highly significant association with days taken to marketable curds (0.673), number of leaves (0.655), gross curd weight (0.876), curd depth (0.731), curd width (0.761) and curd compactness (0.892)

Days taken to marketable curds showed positive and significant association with stalk length (0.473), number of leaves (0.685), gross curd weight (0.762), net curd weight (0.673), curd depth (0.534), curd width (0.581) and curd compactness (0.592). Number of

leaves showed positive and significant correlation with gross curd weight (0.689), curd depth (0.513), curd width (0.573) and curd compactness (0.582). Gross curd weight had significant and positive correlation with number of leaves (0.689), net curd weight (0.876), curd depth (0.589), curd width (0.681) and curd compactness (0.825). The association of curd compactness was positive and significant with curd width (0.744).

4.2.2 Genotypic correlation

The trend of genotypic correlation was almost similar to that of the phenotypic correlation with the increase or decrease in phenotypic correlations, genotypic correlations also increased or decreased in similar fashion. For the correlations between traits i.e., curd depth and curd width; curd depth and curd compactness; stalk length and number of leaves, the genotypic correlation was significantly higher than that corresponding phenotypic correlation.

4.3 Disease reactions

4.3.1 Stalk rot incidence

The stalk rot incidence among various test genotypes was found to be non-significant (Appendix-II). The per cent incidence of stalk rot (Table 2) was minimum in ACC-320 (2.62%) and maximum in Holland Special (19.00%) under natural epiphytotic conditions.

4.3.2 Black rot severity

The black rot severity was also found to be non-significant (Appendix-II) among the genotype studied. The severity of the disease (Table 2) was minimum in ACC-331 (32.96%) and maximum in ACC-329 (56.04%) under natural epiphytotic conditions.

4.4 Effect of genotype on the biology of insect pests

A wide variations were observed in the cauliflower genotypes on the susceptibility to the Diamondback moth (*Plutella xylostella* L.) and cabbage white butterfly (*Pieris brassicae* L.).

4.4.1 Diamondback moth (*P. xylostella*)

The data on various aspects of the biology of *P. xylostella* as affected by genotype are presented in Tables 5a,b,c

4.4.1.1 Oviposition preference The average number of eggs laid per female on different genotypes varied from 75 on KT-25 and 122 on Grodan and thus among the genotypes included in the study Grodan was the most preferred while KT-25 was the least preferred. The check variety, PSBK-1, had an average number of 95.33 eggs. Seven genotypes, viz., Autumn Giant, ACC-328, Lawyna, ACC-330, ACC-331, KT-25 and RS-199 had significantly lower number of eggs than the standard check PSBK-1. While KJ-47 and Holland Special were at par with Grodan, 119 and 117 eggs/plant whereas Lawyna and RS-199 were at par with KT-25; 81 and 81.67 eggs/plant. Ten genotypes had significantly more number of eggs than the standard check variety, PSBK-1.

4.4.1.2 Egg incubation period The egg incubation period on various genotypes varied from 5.33 days (KJ-38, Poonam) to 8 days on Champion (Table 5a). The incubation period on the standard check (PSBK-1) was 7 days. Eight genotypes, viz., EC-103576, Dochligan, ACC-328, ACC-320, Holland Special, KT-25, ACC-331 and PSBK-1 were at par with Champion (Table 5a) while two genotypes, KJ-38 and Poonam had significantly shorter incubation period than PSBK-1. Ten genotypes were found to be at par with KJ-38 and Poonam so far as the incubation period was concerned.

4.4.1.3 Egg hatchability The egg hatchability on various genotypes ranged from 71.51 per cent in Lawyna to 95.11 per cent in ACC-320 (Table 5a). In PSBK-1, the egg hatching was 93.70 per cent Six genotypes, viz., All the year round, Lawyna, ACC-330, KJ-38, KT-25 and RS-199 had significantly lower hatching percentage than the standard check Whereas in nine genotypes the hatchability percentage was at par with the standard check PSBK-1.

Table 2: Mean performance of stalk rot incidence and black rot severity in cauliflower

Name of Genotype	Stalk rot incidence (%)	Black rot severity (%)
Grodan	6.30 (2.47)	52.26 (46.30)
White Impress	8.03 (2.82)	38.02 (37.77)
Autumn Giant	4.99 (2.17)	33.55 (35.32)
EC-103576	3.44 (1.74)	44.94 (42.02)
Dochligan	3.33 (1.47)	37.77 (37.63)
ACC-328	6.48 (2.02)	54.33 (47.49)
KJ-47	6.17 (2.42)	34.22 (35.77)
All the year round	3.89 (1.90)	37.52 (37.74)
Lawyna	2.81 (1.66)	52.09 (46.21)
ACC-330	3.49 (1.84)	39.45 (38.89)
KJ-38	5.59 (2.23)	40.74 (39.41)
Champion	3.77 (1.90)	34.63 (35.96)
ACC-320	2.62 (1.54)	36.07 (36.76)
Holland Special	19.00(4.23)	50.28 (45.14)
ACC-331	3.25 (1.79)	32.96 (35.01)
ACC-329	7.53 (2.56)	56.04 (48.48)
KT-25	12.52 (3.30)	48.40 (44.07)
RS-199	2.88 (1.65)	34.44 (35.92)
Poonam	9.79 (3.07)	48.18 (43.95)
PSBK-1 (Check)	6.92 (2.47)	34.44 (35.52)
	N.S.	N.S.

Figures in parentheses denote transformed values

Table 3: Estimates of Population mean, Range, Phenotypic and Genotypic coefficients of variability, Heritability, Genetic advance and Genetic gain

Characters	Population mean	Range		Phenotypic coefficient of variability (PCV)	Genotypic coefficient of variability (GCV)	Heritability Broad sense (%)	Genetic advance	Genetic gain (%)
		Minimum	Maximum					
Days taken to marketable curds	117.55	102.7	132.1	9.64	9.05	88.10	20.57	17.50
Stalk length (cm)	3.63	3.20	5.10	14.45	12.55	75.40	0.81	22.31
Number of leaves	17.79	14.27	21.47	13.26	10.50	62.80	3.05	17.14
Gross curd weight (kg)	1.57	0.72	2.40	32.69	31.20	91.10	0.96	61.15
Net curd weight (g)	560.83	236.7	808.3	32.59	31.26	92.00	346.32	61.75
Curd depth (cm)	9.74	7.18	11.60	14.89	11.70	61.80	1.85	18.99
Curd width (cm)	14.72	8.83	17.29	13.73	12.68	85.40	3.55	24.11
Curd compactness (g/cm)	56.88	24.87	77.33	25.25	24.10	91.10	26.95	47.38
Stalk rot incidence (%)	6.14	2.62	19.00	92.42	45.44	24.20	2.83	46.09
Black rot severity (%)	42.02	32.96	56.04	27.03	12.96	23.00	5.38	12.80

Table 4: Genotypic (G) and phenotypic (P) correlation coefficients among different traits

Characters		Days taken to marketable curds	Stalk length	No. of leaves	Gross curd weight	Net curd weight	Curd depth	Curd width	Curd compactness
Days taken to marketable curds	P	1.000	0.473*	0.685**	0.762**	0.673**	0.534*	0.581*	0.592*
	G	1.000	0.524*	0.878**	0.828**	0.711**	0.638**	0.629**	0.660**
Stalk length	P		1.000	0.425	0.376	0.213	0.262	0.250	0.142
	G		1.000	0.695**	0.449	0.243	0.394	0.254	0.163
No. of leaves	P			1.000	0.689**	0.655**	0.513*	0.573*	0.582*
	G			1.000	0.855**	0.799**	0.708**	0.766**	0.749**
Gross curd weight	P				1.000	0.876**	0.589*	0.681**	0.825**
	G				1.000	0.915**	0.754**	0.723**	0.865**
Net curd weight	P					1.000	0.731**	0.761**	0.892**
	G					1.000	0.796**	0.802**	0.949**
Curd depth	P						1.000	0.441	0.351
	G						1.000	0.505*	0.568*
Curd width	P							1.000	0.744**
	G							1.000	0.827**
Curd compactness	P								1.000
	G								1.000

* Significant at 5% level of significance
** Significant at 1% level of significance

4.4.1.4 Duration of larval development: The larval duration varied from 14.33 to 22.00 days when fed on twenty different genotypes (Table 5b) of cauliflower, the minimum being on Dochligan and maximum on ACC-320. The larval development was completed in 16.33 days on PSBK-1. Five genotypes, viz., All the year round, ACC-320, ACC-329, KT-25 and Poonam took significantly more time to complete larval development as compared to the standard check (Table 5b). Larval duration in case of three genotypes, viz., All the year round, KT-25 and Poonam were at par with ACC-320, while six other genotypes were at par with Dochligan (Table 5b).

4.4.1.5 Larval survival: Larval survival in different genotypes varied from 89.04 to 96.90 per cent (Table 5b). The minimum survival was in KJ-38 (89.04%) and maximum in ACC-320 (96.90%). The check variety (PSBK-1), exhibited 91.43 per cent survival of the larvae. Fourteen genotypes had the larval survival significantly more than the check variety. Larval survival in Grodan, White Impress, Autumn Giant, EC-103576, Dochligan, ACC-328, All the year round, ACC-330, Champion, Holland Special, ACC-331, ACC-329 and Poonam, was found to be at par with ACC-320 whereas only three genotypes, viz., KJ-47, RS-199 and PSBK-1 were at par with KJ-38. Similarly, larval survival in KJ-47, Lawyna and RS-199 was at par with PSBK-1.

4.4.1.6 Pupal duration

The pupal duration in all the genotypes varied from 6.33 in RS-199 and KT-25 to 8.67 days in Grodan and Dochligan (Table 5b). The pupal duration was found to be 7.67 days in PSBK-1. Nine genotypes including check were at par with Grodan whereas eleven genotypes were at par with RS-199 and KT-25.

4.4.1.7 Pupal survival: The pupal survival in population reared on different genotypes varied from 90.47 to 97.05 per cent (Table 5c) being minimum on KT-25 and maximum on White Impress. In the check genotype, PSBK-1, there was 92.60 per cent survival. None of the genotypes showed significantly lower pupal survival than the check, PSBK-1 while in eight genotypes the survival was significantly higher than the check. Six

genotypes, viz., ACC-328, Holland Special, ACC-331, ACC-329, RS-199 and PSBK-1 were at par with KT-25 and 11 were at par with White Impress.

4.4.1.8 Generation survival The overall generation survival of the pest on different genotypes varied from 64.18 per cent in Lawyna to 87.32 per cent in ACC-320 (Table 5c) as against 79.33 per cent in PSBK-1. Three genotypes, viz., Grodan, White Impress and ACC-320 had significantly higher generation survival than PSBK-1 while Lawyna had significantly less generation survival than the check. Nine genotypes were at par with ACC-320

4.4.2 Cabbage white butterfly (*P. brassicae*)

The effect of cauliflower genotype on various parameters of the biology of *P. brassicae* are summarized in Table 6a,b,c.

4.4.2.1 Larval duration: The average time taken for larval development in different genotypes varied from 22.83 to 31.50 days, being minimum on Dochligan and maximum on KJ-47 (Table 6a) In comparison, the larval development in the standard check, PSBK-1, was completed in 27.67 days. Two genotypes, viz., KJ-47 and Holland Special required significantly more duration than the PSBK-1, while eight genotypes, viz., Grodan, White Impress, Autumn Giant, Dochligan, ACC-328, Lawyna, Champion and ACC-329 required significantly less time to complete larval development in comparison to PSBK-1 (Table 6a) Two genotypes, Autumn Giant and ACC-328 were at par with Dochligan and four genotypes, viz., KJ-38, ACC-320, ACC-331 and Poonam were at par with the standard check (Table 6a)

4.4.2.2 Larval survival. The larval survival was minimum (59.18%) in Grodan and maximum (72.20%) in KJ-47. As against this, in PSBK-1 there was 65.74 per cent survival (Table 6a). Among the twenty genotypes included in the study only KJ-47 showed significantly more larval survival (72.20%) while Grodan and KJ-38 had significantly less survival than PSBK-1 (Check) (Table 6a). Larval survival in five genotypes, viz., Autumn Giant, EC-103576, Dochligan, ACC-331 and ACC-329 was at

Table 5a: Effect of cauliflower genotypes on oviposition preference, incubation period and hatching percentage of *Plutella xylostella*

Name of genotype	Oviposition preference (No. of eggs/female)	Incubation period (days)	Hatching percentage
Grodan	122.0	6.33	92.87 (9.64)
White Impress	100.7	5.67	91.72 (9.58)
Autumn Giant	85.33	5.67	90.69 (9.52)
EC-103576	104.7	6.67	92.34 (9.61)
Dochligan	105.7	7.00	91.86 (9.58)
ACC-328	85.33	7.00	93.42 (9.66)
KJ-47	119.0	5.67	91.85 (9.58)
All the year round	107.3	6.33	89.70 (9.47)
Lawyna	81.00	6.00	71.51 (8.45)
ACC-330	85.67	5.67	89.54 (9.46)
KJ-38	114.3	5.33	87.76 (9.37)
Champion	107.0	8.00	90.24 (9.50)
ACC-320	102.7	7.00	95.11 (9.75)
Holland Special	117.0	7.00	90.87 (9.53)
ACC-331	86.67	7.67	91.54 (9.57)
ACC-329	94.00	6.33	90.10 (9.49)
KT-25	75.00	7.00	89.77 (9.47)
RS-199	81.67	6.00	88.58 (9.41)
Poonam	114.3	5.33	92.08 (9.59)
PSBK-1 (Check)	95.33	7.00	93.70 (9.68)
(p = 0.05)	7.17	1.36	(0.20)

Figures in parentheses denote transformed values

Table 5b: Effect of larval feeding on different genotypes of cauliflower on larval duration, larval survival and pupal duration of *P. xylostella*

Name of genotype	Larval duration (days)	Larval survival (%)	Pupal duration (days)
Grodan	17.33	96.47 (9.82)	8.67
White Impress	15.00	96.76 (9.84)	6.67
Autumn Giant	17.67	95.66 (9.78)	7.33
EC-103576	18.00	94.44 (9.72)	6.67
Dochligan	14.33	95.91 (9.79)	8.67
ACC-328	15.67	96.22 (9.81)	7.67
KJ-47	17.67	91.43 (9.56)	8.00
All the year round	20.00	96.50 (9.82)	7.00
Lawyna	16.33	93.69 (9.68)	8.33
ACC-330	17.33	96.56 (9.83)	8.33
KJ-38	17.00	89.04 (9.44)	6.67
Champion	15.33	94.72 (9.73)	7.00
ACC-320	22.00	96.90 (9.84)	8.33
Holland Special	15.00	95.91 (9.79)	6.67
ACC-331	18.33	94.95 (9.74)	8.00
ACC-329	19.33	96.05 (9.80)	6.67
KT-25	20.00	94.10 (9.70)	6.33
RS-199	17.67	91.25 (9.55)	6.33
Poonam	20.33	96.17 (9.81)	7.33
PSBK-1 (Check)	16.33	91.43 (9.56)	7.67
(p = 0.05)	2.31	(0.14)	1.54

Figures in parentheses denote transformed values

Table 5c: Effect of larval feeding on different genotypes of cauliflower on pupal survival and generation survival of *P. xylostella*

Name of genotype	Pupal survival (%)	Generation survival (%)
Grodan	96.98 (9.85)	86.87 (9.32)
White Impress	97.05 (9.85)	86.15 (9.28)
Autumn Giant	95.00 (9.75)	82.41 (9.08)
EC-103576	95.98 (9.80)	83.70 (9.15)
Dochligan	95.69 (9.78)	84.35 (9.18)
ACC-328	93.52 (9.67)	84.08 (9.17)
KJ-47	96.97 (9.85)	81.49 (9.02)
All the year round	96.42 (9.82)	83.48 (9.13)
Lawyna	95.76 (9.78)	64.18 (8.01)
ACC-330	94.61 (9.73)	81.82 (9.04)
KJ-38	95.90 (9.79)	74.94 (8.66)
Champion	95.31 (9.76)	81.48 (9.02)
ACC-320	94.72 (9.73)	87.32 (9.34)
Holland Special	92.44 (9.61)	80.57 (8.97)
ACC-331	91.16 (9.55)	79.22 (8.90)
ACC-329	92.97 (9.64)	80.52 (8.97)
KT-25	90.47 (9.51)	76.45 (8.74)
RS-199	93.47 (9.67)	75.59 (8.69)
Poonam	93.77 (9.68)	83.09 (9.11)
PSBK-1 (Check)	92.60 (9.62)	79.33 (8.91)
(p = 0.05)	(0.16)	(0.31)

Figures in parentheses denote transformed values

Table 5c: Effect of larval feeding on different genotypes of cauliflower on pupal survival and generation survival of *P. xylostella*

Name of genotype	Pupal survival (%)	Generation survival (%)
Grodan	96.98 (9.85)	86.87 (9.32)
White Impress	97.05 (9.85)	86.15 (9.28)
Autumn Giant	95.00 (9.75)	82.41 (9.08)
EC-103576	95.98 (9.80)	83.70 (9.15)
Dochligan	95.69 (9.78)	84.35 (9.18)
ACC-328	93.52 (9.67)	84.08 (9.17)
KJ-47	96.97 (9.85)	81.49 (9.02)
All the year round	96.42 (9.82)	83.48 (9.13)
Lawyna	95.76 (9.78)	64.18 (8.01)
ACC-330	94.61 (9.73)	81.82 (9.04)
KJ-38	95.90 (9.79)	74.94 (8.66)
Champion	95.31 (9.76)	81.48 (9.02)
ACC-320	94.72 (9.73)	87.32 (9.34)
Holland Special	92.44 (9.61)	80.57 (8.97)
ACC-331	91.16 (9.55)	79.22 (8.90)
ACC-329	92.97 (9.64)	80.52 (8.97)
KT-25	90.47 (9.51)	76.45 (8.74)
RS-199	93.47 (9.67)	75.59 (8.69)
Poonam	93.77 (9.68)	83.09 (9.11)
PSBK-1 (Check)	92.60 (9.62)	79.33 (8.91)
(p = 0.05)	(0.16)	(0.31)

Figures in parentheses denote transformed values

Table 6a: Effect of larval feeding on different genotypes of cauliflower on larval duration and larval survival of *Pieris brassicae*

Name of genotype	Larval duration (days)	Larval survival (%)
Grodan	25.00	59.18 (50.30)
White Impress	25.67	66.46 (54.62)
Autumn Giant	23.50	71.34 (57.64)
EC-103576	27.00	69.88 (56.76)
Dochligan	22.83	66.86 (54.90)
ACC-328	24.17	60.61 (51.13)
KJ-47	31.50	72.20 (58.21)
All the year round	26.67	64.87 (53.67)
Lawyna	25.50	65.42 (54.02)
ACC-330	26.67	62.66 (52.34)
KJ-38	29.00	59.70 (50.60)
Champion	25.67	60.97 (51.36)
ACC-320	28.67	64.35 (53.35)
Holland Special	29.67	61.15 (51.46)
ACC-331	28.00	68.49 (55.87)
ACC-329	24.83	69.81 (56.70)
KT-25	27.17	65.72 (54.17)
RS-199	27.00	62.75 (52.40)
Poonam	28.33	60.11 (50.84)
PSBK-1 (Check)	27.67	65.74 (54.19)
(p = 0.05)	1.76	(3.50)

Figures in parentheses denote transformed values

Table 6b: Effect of larval feeding on different genotypes of cauliflower on the duration of pupa survival of *P. brassicae*

Name of genotype	Pupal duration (days)	Pupal survival (%)
Grodan	11.00	95.52 (9.77)
White Impress	9.67	95.89 (9.79)
Autumn Giant	8.67	98.96 (9.95)
EC-103576	11.50	96.96 (9.85)
Dochligan	11.83	100.00 (10.00)
ACC-328	9.67	96.42 (9.82)
KJ-47	10.17	95.02 (9.75)
All the year round	9.67	90.53 (9.51)
Lawyna	10.00	96.85 (9.84)
ACC-330	9.83	97.78 (9.89)
KJ-38	8.50	98.81 (9.94)
Champion	9.67	98.76 (9.94)
ACC-320	9.33	96.97 (9.84)
Holland Special	8.50	97.85 (9.89)
ACC-331	8.00	98.92 (9.95)
ACC-329	9.33	96.01 (9.80)
KT-25	10.17	93.71 (9.68)
RS-199	9.33	95.61 (9.78)
Poonam	11.00	100.00(10.00)
PSBK-1 (Check)	9.67	92.75 (9.63)
(p = 0.05)	1.33	N.S.

Figures in parentheses denote transformed values

Table 6c: Effect of larval feeding on different genotypes of cauliflower on total number of adults formed and generation survival of *P. brassicae*

Name of genotype	Total number of adults formed	Generation survival (%)
Grodan	27.67	55.33
White Impress	31.67	63.33
Autumn Giant	32.00	64.00
EC-103576	31.33	62.67
Dochligan	31.00	62.00
ACC-328	26.67	53.33
KJ-47	31.33	62.67
All the year round	29.00	58.00
Lawyna	30.00	60.00
ACC-330	29.00	58.00
KJ-38	28.33	56.67
Champion	29.33	58.67
ACC-320	30.33	60.67
Holland Special	28.67	57.33
ACC-331	32.33	64.67
ACC-329	31.00	62.00
KT-25	29.33	58.67
RS-199	29.00	58.00
Poonam	29.67	59.33
PSBK-1 (Check)	29.67	59.33
(p = 0.05)	3.14	6.27

par with KJ-47 while 9 were at par with Grodan. The genotypes White Impress, Autumn Giant, EC-103576, Dochligan, ACC-331, ACC-329 and KT-25 were at par with PSBK-1.

4.4.2.3 Pupal duration: The pupal duration varied from 8 days in ACC-331 to 11.83 days in Dochligan (Table 6b). As against this, the average pupal duration was 9.67 days in PSBK-1 (Check). Two genotypes, viz., EC-103576 and Dochligan took significantly more time to complete pupal development as compared to the check while ACC-331 took significantly less time to complete pupal development than PSBK-1. However, 10 genotypes were at par with the check with regard to pupal duration (Table 6b). The genotypes EC-103576, Grodan and Poonam were at par with Dochligan whereas six others were found to be at par with ACC-331 (Table 6b).

4.4.2.4 Pupal survival: The effect of larval feeding on pupal survival was found to be statistically non-significant (Table 6b). The pupal survival varied from 90.53 in All the year round to 100.00 per cent in Dochligan and Poonam (Table 6b).

4.4.2.5 Adult emergence: The proportion of adults formed in different genotypes varied from 26.67 to 32.33 adults, being minimum in ACC-328 and maximum in ACC-331. However, 29.67 adults were formed in the check PSBK-1. There was no single genotype in which the survival of adult was found to be significantly less than the check. Twelve genotypes, viz., ACC-331, White Impress, Autumn Giant, EC-103576, Dochligan, KJ-47, Lawyna, Champion, ACC-320, ACC-329, KT-25 and Poonam were at par with PSBK-1 (Check).

4.4.2.6 Generation survival: The overall generation survival of the pest on various genotypes varied from 53.33 (ACC-328) to 64.67 per cent (ACC-331) (Table 6c). The average generation survival in the commercial cultivar PSBK-1 was found to be 59.33 per cent. None of the genotypes had significantly less survival than the check. Twelve genotypes including check were found to be at par with ACC-331 whereas ten were at par with ACC-328.

Chapter-5

DISCUSSION

DISCUSSION

Among cole crops, cauliflower (*Brassica oleracea* var. *botrytis* L.) is a most widely grown vegetable in India due to its nutritional value and great production potential. Cauliflower in Himachal Pradesh is grown as an off-season vegetable crop. The evolution of superior genotypes with good horticultural traits requires breeding plans which is the ultimate aim of breeder. Genetic variability is the fundamental necessity of any improvement programme. The present study on genetic variability, correlation, diseases and pests resistance in cauliflower were undertaken for some important characters like days taken to marketable curds, stalk length, number of leaves, gross curd weight, net curd weight, curd depth, curd width, curd compactness, stalk rot incidence, black rot severity and effect of genotype on the biology of Diamondback moth (*Plutella xylostella* L.) and cabbage white butterfly (*Pieris brassicae* L.).

The present investigations were carried out in 20 divergent genotype of cauliflower. The informations were obtained regarding nature and extent of variability, heritability, genetic advance and genetic gain, so as to have guidelines for selection of desirable characters. Similarly, correlation coefficients were worked out to select superior genotypes to help the ongoing breeding programme in particular and future cauliflower improvement in general.

5.1 Mean and variability

Present studies depicted considerable scope for improvement in the cauliflower due to significant differences among the genotypes for all the traits. These results are in line with the findings of Pal and Swarup (1966), Howe and Waters (1984), Sharma *et al.*

(1988), Aditya *et al.* (1989), Jaiswal *et al.* (1992), Thakur (1998) and Anshul (2002), who also reported existence of variability in cauliflower for traits, viz., days taken to marketable curds, stalk length, number of leaves, gross curd weight, net curd weight, curd depth, curd width and curd compactness.

Based on the mean performance of genotypes with respect to various horticultural and quality characters, genotypes viz., Autumn Giant, EC-103576, ACC-328 and Holland Special possessed significantly higher net curd weight than the standard cultivar PSBK-1. These genotypes along with Grodan, Dochligan, KJ-47, ACC-330, KJ-38, KT-25 and Poonam had net curd weight higher than general population mean. These genotypes also gave good performance for stalk length, number of leaves, curd depth, curd width and curd compactness. The gross curd weight was significantly higher than the check, PSBK-1 in genotypes, viz., Autumn Giant, KJ-47 and Holland Special and were at par with EC-103576, ACC-328, KT-25 and Poonam. Days taken to marketable maturity is an important trait of cauliflower breeding for earliness. Among the diverse genotypes Poonam was late and Lawyna was earliest in maturity. Among the high yielding genotypes, EC-103576 was early in maturity and Holland Special was late in maturity. EC-103576 was found to be the best genotype as it gave intermediate stalk length, comparatively lesser leaves, maximum curd depth, curd width, higher gross and net curd weight, lesser days to reach marketable maturity and has higher curd compactness. Since phenotypic and genotypic variances do not have clear cut ceiling and their categorization as high or low is not feasible, therefore, unsuitable for comparison. The range of variability for different traits itself does not show whether it is of genetic or environmental in nature. This is better accomplished by estimating phenotypic and genotypic coefficients of variability which are free from units of measurement and thus helps in comparison among different characters. In the present study the phenotypic coefficients of variability (PCV) were higher than genotypic coefficients of variability, indicating little influence of environmental factors. The estimates of phenotypic and genotypic coefficients of variability were high (>30%) for stalk rot incidence, gross curd weight and net curd weight, moderate (15-30%) for black rot severity and curd compactness and were low (<15%) for days taken to marketable curds, number of leaves, curd width, stalk length and

curd depth. These results are in accordance with the findings of Dadlani *et al.* (1986), Jamwal *et al.* (1992), Dharminder (1999), Anshul (2002), Sanjeev (2002) who have also reported difference in magnitude in the values of phenotypic and genotypic coefficients of variability, indicating more scope for the improvement of characters.

The low phenotypic and genotypic coefficients of variability for earlier mentioned characters revealed that the genotypes of cauliflower possessed less genetic variability for these characters.

5.2 Heritability and genetic advance

The ratio of genetic variance to the total variance is called heritability and is a useful tool in predicting the progress to be achieved through selection. Heritability and genetic advance are two complementary parameters. Genetic advance may be used to estimate expected genetic advance through selection. The efficacy of any selection programme depend upon the extent of heritability and genetic advance which usually changes from population to population and environment to environment. In the present studies all the characters except stalk rot incidence and black rot severity exhibited moderate to high heritability, which indicated that the phenotypic variance was attributable to the genotypic variance and among the genotypes the differences for these traits were real. These results are in accordance with the findings of Jamwal *et al.* (1992) and Radhakrishna and Korla (1994). The heritability estimates ranged from 23.00 per cent to 92.00 per cent being minimum in black rot severity and maximum in net curd weight. The heritability was high for five traits, viz., net curd weight (92.00%), gross curd weight (91.10%), curd compactness (91.10%), days taken to marketable curds (88.10%) and curd width (85.40%), suggesting role of additive gene action and indicating that there is an ample scope for bringing up desirable improvement in these traits and selection for these traits would be effective as phenotypic variance was attributable to the genotypic variance and the difference for these trait among the genotypes were real.

Burton (1952) was of the opinion that the genotypic coefficient of variability along with heritability give the best picture of the genetic advance to be expected from the

selection, whereas Johnson *et al* (1955b) advocated that for effective selection genetic advance along with heritability is more useful. The magnitude of genetic advance ranged from 12.80 to 61.75 per cent. The genetic advance (expressed as percentage of mean) was high (>50%) for net curd weight (61.75%) and gross curd weight (61.15%), medium (25-50%) for curd compactness (47.38%) and stalk rot incidence (46.09%) whereas low (<25%) for rest of the characters. High degree of genetic advance for net curd weight and gross curd weight were reported by Jamwal *et al* (1992) and Sanjeev (1998). The attributes like net curd weight and gross curd weight showed high genetic advance as percentage of mean along with high heritability indicate that selection under such a situation would be more effective for improvement of these characters as these are controlled by additive gene action (Panse, 1957). High heritability coupled with high genetic advance for net curd weight have been reported by Sandhu and Singh (1977). High heritability with medium genetic gain was observed for curd compactness. Heritability was found to be low in black rot severity coupled with low genetic gain indicating the presence of dominance and epistatic effect. The characters as days taken to marketable curds and curd width where heritability is high but low genetic gain indicated the prevalence of non-additive gene action and hence selection as such may not be effective (Wright, 1934, Panse, 1957, Swarup and Pal, 1966; Sharma *et al*., 1988; Mahajan *et al*., 1996, Thakur, 1998 and Anshul, 2002).

5.3 Correlation coefficients (phenotypic and genotypic)

The correlation studies are one of the tools which helps in measuring the degree and magnitude of association between two characters. The breeding programme is considered to be most effective if it is concentrated towards one or at the most few characters. The knowledge of correlation between different characters helps in inter-relationships for indirect selection for characters that exhibit low heritability and gives information regarding the nature, extent and direction of selection pressure among the characters. Therefore, it is necessary to know the concurrent changes which in turn results in the selection of unselected economic characters when selection pressure is applied for the improvement of economic characters. This consideration becomes still important when

one visualized that curd yield being a complex character and is the product of interactions of several component traits. In fact Adam and Grafius (1971) have mentioned that yield should be considered as an end product of number of characters and breeder should not ignore the principle of balance among these components.

In the present investigations, in general, genotypic correlation coefficients, were higher than their corresponding phenotypic one's in most of the pair of traits with little difference in magnitude, indicating that there is strong inherent association among the various traits studied. The net curd weight had positive and significant correlation with days taken to marketable curds, number of leaves, gross curd weight, curd depth, curd width and curd compactness. Lal (1973), Sharma *et al.* (1982), Jamwal (1984), Singh (1984), Pandey and Naik (1986), Aditya *et al.* (1989), Dutta and Korla (1991), Dutta *et al.* (1992), Radhakrishna and Korla (1995), Sanjeev (1998) and Anshul (2002) have also reported positive and significant correlation of net curd weight with gross curd weight, curd depth, number of leaves, days taken to marketable curds and curd compactness, whereas the positive and significant association of net curd weight with gross curd weight, days taken to marketable curds, number of leaves has also been reported by Dhiman *et al.* (1983), Dadlani *et al.* (1983), Pandey and Naik (1991) and the present findings are almost in accordance with their results.

From the above discussion, it may be concluded that by making selection for days taken to marketable curds, increased number of leaves, gross curd weight, curd depth, curd width and curd compactness the net curd weight will be effected. The present results are in agreement with findings of Jamwal (1984) and Sanjeev (1998).

5.4 Disease reaction – stalk rot

Various genotypes of cauliflower were almost at par statistically for disease reaction to stalk rot (Appendix-II). However, on the basis of percentage disease incidence under natural epiphytotic conditions, the maximum incidence of disease was in Holland Special (19.00%) and lowest in ACC-320 (2.62%). Two genotypes namely Holland Special (19.00%) and KT-25 (12.52%) showed moderate resistance (11-20%), while rest

of the genotypes showed resistant reaction (0-10%). These findings were in accordance with Dharminder (1999), Kapoor (1986) and Harinder Singh *et al.* (1995). However, cv. PSBK-1 which was found resistant in the present studies is contrary to the earlier findings of Sharma *et al.* (2000) who observed this cultivar as highly susceptible. It may be due to unfavourable weather conditions for disease development prevailed during the crop season.

5.5 Disease reaction – black rot

In case of black rot all the genotypes were statistically at par (Appendix-II) for disease reaction to black rot under natural epiphytotic conditions. The maximum severity of disease was recorded in ACC-329 (56.04%) while least severity was shown by ACC-331 (32.96%). On the basis of per cent disease severity, all the genotypes showed highly susceptible reaction (>20% severity). The present finding are in agreement with Thakur (1998) who has also found majority of lines as susceptible including genotypes Holland Special, PSBK-1, KJ-47 and KJ-38.

5.6 Effect of genotype on the biology of insect pests

It was found that the genotypes of cauliflower used in the present study had considerable effect on the biology of both the pests, viz., Diamondback moth (*Plutella xylostella* L.) and cabbage white butterfly (*Pieris brassicae* L.). Similar variations were also observed by Lin *et al.* (1983), Asyakin *et al.* (1988) and Lal (1991).

5.6.1 Diamondback moth (*Plutella xylostella*)

5.6.1.1 Oviposition preference: Genotype KT-25 showed the least preference for oviposition, whereas Grodan was the most preferred genotype for oviposition by the pest. Lawyna and RS-199 were at par with KT-25 showing minimum preference for oviposition. While KJ-47 and Holland Special were at par with Grodan showing maximum oviposition preference. The genotypes, viz., KT-25, Lawyna, RS-199, Autumn Giant, ACC-328, ACC-330 and ACC-331 showed significantly less oviposition preference than the standard check, PSBK-1.

5.6.1.2 Egg incubation period: The incubation period was found to be maximum on Champion, at par with EC-103576, Dochligan, ACC-328, ACC-320, Holland special, KT-25, ACC-331, while PSBK-1 (check) showed least susceptibility for the pest. However, minimum incubation period was found on Poonam and KJ-38 which had significantly shorter incubation period than the check.

5.6.1.3 Egg hatchability: The minimum hatching percentage was found on Lawyna whereas maximum egg hatchability was on ACC-320. Six genotypes, viz., All the year round, Lawyna, ACC-330, KJ-38, KT-25 and RS-199 had significantly lower hatching percentage than the standard check, PSBK-1.

5.6.1.4 Duration of larval development: Maximum duration for larval development was taken by genotype ACC-320, at par with All the year round, KT-25 and Poonam. Five genotypes, viz., All the year round, KT-25, Poonam, ACC-320 and ACC-329 took significantly more time to complete larval development as compared to the standard check, PSBK-1. The genotypes at par with Dochligan were White Impress, Holland Special, Champion, ACC-328, Lawyna and PSBK-1 (Check).

5.6.1.5 Larval survival: The minimum larval survival was in KJ-38, whereas maximum survival was found in ACC-320. Larval survival was found to be at par with ACC-320 in genotypes like Grodan, White Impress, Autumn Giant, EC-103576, Dochligan, ACC-328, All the year round, ACC-330, Champion, Holland Special, ACC-331, ACC-329 and Poonam. Whereas, KJ-47, RS-199 and PSBK-1 were at par with KJ-38.

5.6.1.6 Pupal duration: The maximum pupal duration was found on Grodan and Dochligan which was at par with Lawyna, ACC-330, ACC-320, KJ-47, ACC-331, ACC-328, Poonam, Autumn Giant and the standard check, PSBK-1.

5.6.1.7 Pupal survival: The pupal survival when reared on different genotypes was found to be minimum in KT-25 and maximum in White Impress. The genotypes found to be at par with KT-25 were ACC-328, Holland Special, ACC-331, ACC-329, RS-199 and PSBK-1 (Check).

5.6.1.8 Generation survival The overall generation survival of the pest was found to be minimum in Lawyna and maximum in ACC-320. Lawyna was the only genotype which showed significantly less generation survival than the check (PSBK-1). Grodan, White Impress, Dochligan, ACC-328, EC-103576, All the year round, Poonam, Autumn Giant and ACC-330 were at par with ACC-320

From the above results, it was found that KT-25 was the least preferred genotype for oviposition, egg took maximum time to hatch, less hatching percentage, maximum larval duration and least pupal survival when compared with standard check, PSBK-1. The standard check, PSBK-1 showed high incubation period, less larval survival, maximum pupal duration and less pupal survival The genotype KT-25 was followed by Lawyna, RS-199, KJ-38 and ACC-331 which were found to be less susceptible to Diamondback moth (*P. xylostella*) than the check PSBK-1 However, the most susceptible genotype was ACC-320 with maximum hatching percentage, maximum larval survival and maximum generation survival when compared with PSBK-1 (Check). It was followed by Grodan, White Impress, Dochligan, ACC-328, EC-103576, All the year round, Poonam, Autumn Giant and ACC-330 Variations with regard to susceptibility to *P. xylostella* in different genotypes can be attributed to some specific chemical components present in the foliage like sinigrin content (Peterka *et al*., 1986), presence of triterphenols, α- and β-amyrin (Eigenbrode *et al*., 1991b) and allyl components of leaves (Eigenbrode and Pillai, 1998). Whereas, Stoner (1990) expressed the opinion that allelic genes were responsible for glossiness of leaves which in turn was responsible for providing resistance to *P. xylostella*.

5.6.2 Cabbage white butterfly (*Pieris brassicae* L.)

5.6.2.1 Larval duration The duration for larval development was maximum on KJ-47 and minimum on Dochligan It was found that genotypes KJ-47 and Holland Special took significantly more duration to complete their development as compared to the standard check PSBK-1 ACC-328 and Autumn Giant were found to be at par with Dochligan which had minimum larval duration.

5.6.2.2 Larval survival: The larval survival was minimum in Grodan which was at par with KJ-38, Poonam, ACC-328, Champion, Holland Special, ACC-330, RS-199, ACC-320 and All the year round. Only two genotypes were found to have significantly less larval survival than the standard check PSBK-1, whereas maximum survival was found in Autumn Giant, EC-103576, Dochligan, ACC-331 and ACC-329.

5.6.2.3 Pupal duration: The genotype Dochligan resulted in maximum pupal duration whereas minimum pupal duration was found on ACC-331. The genotypes found to be at par with Dochligan were EC-103576, Grodan and Poonam exhibited maximum pupal duration. EC-103576 and Dochligan took significantly more time to complete pupal development than PSBK-1 (Check). Minimum pupal duration with regard to ACC-331 found in Holland Special,KJ-38, Autumn Giant, ACC-320, RS-199 and ACC-329.

5.6.2.4 Pupal survival: Pupal survival was minimum in Dochligan and maximum in Poonam. Though the data were statistically non-significant.

5.6.2.5 Adult emergence: The minimum number of adults was formed in ACC-328 which was found to be at par with Grodan, KJ-38, Holland Special, ACC-330,RS-199, All the year round, KT-25, Champion, Poonam and PSBK-1 (Check). No single genotype had significantly less number of adults than check. However, maximum adult emergence was in ACC-331.

5.6.2.6 Generation survival: Minimum generation survival was found in ACC-328 and maximum in ACC-331. Ten genotypes, viz., Grodan, KJ-38, Holland Special, ACC-330, RS-199, All the year round, KT-25, Champion, Poonam and PSBK-1 were at par with ACC-328 possessing minimum generation survival. No single genotype had less generation survival than the check PSBK-1.

From the above results, it was found that ACC-328, Grodan, KJ-38, Holland Special, ACC-330, RS-199 and All the year round were resistant genotypes against *P. brassicae* as they had minimum larval survival, minimum number of adult emergence and minimum generation survival and were found to be at par with PSBK-1 (Check). Besides,

the most preferred genotype was ACC-331 having maximum larval survival, minimum pupal duration, maximum pupal survival, maximum adult emergence and highest generation survival. No genotype had significantly less generation survival than PSBK-1 (Check).

The results are in conformity with Asyakin *et al* (1988), Anshul (2002) who reported higher mortality in larval stage in resistant genotypes. Early maturing genotypes such as Grodan, All the year round and RS-199 had less number of larvae of *P. brassicae* confirmed the findings of Vail *et al* (1991) who have observed less number of larvae of *P. brassicae* on early maturing cultivars.

It may be concluded that EC-103576, Holland Special, Autumn Giant and ACC-328 were significantly better genotypes as compared to the standard check PSBK-1 for horticultural and quality traits, i.e., net curd weight, stalk length, number of leaves, gross curd weight, curd depth, curd width and curd compactness. These genotypes also showed tolerant reaction against stalk rot but were less tolerant to black rot. The genotypes found to have less preference for Diamondback moth (*P. xylostella*) were KT-25, Lawyna, RS-199, KJ-38 and ACC-331, whereas ACC-328, Grodan, KJ-38, Holland Special, ACC-330, RS-199 and All the year round for cabbage white butterfly as compared to other genotypes as well as standard check.

Chapter-6

SUMMARY & CONCLUSION

SUMMARY & CONCLUSION

The present study entitled "Evaluation of cauliflower genotypes for horticultural traits and resistance to some diseases and insect pests" was carried out at the Vegetable Research Farm, Nauni of the Department of Vegetable Crops, Dr. Y.S. Parmar University of Horticulture and Forestry, Nauni, Solan during 2002-2003.

The materials consisted of twenty divergent genotypes of cauliflower including check viz., PSBK-1. Genotypes were raised in a Randomized Block Design with three replications to study their mean performance for horticultural and quality characters. Susceptibility reaction of all the genotypes against Diamondback moth and cabbage white butterfly was studied in PG laboratory of Department of Vegetable Crops, UHF, Nauni, Solan. For Diamondback moth two pairs of newly emerged moths were released in a glass chimney (20x13 cm) containing fresh leaves of particular genotype. Similarly, egg masses of cabbage white butterfly were collected and placed on the leaves of particular genotype in similar glass chimneys. All the developmental stages of the pests were studied in the experiments which were laid in Completely Randomized Design and analysed accordingly.

The analysis of variance showed significant genotypic differences for all the horticultural and quality characters except for disease reactions to stalk rot and black rot. Data of horticultural and quality characters was analysed and then the coefficients of variability, heritability, genetic gain and correlation coefficients were worked out individually. Observations were recorded for days taken to marketable curds, stalk length, number of leaves, gross curd weight, net curd weight, curd depth, curd width and curd compactness.

Analysis of variance revealed significant differences among genotypes for all the horticultural characters and for stalk rot incidence and black rot severity. However, stalk rot incidence and black rot severity was found to be non-significant. Highest net curd weight was shown by genotype EC-103576 followed by Holland Special, Autumn Giant and ACC-328 which were statistically at par with EC-103576.

Besides showing superiority to the standard check PSBK-1 and general population mean in terms of net yield, EC-103576 also showed superiority over the standard check for traits like stalk rot incidence and less preference for Diamondback moth and for cabbage white butterfly. The coefficients of variability were low for majority of characters under study, however, it was moderate for black rot severity and curd compactness, while it was high for gross curd weight, net curd weight and stalk rot incidence. Phenotypic coefficients of variability were higher for all the characters under study with smaller magnitude than genotypic coefficients of variability with the exception of stalk rot incidence and black rot severity. Majority of characters estimated for heritability fell in the category of moderate to maximum while only two characters i.e. black rot severity and stalk rot incidence showed low quantum of heritability. Genetic advance as per cent of mean was on lower side in majority of characters, however, highest genetic advance was shown by net curd weight and gross curd weight. High additive genetic action was shown by net curd weight and gross curd weight due to high heritability and high genetic gain and that the straight selection for these trait would be effective. Correlation studies among different traits revealed that net curd weight had positive and significant association for all the characters except stalk length. In general, genotypic correlation coefficients were higher in magnitude than the phenotypic ones. Studies on the susceptibility of cauliflower genotypes to *P. xylostella* and *P. brassicae* revealed that feeding on different genotypes affected the development of the larval stages of the pests. KT-25, Lawyna, RS-199, KJ-38 and ACC-331 were found to be less susceptible by Diamondback moth while, ACC-328, Grodan, KJ-38, Holland Special, ACC-330, RS-199 and All the year round were less preferred by cabbage white butterfly.

Conclusion

It may be concluded that genotypes viz., EC-103576, Holland Special, Autumn Giant and ACC-328 were significantly superior as compare to the standard check, PSBK-1 for horticultural and quality traits. These genotypes also exhibited high estimates of heritability and genetic gain for gross and net curd weight which revealed that there is possibility for improvement of these characters by selection. These genotypes also showed tolerant reaction against stalk rot but were less tolerant to black rot. The genotypes found to have less preference for Diamondback moth (*P. xylostella*) were KT-25, Lawyna, RS-199, KJ-38 and ACC-331, whereas ACC-328, Grodan, KJ-38, Holland Special, ACC-330, RS-199 and All the year round for cabbage white butterfly as compare to other genotypes as well as from standard check. The genotypes which performed well for horticultural traits, diseases reaction and insect pest tolerance could be effectively used as parents in hybridization programme for improvement of these cauliflower genotypes.

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* **Original not seen**

APPENDICES

Appendix -I

Month	Rainfall (mm)	Temperature		Relative humidity	
		Maximum	Minimum	Maximum	Minimum
2002					
August	302	27.9	19.9	90	73
September	230.6	26.6	15.3	82	70
October	15.0	26.4	10.4	67	47
November	Nil	23.9	6.1	67	42
December	Nil	20.7	3.5	67	47
2003					
January	39.6	19.9	1.8	75	40
February	101.6	19.6	5.0	86	48
March	57.6	23.5	8.3	74	41
April	43.4	29.2	12.3	65	34
May	33.0	31.8	15.6	52	24

Source : Agrometeorological Section, Department of Soil Science, UHF, Nauni, Solan

Appendix-II

Analysis of variance for different traits

Source	d.f.	Mean sum of squares									
		1	2	3	4	5	6	7	8	9	10
Treatment	19	355.00*	0.690*	12.554*	0.741*	9487.200*	4.705*	11.051*	582.250*	1.424	65.217
Replication	2	76.995	0.155	0.061	0.018	3450.400	2.178	0.345	25.484	0.530	41.677
Error	38	15.303	0.068	2.073	0.023	2682.400	0.805	0.596	18.426	0.871	35.605

1. Days taken to marketable curds
2. Stalk length
3. Number of leaves
4. Gross curd weight
5. Net curd weight
6. Curd depth
7. Curd width
8. Curd compactness
9. Stalk rot incidence
10. Black rot severity

Appendix-III

Analysis of variance for different traits

Source	d.f	Mean sum of squares													
		11	12	13	14	15	16	17	18	19	20	21	22	23	24
Treatment	19	614.320*	1.758*	0.207*	12.435*	0.040*	1.890*	0.029*	0.269*	13.932*	17.659*	2.976*	0.047	6.750*	27.004*
Error	40	18.867	0.683	0.014	1.967	0.006	0.867	0.009	0.035	1.137	4.504	0.654	0.030	3.617	14.467

11.Oviposition preference (No. of eggs/female)
12 Egg incubation period
13 Hatching percentage
14 Larval duration
15 Larval survival
16 Pupal duration
17 Pupal survival
18 Generation survival
19 Larval duration
20 Larval survival
21 Pupal duration
22 Pupal survival
23 Total number of adults formed
24 Generation survival

CURRICULUM VITAE

Name	:	Alaksh Pathania
Father's name	:	Shri Ambrish Singh
Date of birth	:	01-06-1978
Sex	:	Male
Marital status	:	Single
Nationality	:	Indian

Educational qualifications

Certificate/Degree	Percentage/ grade	Board/University	Year
10+2	First	HP Board	1996
B.Sc.(Hort.)	First	Dr. YS Parmar University	2001

Whether sponsored by some State/ Central Govt/Univ/SAARC : No

Scholarship/Stipend/Fellowship/ any other financial assistance received during study period: : Stipend during M.Sc.