

STUDIES THE RELATION OF GENETIC BEHAVIOUR AND DIVERGENCE ANALYSIS FOR SOME QUALITY ATTRIBUTES FOR SOME CROSSES IN PEA (*Pisum sativum* L.)

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ABSTRACT

The present investigation was carried out to study gene effect and genetic divergence for nutritional quality attributes. Six parents of pea, named (P1) Master pea, (P2) Little marvel, (P3) Lincoln, (P4) Allepo, (P5) Alaska, (P6) Early perfection were randomly sampled among a large collection germplasm. The seeds of parents were introduced from different sources. The six parental genotypes were crossed according to half diallel crosses design. Total carbohydrates, total seed protein and amino acid compositions were determined for the studied pea genotypes.

The results revealed considerable variation for all studied quality attributes. The mean performances of F₁ hybrids for protein, carbohydrates and essential amino acids varied according to parental combinations and manifested heterotic effects. The results also revealed that cysteine content was low in Little marvel (P2) variety and controlled by recessive genes, while the high cysteine content of Alaska, (P6) was dominant in crosses.

In the analyzed set of pea genotypes, all essential amino acids contents except tryptophan were lower than those the recommended pattern of FAO/WHO reference protein. Based on nutritional quality attributes, the pea populations were grouped into five clusters. The data indicated that considerable genetic divergence was induced by hybridization and the F₁ hybrids were widely dispersed from their parents. The study revealed that there was no association between genetic divergence among parents and heterosis response of F₁ hybrids. It could be also regarded that non-additive gene effects were more important than those additive gene effects in determining the expression of all nutritional quality attributes. The average level of dominance for genes controlling these attributes was in the over dominance range. The association analysis revealed that total carbohydrate content was negatively correlated with seed protein content, while was positively correlated with total amino acids and all studied essential amino acids.

The obtained results suggested the possibility of development of high yielding and nutritionally superior pea genotypes through suitable breeding programs.