REVIEW OF LITERATURE

Genetic variability of medicinally plants is extremely very important (Letessi, 1991). Wild ecotypes selected for their high dry weight and/or active components contents and/or resistance to pathogens are often used in cultivation. Pank et al., 2003. Several studies have been performed to characterize different accessions of medicinal...
The literature pertaining of impact on oil yield, herb yield and other characteristics of *Ocimum* species is described below.

2.1 Variability, Heritability and Expected Genetic Advance

2.1. Variability

The extent of diversity present in the existing germplasm determines the limit of selection for improvement. The characters of economic importance are generally quantitative in nature and exhibit considerable degree of interaction with the environment. Thus, it becomes imperative to compute variability present in the breeding material. The total variability in a population can be partitioned into two main categories, i.e. genotypic variability and environmental variability. Genotypic variability results from the actual differences between the genotypes which are due to genes, whereas environmental variability results from the effects of environmental factors to which the genotypes are subjected to. The former kind of variability is heritable and is the basis for a plant breeding program, whereas the latter one is non-heritable. The relative proportion of these two components of total variability gives information about the degree of transmissibility of a trait from one generation to the next, which is referred to as heritability. Statistically, the total variability is expressed in terms of phenotypic coefficient of variation (PCV) and the genotypic variability is expressed in terms of genotypic coefficient of variation (GCV). These parameters of variability are particularly very informative when a breeder is interested in having a stock of the comparative account of variability present in different traits which might have been measured in different units.

Genetic variability of medicinal plant is generally very important (Tetenyi, 1991). Wild ecotypes selected for their high dry weight and/or active components contents and/or resistance to pathogen are often used in cultivation Pank *et al.*, 2003. Several studies have been performed to characterize different accession of medicinal
plant. Some plant are harvested directly from their natural site (Kartnig et al., 1989; Umek et al., 1999; Girzu et al., 2000, Bergonzi et al., 2001; Pietta et al., 2001; Walker et al., 2001). Their chemical characteristics may be of poor scientific value because the environment factor which are not accurately defined affect the result, so the best way to compare accession is to cultivate them on the same site (Southwell and Campbell, 1991; Oravec Sen et al., 1994; Buter et al., 1996, 1988a, 1998b; Seidler-Lozkowska and Debrowska et al., 1996; Cellarova et al., 1997; Debrunner et al., 1997 Franke et al., 2000; Pluhar et al., 2002 and Bindu et al., 2006).

Szabo et al. (1996) investigated the morphological and chemotaxonomic variability of 13 basil (Ocimum basilicum) genotypes. They also studied plant height, secondary branches, leaf stem, flower ratio and essential oil content in difference plant organs.

Kritikar and Basu (1984) Studied leaf area, plant height, number of racemes per plant, number of flowers per raceme, 1000 seeds weight and days to maturity and their large diversity among genotypes. The large variability seemed to be more genetic rather than environment. Great variability occurred for morphological characters i.e. leaf area, number of racemes per plant, number of flower per raceme, plant height 1000 seeds weight and days to maturity. The value for plant height indicating more genetic influence on the different genotypes of Ocimum. The wide range of genetic variability and additive gene effect for the character.

2.1.2. Heritability

Heritability \( (h^2) \) of a trait is an important quantitative measure in determining its response to selection. At first Lush, 1945 defined heritability as the ratio of genetic variance to the phenotypic variance, which is termed as broad sense heritability. In contrast, the narrow sense heritability is the ratio of additive genetic variance to the phenotypic variance. Robinson et al., 1949 considered that additive genetic variance indicates the degree to which the progeny is likely to resemble the parents. In segregating population, only this component is transmitted to the next generation. The total genetic variance consists of additive, dominance, and epistatic variances. The
detailed account of components of genetic variance is presented elsewhere in this manuscript.

The knowledge of heritability provides important information to the breeder. If the value of heritability in broad sense is high, it indicates that the character is least influenced by the environmental effects, and there exists sufficient genetic variability for that trait leading to the proposition that selection would be effective for improvement of such character. Broad sense heritability is based on total genetic variance which includes both fixable (additive) and non-fixable (dominance and epistatic) variances. If broad sense heritability is low, it reveals that the character is highly influenced by environmental effects and genetic improvement through selection will be difficult due to masking effects of the environment on the genotypic effects.

_Vieria et al., (2001)_ observed Morphological, chemical and genetic differences of 12 tree basil (*Ocimum gratissimum* L.) accessions to determine whether volatile oils and flavonoids can be used as taxonornical markers and to examine the relationship between RAPDs to these chemical markers. The accessions morphologically described as *O. gratissimum* var. *gratissimum* contained eugenol as the major volatile oil constituent, and cirsimaritin as the major flavone. *Ocimum gratissimum* var. *macrophyllum* accessions contained thymol as the major volatile oil constituent, and xantomicrol as the major flavone. A distinct essential oil and flavone chemotype (producing geraniol and a mixture of the flavones cirsimaritin, iso eumusin, xanthomicrol, and luteolin) was found in an accession genetically more distant from the other two groups when analyzed by molecular markers. The accessions could be divided based on volatile oil constituents into six groups: (1) thymol: α-copaene (ot24, ot25, ot26, and ot28); (2) eugenol: spathulenol (ot17, ot63, and ot52); (3) thymol: p-cymene (ot65); (4) eugenol: γ-murolene (ot27 and ot29); (5) eugenol: thymol: spathulenol (ot85); and (6) geraniol (ot 84). Cluster analysis of RAPD markers showed that there are three groups that are distinct genetically and highly correlated (r=0.814) to volatile oil constituents.
Supat (1996) studied effect of planting date and spacing on seed yield and seed quality of sweet basil grown in December, January and February. Planting dates had an effect on plant width, height, number of primary branches, days to flowering seed yield and seed quality. The widest bush, early flowering and maximum number of primary branches, highest seed yield and seed germination was obtained from plant grown in December.

Verma et al., (1989) observed great variation in different Ocimum species for different morphological traits, essential oil content between 0.16% in Ocimum basilicum EC-112807 and 0.43% in Ocimum basilicum Indian basil. The highest total essential oil yield (280.4lt./ha) was obtained from Indian basil followed by French basil- Bangalore selection (229.4lt./ha).

Kritikar and Basu (1984) observed Highest herb and oil yield was recorded from O. basilicum (French basil), followed by O. citriodorum (EC 110586) yielding 394.2 quintal herb and 157.8 liter oil /ha. Oil content of fresh weight basis varied from 0.21 to 0.51 per cent. It was highest for O. canum, followed by O. carinosum (0.48%) and O. basilicum - Indian basil (0.46%). High heritability broad sense and high genetic gain for oil yield, fresh herb yield and oil content indicates great possibility of further improvement for these characters through appropriate plant breeding methods. High range of variability was recorded for all these characters earlier by Verma et al., (1989). However, the range was much wider for fresh oil yield in comparison to plant height and oil percent. This difference was attributed to the changed environmental factors viz., time of planting. Higher value of heritability showed lesser environmental and greater genetic effect the estimate of the higher vales of heritability for characters i.e. leaf area, number of racemes per plant, number of flower per raceme, plant height, 1000 seeds weight and days to maturity.

2.1.3. Expected genetic advance

Improvement in the mean genotypic value of selected plant progeny over the parental (base) population is known as genetic advance. It is the measure of genetic gain under selection. The genetic advance from the mixtures of pure lines or clones should be
calculated using broad sense heritability estimates and from segregating population using narrow sense heritability.

Heritability and genetic advance are important selection parameters. Heritability estimates along with genetic advance are more helpful in predicting the gain under selection than heritability estimates alone. However, it is not necessary that a character showing high heritability will also exhibit high genetic advance. Johnson et al., (1955). The estimates of heritability and genetic advance help in deciding the most appropriate breeding methodology in any crop improvement program.

Sharma (2005) observed significant differences among the genotypes for all the characters except days to seed maturity and essential oil content. Genetic variability was maximum for spikes per plant and minimum for essential oil content, as reflected by their genotypic coefficient of variations. The heritability estimates in broad sense were high for seed yield per plant, plant height, 1000-seed weight and spikes per plant, while moderate heritability were observed for primary branches per plant, lamina length and days to flower initiation. Days to seed maturity showed lowest heritability. Expected genetic advance as per cent of mean was high for seed yield per plant, plant height, spikes per plant. Medium value of expected genetic advance was obtained for 1000-seed weight, plant height and spikes per plant while high heritability coupled with medium value of genetic advance was observed for 1000-seed weight. Moderate heritability coupled with medium value of genetic advance was observed for primary branches per plant.

Ahmad and Khaliq (2002) studied morpho-molecular variability and heritability in Ocimum genotypes in Himalayan regions of Pakistan. The seeds of four genotypes from different localities of district Poonch were sown in pots and transplanted to the field. They found large diversity among genotypes for leaf area, number of racemes per plant, number of flowers per raceme, plant height, 1000-seed weight and days to seed maturity. Total seed protein in SD-PAGE. 1000 seed weight and days to maturity indicated large diversity among the genotypes.
Singh et al., (2002) analyzed variations for morphological, phonology and essential oil composition in germplasm accessions of sweet basil (*Ocimum basilicum* L.) an important medicinal and aromatic crop. Significant variations were observed for morphological and essential oil traits. Texi and Lenzi (2002) described the behavior of some dwarf genotypes of basil. They also studies plant growth and seed production of basil genotypes. The dwarf genotypes showed a large decrease in the length of spike and seed production.

Vieria et al., (2001) Studied morphological, chemical and genetic differences of 12 tree basil (*Ocimum gratissimum*) accession to determine whether volatile oils and falconoid can be used as taxonomic markers and to examine the relationship between random amplified polymorphic DNA and these chemical markers cluster analysis showed that there were three groups genetically distinct and highly correlated to volatile oil constituents.

Putievsky et al., (1999) studied crossability and relationship between morphological and chemical varieties of *Ocimum basilicum*, in their studies on F1 and F2 progeny of fourteen accessions of four *Ocimum basilicum* varieties, the crossability between and within these varieties was found 30-90% and viability was 28-50% while pollen fertility was observed above 70%.

Karlovic et al., (2001) observed great variability of morphological characteristics among 10 basil accessions. Considerable variation was recorded for all agronomic traits except for plant height and number of branches per plant.

Lachowicz et al., (1997) showed differences in morphological features, growing characteristics and yields of essential oil produced per-unite area of land anise basil was most was production in terms of biomass, while cinnamon basic produced the most essential oil.

Gupta (1996) studied on variation in herbage yield, oil yield and major component of various *Ocimum* species varieties (chemotypes) harvested at different stages of maturity were reported high degree of variation in *Ocimum* species for herbage and
oil field composition depending upon the ontogenetically stage of *basilicum var. glabratum*, *Ocimum basilicum var. purpureascens*, *Ocimum basilicum var. thyrsiflorum*, *Ocimum basilicum var. minima*, *Ocimum americanum*, *Ocimum gratissimum*, *Ocimum sanctum*, *Ocimum viride*, and *Ocimum kilimandscharicum*, the effect of growth stage on oil yield, herbage yield and oil composition was examined over three consecutive seasons. It was found that although the herbage yields for all *Ocimum* species/varieties (chemotypes) around the initiate of seed formation (180 days after planting), the maximum oil yield for only *Ocimum basilicum var. purpureascens*, *Ocimum viride* for only, *Ocimum sanctum*. For the other species/varieties (chemotypes) examined, the maximum oil yield was found to be the 50% seed set stage (210 days) or between the 50% seed set stage and full seed maturation stage (210-240 days). For *Ocimum basilicum var. glabratum* (camphor type), *Ocimum basilicum var. purpureascens* methyl (cinnamate-type), *Ocimum gratissimum* (eugenol-type), *Ocimum viride* (thymol-type) and *Ocimum sanctum* (eugenol-type), the major component reached its maximum around 180 days after planting. For *Ocimum canum* (linalool type) the linalool content did not change throughout its complete life cycle. The maximum content of the major constituent of all over *Ocimum* species/varieties (chemotype) except *Ocimum viride* (thymol-type) occurred at the 50% seed set stage (210 days). Finally for *Ocimum viride* (thymol-chemotype) the phenophase for maximum content of the major constituent was between 180-240 days.

Hammer et al., (1996) studied evaluation of a variable collection of *Ocimum spp* were evaluated 182 *Ocimum* accession for growth characterized and yield components and observed wide range of differences within the different species and races.

Randhawa and Gill (1995) was conducted during the spring season of 1988 and 1989. The treatment of the study consisted of five transplanting dates, March 10, March 25, April 10, April 25 and May 10 as main plot treatment and three stages of harvesting (vegetative, 50 percent flowering and complete flowering) as sub plot treatment. The results of the study revealed that to get maximum herb and oil yield.
French basil should be transplanted from end of March to first week of May. The oil content in herb was maximum at the vegetative stage.

**Thoppin and Jose (1994)** observed inter specific variation in the quantity and quality of the essential oils in the four botanical varieties (all 2n=48) of the aromatic herb *Ocimum basilicum*.

**Putiesky (1993)** observed variation in seed yield per plant from green and dried plant. **Lee et al., (1994)** reported higher essential oil content of leaves and greater total oil content per plant.

**Sarvin et al., (1992)** developed a new variety of *Ocimum americanum* L. by natural selection and raised for two successive growing season to examine the seasonal variation in here yield and oil content chemical variation and citral content. The new strain was selected because it was a short duration crop (100days) for the production of citral rich oil.

**Bonnaerdeoux (1992)** studied the effect of different harvesting methods on the yield and quality of basil oil in the river irrigation area were extracted essential oils by stem distillation from whole plant or from flower only. Essential oil yield were higher from plants harvested when they were 3-11 cm in length.

**Karitikar and Basu (1984)** the higher value of genetic advance in association with higher heritability showed that additive gene effect were more important for these trait as will higher heritability revealed less environment and greater genetic effect on four genotypes/ land races, while value of covariance genetic advance and relative genetic advance showed that range of variability was low. Low values of genetic advance for these traits indicated non-additive gene effect.

### 2.2. Correlation Analysis

The association of various characters gives an information to breeder that how association are the important directly or indirectly to ameliorate the yield and how
other association which are responsible for reducing yield reflecting the negative trend. Correlation between different traits is generally due to the presence of liked genes and epistasis effect of different genes. Correlation coefficient analysis determines component characters on which selection can be based for improvement in yield.

Johnson et al., (1955) stated that estimates of genotypic and phenotypic correlation among characters are useful in planning and evaluating breeding programme, the correlation studies provide an opportunity to study magnitude and direction of association of one character with another character.

Sharma, (2005) found positive and significant correlation of seed yield per plant with days to flower initiation, days to seed maturity, plant height, primary branches per plant, lamina length, Spikes per plant spikes length, 1000-seed weight and essential oil content both at phenotypic and genotypic levels. Lamina width showed positive correlation at phenotypic level was found to be negatively with seed yield per plant at genotypic level. The positive and significant correlation between plant height and spike length, lamina length and lamina width, lamina length and 1000-seed weight, spike length and number of flower whorls per spike and 1000-seed weight and seed yield per plant were recorded. The genotypic correlation coefficients were in general, higher in magnitude than phenotypic correlation coefficient. The path coefficient analysis at phenotypic level revealed that 1000-seed weight had the largest positive direct effect on seed yield per plant followed by spike length, lamina length, spike per plant, primary branches per plant, days to flower initiation, plant height and days to seed maturity. At genotypic level, days to flower initiation had highest positive direct effect on seed yield per plant followed by plant height, lamina width and essential oil content, At phenotypic level, the largest negative direct effect was observed for number of flower whorls per spike. At genotypic level, the negative direct effect on seed yield per plant was observed for spike length.

Javanmardi et al., (2002) horticultural characteristics, including quantitative and qualitative traits along with the chemical variation of phenolic acids of 23 accessions
of basil (*Ocimum basilicum* L.) from Iran were studied. Morphological studies of accessions showed a high level of variability in recorded traits. Quantification of phenolic acids was determined using high-performance liquid chromatography and showed drastic variations between accessions. Chemical studies revealed that romaine acid is the predominant phenolic acid present in both flower and leaf tissues. Unusual basil accessions were identified that can serve as genetic sources of phenolic acids for crop improvement in *Ocimum* species.

Gupta, (1996) observed the phonological stages of the crop have a positive correlation with temperature and humidity; therefore harvest schedule should be based on the stage of crop rather than on calendar date for harvesting. Thus the crop is to seed set, any further delay is undesired. Harvest taken after 15th November exhibit heavy leaf fall and also the phenolic constituents show considerable decrease as result of physiological changes brought about by maturation of seed, therefore, harvesting must be carried out well before seed maturation in all the *Ocimum* species.

Sceu et al., (1991) obtained oils from various parts i.e. leaf, flower, stem. Whole plant and leaf flower of *Ocimum basilicum*, which were categorized into five groups by preference raking test of their aromas. High statistical correlation was found among the volatile components of the oil, duration, sensory evaluation.

Fisher (1918) gave an idea of correlation. The correlation analysis is used as measure of the degree of association between characters worked at same time. The correlation coefficient helps the breeder to choose superior genotypes from a genetic population. Burton (1951) elucidated the usefulness of correlation study and focused the estimates of correlation among various traits were much important foe flowering and evaluating the breeder program of Indian basil.

The Pearson correlation analysis showed that there are highly significant correlations between concentrations of certain phenolic acids in leaves and flowers of *O. basilicum*. In the case of leaves, there were positive correlations between RA and p-coumaric acid, and vanillic acid and ferulic acid. A highly significant correlation
between correlation between flower and leaf tissue was observed for hydroxybenzoic acid with its occurrence in minimum endogenous concentrations in both leaf and flower tissues in all the tested accessions.

2.3. Heterosis and Inbreeding depression

Shull (1952) defined the term heterosis as "the interpretation of increased vigor, size, fruitfulness, and speed of development, resistance to disease and to insect pests, or to climatic rigors of any kind, manifested by crossbred organisms as compared with corresponding inbreds, as the specific results of unlikeness in the constitutions of the uniting parental gametes." This definition, however, is often interpreted as not implying a genetic basis for heterosis, because the definition basically describes the phenotype that results from crossing two different inbred lines. Therefore, the definition of heterosis or hybrid vigor as the difference between the F₁'s and the mean of the two parents (Falconer (1981)) is commonly used in the literature, and this heterosis is often called mid parent heterosis.

The plant breeders recognized the benefits of mating diverse individuals in terms of increased luxuriance, superior expression of economic traits, and wider adaptability (Kolreuter, 1761; Knight, 1799; Gartner, 1849, and others). This, along with experiments showing the injurious effects of self-fertilization Darwin, (1876) and Beal, (1880), prompted breeders to consider prevention of the injurious effects of inbreeding or cross-fertilization between closely related plants as a major crop improvement objective. During this early phase, Shull (1908) coined the term heterosis, a synonym for hybrid vigor, to describe the stimulus resulting from increased heterozygosis.

Heterosis or hybrid vigor is manifested as improved performance for F₁ hybrids generated by crossing two inbred parents. Heterosis can be defined quantitatively as an upward deviation of the mid-parent, based on the mean values of the two parents Johnson and Hutchinson, (1993). Heterosis may be positive or negative. Depending upon breeding objectives, both positive and negative heterosis is useful for crop improvement, such as positive heterosis is desired for yield and
negative heterosis for early maturity. Depending upon the criteria used to compare the performance of a hybrid, heterosis is expressed in three ways: mid parent heterosis, standard/commercial heterosis and better parent heterosis (heterobeltiosis). However, from the plant breeder’s viewpoint, better parent and/or standard heterosis is more useful. The former is designated as heterobeltiosis (Fanseco and Petterson, 1968) and the latter as standard variety heterosis Virmani, (1994). From a practical point of view, standard heterosis is most important because it is aimed at developing desired hybrids superior to the existing high yielding commercial varieties. Application of heterosis in agricultural production yields multi-billion dollar returns and represents a single greatest applied achievement in the discipline of genetics.

Heterosis is usually unfixable from generation to generation as the heterozygote advantage is confined to F₁ population only. But some natural contrivances which favor the existence of heterozygote or those which preserve the heterozygote condition from generation to generation could fix it. Since such mechanisms in nature are the existence of homozygous lethal factors, balanced heterozygote, apomixes or the use of vegetative reproduction. Heterosis of these crops has been exploited only over the past few decades Miller (1998). Hybrids of sunflower became a reality with the discovery of cytoplasm male sterility and effective male fertility restoration system during 1970. hybrid vigor has been the main driving force for acceptance of this oilseed crop. Utilization of heterosis has allowed sunflower to become one of the major oilseed in many countries of Eastern and Western Europe, Russia and South America and is an important crops in the USA, Australia South Africa, china, India and Turkey. Heterosis plays important role in improving crop productivity and quailt in order to feed the ever- increasing human population, particularly in developing countries. Heterosis in significant for oil yield and is one of the driving forces behind the hybrid seed industry in cultivated and medicinal crops.

Inbreeding depression (ID) is usually defined as the lowered fitness or vigor of inbred individuals compared with their non-inbred counterparts. Its converse is heterosis; the ‘hybrid vigor’ manifested as increased size, growth rate or other
parameters resulting from the increase in heterozygosis in F₁ generation crosses between inbred lines. Inbreeding depression, the depressive effect, is the expression of traits arising from increasing homozygosity Allard, (1960). In quantitative genetics theory, inbreeding depression and heterosis are due to non-additive gene action, and are considered to be two aspects of the same phenomenon (Mather and Jinks, 1982, Li et al., 1997b) suggested that hybrid breakdown in rice was part of inbreeding depression largely related to additive epistasis. Heterosis and inbreeding depression were studied for selecting good materials for developing superior hybrid wheat variety.

Goneceariue, (2008) observed the inbred lines with a high combining capacity have been selected. The different types of hybrids developed manifest heterosis in F₁ but their use is not effective. Some of the hybrids produced manifest heterosis not only in F₁ but also in F₂ generation. The hybrids that manifest heterosis for plant height, inflorescence length, inflorescence ramification number and essential oil content have been used to develop productive cultivars of hybrids origin that ensure an increased inflorescence and essential oil production.

Bindu et al., (2006) studied of extent of heterosis for morphological yield trait and forskolin content in coleus forskolin in their investigation percentage of heterosis poor standard cheek in desirable direction was greater for dried root weight in hybrid nine (65.38), followed by hybrids three (37.56) while hybrid seeds was yielded forskolin content eight part with check variety K-8.

Goneceariue, (2004) studied on heterosis effect in all backcross hybrids of salvia sclarea displayed heterosis for plant height (4.9-55.0%), and length of inflorescence (5.4-57.6%). The mail axis of inflorescence (2.0-18.7%) and for number of inflorescence ramifications (1.9-100.0%). The availability of an increase in the number of hybrids permits creation of male sterility lines, fertile hybrid population and cultivars with high content and yield of essential oils.
Ouborg and Treuren, (1994) observed a significant between population size (or level of genetic variation) and level of additional inbreeding depression, here referred to as inbreeding load, may be expected. In previous study on the rare and threatened perennial salvia pretentes, a positive correlation between population size and level of aliozyme variation has been demonstrated. In a field experiment with the two largest and the two smallest population, survival of selfed progeny was lower than survival of outcrosses progeny. In addition, survival of out crossed progeny was, with the excepted of the largest population, lower than of hybrid progeny, resulting from crosses between populations. Effect on plant size was qualitatively similar to the effects on survival, but these effects were variable in time because of differential survival of largest individuals. In all populations the total inbreeding load that is, the effects on size and survival multiplicd, increased in time. It was demonstrated that inbreeding load in different traits may be independent. At no time and foe no trait was inbreedings load or heterosis effect correlated with mean number of alleles/locus, indicated that aliozyme variation is not representative for variation investigation.

Khosla, (1993) observed that hybrids between Ocimum gratissimum (with a high eugenol content) and Ocimum viride (with a high thymol content) showed heterosis for vegetative and floral traits and were vigorous in growth. Data are tabulated on values for height, leaf blade size, herbage yield per plant, seed set and percentage of essential oil content and its main constituents in the parents and F1 reciprocal hybrids.

Oh and Hahn, (1989) the study on inbreeding load and heterosis in relation to population size in the mint salvia pratensis were found for eight quantitative traits related to yield in a cross involving six parents. Analysis of variance revealed that there were highly significant differences between the parents and there F1 hybrids for all the traits except internodes per main stem. Heterosis was significant and positive for plant height, leaves per plant dry weight of leaves per plant and stem diameter.

Visloukhova and Romanenko, (1988) study of interline hybrids indicated that the greater the homozygosity of the inbred progenies, the higher were the degree of heterosis in the F1 and the percentage of crosses uniform in height, plant diameter,
and peduncle and inflorescence length. Crossing lines of advance inbreed generations increased the percentage of early hybrids and reduced that of late ones, necessitating selection for lateness. Selection of winter-hardy lines increased the hardiness of the hybrids bred from them. The maternal parent had the greater effect on plant shape and winter hardiness in the hybrids. Interlines hybridization combined with selection improved autumn regrowth.

2.4. Nature of gene action

Selection of an appropriate breeding strategy for yield improvement in any crop requires knowledge of nature and magnitude of gene action and association of characters with yield and also on the extent of partitioning the overall variability into heritable and non-heritable components with the help of a suitable statistical technique. Fisher 1918 partitioned the hereditary variance for the metric and additive portion resulting from the average effect of gene, a dominant portion resulting from the intra-allelic interaction and epistatic part associated with inter-allelic interaction. Cockerhan 1961 further showed that epistatic variance can be partitioned into digenic interaction of the additive, additive x additive, additive x dominance and dominance x types and of higher order interaction. Such partitioning of variability into components requires rising of a number of related generation and their evaluation in an appropriate statistical design.

In polygenic inheritance, the effect of individual gene can not ordinary is distinguished from one another. Consequently, it is not possible to determine the mode of action of each gene. By studying their combined effect in segregating population, however, one can get some insight into their behavior and can draw inference about the average level of the dominance involved in the expression of a particular character. Fisher et al., (1936) presented a method for estimating the deviation relative to that of additive genetic variance, furnished another basis for estimating the degree of dominance Comstock et al., (1949).
2.5. Joint Scaling Tests

Instead of testing the various expected relationships one at a time, a procedure called joint scaling test was proposed by Cavalli (1952). The combines the whole set of scaling test into one and thus offers a more general, more convenient, more adaptable and more informative approach. It consists of two steps viz (i) estimation of the model’s three parameters m, (d) and (h) from the mean of all types of families available (at least four types of families are required to test the goodness of fit of the model) by weighted least square technique and (ii) comparison of these means as observed with their expected values derived from the estimates of the three parameters. The significance of the chisquare test between observed and expected means of different generations indicates the presence of epistasis.

2.6. Generation Mean Analysis

The generation mean analysis is employed in studies of inheritance of quantitative traits, and is a simple and useful technique for estimating gene effects for a polygenic trait; its greatest merit lying in the ability to estimate epistatic gene effects such as additive x additive (aa), dominance x dominance (dd) and additive x dominance (ad) effects (Singh and Singh 1991; Hayman 1958; Jinks and Jones 1958 and Mather and Jinks 1982) independently formulated the exact fit solutions for estimating mean (m), additive (d), dominance (h), additive x additive (i), additive x dominance (j), and dominance x dominance (l) gene effects from the means of six basic generations viz., P₀, P₁, F₁, F₂, B₁ and B₂ of a cross between two true breeding lines. Mather 1949 and Jinks and Jones 1958 developed three parameter model (m, d, and h) for the estimation of various components of genetic variance. Estimates of gene effects based on generation mean analysis are the simplest procedure and it yields to a satisfactory degree of statistical precision.

The generation mean analysis has been suggested to estimate epistasis but it can only measure net epistatic effects and has nothing to do with the effects at the individual genetic locus level (Falconer and Mackay, 1996). Also, without considering the mechanistic basis of epistasis Whitlock et al., 1995, results from
such an analysis may be very difficult to interpret. The use of a well-designed pedigree and violation of the genetic assumption about two alleles at single loci have made this method less useful for out crossing species, e.g., forest trees and medicinal plants

2.6.1. Additive and non-additive gene actions

The additive type of gene action is operative when complete absence of allelic interactions, both at inters and intra-allelic levels are envisaged. So is the case for all genes controlling that character? Non-additive type of gene action may result from interaction between alleles of the same gene or locus (dominance) and that between the alleles of different genes or loci (epistasis). Thus, the former is indeed the dominance action of gene and the latter is the epistatic or non-allelic interaction. Thus, non-additive type of gene action entails: (i) dominance action (ii) non-allelic interaction.

2.6.2. Complementary and duplicate epistasis

Complementary epistasis involves two non-allelic genes complementing each other to produce a new phenotype, which is not ascribable to them individually. They mutually reinforce each other’s effect. Such a variation is created by the interaction of two homozygotes for the two genes, each acting additively, that is, and additive x additive (AA) interaction.

Duplicate epistasis involves two non-allelic genes which tend to cancel or weaken the effect of each other when they occur in combination (hybrid). They act in opposite directions hence dilute each other’s effects. Such a variation arises from an interaction between a homozygote and a heterozygote or between two heterozygotes. Accordingly, they are termed as additive x dominance (AD) and dominance x dominance (DD) epistatic interactions, respectively.

Epistasis is a genetic phenomenon resulting from non-additive interactions of alleles at different but functionally related loci (Falconer and Mackay, 1996). It has been demonstrated that non-allelic interactions are ubiquitous in the genetic control of quantitative traits Jinks and Jones, 1958 and Rieseberg et al., 1996 and may play a
central role in affecting two major evolutionary processes of speciation, founder effects (Giddings et al., 1989) and hybridization (Harrison, 1993). Despite its importance in evolution, however, epistasis has received little attention by empiricists. One of the important reasons is that virtually no powerful method has been developed to quantify the contribution of epistasis to genetic variance in a population (Cheverud and Routman, 1995). Epistasis is extremely difficult to handle by traditional biometrical genetic approaches (Mather and Jinks, 1982).

Sharmila et al. (2007) observed the nature and magnitude of gene effects for yield and its components in sesame. We carried out generation mean analysis using the different crosses of sesame. The P₁, P₂, F₁, F₂, BC₁ and BC₂ of these generations were studied for seven quantitative traits. The analysis showed the presence of additive, dominance and epistatic gene interactions. The additive dominance model was adequate for plant height and capsule length. An epistatic digenic model was assumed for the remaining crosses. Duplicate-type epistasis played a greater role than complementary epistasis. The study revealed the importance of both additive and non-additive type of gene action for the traits studied. The presence or absence of epistasis can be detected by the analysis of generation mean using the scaling test, which measures epistasis accurately whether it is complimentary (Additive x additive) or duplicate (Additive x Dominance) and (Dominance x Dominance) at the digenic level. The obtained information on the nature of gene action in sesame to provide a basis for an evaluation of selection methods for the improvement population.

Marinkovic et al. (2006) were estimates the effects of additive and dominance genes and their interaction on the inheritance of hectoliter weight in 10 sunflower hybrids developed by crossing five inbred lines derived from the synthetic-NS-S-1 were analyzed in 2001 and 2002. The linkage among the expected progeny means was tested using the scaling tests method (Mather, 1949), while the estimates of gene effects and mode of inheritance were made by generation mean analysis (Mather and Jinks, 1982). The additive-dominance model was not adequate for all crosses from the two years. In the hybrids for which the model was not adequate, epistatic gene effects
were important in the inheritance of the studied characters. In the first years of study, duplicate epistasis between dominant increased while duplicate epistasis between dominant decreased. In the second year of study duplicate epistasis between dominant increased while duplicate epistasis between dominant deceased. In second year of investigation the type of epistasis could not be determined, because the values of the non-fixable components (dominant and dominant x dominant) were in significant.

**Dass and Griffey (1995)** studied the genic control of wheat adult-plant resistance to powdery mildew. Additive effects were predominant in all six crosses. In relation to five crosses there was evidence of digenic epistasis. Dominance effects were significant in four crosses. Barakat, (1996) employed generation mean analysis in combination with an analysis of variation to study the inheritance of wheat characters related to immature embryo regeneration capacity. The author found that epistatic effects were more important than either additive or dominance genic effects to determine the five *in vitro* traits.

**Balatero et al., (1995)** did not verify epistatic effects determining the androgenic response in hexaploid triticale. The results showed that dominance was an important cause of high embryo induction. Absence of epistasis was also verified by Gingera *et al.,* (1995) in a study of inheritance of delayed first pustule appearance to common leaf rust in sweet corn, and Holtom *et al.,* (1995), in relation to maturity and seed characters in sunflower.

**Rahman et al., (1994)** studied the genic control of seedling root characteristics in maize. The analyses showed that dominance effects were greater than additive genic effects, and epistasis was an important component of the genotypic values of individuals. Ramsaha *et al.,* (1994) combined generation mean analysis and triple test cross to study the inheritance of yield and its components in Swede. In relation to direction of dominance, reciprocal effects and epistasis, relevant differences between the polygenic systems were evidenced.
Mgonja et al., (1994) and Saha Ray et al., (1994) studied generation mean analysis in rice obtained evidence of duplicate epistasis in the polygenic systems responsible for stem and mesocotyl length, respectively. Both additive and non-additive genic effects were important.

As seen, this methodology provides information on the relative importance of average effects of the genes (additive effects), dominance deviations, and effects due to non allelic genic interactions, in determining genotypic values of the individuals and, consequently, means genotypic values of families and generations. It is interesting to note that in most of the papers there was evidence of epistasis. Thus, in genetic studies assuming additive-dominance model, the estimates of the linear components of means can be biased due to epistatic effects. This has been shown for the case of polygenic system without fixed genes. This work was carried out to assess the consequences of epistasis in polygenic systems with fixed genes and is an extension of part of the paper of Pooni and Treharne, (1994).

2.7. Oil Content:
The genus Ocimum, (Lamiaceae formerly Labiatae), collectively called basil has long been recognized as a diverse and rich source of essential oils. The essential oil, mainly used in food industries and perfumery, also possesses antimicrobial activity Prasad et al., (1985) and some of its components, such as 1,8-cineole, linalool and camphor are known to be biological activity Morris et al., (1979). Comphor and 1, 8-cineole seems also to be involved as agents in alelopathic reactions Rice (1979).

The essential oils of basil extracted via steam distillation from the leaves and flavoring tops are used to flavor foods, dental and oral products, in fragrances, and in traditional rituals and medicines (Guenther 1949; Simon et al., 1984). Extracted essential oils have also been shown to contain biologically-active constituents that are insecticidal Deshpande and Tipnis (1977), Chavan, and Nikam, (1982), Chogo and Crank, (1981), nematicidal Chatterjee et al., (1982), fungistatic Reuveni et al., (1984) or which have antimicrobial properties Ntezurubanza et al., (1984). These properties can frequently be attributed to predominant essential oil constituents, such as methyl
chavicol, eugenol linalool, camphor, and methyl cinnamate. Two minor components of the essential oil of sweet basil, juvocimene I and II have been reported as potent juvenile hormone analogs Nishida et al., (1984).

There are several types of basil oil in international commerce, each derived principally from different cultivars or chemotypes of sweet basil. The oils of commerce are known as European French or Sweet Basil, Egyptian, Reunion or Comoro; and to a lesser extent Bulgarian and Java basil oils (Heath, 1981). The European type of basil oil considered to be the highest quality, and producing the finest odor, characteristically contains: linalool; methyl chavicol; and to a lesser extent 1,8-cineole, alpha-pinene; beta-pinene; myrcene; ocimene; terpinolene; camphor; terpinen-4-ol; alpha-terpineol; eugenol; and sesquiterpenes (Guenther 1949; Simon et al., 1984). Egyptian basil oil of commerce is similar to European basil oil except that the concentration of d-linalool is significantly lower while the concentration of methyl chavicol is significantly higher Fleischer, (1981). In contrast, Reunion or Comoro basil oil contains little if any d-linalool and is a harsher, spicy oil due to the very high concentration of methyl chavicol, and to a lesser extent, 1,8-cineole, borneol camphor and eugenol (Lawrence et al., 1972; Simon et al., 1984). Bulgarian and Java basil oils are rich in methyl-cinematic and eugenol respectively Heath, (1981).

Zheljazkov et al., (2008) was conducted to assess yield, oil content and composition of 38 genotypes of sweet basil (Ocimum basilicum L.). Overall, biomass yields were high and comparable to those reported in the literature. However, basil genotypes differed significantly with respect to oil content and composition. Oil content of the tested accession varied from 0.07% to 1.92% in dry herbage on the basis of the oil composition, basil accession were divide into seven groups. high-linalool chemo type (19-73%), linalool-eugenol chemotype (six chemotype with 28-72%, chavicol and 5-29% eugenol, methyl chavicol chemotype (six accession with 20-72% methyl chavicol and no linalool, methyl chavicol- linool chemotype (six accession with 8-29% methyl chavicol and 8-53% ionalool, methyl eugenol- linalool chemotype (two accession with 37% and 91% methyl eugenol and 60% and 15% linalool, methyl
cinnamate-linalool chemotype (one accession with 9.7%, methyl cinnamate and 31% linalool and bergamotene chemotype (one accession with bergamotene as major constituent, 5% eucalyptol, and <1% linalool). Our results demonstrated that basil could be a viable essential oil crop in Mississippi. The availability of various chemotypes offers the opportunity for production of basil to meet the market requirement of specific basil oils or individual compounds such as linalool, eugenol, methyl, chavicol, methyl cinnamate, or methyl eugenol.

Javanmardi et al., (2002) were found Ocimum species are used in traditional Iranian medicine, as a culinary herb and as a well known source of flavoring principles. Horticultural characteristics, including quantitative and qualitative traits along with the chemical variation of phenolic acids, of 23 accession of basil (Ocimum basilicum L.) from Iran were studied. Morphological studied of accession showed a high level of variability in recorded traits. Quantification of phenoliv acids was determined using high-performance liquid chromatography and showed drastic variation between accessions. Chemical studied revealed that rosmarinic acid is the predominant phenolic acid present in both flower and leaf tissues. Unusual basil accessions were identified that can serve as genetic sources of phenolic acids for crop improvement.

Ozcan and Chalchat (2002) were observed the constituents of essential oils isolated by hydro distillation of the over ground parts of Ocimum basilicum L. and Ocimum minimum L. from turkey were examined by GC-MS. A total of 49 and 41 components, respectively, were identified accounting for 88.1% and 74.4% of the oils of O. basilicum and O. minimum, respectively. The oil of O. basilicum contained, as main components, methyl eugenol 78.02%, α-cubebene 6.17%, nerol 0.83% and e- muuurolene 0.74%. Major compounds in the volatile oil of O.minimum were geranyl acetate 69.48%, terpinen-4-ol 2.35% and octan-3-yl- acetate 0.72%. The essential oil of O. basilicum was characterized by its high content of methyl eugenol 78.02%, whereas the most important essential oil constituent of O. minimum was geranyl acetate 69.485.
Marotti et al. (1996) were found ten cultivars of basil were studied to establish a possible relation between morphological characteristics and essential oil composition. The morphological parameters were recorded at the beginning of the flowering stage and the essential oils, obtained by hydrodistillation, were analyzed by gas chromatography (GC) and GC/ mass spectrometry (GC/MS). Among the cultivars, four phenotypes were distinguished on the basis of leaf size, shape and color and plant height, weight, branching and leafing. The composition of essential oil all characterized by a high content of linalool, including three chemotypes, linalool and methylchavicol and linalool and linalool and linalool and eugenol. Two chemotypes each had their own suite of morphological characters, whereas two groups of cultivars, with different morphological parameters belonged to the same chemotype.

2.8. Transgressive Segregation:

Transgressive breeding aims at isolating gene combinations (Recombinants) which posses new characters or new (higher or lower as is desirable) intensity of trait. These genotypes are superior to either parent. Heaney and Smith stated that though all quantitative characters can manifest transgressive segregation, flowering time and plant height are the two traits which are most frequently transgressed. Transgressive breeding aims at improving yield or its contributing characters through transgressive segregation. Transgressive segregation refers to the appearance of such plants in an F₂ generation that are superior to both the parents for one or more characters. The appearance of transgressive sergents for a trait in F₂ is the function of the following favorable genetic situations associated with parents involved in hybridization: (1) The character must be polygenic ally controlled. (2) Parents should be completely homozygous. (3) Parents should be complementary to each other for the (+) and (-) genes conditioning the traits in point. (4) There should be no linkage.

Loren et al. (2002) from a survey of 171 studies that report phenotypic variation in segregation hybrid populations, stated that transgression is the rule rather than the exception and observed that 155 out of 171 studies (91%) report at least one transgressive trait and 44% of the 1229 traits examined were transgressive segregants.
Studies of quantitative traits in segregating hybrid populations sometimes report
the presence of phenotypes that are extreme relative to those of either parental line
(Devicente and Tanksley, 1993; Rieseberg and Ellstrand, 1993; Cosse et al., 1995).
The generation of these extreme phenotypes is referred to as transgressive
segregation, and this is a major mechanism by which extreme or novel adaptations
observed in new hybrid ecotypes or species are thought to arise. If transgressive
segregation is frequent, then an important evolutionary role for hybridization is more
easily explained. Note that transgressive segregation is a phenomenon specific to
segregating hybrid generations and refers to the fraction of individuals that exceed
parental phenotypic values in either a negative or positive direction. This is caused in
part by heterosis, which is most pronounced in first-generation hybrids, and is
implicated when the mean trait value of the hybrids exceeds (in a positive direction
only) the phenotypic values of both parental lines. As will be shown below, the
 genetic basis of transgressive segregation appears to be largely distinct from that
 underlying heterosis.

2.8.1. The nature of transgressive segregation

A remarkable diversity of traits has been shown to exhibit transgression in plants.
The bulk of these are morphological traits (65%), whereas the remainder are fairly
evenly divided among trait categories such as fecundity, the biochemical composition
of organs and tissues, physiology, life history, and tolerances to various biotic and a
biotic factors. This latter category may be most important to the success of hybrids,
because transgressive segregation for ecological tolerances seems most likely to
facilitate niche divergence. Transgressive segregation has also been reported for
potential permitting barriers such as flowering time and floral differences that
contribute to pollinator discrimination. In this context, it is noteworthy that the
reproductive barrier between a well-documented natural hybrid species, H. paradoxus,
includes habitat isolation (salt tolerance) and a shift in flowering time
Rieseberg, (1997). However, it has not yet been shown that transgressive segregation
has facilitated the development of either adaptation.
2.8.2. The genetic basis of transgressive segregation

As per the hypothesis of classical genetic, studies transgressive segregation can result from the expression of rare recessive alleles Rick, and Smith, (1953) and/or from complementary gene action Vega, and Frey, (1980). The best evidence that rare recessive alleles exist in wild populations whose phenotypes are masked by common alleles comes from crosses between the domesticated tomato, Lycopersicon esculentum and its wild relative, L. chilense Rick and Smith, (1953). A single plant from an F₂ population between the species was found to have dull orange flowers, a phenotype never before seen in either parental species or for that matter any other species of Lycopersicon. Additional crosses revealed that this trait is controlled by a rare recessive allele in the self-incompatible wild species, L. chilense, as predicted by the recessive allele theory. However, it seems unlikely that rare recessives account for more than a small fraction of the transgressive phenotypes reported in the literature because transgressive segregation is most frequently reported in crosses involving inbred lines in which recessive alleles are likely to be fixed in the homozygous condition.