Table 4 Estimates of variance components and degree of dominance for yield, yield contributing characters in F1 generation

	Days to 5	0% Days to	Plant height	Number of primary	Number of	Number of	Number o	of Pod length (cm)	100 seed weight (gm)	Yield/plant
	flowering	maturity	(cm)	branches/plant	clusters/plant	pods/plant	seeds/pod			(gm)
$\sigma^2 GCA$	0.0911	0.1756	0.1926	0.0030	0.0094	0.1814	0.0257	0.0130	0.0034	0.0267
$\sigma^2$ SCA	3.5817	7.8034	2.6732	0.0085	0.1417	0.9816	0.0792	0.0449	0.0587	0.1439
$\sigma^2 GCA / \sigma^2 SCA$	0.0254	0.0225	0.0720	0.3486	0.0664	0.1848	0.3247	0.2888	0.0575	0.1853
$\sigma^2 A$	0.1822	0.3512	0.3852	0.0060	0.0188	0.3628	0.0514	0.026	0.0068	0.0534
$\sigma^2 D$	3.5817	7.8034	2.6732	0.0085	0.1417	0.9816	0.0792	0.0449	0.0587	0.1439
h <sup>2</sup> <sub>bs</sub>	94.6797	94.7856	85.5424	83.8150	89.1171	84.2461	75.4477	76.2365	83.4394	77.7690
h <sup>2</sup> <sub>ns</sub>	4.5831	4.0822	10.7739	34.6820	10.4386	22.7346	29.6938	27.9569	8.6624	21.0484

Note:  $\sigma^2 A$ =Additive variance,  $\sigma^2 D$ = Dominance variance. Where,  $\sigma^2 GCA = Vg =$  variance due to GCA;  $\sigma^2 SCA = Vs =$  variance due to SCA; Ve = environmental variance p = number of parents. These variances were translated into different components of phenotypic variance as: Additive genetic variance VA = 2 Vg, Total genetic variance VG = 2 Vg + Vs, Phenotypic variance Vp = 2 Vg + Vs + Ve, Heritability in broad sense (h<sup>2</sup>b) and narrow sense (h<sup>2</sup>n) were estimated as: h<sup>2</sup>b = (VG / Vp) × 100, h<sup>2</sup>n = (VA / Vp) × 100