This indicated that though there was high degree of association between two variables at genotypic level, its phenotypic expression was deflated by the influence of environment. It has also indicated that there was an inherent relationship between the characters studied which is in agreement with the conclusions of Venkataravana *et al.* (2000) and Suneetha *et al.* (2004). In most of the cases the direction and magnitude of phenotypic and genotypic correlation between various characters remained almost same. The phenotypic correlation coefficients in very few cases were higher than their corresponding genotypic correlation coefficients which might be due to the non-genetic causes probably environment inflated the value of phenotypic correlation.

Correlation coefficient were estimated between total kernel yield and other traits under study indicated that total kernel yield per plant was positively and significantly correlated with all the characters except SCMR, SLA and root diameter.

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High yielding early maturing inbred lines of safflower wild species, *Carthamus palaestinus*

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Carthamus palaestinus is a late maturing, poor yielding wild species of safflower. The diversity observed in the parental accession of *C. palaestiuns* for agronomic and yield traits has been exploited to improve *C. palaestiuns* for earliness and yield through intercrossing and pedigree breeding. Thus developed improved inbred lines were early in maturity and high yielders than the parental accession.

Carthamus palaestinus was identified as a source of resistance to Fusarium wilt and Alternaria leaf spot (Pallavi et al 2007; Prasad and Anjani 2008), for which resistance is not available in cultivated safflower (C. tinctorius) genepool. It produces fertile hybrids when crossed to cultivated species. The frequent problem encountered, while transferring the disease resistance from *C. palaestinus* to safflower, was simultaneous transfer of undesirable traits like late flowering and low yielding ability along with diseases resistance in interspecific derivatives of the cross *C. tinctorius,* $2n$=24 x *C. palaestinus*, $2n$=24. In order to overcome this problem, an attempt was made to reduce time taken to reach flowering and increase productivity of *C. palaestinus*. The results of this investigation were presented in the present paper.

Diverse *C. palaestinus* phenotypes identified in the population of *C. palaestinus* accession, PI235663 introduced from USDA were advanced progeny-wise through self-pollination for three generations and then through conscious selection for desirable traits, intercrossing and pedigree method. Data on rosette duration, days to 50% flowering and maturity, 100-seed weight, seed yield/plant were recorded on each plant-progeny. Pollen contamination through honeybee was avoided by growing the material under pollination nets.

The parental accession of *C. palaestinus* has exhibited diversity for main traits (Table 1). The improved *C. palaestinus* inbred lines exhibited 10-15 days reduced rosette duration, short plant height, 10-15 days early flowering and maturity, and higher 100-seed weight and seed yield/plant than the original parental population of *C. palaestinus* (Table 1). These improved inbred lines have been further stabilized through inbreeding for the desirable traits identified.

Table 1. Agronomic and yield traits in parental line and improved inbred lines of *C. palaestinus*

Trait	Parental *C. palaestinus*	Improved inbred lines of *C. palaestinus*
Duration of rosette period (days)	45-50	30-35
Plant height (cm)	85.6-135.7	85.2-90.8
Days to 50% flowering	90-95	80-85
Days to maturity	135-140	120-130
100-seed weight (g)	3.3-4.1	4.7-5.1
Seed yield/plant (g)	7.6-22.7	41.4-110.8

The improved inbred lines exhibited more than 100% higher yield potential than the parental *C. palaestinus* accessions under minimal irrigated conditions. By using these improved inbred lines, the frequently encountered problem of late flowering and low yield potential of progenies of *C. tinctroius* x *C. palaestinus* could be overcome successfully.

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Genetic variability for nutritional traits in Indian-mustard (*Brassica Juncea* L.)

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Tocopherols represent a group of naturally occurring lipid soluble compounds collectively known as Vitamin E which can't be produced in humans and animals. Thus, vitamin E has been recognized as an essential nutrient for the growth and health of all species of animals. Among all forms of tocopherol, -tocopherol has the highest vitamin E activity. Vegetable oils are the most abundant source of naturally occurring tocopherols. Indian-mustard represents the best target for the enhancement of tocopherols by breeding, because it plays an important role in oilseeds crops of India. Although, the genetic variability for nutritional traits has been extensively studied in *Brassica napus*, but such information in *Brassica juncea* (Indian-mustard) is very limited. Therefore, the aim of the present investigation was to study the genetic variability for nutritional traits including tocopherol content in seeds of Indian-mustard genotypes.

For the estimation of quality parameters, fifty genotypes of Indian-mustard were selected and seeds from each genotype were collected from self-fertilized plants. Individual tocopherol content was quantified by HPLC system (Model Waters e2695, e-alliance, autosampler) attached with a photodiode array detector (Waters, Milford, MA, USA) using external standards and separated by LiChrospher Si60 (5 m, 150mm x 4.6mm) column connected with Guard cartridge (32mm x 4.6mm). Total tocopherol content in a sample was computed by summing the amounts of the individual tocopherol (-, -, and -tocopherol). The extraction of the total oil content was performed by soxhlet method AOAC using SOCS PLUS system (Pelican Equipments, Chennai) using petroleum ether whereas protein content was determined by microKjeldahl method.

Analysis of Variance (ANOVA) exhibited highly significant differences among the genotypes for individual as well as total tocopherol, oil and protein content. The level of -tocoperol, -tocopherol, -tocopherol and total tocopherol