5. SUMMARY AND CONCLUSIONS

The present investigation entitled “Genetic analysis for seed yield and other traits with molecular characterization for disease resistance in flax, *Linum usitatissimum* L.” was undertaken to get the information on the nature of gene action for seed yield, fibre, quality traits and to study the inheritance of wilt, rust resistance and to identify molecular markers linked to the wilt disease. The investigation was carried out at the Experimental Farm of the Department of Crop Improvement, CSK HPKV Palampur and Research Stations Kangra and Kukumseri and Molecular Cytogenetics and Tissue culture Laboratory of the Department.

The experimental material comprising P$_1$, P$_2$, F$_1$, F$_2$, BC1 and BC$_2$ generations of three crosses viz., Turkey x Binwa, TL-11 x Him Alsi-2 and TL-43 x Binwa was evaluated in Compact Family Randomized Block Design with three replications during *rabi* 2008-09 at two locations viz., Palampur (E1) and Kangra (E2). Two released varieties viz., Him Alsi-2 (dual type) and Binwa (seed type) were used for their further improvement for wilt, rust resistance, yield and quality traits with three exotic varieties viz., TL-11, TL-43 and Turkey. The observations were recorded on ten randomly taken plants per entry per replication in case of parents and F$_1$s, thirty in case of back crosses (B$_1$ and B$_2$) and fifty plants in case of F$_2$ generations.

For inheritance studies separate experiment consisting of F$_1$, F$_2$ and backcross generations was raised. Inoculation of each plant was taken from rust infected plants and for wilt grown in wilt sick plots. A molecular study was carried out through RAPD. The data was analyzed by using simple scaling test given by Mather (1949) and Joint scaling test of Cavalli (1952), and the estimation of various genic effects by Jinks and Jones (1958). The mode of inheritance was ascertained by applying chi-square test of goodness of fit.
The results of scaling tests revealed that additive dominance model was fit in cross Turkey x Binwa for biological yield per plant, straw weight, retted straw weight, total fibre, line fibre, seeds per capsule, seed yield per plant in E1; seed yield per plant in cross TL-43 x Binwa (E2), which suggested the absence of epistasis in these crosses. Dominance component was found to be predominant over additive component hence breeding strategy should be hybridization in above crosses followed by deffering selection to later generations. The above model was a failure thereby indicating presence of non allelic interactions for remaining traits in all the crosses.

Complementary type of gene action was observed for biological yield per plant and seed yield per plant in E1, biological yield per plant in E2 in cross TL-11 x Him Alsi-2; seed yield per plant and plant height in E1, days to maturity and plant height in E2 in cross Turkey x Binwa, days to 50 per cent flowering and biological yield per plant in cross TL-43 x Binwa (E2). Such type of gene action was not observed for remaining traits in all the crosses. The traits for which the above gene action was observed, the breeding strategy should be selection in early generation by adopting biparental matings for isolation of transgressive segregants.

Duplicate type of gene action was observed for days to 50 per cent flowering, plant height, technical height in E1 and days to 50 per cent flowering, seed yield per plant, plant height, technical height, straw weight, retted straw weight, total fibre, per cent fibre, line fibre in E2 in cross TL-11 x Him Alsi-2; technical height in both E1 and E2 in cross Turkey x Binwa, secondary branches per plant, 1000 seed weight, plant height in E1 and technical height in E2 in cross TL-43 x Binwa. Duplicate type of gene action was not observed for the remaining traits in all the crosses. The traits for which the above gene action was observed, the breeding strategy would be by growing large segregating populations and adopting biparental mating to get transgressive segregants.
All the components of gene action i.e., d, h, i, j and l in cross Turkey x Binwa were found to be significant for days to maturity and plant height in E2 whereas in other crosses in both the locations and above cross in E1 the similar behaviour was not observed. In addition in the above cross significantly positive value of d and significantly negative value of [i] for the above traits was observed. This indicates negative alleles are dispersed in the parents for the inheritance of these traits which suggests that the selection should be delayed to later generation.

Out of the three crosses TL -11 x Him Alsi-2 is the best cross in both the locations. This cross invariably has given 2-3 times higher yield than the remaining crosses. Therefore, the results obtained in the present investigation with respect to the above best cross for generation mean analysis suggested that both additive and dominance gene effects were important for most of the traits but dominance was predominant as compared to additive effects. Duplicate type of gene action was observed in the expression of days to 50 per cent flowering, seed yield per plant, plant height, technical height and fibre traits in E2 for the above cross which implies the use of biparental approach and selection to be deferred to later generation. Complimentary type of gene action was seen for biological yield per plant, seed yield per plant which implies the use of biparental approach and early generation selection.

Keeping in view, the presence of both fixable and non fixable type of gene effects for most of the traits as well as duplicate type of gene action for few traits in cross TL-11 x Him Alsi- 2, it appears worthwhile to go for biparental matings or few cycles of recurrent selection for the accumulation of favourable genes for seed yield and its components in linseed.

Moreover, for cross TL-11 x Him Alsi-2 in E2, additive x additive (i), additive x dominance (j) and dominance x dominance (l) interaction effects with duplicate nature are contributing in the inheritance of these traits viz., days to 50 per cent flowering, seed yield per plant, plant height, technical height, straw
weight, retted straw weight, total fibre, per cent fibre, line fibre and capsules per plant, 1000 seed weight, plant height, technical height, oil content indicating recurrent selection could be employed for genetic improvement of these traits. The method is helpful in breaking up undesirable linkages.

The contradiction between heterosis and inbreeding depression for days to 50 per cent flowering, days to maturity, harvest index, plant height, per cent fibre for cross TL-11 x Him Alsi-2 could be due to the presence of linkage between genes. Negative value of heterosis for days to 50 per cent flowering is desirable in TL-11 x Him Alsi-2 since earliness is an important objective for linseed breeding. Significantly positive inbreeding depression were obtained for days to 50 per cent flowering, primary branches per plant, secondary branches per plant, capsules per plant, 1000-seed weight, plant height, technical height, straw weight, retted straw weight, total fibre, line fibre, per cent fibre, protein content in E1 and primary branches per plant, secondary branches per plant, capsules per plant, biological yield per plant and technical height in E2 in the above cross.

The results of this study demonstrated that gene effects obtained by generation mean analysis differed with genetic backgrounds of the crosses, and were also influenced by environmental conditions. There is an involvement of epistasis in genetic control of some of the traits studied in the present findings which revealed separate breeding strategies crosswise as well as environment wise.

For wilt the results obtained revealed that out of five parents, two were categorized as resistant in both the locations (Him Alsi-2, Binwa). Turkey was found to be highly susceptible in E1 and E2. The segregation pattern studies indicated that the wilt and rust diseases in linseed are controlled by single dominant gene, and inherited in the ratio of 3:1. The segregation pattern studies indicated that the seed colour and flower colour in linseed were controlled by single dominant gene, whose expression is subject to the genetic background of the genotype involved in the cross.
All the genotypes used in the present investigation were found to have high fatty acid content (α-Linolenic-acid). Higher amount of linolenic acid in the experimental material shows its unsuitability for edible purpose but suggests its usefulness for industrial purposes.

Of the 60 RAPD primers used in the present studies for identification of molecular markers linked to the wilt disease, only 12 primers were polymorphic but did not generate polymorphism among the bulks. Hence, proposed primers used in the present study were not useful and more random primers should be used to identify markers linked to the disease in future breeding programme.

Another important aspect from practical point of view was the identification of a potential cross for the simultaneous improvement of linseed with respect to seed yield, oil content and fibre. TL-11 x Him Alsi-2 was found to be the promising cross because of its high yield, quality and disease resistance among the three crosses studied and thus could be utilized in future breeding programme. The outcome of the present endeavour suggests different breeding strategy crosswise as well as location wise because of different gene actions in various crosses and locations.