Chapter 2

REVIEW OF LITERATURE

Bitter gourd (*Momordica charantia* L.) is a tropical and subtropical important commercial vegetable crop of the family Cucurbitaceae and Genus Momordica. It is locally known as karala an important home garden vegetable. It is a fast growing climbing annual, native to south Asia. Compared to other cucurbits, bitter gourd has relatively high nutritional value, in respect of iron and ascorbic acid contents. It is one of the most common fruit vegetables having a great demand in Bangladesh. It has export potentiality because of its excellent keeping quality and grows year-round due to its photo insensitivity.

The main goal of most of the plant breeding programs is to increase the yielding ability of crop plants. Information on various quantitative traits, particularly of those that contribute to yield will be most useful in planning and successful implementation of the breeding program. Hybridization is one of the means of obtaining increased yield and exploitation of heterosis, is proving an efficient approach for improvement of vegetable crops. Therefore, the literatures on Line X Tester, heterosis, cross compatibility, combining ability, heritability and genetic improvement studied in bitter gourd and other relevant crops under the family Cucurbitaceae have been reviewed and presented under the following headings:

2.1 Morphological Evaluation of Inbred Lines

According to the last taxonomic description of Jeffery (1990), the Cucurbitaceae consists of 118 genera and 825 species. Robinson and Walters (1997), there is wide genetic variability in bitter gourd (Ahamed *et al.* 2014) and thus, the utilization of such variability in the crop's breeding programs is possible.

The genous *Momordica* includes about 42 species of the old-world tropics mainly in African. A few of these are widely cultivated for their edible fruits in India, Indonesia, Sri Lanka, Malaysia, the Philippines, China, the Caribbean and Pakistan. There are two fruit morphotypes of bitter gourd grown in this country. The dwarf plant types producing small sized fruits are known as Uchha and large fruit types are called Karalla (Rashid, 1999). Different bitter gourd genotypes were introduced over the years, cultivated for centuries and adapted to varied agro-ecological zones of Bangladesh. Such situations contributed for the evolvement of local genotypes with different types of fruit bitter gourd genotypes have been introduced from all over the world and local collections were made in the entire country. The introduced genotypes have diverse origin and contain many useful traits that are essential for the variety development and in addressing the critical varietal problem of the sector.

Sex expression in the cucurbitaceous vegetables is controlled by environmental as well as genetic factors. In melon, cucumber and many other cucurbits, two or more genes are involved in sex expression, sometimes with each gene having three or more alleles (e.g., luffa). It was further revealed that unfavorable growing conditions such as water stress could cause a slowdown in flower production. In general, female sex expression was reported to be promoted by low temperature, low nitrogen supply and high moisture availability. These environmental factors influence the levels of endogenous hormones, particularly ethylene, auxin and gibberellic acid, which ultimately influence sex expression (Robinson and Walters, 1997). Bleasdale (1984) stated that in cucumber or squash all the first formed flowers were usually male. Then a mixture of male and female flowers was produced, with an ever-increasing proportion of female flowers for the rest part of plant life. In all the species of cucurbits, the production of staminate flower was much more in number than the pistillate flower. In bitter gourd, staminate flower always came earlier than the pistillate flowers. Anderson (1984) observed that fruit shape was more or less evident in the shape of the immature ovary, with the developmental changes that affected ultimate shape due to both genetic and environmental factors. Also, a few fruits on a plant, particularly the earliest ones, might be shape a little differently than the rest, with the difference being evident in the ovaries. Seeds of cucurbit vegetables are relatively large, varying from about 20 mg per seed for muskmelon to 150 mg for squash and pumpkin (Lorenz and Maynard, 1980).

Pandey *et al*. (2019) evaluated of 29 bitter gourd accessions in this study. Genetic variation among 29 bitter gourd genotypes was assessed using morphological and ISSR markers during 2013–14. Data were recorded on 08 quantitative traits, viz. plant height (cm), fruit length (cm), fruit diameter (cm), fruit weight (g), seeds per fruit (number), number of branches per plant, number of fruits per plant (number) and yield per plant (g). High genetic variability was observed for yield per plant (397–1990 g), number of fruits per plant (9.18–43), individual fruit weight (25.47–125.67 g), plant height (110–503 cm), fruit length (6.39–25.97 cm), fruit diameter (2.53–6.1 cm), number of seeds (5–22.33) and number of branches per plant (4.67–16.44). The pair-wise Jaccard's similarity coefficient ranged between 0.22–1.00 based on morphological traits. These data revealed that large amount of genetic variability exist among the examined genotypes of bitter gourd.

Sureshkumara *et al*. (2017) conducted an experiment at University of Agricultural Sciences, GKVK, Bengaluru, India to study the performance of 24 bitter gourd hybrids. Among these hybrids Coimbatore Long x Panurthy was recorded highest yield per vine (2.32 kg), average fruit weight (85.10 g), percent fruit set (93.28), days to opening of first male flower appearance (37.32 days), day to fifty per cent flowering (83.12 days) and days to first harvest (64.07 days). Lesser number of seeds fruit-1 was recorded in Arka Harit x Coimbatore Small (12.30), maximum average fruit length in Green Long x Panurthy (25.15 cm), maximum sex ratio was recorded in Green Long x Nanjan good Local. Maximum productive vine length was recorded in White Long x Panurthy at 45 DAS (114.47 cm), 60 DAS (159.91 cm) and 90 DAS.

Resmi and Sreelathakumary (2017) evaluated 33 genotypes of bitter gourd collected from different agro-climatic regions of India. The analysis of variance revealed considerable genetic diversity among elite genotypes of M. charantia for aggregate effect of most of the characters studied. Among the genotypes evaluated, MC 9 was the earliest to emerge, MC 1 was the most vigorous registering the highest values for vine length and MC 20 for internodal length. Significantly maximum number of primary branches was recorded by MC 32 and was the earliest to harvest. Maximum fruit length, fruit girth, average fruit weight and yield per plant were recorded in MC 20. Highest number of fruits per plant was recorded in MC 10. MC 32 had higher number of seeds per fruits while MC 24 recorded higher seed weight.

Rashid *et al.* (2014) evaluated eight cultivars of snake gourd (*Trichasanthes anguina* L) collected from test F1 genotype and different seed company were evaluated under Randomized Block Design with three replications at Research & Development (Vegetable) Farm, Supreme Seed Company Limited, Bhaluka, Mymensingh in kharif-1 for correlation coefficient analysis between yield and first attributing characters. days to female flowering, days to male flowering, node number of 1st female flowering, number of nodes at 1st male flowering, days to 1st harvest, number of fruits per plant, Total number of fruits, total weight of fruit per plant and yield (gm), Individual fruit weight (gm), fruit length (cm) and fruit diameter (cm) were major contributing factors towards yield and selection based on these characters can be effective for developing high yielding varieties.

Yadav *et al.* (2008) reported in bitter gourd that Maximum vine length was recorded in IC-85635A. Significantly higher number of primary branches per vine and intermodal length were observed in IC-85639. Maximum number of nodes was observed in JMC-4. Significantly minimum numbers of days for first appearance of male flower and maximum fruit length, fruit width, yield per vine, yield per plot were recorded in MC-84. Highest number of fruits per vine was recorded in GY-I.

Variability

Sahoo and Singh (2020) conducted an experiment to estimate heritability, genetic advance and genetic variability for yield and yield contributing components of cucumber. High heritability coupled with high genetic advance as percent of mean was observed for fruit length (cm), fruit weight (g), number of fruits per plant, plant height (m), yield per plant (kg), yield per hectare (q/ha), days to first male flower, node to first male flower, node to first female flower and sex ratio (M/F). These characters had additive gene effects and therefore, these are more reliable for effective selection. Yield of parthenocarpic and gynoecious cucumber lines could be improved upon by selecting superior characters for further improvement in cucumber breeding. Heritability in broad sense may play greater role about information of relative value of selection. The results in the experiment revealed higher heritability estimate for all the characters. High heritability indicates less influence of environment and is governed by additive gene effects.

Maurya *et al.* (2018) reported in bitter gourd that the presence of high heritability in broad sense (h2bs) coupled with high genetic advance in percent of mean were observed for average fruit weight, whereas high heritability in broad sense (h2bs) were observed for no. of fruits per plant followed by fruit yield per plant (kg), vine length (m), fruit length (cm), node no. of first staminate flower and in case of high genetic advance in per cent of mean were observed for no. of fruits per plant, followed by fruit yield (kg) and vine length showing additive gene effect. The high estimates of heritability in broad sense (h2bs) were observed for all the character except days to anthesis of first pistillate flower (68.62%), node no. of first pistillate flower (64.97%), which indicated moderate heritability, while days to first fruit harvest (61.07%) and fruit diameter (54.59%) indicated low heritability. High estimates of genetic advance in per cent of mean was recorded for no. of fruit per plant (44.52%) followed by fruit yield per plant (42.00%), vine length (40.30%), fruit length (34.25%), average fruit weight (26.47%), while, no. of nodes per vine (25.62%) and showed moderate genetic advance in per cent of mean. Whereas, node no. of first pistillate flower (21.33%) followed by days to anthesis of first pistillate flower (15.93%), fruit diameter (13.78%), and days to first fruit harvest (11.35%) recorded the low genetic advance in per cent of mean.

Pathak *et al.* (2014) explained that high GCV and PCV were recorded in bitter gourd for number of fruits per plant (37.61% and 39.92%, respectively), average fruit weight (31.73% and 32.26%, respectively) and fruit length (24.05% and 25.18%, respectively) whereas, low GCV and PCV were observed for days to first male (4.75% and 5.60%, respectively) and female flower opening (4.03% and 5.63%, respectively). High heritability with high GA was observed for fruit weight (96.74% and 64.29%, respectively), fruit length (91.25% and 47.33%, respectively) and number of fruits per plant (88.75% and 72.99%, respectively) which is an indicative of greater proportion of additive genetic variance and consequence a high genetic gain from selection. Moderate heritability and GA were recorded for yield per plant (54.93% and 17.25%, respectively). High heritability with low GA was observed for days to first male (72.02% and 8.30%, respectively) and female flower opening (51.19% and 5.94%, respectively) indicated that non-additive gene effects were involved for the expression of these characters.

Islam *et al*. (2009) evaluated 20 bitter gourd genotypes and observed high genotypic co-efficient of variation (GCV) for branches per vine, yield per plant and number of fruits per plant whereas low genotypic co-efficient of variation was observed for days to first male and female flowering. Differences between genotypic and phenotypic coefficient of variation revealed that major portion of the phenotypic variance was genetic in nature. Hossain *et al.* (2010) reported highest GCV for yield per plant (42.75%), number of fruits per plant (33.41%), fruit length (27.57%), number of lateral shoots (24.19%), average fruit weight (22.14%), petiole length (16.10%) and node order at which male and female flower opened (13.28% and 12.62%) in 58 evaluated long type cucumber genotypes.

Some available literatures on various aspects of genetic advance and heritability are given in Table 2.1

Table 2.1 Literature on genetic advance (GA) and heritability (h^2) in bitter gourd and other related species for yield and yield components

Crop	GA%	H^2 %	References
1. Days to first female flower opening • Bitter gourd	• 15.93	• 68.62	• Maurya *et al.* (2018)
2.Node no. of first female flower anthesis • Bitter gourd • Bitter gourd	• 21.33 • 21.47	• 64.97 • 61.72	• Maurya *et al.* (2018) • Tyagi *et al.* (2018)
3.Days of first fruit harvest • Bitter gourd • Bitter gourd	• 11.35 • 8.31	• 61.07 • 40.65	• Maurya *et al.* (2018) • Tyagi *et al.* (2018)
4. Average fruit weight • Bitter gourd	• 26.47	• 80.3	• Maurya *et al.* (2018)
5. Length and diameter of fruit • Bitter gourd	• 80.2 (Length) & 54.59 (diameter)	• 80.2 (Length) & 54.59 (diameter)	• Maurya *et al.* (2018)
6. Number of fruits per plant • Bitter gourd	• 44.52	• 90.52	• Maurya *et al.* (2018)
7. Yield per plant • Bitter gourd	• 42.00	• 89.09	• Maurya *et al.* (2018)
8. Number of seeds per fruit • Pumpkin	• -	• High	• Aruah *et al.* (2012)
9. Weight of 100 seeds • Bitter gourd	• Considerable (20.81)	• Moderate (53.4)	• Tyagi *et al.* (2018)

2.2 Correlation Studies and Path Coefficient Analysis

Yield, a complex character which is associated with many morphological, physiological and anatomical plant characteristics. Study of relationships (usually by correlations and path coefficient analysis) between the traits associated with yield is very much important in identifying important characters for selection for yield improvement in bitter gourd. Usually, more than one trait is measured on progenies evaluated either for a specific trait in cyclical selection programs or in applied breeding programs that require a combination of traits to satisfy growers. Although yield is usually the primary trait of interest, yield contributing traits are all corollary traits that a breeder must consider for eventual usefulness of genotypes evaluated. It is only natural; therefore, that attention is given to associations among traits during selection and testing of genotypes.

Correlation measured by a correlation coefficient is important in plant breeding because it measures the degree of association, genetic or non-genetic between two or more characters. If genetic association exists, selection for one trait will cause changes in other traits called the correlated response. The cause of correlation can be genetic and/or environmental. Genetic causes may be attributed to pleiotropism and/or linkage disequilibrium. When genes are not closely linked, linkage disequilibrium is not an important cause of correlation between characters in random mated populations. In such cases the existence of genetic correlations is mostly attributable to pleiotropy (Hallauer and Miranda, 1982).

Phenotypic correlations between traits are calculated by using directly observed measurements. There are two causes of phenotypic correlation between traits: genetic and environmental. Statistical techniques are used to estimate these correlations from directly observed measurements (Cruz and Regazzi, 1997; Hallauer and Miranda, 1982).

Genetic correlations are particularly important because they provide the plant breeder with information about heritable associations between traits. This information is useful in the development of appropriate strategies for breeding for multiple traits in a plant improvement program or for employing indirect selection for a particular trait such as yield. Selection for one trait will result in a response in genetically correlated traits.

Path coefficient analysis is a statistical tool that helps the plant breeder to better understand what types of relationships exists between two variables. Such that one variable directly causes an effect on the other variable. Alternatively, a variable can cause an indirect effect by way of (via the "path" of) a third, or more variables. In general, the path coefficient analysis consists of partitioning the correlation coefficient into the direct and indirect effects (Cruz and Regazzi, 1997; Vencovsky and Barriga, 1992).

The study of relationships among quantitative traits is important for assessing the feasibility of joint selection of two or more traits and hence for evaluating the effect of selection for secondary traits on genetic gain for the primary trait under consideration. A positive genetic correlation between two desirable traits makes the job of the plant breeder easy for improving both traits simultaneously. Even the lack of correlation is useful for the joint improvement of the two traits. On the other hand, a negative correlation between two desirable traits impedes or makes it impossible to achieve a significant improvement in both traits. However, simple correlations do not give an insight into the true biological relationships of these traits with yield. Yield, being quantitative in nature is a complex trait with low heritability and depends upon several other components with high heritability (Grafius, 1959). These traits are in turn interrelated. Their interdependence influences the direct relationship with yield and as a result, the information obtained on their association becomes unreliable (Khairwal *et al.*, 1999). The path coefficient analysis initially suggested by Wright (1921) and described by Dewey and Lu (1959) allows partitioning of correlation coefficient into direct and indirect contributions (effects) of various traits towards dependent variable and thus, helps in assessing the cause-effect relationship as well as effective selection.

Generally, a path coefficient analysis is needed to clarify relationships between characteristics, because correlation coefficients describe relationships in a simple manner. Path coefficient analysis shows the extent of direct and indirect effects of the causal components on the response component. In most studies involving path analysis, researchers considered the predictor characters as first-order variables to analyze their effects over a dependent or response variable such as yield (Gunel *et al.*, 1991; Gopal *et al.*, 1994; Yildirim *et al.*, 1997; Bhagowati and Saikia, 2003).

The knowledge of certain genetic parameters is essential for proper understanding and their manipulation in any crop improvement program. Grain yield is the result of the expression and association of several plant growth components. Correlation coefficients, although useful in quantifying the size and direction of trait associations, can be misleading if the high correlation between two traits is a consequence of the indirect effect of the traits (Dewey and Lu, 1959). The advantage of path analysis is that it permits the partitioning of the correlation coefficient into its components, one component being the path coefficient that measures the direct effect of a predictor variable upon its response variable, the second component being the indirect effect(s) of a predictor variable on the response variable through another predictor variable (Dewey and Lu, 1959). In agriculture, path analysis has been used by plant breeders to assist in identifying traits that are useful as selection criteria to improve crop yield (Milligan *et al.*, 1990).

Yield is a complex phenomenon, entailing several contributing factors. These factors influence yield both directly and indirectly and the breeder is naturally interested in investigating the extent and type of association of such traits. Towards a clear understanding of the type of plant traits, correlation and path coefficient analysis are logical steps. Phenotypic and genotypic correlations within varieties are of value to indicate the degree to which various characters are associated with economic productivity. Path coefficient analysis is a reliable statistical technique that provides means not to quantify the interrelationships of different yield components but also indicates whether the influence is directly reflected in the yield or takes some other pathway for ultimate effects. As a guideline for interpretation of path analysis results, the following broad points may be kept in view (Singh and Chaudhary, 1977)

Firstly, if the correlation coefficient between a causal factor and the effect is almost equal to its direct effects, and then correlation explains the true relationship through this trait will be effective.

Secondly, if the correlation coefficient is positive, but the direct effect is negative or negligible, the indirect effects seem to be cause of positive correlation. In such situations, the indirect causal factors are to be considered simultaneously for selection.

Thirdly, correlation coefficient may be negative but the direct effect is positive and high. Under these circumstances, a restricted simultaneous selection model is to be followed i.e., restrictions to be imposed to nullify the undesirable indirect effects in order to make use of the direct effect.

Fourthly, if the correlation coefficient is negative and direct effect is also negative, then we have to drop the selection based on that character.

Fifthly, the residual effect determines how best the causal factors account for the variability of the dependent factor. If residual effect is high, some other factors, which have not been considered here, need to be included in this analysis to account fully for the variation in yield.

Maurya *et al*. (2019). carried out an experiment to study the correlation coefficient and path coefficient for the yield and yield component of bitter gourd (*Momordica charantia* L.) to estimate the correlation coefficient and to work out the path coefficient analysis for yield and its component traits of 30 genotypes. Thirty genotypes of bitter gourd were evaluated for yield contributing characters to observe their associations and direct and indirect effect on fruit yield. In most cases, the genotypic correlation coefficient was higher than the respective phenotypic correlation coefficients indicating the suppressive effect of environment modified phenotypic expression of these characters by reducing phenotypic correlation values. The higher magnitude of coefficient of variation at phenotypic as well as genotypic levels were observed for phenotypic in no. of fruit per plant followed by fruit yield per plant (kg), fruit length (cm), node no., average fruit weight (g), node no. to anthesis of first pistillate flower, no. of nodes per vine and lower value in days of first fruit harvest followed by days to anthesis of first pistillate flower, fruit diameter. The phenotypic correlation coefficients between different characters were generally similar in magnitude and nature to the corresponding genotypic correlation coefficient. The significant and positive correlation with yield per plant was observed at phenotypic level with average fruit weight and no. of fruits per plant. The analysis of path coefficient indicating appreciable amount of direct positively effect of no. of fruits per plant and fruit yield per plant followed by vine length on fruit yield per plant.

Kumar *et al*. (2018) conducted an investigation entitled "Correlation and characters association studies in bitter gourd (*Momordica chantia* L.)" was carried out at Horticulture Research Farm, Department of Horticulture, Babasaheb Bhimrao Ambedkar University (A Central University), Vidya- Vihar, Rae Bareli Road, Lucknow (U.P.), India during summer season of the year 2014-2015. The experiment was laid out in Randomized Block Design with three replications. The experimental materials consisted fifteen genotypes of bitter gourd i.e., HABG-22, NDBT-07, NDBT-09, Meghana-2, Selection-5, Preethi, Phul Ujjwala, Priya, Nakhara, Pant Karela-1, Hirkani, VRBT-23, Pusa Vishesh, Pusa Ashaudhi and Arka Harit. Correlation coefficient and direct and indirect effect of fruit yield attributing traits, it is clear that for bring out designed improvement towards fruit yield in bitter gourd. Average fruit weight and fruits per vine can be used as direct selection parameters.

Ananthan and Krishnamoorthy (2017) conducted an experiment to study the correlation and path analysis for yield and yield attributing characters namely first female flower node, days taken for first female flowering, number of fruits per plant, fruit length, fruit weight (g), fruit yield per plant (kg) of twenty ridge gourd. The genotypic and phenotypic correlation coefficients showed that the fruit yield per plant significantly contributed by fruit weight (0.722 and 0.681), fruit diameter (0.426 and 0.393), number of fruits per plant (0.504 and 0.477) and first female flower node (0.467 and 0.428). The path coefficient analysis showed that number of fruits per plant exhibited significant positive direct effect on yield per plant (1.4792) followed by fruit weight directly (0.9346) and indirectly (0.7220).

Anjali *et al.* (2017) studied with character association and revealed that fruit yield had positive and significant correlation with average fruit weight (0.774), number of fruits per plant (0.945), vine length (0.547), number of primary branches (0.472), fruit length (0.390), seed length (0.240) whereas, fruit yield had negative and significant correlation with number of node of first female/hermaphrodite female flower (-0.458), days of first female/hermaphrodite flower anthesis (-0.314) and days of first fruit harvesting (-0.401) in ridge gourd.

Durga *et al*. (2017) carried out an investigation of bitter gourd at Vegetable Research Farm of Department of Horticulture, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi, India during the kharif season of 2014. The present experiment was under taken with 20 genotypes in Randomized Complete Block Design (RBD) in three replications. The yield of the crop is a complex character and is the ultimate product of action and interaction of various component characters. Taking the phenotypic correlation coefficient into consideration in the present investigation, characters namely node number of first staminate flower appearance (0.321), node number of first pistillate flower appearance (0.472), vine length (0.338), fruit circumference (0.613), fruits per plant (0.467), average fruit weight (0.641), fruit diameter (0.491) and internodal length (0.225) are positively and significantly correlated with yield per plant while on the other hand, days to anthesis of first staminate flower (- 0.302) and days to first harvest (- 0.294) are negatively and significantly correlated with yield per plant.

Jatav *et al.* (2016) reported on twenty-four genotypes of bitter gourd were grown in Randomized Block Design with three replications including two checks (Pant Karela-1 and Pant Karela-2) to assess correlation co-efficient and path co-efficient analysis at G.B. Pant

University of Agriculture and Technology, Pantnagar, during summer 2014., Correlation co-efficient studies indicated that fruit yield per plant had highly significant and positive correlation with number of fruits per plant (0.577) followed by average fruit weight (0.551), fruit diameter (0.550), main vine length (0.470), while it was significantly and negatively associated with days to first female flower (-0.459), days to first harvest (-0.444) and number of node to first male flower (-0.425). Path co-efficient analysis revealed that number of fruits per plant (0.875) exerted high order of positive direct effect towards yield followed by average fruit weight (0.797), days to first harvest ((0.190)); however, days to first female flower (-0.201) followed by weight of seed per fruit (0.150), number of node to first female flower (-0.116). number of branches per vine (-0.064), exerted negative direct effect towards yield. Based on overall findings of the present study, it was concluded that for selection of superior genotypes primary emphasis should be given on fruit yield per plant followed by number of fruits per plant, average fruit weight and fruit diameter.

Mahabubur *et al*. (2016) studied genetic variability, heritability and path coefficient analysis in 21 genotypes of snake gourd. Correlation studies revealed that the fruit yield had a significant, positive correlation with the number of fruits per vine, length of fruit and single fruit weight. Importantly, more than 90% of the genotypic total variation was contributed by the characters included in the path analysis. The highest direct positive effect was recorded for the number of fruits per vine

Pathak *et al.* (2014) explained that correlation analysis revealed that number of fruits per plant had significant positive correlation for yield in bitter gourd. Further, path coefficient analysis partitioned the correlation into direct and indirect effects. Yield was found to be directly correlated with fruit weight, number of fruits per plant and fruit length, hence selection based on these characters would more rewarding.

Kumar *et al*. (2013) studied correlation and path analysis for yield and yield contributing characters namely total yield per vine (kg), number of fruits per vine, average weight of fruit (g), average length of fruit (cm), average diameter of fruit (cm), to anthesis of first male flower, days to anthesis of first female flower, node number at which first female flower appeared, days to maturity, number of primary branches, vine length of 20 sponge gourd genotypes were studied. Total yield per vine was found to be positively and significantly correlated with number of fruits per vine, average weight of fruit and number of seeds per fruit. Path coefficient analysis revealed that average diameter of fruit, number of primary branches, number of fruits per vine and average weight of fruit showed positive direct effects on total yield per vine.

Hossain *et al.* (2010) mentioned that the correlation co-efficient revealed yield per plant had highly positive and significant association with fruit length and diameter, average fruit weight and number of fruits per plant. Path analysis showed that the fruit length and diameter, average fruit weight and number of fruits per plant directly contributed towards the yield per plant in cucumber.

Kupper and Staub (1988) observed moderate to large negative correlation between fruit number. Number of female flowers per vine, fruit length, and fruit diameter and fruit weight were positively associated with yield. Number of days for first female flower emergence was negatively associated with number of fruits per vine and yield per vine in cucumber (Choudhary *et al.*, 1985). It was also observed that a positive correlation of length and diameter of the fruits with that of the fruit weight.

2.2.1 Heritability

Heritability in the "broad sense" is the ratio expressed in percent of genetic variance to the total phenotypic variance. Narrow sense heritability is the ratio of additive genetic variance to total phenotypic variance. The success of breeding program depends largely upon the combining ability of the genotypes and the extent to which the desirable traits are heritable. The knowledge of heritability helps plant breeders in predicting the behavior of the succeeding generation, making desirable selection and assessing the magnitude of genetic improvement through selection. Yield is the most important agronomic trait in the selective process; however, this characteristic has low heritability. This problem is overcome through the indirect selection of agronomic characters that are positively correlated with productivity (Cruz and Carneiro, 2003).

High heritability with high genetic gain is associated with additive gene effects (Panse, 1957). On the contrary, non-additive gene effect (dominance or epistasis) is associated with characters exhibiting high heritability and low genetic advance.

If a particular character is controlled by recessive genes, selection should be delayed until the generations are more homozygous. If heritability is low then either increased replication is required, or else selection for a correlated character may be practiced to increase the chances of identifying superior genotypes (Hill *et al*., 1999). Heritability in the narrow sense is important to the plant breeder, because the effectiveness of selection depends on the additive portion of genetic variance in relation to total variance (Falconer, 1960).

Since the value of heritability depends on the magnitude of all the components of variance, a change in any of those factors will affect it. Therefore, change of conditions of culture or management, such as plant date, density, number of replications and years, will affect environmental variance (Wricke and Weber, 1986). Selection of a trait should fairly be easy if it is highly heritable. This is because there would be a close correspondence between genotype and phenotype due to a relatively smaller contribution of environment to the phenotype. Nevertheless, for a trait with low heritability, selection may be considerably difficult or virtually impractical due to the masking effect of the environment on the genotypic effects (Singh, 1990).

Heritability is useful to study genetic change of a population undergoing selection (Falconer, 1981) and to choose among alternative breeding programs (Robertson, 1957; Hill, 1971). High heritability accompanied by high genetic advance is more useful than heritability alone and considerable importance could be made in these characters by predicting the result and selecting the best individual (Johnson *et al.,* 1955). This is the only method that has been proved unbiased in the presence of selection. The findings of different investigators are presented as follows:

Tyagi *et. al*. (2018) reported in bitter gourd that the estimates of heritability in broad sense (h^2_{bs}) ranged from 31.21 percent (vine length) to 92.41 per cent (fruit length). Highest estimates of heritability were observed for all the characters fruit length (92.14), number of nodes per vine (89.27), fruit diameter (82.30), fruit yield per plant (72.67). However, node number to anthesis of first pistillate flower (61.72%) and number of fruits per plant (50.50%) which indicated moderate heritability, while days to anthesis of first pistillate flower (44.99%), days to first fruit harvest (40.65%) and vine length (31.21%) indicated lower heritability. Highest estimates of genetic advance in per cent of mean was recorded for average fruit weight (42.82%), vine length (42.39) fruit length (41.50%), fruit yield per plant (34.58%), while number of nodes per vine (28.51%), fruit diameter (24.97%), node number to anthesis of first pistillate flower (21.47%), and number of fruits per plant (20.14%) showed moderate genetic advance in per cent of mean, whereas, days to anthesis of first pistillate flower (11.34%), and days to first fruit harvest (8.31%) recorded the lower genetic advance in per cent of mean.

Yadav *et. al*. (2012) conducted a field experiment with 20 diverse cucumber genotypes (BSC-1, BSC-2, CH-122, 126,128, CHC-1, Swarna Ageta, VRC-11-2, CC-3, CC-8, DR/NKV/02, VRC-19, CC-2, 4, 5, 6, 7, 9, 1 and Ranchi-1) in randomized block design with three replications. Analyzed data revealed that among all the genotypes CC-5, BSC-2, BSC-1, CH-128, CHC-2 and CC-2 gave promising results. Heritability estimated were high > 90% for days to first male flower anthesis, nodes no. bearing first female flower, vine length, numbers of branches/ vine, no. of fruits/vine, fruit diameter at edible stage, fruit length, fruit weight at edible stage, 100 seed weight, days to first fruit harvest and fruit yield/vine. In the present study, high genetic advance coupled with high heritability was observed for no. of branches/vine followed by cavity of fruit at edible stage, fruit yield/vine, no. of fruits/vine, fruit length and 100 seed weight. It indicated that additive gene effects were more important for these traits.

2.3 Parent Selection

Plant breeding deals with high-yielding genotypes and parental selection is the first step in any plant-breeding program. However, how the best to choose parents of these genotypes, remains an unsolved question. Research on parent selection may be approached in two ways: a priori and a posteriori choice. The former consists of selection methods based on *per se* parent performance, such as mid-parental value, divergence according to coefficient of parentage, character complementation, multivariate analysis and parental distances, least squares, parental complementation, and ideal genotype. A long period is necessary to choose parents by the second way, especially in perennial plants (Dias *et al.*, 2004). Seven different genotypes were selected using statistical analysis basis on ranking of mean value and GCA. In breeding programmes, the common approach of selecting parents on the basis of per se performance dose not lead to fruitful results. Hence, potential parents need to be selected based on their genetic architecture and combining ability (Sundharaiya and Venkatesan, 2007)

Line x tester analysis is one of the most powerful tools for predicting the general combining ability (GCA) of parents and selecting of suitable parents and crosses with high specific combining ability (SCA) (Rashid *et al*., 2007). The most commonly used designs for combining ability studies are line x tester (L x T) and diallel analysis. Combining ability analysis following the diallel analysis was given by Griffing (1956) is frequently used for testing the performance of parents in hybrid combinations.

In case of parent selection, the highest GCA and the lowest GCA have been considered to know the behavior of gene action.

2.3.1 Line x Tester Analysis

The concept of Line x Tester was developed by Kempthorne (1957). It is a modified form of a top cross scheme. In case of top cross only one tester is used, while in case of Line x Tester several testers are used. Line x Tester is one of the most powerful tools for predicting the general combining ability (GCA) of parents and selecting of suitable parents (Rashid *et al.,* 2007). The first step in evaluating the potential of new inbred lines is to cross them to a common parent and compare the performance of their hybrids. The common parent referred to as the tester and the hybrids produced are known as test crosses or top crosses. The tester is the same for all the inbred lines under evaluation (Singh and Narayanam, 2006). In breeding programs, the common approach of selecting special parents on the basis of *per se* performance does not lead to fruitful results. Hence, potential parents need to be selected based on their genetics architecture and combining ability (Sundharaiya and Venkatesan, 2007).

However, to breed high yielding varieties, breeders often face the problem of selecting parents. In this context various breeding approaches have been suggested. The line × tester analysis method is one of the powerful tools available to estimate the combining ability effects and aids in selecting desirable parents for exploitation in breeding (Fellahi *et al.* 2013).

Abebe *et al*. (2020) carried out an experiment to evaluate the heterotic performances of the F_1 hybrids over the standard checks (Kolba and Jibat) in maize. Fifty entries consist 48 F_1 single crosses developed from 24 inbred lines and 2 testers using line x tester design and two commercial check hybrids used in the study. Analysis of variance revealed existence of significant genetic variation among genotypes for all studied traits except for plant aspect. Location x entry interaction for most of the traits was not significant which suggests hybrid performance was consistent across tested locations. The magnitude of standard heterosis over Kolba and Jibat for grain yield ranged from -40.31 (L13 x T1) to 32.44% (L23 x T1). The testcrosses (48) were generated from crossing of 24 inbred lines (female parents) with two testers (male parents) in line x tester mating design during 2015/2016 cropping season at AARC. The inbred line testers used for the formation of the testcrosses were FS59 (Tester 1) and FS67 (Tester 2). Ambo maize breeding program commonly uses these testers in the identification of promising inbred lines.

Daleep and Mamta (2018) conducted an experiment to estimate the effects of combining ability and heterobeltiosis in bitter gourd under rainy season, 2013 at Vegetable research farm, Department of Vegetable Science, PAU, Ludhiana. The seven line and six tester which were mated in a line x tester manner to produce forty-two hybrids. The sca effect greater than gca effects that indicates that non additive effect for carotene, vitamin-C, total Sugar and reducing sugars. Parents PAUBG-13 and PAUBG-50 Significant gca for Vitamin-c and total Sugar and cross combination Punjab-14 x PAUBG-50 significant sca effect for total and reducing sugar. The heterosis over batter parent significant in crosses PAUBG-4 x PAUBG-50 (18.58%), Punjab-14 x PBIG-56 (52.92%) and Punjab-14 x PAUBG-50 (-57.73) for vitamin-C, carotene and total sugar, respectively.

Shashikumar and Pitchaimuthu (2016) conducted an experiment to understand the nature of gene action of quantitative traits and to identify promising parents for breeding programme in muskmelon. Six female and five male parents were crossed in line x tester mating fashion to produce thirty F1s and were grown in a randomized complete block design with three replications. Analysis of variance showed high magnitude of GCA over SCA variance indicating predominance of additive gene effects for all the traits. RM 43 and IIHR122 were the best general combiner for most of the quantitative traits. Strong phenotypic correlation between GCA and parent per se performance for all traits except for number of primary branches per vine and fruit yield per vine indicated the possibility of selection of traits at the level of parents. Hybrids ms-1 x IIHR 616, RM 43 x IIHR 718 and RM 43 x IIHR 121 out yielded commercial check NS 910 with significantly larger fruits, significantly sweeter and earlier in picking could be commercially viable for hybrid seed.

Shivanand *et al.* (2015) carried out an experiment to know the influence of physiological traits on the total fruit yield per vine in *Luffa acutangula* during 2012 -2014. The genotype L4 and T4 were found to be good general combiners. The crosses L4 x T2 (1581.69g), L5 x T4 (1365.00g), L6 x T4 (1359.65g) and L2 x T4 (1224.48g) have been identified as good specific combiners for fruit yield per vine. The best performing parents can be used for further breeding programmes a hybrid could be exploited for cultivation.

Narasannavar *et al*. (2014) studied 51 F_1 crosses of ridge gourd in a Line × Tester set involving 20 parents to study heterosis for growth, earliness, yield and quality parameters. Maximum standard heterosis for vine length (9.20%) was observed in KRG-7 x ASM, for number of leaves in KRG-11 x PN (172.12%), for number of branches in KRG-11 x PN (141.38%), for days to first male flower appearance in KRG-3 x PN (-19.48%), for node to first female flower appearance in KRG-9 x ASJ (-56.92%), for node to first female lower appearance in KRG-2 x ASM (-19.35%), for sex ratio in KRG-17 x PN (-40.34%), for average fruit weight in KRG-6 x ASJ (36.34%), for fruit length in KRG-1 x ASJ (36.91%), for fruit diameter in KRG-12 x PN (55.09%), for fruit yield per plot in KRG-3 x ASM (26.53%), for fruit yield per hectare in KRG-3 x ASM (26.46%),and for seed yield per fruit in KRG-4xASM (201.11%). The four best performing F1 hybrids *viz*., the cross KRG-3×ASJ (23.61%) followed by KRG-3×PN (13.80%), KRG-10×PN (12.45%) and KRG-11×PN (6.00%) exhibited the highest standard heterosis for total yield per vine.

Kumara *et al.* (2011) studied on combining ability in bitter gourd for quantitative characters by using six lines and four testers in a line x tester mating design. They observed that two characters (number of primary branches and fruit yield per vine) were found significant differences and variances due to *SCA* were higher than the corresponding GCA for all the characters except for vine length, it indicates predominance of non-additive gene action.

Sundharaiya and Venkatesan (2007) studied on combining ability in eight bitter gourd lines, to identify suitable parents and crosses for further exploitation, indicated that the lines MC 13 (L1) and Panruti Local (L2) were good general combiners for yield per vine. The lines Ayakudi Local (L3) and Mithipagal (L5) recorded negative general combining ability and lower per se for days to first female flowering and days to fruit maturity. This can be utilized in breeding programme to develop earliness in bitter gourd. The hybrids MC 13 x Arka Harit (L1 x T3), Panruti Local x VK 1 Priya (L2 x T2) and MC 13 x Co 1 (L1 x T1) registered higher per se and specific combining ability for fruit length, individual fruit weight and yield per vine. The study revealed that additive x additive and additive x dominance type of interactions played a major role for days to first female flowering, days to fruit maturity, number of fruits per vine, fruit length, fruit size index, cavity size index, single fruit weight and yield per vine. The lines L1, L2, L3 and L5 expressed higher per se and general combining ability for most of the characters can successfully be utilized for developing superior hybrids in bitter gourd hybridization programmes.

2.4 Diallel Cross Analysis for Yield and Yield Contributing Traits

The term "diallel cross" has been attributed to a Danish geneticist, J. Schmidt (Wricke and Weber, 1986), who used it in livestock breeding to designate a cross of two males with two females. The term came into use in plant breeding and genetics during the 1950s (Christie and Shattuck, 1992), with the first written report of a diallel cross applied in plants released by Jinks and Hayman in 1953.

The diallel cross is defined as all possible crosses among a group of parents. A diallel cross with n parents would generate n^2 progeny families (Jinks and Hayman, 1953). This is also called a complete diallel (Griffing, 1956b). Since the advent of the diallel mating design, it has been widely used in plant breeding research to obtain genetic information. It is used in both self-pollinating and cross-pollinating species, as well as homozygous or inbred parents (Jinks and Hayman, 1953; Griffing, 1956b) and non-inbred parents (Gardner and Eberhart, 1966).

Christie and Shattuck (1992) concluded that diallel analysis is a sophisticated form of progeny testing from which information can be obtained that is not available from any other analysis of mating, and can be used by plant breeders as an aid in selection of parents or crosses. According to Hallauer and Miranda (1981), the diallel mating design has been used and abused more extensively than any other mating design. However, they noted that it is very useful, if properly analyzed and interpreted. Sokol and Baker (1977) suggested that genetic interpretation of data from diallel experiments is valid only if the following assumptions about the parental material are true: diploid segregation, homozygous parents, gene frequencies are equal to one-half at all segregating loci, genes are independently distributed between parents and no non-allelic interaction.

Some of the assumptions regarding diallel analysis are easily accepted while others are more critical. Kempthorne (1956) suggested that no valid information would be derived from genetic analysis of diallel crosses, if genes were not independently distributed among the parents. According to Hayman and Mather (1955), gene frequencies that are not equal to one-half confound the statistical estimates. Horner *et al.,* (1955); Gilbert (1958) and Cockerham (1959) agreed that the absence of epistasis cannot be assumed when dealing with quantitative traits until experimentally proven otherwise. Sokol and Baker (1977) further asserted that no epistatic assumption is biologically unrealistic. According to Hallauer and Miranda (1981), the assumptions of independent distribution of genes in the parents used and no epistasis are not valid for the small number of parents usually used in diallel crosses. They stated that independent distribution of genes could not occur unless a minimum of 2n parents are included in the diallel set of crosses.

There are several methods of diallel analysis and modification but the basic methods have been described by Jinks and Hayman (1953), Griffing (1956b), Gilbert (1958) and Gardner and Eberhart (1966). Each analysis requires certain assumptions that may limit its use or interpretations of its results, therefore, criticism of diallel analysis and perceptions of abuse arise from the interpretations of results (Christie and Shattuck, 1992). Nevertheless, diallel analyses are of great benefit to breeders and geneticists. Plant breeders and geneticists have used diallel mating designs extensively to investigate genetic properties of plant cultivars and populations.

Hayman's (1954) and Griffing's (1956b) analyses are frequently used together to complement interpretation of data. Diallel analyses differ in three main ways (Hayman, 1960a) 1) in the material under investigation 2) in the postulated underlying genetic mechanism and 3) in the methods of estimation. For example, some studies are aimed at a particular set of lines while others target populations from which these lines are sampled.

Diallel analysis provides information on average performance of individual lines in crosses known as general combining ability (GCA). It also gives information about the performance of crosses relative to the average performance of parents involved in the cross known as specific combining ability (SCA). Ghosh and Das (2003) explained that a cross between two lines has an expected value, which is the sum of the general combining abilities of its two parental lines. However, some crosses deviate from this expected value to a greater or lesser extent, and this deviation is what is known as the specific combining ability of the two parents in combination.

In statistical terms, general combining abilities are the main effects and specific combining ability is an interaction. Zary (1980) elaborated that the term 'interaction' should not be confused with any form of genetic interaction between postulated genes. The term is used to refer to the departure from additivity represented by main effects. There are no genetic assumptions with Griffing's analysis on combining ability (Wright, 1985), and several scientists believe that this method conveys reliable information on the combining potential of parents (Nienhuis and Singh, 1986).

Griffing (1956b) also postulated two models for analysis of variance of the diallel design. Model I (fixed effects) is used in assumption that the parents are the population, i.e., parents are a fixed set of lines. Estimates from this model apply only to the genotypes included and cannot be extended to some hypothetical reference population (Hallauer and Miranda, 1981). In this model, estimation of components of variance is not appropriate, but estimation of GCA and SCA effects is valid and informative. Model II (random effects) is used where parents are a sample of randomly chosen lines from a reference population and the estimates are interpreted relative to the reference population. With this model, estimates of variance components are the main interest.

According to Griffing (1956a) a large GCA: SCA variance ratio suggests importance of additive gene effects, while a low ratio signifies presence of dominant and/or epistatic gene effects. Wassami *et al.,* (1986) noted that the GCA component contains additive effects in addition to additive x additive effects when present. Christie and Shattuck (1992) concluded that it is easy to select the appropriate analysis if the breeder decides on the purpose or level of the analysis desired and reference population before initiating a diallel cross. They also reported that diallel or other complicated designs do not assure success in reaching plant breeding goals, but will increase the chances of success if properly utilized. Diallel cross analysis has been found as a useful biometrical technique for understanding the nature of quantitatively inherited traits and to ascertain the property of parents by estimation of general and specific combining abilities.

2.4.1 Combining ability for yield and yield related traits in bitter gourd

The combining ability analysis gives useful information regarding the selection of parents in terms of the performance of their hybrids. Richey and Mayer (1925) gave the concept of combining ability. The concept of combining ability in terms of genetic variation was first given by Sprague and Tatum (1942) using single crosses in maize. They defined the term of general combining ability to indicate the performance of a line or population in several hybrid combinations and specific combining ability was used to designate those effects in certain combinations which significantly departed from what would be expected on the basis of average performance of the lines involved.

General combining ability (GCA) is the average performance of a line in hybrid combinations and specific combining ability was used to designate those cases in which certain combinations do relatively better or worse than expected on the basis of average performance of lines involved. On general combining ability, genes with additive effects are more important, while specific combining ability is more dependent on genes with dominance and epistatic effects.

General and specific combining ability effects are important indicators of the potential value of inbred lines in hybrid combinations. General combining ability is the average performance of a line in hybrid combinations, while SCA is used to designate deviations of certain crosses from expectations on the basis of the average performance of the lines involved (Sprague and Tatum, 1942). Genetically, GCA is primarily associated with genes, which are additive in their effects, whereas SCA is attributed to the non-additive genetic portion of the total genetic effects (Rojas and Sprague, 1952). Additive effects are the predictable portion of the genetic effects and are therefore useful to plant breeders.

Diallel crosses represent the best strategy for determining the general (GCA) and specific (SCA) combining ability between putative parents. However, the major barrier for their use is the need of a large number of crosses for evaluation. The interpretation can be affected by the number and quality of data needed to obtain a precise estimate (Burow and Coors, 1993). Diallel cross designs are frequently used in plant breeding research to obtain information on genetic effects for a fixed set of parental lines or to estimate general combining ability (GCA), specific combining ability (SCA), variance components and heritability for a population from randomly chosen parental lines.

Diallel analysis provides information on average performance of individual lines in crosses known as general combining ability (GCA). It also gives information about the performance of crosses relative to the average performance of parents involved in the cross known as specific combining ability (SCA). Ghosh and Das (2003) explained that a cross between two lines has an expected value, which is the sum of the general combining abilities of its two parental lines. However, some crosses deviate from this expected value to a greater or lesser extent, and this deviation is what is known as the specific combining ability of the two parents in combination. The concept of combining ability (CA) is very important in heterosis breeding program. General combining ability (GCA) is the average performance of a strain in a series of crosses. Specific combining ability (SCA) is the deviation from performance predicted on the basis of GCA.

It has been established that a high yielding line may not necessarily be able to transmit its superiority to the hybrids (Allard, 1960). Hence an estimate of gca (worth of parents) and sca (worth of hybrids) effects may be more reliable test rather than *per se* performance. For estimate of the general and specific combining ability, different workers have used several methods. Among them poly cross (Tysdal *et al.* 1942), line x tester (Kempthorne, 1957), diallel cross (Griffing, 1956 b) and triallel crosses (Rawling and Cockerham, 1962) have most commonly used. Griffing (1956 a and 1956 b) emphasized the statistical concept of gca and sca and provided a technique of estimating these. Kempthorne (1957) defined the general and specific combining ability variance σ2 gca and σ2 sca, respectively, in terms of half and full sibs. Jinks (1954) and Hayman (1954a and 1954 b) provided the genetic basis and analysis of diallel cross. Knowledge on the effects of general combining ability (GCA) and specific combining ability (SCA) is useful in the selection of parental genotypes. The main goal of hybrid breeding is the identification of parents with high SCA for technological quality and agronomic traits. Such data facilitate the choice of pairs of parental genotypes with a high probability of heterosis in their F_1 progeny. The available literature on combining ability variances and their effects in bitter gourd has given as follows:

Acharya *et al.* (2019) were evaluated of ten parents of bitter gourd viz., Solan Hara, Pusa Do Mousmi, BG-14, Green Long, MDU-1, IC-85605, IC-45346, IC-68272-1, IC-68237 and Solan Collection and their forty-five crosses (using half diallelic system) along with check viz., Jhalri, US-6214 and US-6203. Good general combiners for various economic traits IC-68237 for number of primary branches per vine (0.09), fruit length (0.52), fruit diameter (0.17) & number of fruits per vine (0.22) over the pooled environments. SCA (Specific Combining Ability) for economic traits were observed in Solan Collection x IC 68237 (1.24) for number of fruits per vine, IC 68237 x MDU-1 for fruit length (1.82) and fruit weight (7.81). These results indicate that both additive and non-additive gene effects are involved in the inheritance of the studied traits. The additive gene action was more important than the non-additive ones in the genetics of most studied traits.

Bhatt *et al.* (2017) evaluated 36 hybrids in diallel design (excluding reciprocals) along with the parents in bitter gourd. The analysis of variance for experimental design revealed the existence of adequate genetic variability in experimental material for all traits under study.

Variance due to parents Vs F1's were significant for all characters, except days taken to opening of first female flower, days taken to first fruit set, fruit weight and total fruits yield per vine, thereby indicating the presence of overall average heterosis for all characters. Combining ability analysis revealed importance of both additive and non-additive gene action. On the basis of overall performance, the three best crosses were, namely Panipat Local x Phule Green, Phule Green x Pusa Do Mausami and Punjab-14 x Pusa Do Mausami. Panipat Local x Phule Green was superior in respect of days taken to opening first female flower, vine length, days to first fruit harvest, fruit length. Phule Green x Pusa Do Mausami was took fruit length, fruit weight, fruit diameter and total fruits yield per vine. Punjab-14 x Pusa Do Mausami was better with regard to superior for number of node at which first female flower appeared, number of fruits per vine and days to first fruit harvest.

Rani (2014) evaluated twenty-eight F1 hybrids developed during summer, 2010 by crossing 8 diverse parents in all possible combinations without reciprocals for diallel analysis for genetic parameters and graphic representation for yield and yield attributing traits in bitter gourd. The validity of the assumptions of diallel analysis was confirmed for all the traits studied except number of fruits/vine other traits such as average fruit weight, pulp thickness and yield/vine as t2 values for these traits were found to be significant. The dominance variance was found to be greater in magnitude than additive variance for all the traits indicating the presence of over dominance controlling the traits which was further confirmed from the regression line of Wr-Vr graph was found to cut the ordinate below origin. The distribution of array points along and around the regression line for yield/vine indicated that the parents IC-470560, IC-470550 and IC-033227 had an excess of dominant genes whereas IC-045339 being farthest from the origin carrying maximum recessive genes. The predominance of dominant gene action coupled with low heritability observed for all the traits except average fruit weight suggesting the importance of heterosis breeding for improvement of yield and yield attributing traits in bitter gourd.

Sing *et al*. (2013) studied on twenty-one crosses along with their parents for combining ability, heterosis and gene action for eight yield and yield components in bitter gourd. Except days to 50% flowering significant differences were observed for all the characters under study. All the traits were found under the control of non-additive gene action except for fruit length and fruit breadth which showed significant differences due to both gca and sca with preponderance to additive gene action. HABG-30 was found to be good general combiner for most of the characters (yield/plant, yield t/ha, fruit weight, fruit length, fruit breadth and vine length). HABG-24XHABG-30 exhibited significant sca effect for all characters except days to 50% flowering and HABG-23XHABG-34 showed significant sca effect for number of fruits per plant, yield/plant, yield t/ha and vine length. These crosses were also found to show significant heterosis in the desired direction for most of the yield characters. Hence, they can be exploited as desirable hybrids.

Verma *et al*. (2013) carried out an investigation in bitter gourd to get information regarding magnitude of combining ability and nature of gene action for fruit yield and several other yield attributing traits following line x tester mating design involving 12 lines and 3 testers and their 36 hybrids. From the estimate of gca effects, among the parental lines NDBT-13, NDBT-15 and NDBT-19 were identified as superior donor for both seasons and NDBT-10 for summer season and among the testers Kalyanpur Sona for summer season and Pusa Do Mausami for rainy season for fruit yield per plant and its yield contributing traits like number of fruits per plant and average fruit weight. Eight crosses displayed desirable significant sca effects in both seasons for fruit yield per plant. Among these eight crosses the best cross combinations based on desirable sca effects for fruit yield per plant were NDBT-19 × Pusa Do Mousami in summer season while NDBT-8 × Pusa Do Mousami, NDBT-15 × NDBT-12 and NDBT-10 × Pusa Do Mousami in rainy season. These crosses have more number of fruits per plant, average fruit weight, fruit diameter and other component traits in both seasons

Naliyadhara *et al.* (2010) explained that combining ability analysis was carried out in 9 X 9 diallel cross of sponge gourd. The estimated component of variance of SCA was higher than GCA for most of the characters which indicated the predominance of non-additive gene action for characters under study. Three parents were found good general combiners for fruit yield and some of fruit yield contributing characters which offer the worth considering in further breeding program. Three cross combinations were found as promising which can be tested for promotion of F_1 hybrid.

2.4.2 Hybrid performance and heterosis study for yield and other traits of bitter gourd

For the first time, the term heterosis was coined by Shull (1914) for the specific stimulus of heterozygosis upon cell division, growth and other physiological activities of an organism and defined heterosis "to cover the real observable phenomenon" when unlike gametes are brought together to form a hybrid. The term heterosis is now widely used, which refers to the phenomenon in which the F_1 hybrid obtained by crossing the two genetically dissimilar homozygous gametes or individuals shows the increased or decreased performance for any character over its parental values. Shull (1948) referred to this phenomenon as the stimulus of heterozygosis. The expression of heterosis may be due to factors such as heterozygosity, allelic interaction such as dominance or over dominance, non-allelic interaction or epistasis and maternal interactions. The degree of heterosis depends upon the number of heterozygous alleles. The higher number of heterozygous loci, more the heterosis expected (East and Hayes, 1912). Heterosis was first noted in cucurbits by Hayes and Jones (1916) in cucumber.

Allard (1960) considered heterosis as "hybrid vigor such that F1 hybrid falls outside the range of the parents with respect to some character or characters". Heterosis in common use represents the phenomenon in which the F1 population obtained by crossing of two genetically dissimilar individuals which shows increased vigor over mid-parent value (relative heterosis) or over better parent value (heterobeltiosis). A third type of heterosis is expressed as the increased or decreased vigor over the popular/standard check variety called as standard heterosis or economic heterosis has practical importance.

Heterosis breeding has led to a breakthrough in yield in several crop plants. Heterosis is more pronounced in cross pollinated species (Hays and Footer, 1976). For the exploitation of heterosis, it is imperative to study the magnitude of genetic differences among parents involved in the crosses as well as genetic worth of the crosses. The parents with optimal to intermediate genetic diversity are supposed to show maximum heterosis (Moll and Stuber, 1974).

Heterosis breeding in crop plants has been the most successful approach among various technological options available to the geneticist and plant breeders and hybrids offer opportunities for improvement in productivity, earliness, uniformity, quality and wider adoptability and for rapid deployment of dominant genes (Riggs, 1988). A considerable degree of heterosis has been documented in bitter gourd and other cucurbits for various characters. The heterosis of some traits as reported by various scientists is reviewed below:

Naik *et al.* (2020) conducted an experiment to study the performance of 10 F_1 crosses of bitter gourd obtained from half diallel were studied to investigate the extent of heterosis for yield and its contributing characters. The analysis of variance showing all treatments are significant except days to opening of first female flower. The negative heterosis which is desirable for days to opening of first male flower, number of node bearing first male flower, number of node bearing first female flower in most of the crosses. Significant heterosis was recorded over better parent. The F_1 crosses Galaxy (Selection 9) x Special Bolder Uccha had identified most important parameter like number of fruits per vine and yield per vine. The crosses Shivam (Selection 12) x Special Bolder Uccha, Galaxy (Selection 9) x Meghdut Korola and Galaxy (Selection 9) x Special Bolder Uccha were noted to be the top performing crosses with respect to earliness and yield parameter.

Acharya *et al.* (2019) studied on ten parents of bitter gourd viz., Solan Hara, Pusa Do-Mousmi, BG-14, Green Long, MDU-1, IC-85605, IC-45346, IC-68272-1, IC-68237 and Solan Collection and their forty-five crosses along with check viz., Jhalri, US-6214 and US-6203. Economical heterobeltiosis for yield per vine (kg) were recorded in IC 85605 x IC 45346 (38.94%) and MDU 1 x IC 85605 (34.98%) over the environments. Good general combiners for various economic traits IC-68237 for number of primary branches per vine (0.09), fruit length (0.52), fruit diameter (0.17) & number of fruits per vine (0.22) over the pooled environments. SCA (Specific Combining Ability) for economic traits were observed in Solan Collection x IC 68237 (1.24) for number of fruits per vine, IC 68237 x MDU-1 for fruit length (1.82) and fruit weight (7.81).

Daleep and Mamta (2018) conducted a study to estimate the effects of heterobeltiosis in bitter gourd under rainy season, 2013 at Vegetable research farm, Department of Vegetable Science, PAU, Ludhiana. The seven line and six tester which were mated in a line x tester manner to produce 42 hybrids. The sca effect greater than gca effects that indicates that non addative effect for carotene, vitamin-C, total Sugar and reducing sugars. Parents PAUBG-13 and PAUBG-50 Significant gca for Vitamin-c and total Sugar and cross combination Punjab-14 x PAUBG-50 significant sca effect for total and reducing sugar. The heterosis over batter parent siganificant in crosses PAUBG-4 x PAUBG-50 (18.58%), Punjab-14 x PBIG-56 (52.92%) and Punjab-14 x PAUBG-50 (-57.73) for vitamin-C, carotene and total sugar, respectively.

Rao *et al.* (2017) studied on heterosis by using diallel analysis (without reciprocal) of the 21 crosses derived by crossing seven diverse bitter gourd inbreeds for earliness and yield components. Data was recorded for eleven quantitative traits. Proportion of genes with positive and negative effects at all loci (H2/4H1) in the parents were found to be less than 0.25 for most of the traits revealed the asymmetrical distribution of the positive and negative alleles. Days to 50% flowering, days to first harvesting, fruit length (cm), fruit diameter (cm), number of fruits per plant and yield per plant (g) exhibited below 50% narrow sense heritability, which indicated the predominance of non-additive gene action. The average degree of dominance (H1/D)1/2 revealed that over dominance gene action for most of the yield related traits. Heterosis over standard check (Pusa Do Mousami) was also observed for all the traits under study. The best performing F1 hybrids with high standard heterosis and mean performance for yield were found in crosses DBGS-54 × DBGS-2 (43.00%), DBGS-54 × Pusa Vishesh (37.89%) and Pusa Aushadhi × DBGS-54 (34.57%). Pusa Aushadhi × DBGS-54, Pusa Aushadhi × DBGS-57 and Pusa Aushadhi × DBGS-37 were the best early yielding hybrids.

Kalidas *et al*. (2015) studied heterosis in cucumber for yield and yield related traits in 28 F_1 hybrids of cucumber obtained by 8 x 8 diallel crosses involving eight parents including one gynoecious line (GBS-1).The F_1 hybrids developed using gynoecious line as one parent were found to be superior in performance over top parents for various characters node number of first female flower (-2.61%),days to first female flower anthesis (-3.45%),number of fruits/plant (57.49%) and yield/plant (66.40),whereas GS-4 X Pusa Uday showed better heterosis for fruit length (20.34%),fruit diameter (17.04%) and fruit weight (12.24%).The best three heterotic hybrids identified over the top parent for yield/plant GBS-1XPusa Uday (66.40%),GBS-1 X Punjab Naveen (54.44%) and GS-4 X Pusa Uday (41.29%) and these may be exploited for commercial cultivation. Adjoumani *et al*. (2016) evaluated various components of variation, heritability and genetic of fruit characters. Parents, F1, F2 and BC1 hybrids were showed in the same environments at two locations, with statistically significant performance observed in d (Manfla) than forest (Abidjan), and large variability was found between fruits of parental and hybrid F1, BC1 and F2 families. Parental and individuals were homozygous while F1 and BC1 generations were heterozygous. Fruit maturity period and number of hybrids F1, BC1 and F2 families were intermediate to those parents. Percentage heterosis to mid parent average was negative for fruit maturity period and fruit number but positive for fruit size characters. Percentage heterosis according to better parent average was negative for fruit maturity period and fruit number but positive for fruit size. The genotype, phenotypic and additive variance was larger than the environmental variance in the majority of the families at both locations. This involved high broad and narrow-sense heritability for all characters. In conclusion, this study showed a homogeneity between parental and F1 genotype but a heterogeneity between BC1 and F2 one. In addition, heterosis was observed in F1 fruit size and high heritability was observed for all characters

Kandasamy (2015) conducted a study in bitter gourd where twenty F1 hybrids of bitter gourd in a diallel set involving five parents including reciprocals were evaluated to assess the extent of hybrid vigor in the yield contributing traits. Appreciable amount of heterosis was observed for all the characters under this study except node number of first female flower. The F1 hybrids P5 × P3 (Panruti local × VK-1 Priya), P4 × P2 (MC -13 × Arka Harit) and P2 × P1 (Arka Harit × CO-1) were observed best performing for yield and they showed 46.21, 29.31 and 14.30 per cent heterosis, respectively better parent Arka Harit (P2).

Singh *et al*. (2013) studied heterosis for eight yield and yield components in bitter gourd. Most of the crosses were proved to be highly heterotic for all the characters except days to 50% flowering. Only two crosses viz., HABG-24XHABG-30 and HABG-29 X HABG-30 showed significant negative heterobeltosis for days to 50% flowering. The extend of percent heterosis for number of fruits per plant ranged from 2.51 to 48.75. Twenty crosses out of 21 cross combinations showed significant positive heterosis. Seventeen hybrids out of the 21 crosses showed positive significant heterobeltosis for yield. These crosses were showed significant heterosis in the desired direction for most of the yield characters.

Talekar *et al*. (2013) conducted a study in bitter gourd *(Momordica charantia* L.) to assess the extent of heterosis for twelve quantitative traits including fruit yield per vine. Eleven lines and four testers were crossed in a line x tester fashion to develop 28 F1 hybrids. The analyses of variance for experimental design for twelve characters revealed that the differences among the mean square due to genotypes were found highly significant for all the traits. Further variance due to parents and hybrids (within group) were also found significant for all the studied characters. Differences due to parents Vs hybrids were also found highly significant for most of the characters. Heterosis was worked-out over better parent and standard variety, Priya. The standard heterosis for fruit yield per vine ranged from -55.65 to 73.79%. The crosses Preethi x HABG-22, Ujjwala x HABG-22, Hirkani x CO-4, Hirkani x HABG-22 and Kalyanpur Baramasi x HABG-21 were the best heterotic combinations for fruit yield per vine, which recorded 73.79, 63.10, 57.26, 53.83 and 52.22% standard heterosis, respectively and could be utilized for hybrid development in bitter gourd The heterosis for fruit yield per vine was associated with the heterosis expressed by its component characters.

Rani (2012) conducted an experiment to estimates of heterosis, heterobeltiosis and standard heterosis and found variable among the crosses in the present study. Heterosis over mid-parent in desired direction was recorded for yield and yield attributing traits viz., vine length (41.34%), number of laterals/vine (21.21%), internodal length (-23.28%), days to 1st male flower (-9.33%), days to 1st female flower (-9.57%), Node number at 1st male flower appeared (-27.15%), node number at 1st female flower appeared (-20.34%), sex ratio (-21.93%), number of fruits/vine (37.55%), average fruit weight (51.41%), fruit length (40.0%), fruit girth (24.36%), pulp thickness (26.34%), number of seeds/ fruit (-20.49%) and yield/vine (96.03%). Based on overall results, heterosis breeding for the crosses viz., IC-044438 × IC-045339 (vine length, fruit weight, fruit length, pulp thickness and yield) and IC-045339 × IC-085622 (number of fruits/vine, fruit weight, fruit girth and yield) while pedigree method of selection and recurrent selection for the crosses like IC-044438 × IC-470560 (days to 1st male flower appeared), IC-044438 × IC-045339 (number of fruits/vine), IC-044417 × IC-470558 and IC-044417 × IC-085622 (fruit length) and IC-044438 × IC-045339 and IC-045339 × IC-470558 (yield/vine) can be successfully employed for attaining higher yields with desirable properties in bitter gourd.

Bimal (2008) reported in bitter gourd that the significant desirable heterosis was observed for days to first male flower opening -19.97% (P1XP3); days to first female flower opening -14.39% (P1XP3); number of fruits per vine or plant 85.76% (P5XP2), average single fruit weight 52.10% (P3XP2); fruit yield per vine or plant 85.71% (P5XP3); fruit length 9.73% (P1XP2); fruit diameter -46.93% (P3XP5); Seed weight per fruit -51.66% and 100 seed weight -29.16 (P5XP6).

Some available literature on various aspects of heterosis are given in Table 2.2

Table 2.2 Literature on heterosis in bitter gourd and other related species for yield and yield components

Crop	Heterosis (%)	References
1. Days to first female flowering		
• Bitter gourd • Bitter gourd	• -17.51 • -14.39	• Talekar *et al*. (2013) • Bimal (2008)
2. Node no. of first female flower anthesis		
• Bitter gourd • Bitter gourd	• -3.33 to -24.81 • -16.41 to 23.08	• Kandasamy (2015) • Talekar *et al*., (2013)
2. Days of first fruit harvest		
• Bitter gourd • Bitter gourd	• -2.25 to -30.40 • -17.27 to 11.20	• Kandasamy (2015) • Talekar *et al*. (2013)
3. Number of primary branches		
• Bitter gourd	• -26.23 to 13.70	• Talekar *et al*. (2013)
4. Average fruit weight		
• Bitter gourd • Bitter gourd	• 27.31 • 53.33	• Talekar *et al*. (2013) • Bimal (2008)
5. Length and diameter of fruit (cm)		
• Bitter gourd • Bitter gourd	• 40.92 length & 22.52 diameter • 9.73 length, -46.93 diameter	• Talekar *et al*. (2013) • Bimal (2008)
6. Number of fruits per plant		
• Bitter gourd	• 100.4	• Talekar *et al*. (2013)
7. Yield per plant		
• Bitter gourd	• 73.79	• Talekar *et al*. (2013)
9. Number of seeds per fruit		
• Bitter gourd	• -1.17 to -46.93	• Bimal (2008)
10. weight of 100 seed (g)		
• Bitter gourd	• -1.97 to -29.16	• Bimal (2008)