SUMMARY

The diallel analysis of protein percent, yield, panicle length, number of grains, weight of the grains, flag leaf index, second leaf index revealed that additive and dominance effect are both important in the inheritance of all the traits studied except second leaf index where only additive effect is important. Preponderance of additive effects are prevalent in percent protein, height, grain weight and flag leaf index. Non-additive components have greater effect than additive components in yield per plant, number of grains per panicle and length of panicles. Dominance deviations are apparent in all characters except second leaf index. Effect of environment is found to be significant only in the second leaf index. The magnitude of dominances is mostly partial but overdominance is also found in the inheritance of yield per plant, number of grains per panicle and length of the panicle. Asymmetry of the positive and negative genes are observed for all traits except second leaf index. Recessive genes are more frequent and important for the inheritance of protein and grain weight both of which are due to excess of positive genes. Dominant genes are prevalent and important for rest of the characters. Low protein is dominant over high protein; like wise high yield over low yield, tall plant over short plant, high number of grains per panicle over low number, long panicle over short panicle, small grain weight over high grain weight, high flag leaf index over low flag leaf index and low second leaf index. Heritability in the
broad sense has been estimated for each of the above characters and found to be high, and moderately high in the narrow sense, and are apparent in all the above characters. It is suggested that the following crosses would be advantageous for high protein; P-III x P-VII, P-V x P-III, P-I x P-VII, P-III x P-VII, P-V x P-VII for both protein and yield. P-I x P-VI, P-II x P-VII, P-I x P-VII and P-VI x P-VII, are important.

The test cross analysis P-III x P-VII (F_2 kernel generations) showed unimodal frequency distribution with transgression at both high and low percent protein ends. Mean protein percent of F_2 indicated additive x additive type of interaction with high heritability and genetic advance. Genetic coefficient of variation was high due to heterozygosity of the F_2 population since protein percent is highly polygenic in nature.