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ASSESSING GENETIC WORTH OF SEGREGATING POPULATIONS TO DERIVE TRANSGRESSIVE RECOMBINANT INBRED LINES IN CHILLI (*CAPSICUM ANNUUM* L.)

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ABSTRACT

Identifying and restricting productive crosses and management of large segregating populations generated from a few crosses can enhance crop breeding efficiency. Breeders can better allocate resources by identifying and eliminating unproductive populations in early generations. In order to maximize the likelihood of producing good RILs from a small number of crosses with high breeding potential. Breeding potential of three (LTL7 × S343, AP × S343 and PDL1 × S343) F_2 populations derived from parents differing for fruit yield was assessed based on trait mean, absolute range (AR), standardized range (SR), phenotypic coefficient of variation (PCV), transgressive segregation index (TSI) and usefulness index (UI), which combines, mean, phenotypic standard deviation and standardized selection differential at different selection intensities. The cross with high quantitative traits' mean, AR, SR, PCV, TSI and UI in F_2 generations was considered as that with better breeding potential. Based on descriptive statistics, TSI and Uc, breeding potential of (LTL7 × S343) F_2 population was better than remaining two (AP × S343 and PDL1 × S343) F_2 population for green fruit yield plant^{-1}. In light of the findings and those of other researchers, UI may be a useful tool for objectively choosing segregating populations of chilli with promising breeding prospects.

Keywords: Breeding potential, Usefulness index, Transgressive segregation index, Phenotypic coefficient of variation

Introduction

Chilli (*Capsicum annuum* L.) is one of the most important spice and vegetable crops grown in India with great export potential. Chilli is used in both green and dry forms in all culinary preparations. It is an indispensable condiment of every home as used in the daily diet (Shankargouda, 2017). It is known as wonder spice owing to its nutritional and pharmaceutical values. It belongs to the nightshade family, Solanaceae with diploid chromosome number of 2n=2x=24. It is the second most important solanaceous vegetable after tomato grown worldwide both as a spice or vegetable crop (Hasan *et al.*, 2014). There are over 35 recognized Capsicum species, the most common of which comprise the cultivated type *Capsicum annuum*, and four domesticated namely *C. frutescens, C. chinense, C. baccatum* and *C. pubescens* (Di Dato *et al*., 2015). Among these, *Capsicum annuum* and *Capsicum frutescens* are most widely cultivated in India mainly in southern parts of the country where temperature is favourable for *C. annuum*. Chilli is one of the most popular vegetables, originated from South and Central America (Bahurupe *et al.*, 2013). At global level, chilli is one of the spices that generate huge revenues for producers and therefore contributes to poverty alleviation and improvement of women's social status (Karungi *et al*., 2013). It is an often-cross-pollinating species with out-crossing of 7 to 90 % (Singh *et al*., 1992).

Since resources are obviously restricted, it is not possible to advance all the progenies generated to later generations. Often, a crop breeder must choose a small number of segregating (breeding) populations derived from bi-parental/multi-parental crosses in order to use pedigree selection to identify superior/transgressive RILs for use as pure line cultivars. Removing poor crosses in the early generations maximizes the likelihood of deriving desirable RILs from large segregating populations derived from a few crosses with good breeding potential (Ramesh and Byregowda, 2016; Suresh *et al*., 2017; Bernardo, 2020 and Anilkumar *et al*., 2021).

Among the many segregating populations that are often created in crop breeding programs, breeders employ first-degree statistics like mean and range and second-degree statistics like absolute variance and standardized variance (PCV) to select the better segregating populations. For a given trait, the best breeding populations would be those that have high mean and a large genetic variance. A high mean at the beginning helps guarantee that, even in cases when selection is flawed, the chosen offspring will also have a high mean. The selection of genotypes with an optimal combination of traits is facilitated by high genetic variance. A substantial genetic variance combined with a relatively high mean ensures the maximum performance of selected offspring. The Transgressive Segregation Index (TSI) (Koide *et al*., 2019), which considers "AR" in segregating populations in relation to parental AR, and the usefulness criterion (Uc) (Melchinger, 1987), a summary statistic that combines mean, variance, and heritability, offer an objective way to choose segregating populations with superior breeding potential. Choosing breeding populations with strong breeding potential in terms of recovering RILs for use as parents in hybridization program is a challenge for crop breeders (Witcombe and Virk, 2001). The current investigation is to determine which possible cross, based on first- and second-degree descriptive statistics, Uc, and TSI estimable in their early segregating generations, are likely to produce a high frequency of better RILs in advanced generations.

Materials and Methods

Parental genotypes differing for fruit yield were used to generate three biparental crosses. The F_1 s of three crosses were raised and hybridity was confirmed using male parent-specific traits. The size of the F_2 population varied from 110 to 196. The true hybrids of these crosses were forwarded to generate three F_2 populations, which were sown at the Experimental plots of 'K' block, Department of Genetics and Plant Breeding, University of Agricultural Sciences (UAS), GKVK, Bengaluru (N12 º58, E77 º35'). Three F_2 segregating populations were planted separately in contiguous blocks with a spacing of 75 cm between rows and 45 cm between plants within a row during the last week of November, 2023. Recommended package of practices was followed to raise a healthy crop. The data were recorded on each F_2 individual plant at their maturity for fruit yield expressed as green fruit yield plant^{-1} (g).

Estimation of Descriptive Statistics and Quantitative Genetic Parameters

To compute descriptive first-degree statistics like mean, absolute range (AR) (highest-lowest) and standardized range (SR) [(highest-lowest)/mean], and second-degree statistics like absolute phenotypic variance σ^2_p, phenotypic standard deviation (σ_p), and standardized phenotypic variance, i.e., phenotypic coefficient of variance (PCV) = [(σ_p / mean) × 100] (Burton and Devane, 1953), data recorded on ten randomly selected plants of four parents, F_1s, and each F_2 plant. "F" test and Levene's test (Levene, 1960) were used to analyse the significance of trait means and σ^2_p comparing the three crosses. These tests were implemented using statistical options in Microsoft Excel program and R studio. It was calculated that the transgressive segregation index (TSI) was equal to the AR/trait mean difference between parents (Koide *et al.,* 2019). The 'σ_g' was estimated as the square root of σ^2_g; The σ^2_g was estimated as σ^2_p - σ^2_e, where, σ^2_e for F_2 populations was estimated as the average of phenotypic variance in non-segregating populations (F_1, P_1, P_2). Usefulness index (UI) for each trait was estimated as trait mean + (k × σ^2_g/ σ_p), where, k = standardized selection differential at different selection intensities; k = 2.67 and 2.06 at 1 *per cent* and 5 *per cent* selection intensities, respectively (Bernardo, 2020).

Criteria to Assess the Breeding Potential of Crosses

The cross with high quantitative trait mean, AR, SR, PCV, TSI and Uc in F_2 generations was considered as those with better breeding potential.

Results and Discussion

The arithmetic mean is a widely used metric for assessing central tendency when summarizing data points. Mean and range are commonly employed as descriptive statistics to capture observed patterns of variation in target traits. A high mean and range for the target characteristic or traits provide an advantage in selecting favourable genotypes from segregating populations. Breeding population derived from LTL7 x

S343 having highest trait mean which was followed by the population derived from AP x S343 among three crosses. Significant differences were observed between mean performances of AP x S343, PDL1 x S343 and LTL7 x S343 crosses derived segregating populations for green fruit yield plant^{-1} (Fig. 1). However, LTL7 x S343 is better than AP x S343 and PDL1 x S343 for green fruit yield plant^{-1} with respect to AR (Table 1). On the contrary, LTL7 x S343 is better than those derived from remaining crosses in terms of unit-independent estimates of SR for green fruit yield plant^{-1} (Table 1).

Greater variance expands the range for selecting genotypes with the desired combination of traits. Selected offspring can reach their full potential if the genetic variance and mean are both relatively large (Bernardo, 2020 and Anilkumar *et al*., 2021). Phenotypic variability, as a measure of dispersion, combines genetic and environmental variability. A small difference between PCV (phenotypic coefficient of variation) and GCV (genotypic coefficient of variation) indicates that environmental factors have minimal influence on trait expression. These variations can be interpreted as reflecting another measure of variability: broad-sense heritability. The variability measures PCV and GCV which are true reflections of variability were found to be higher in LTL7 x S343 for green fruit yield plant^{-1}. While broad sense heritability was found to be high in the F_2 population from a cross LTL7 x S343 (Table 1). The crosses whose parents differ for a larger number of dispersed genes are likely to exhibit higher traits means and variances than those whose parents differ for fewer genes (Kearsey & Pooni 1996 and Bernardo 2020).

The estimates of $\sigma^2{}_p$ were comparatively higher in F_2 derived from the cross LTL7 × S343 than other crosses for green fruit yield plant^{-1} (Table 2). Levene's test for homogeneity of variances is used when comparison is to be made among populations based on trait variances and when number of individuals among population being compared are not same. The variances among three segregating populations derived from crosses significantly differed for green fruit yield plant^{-1} (Table 2). The results suggest that selection would be more effective and consequently greater genetic gain from F_2 derived from the cross LTL7 × S343 than other crosses for marketable and consumable product, i.e., fruit yield. Similar results were reported by Tirupathamma *et al*. (2021) for green fruit yield plant^{-1} in biparental derived segregating populations of chilli.

The process known as transgressive segregation (TS) occurs when a small number of genotypes in F_2 or later Phenotypes that are outside of both parents' range are displayed by segregating generations. Plant breeding cannot succeed without transgressive segregation (TS); when plant breeding is successful, TS thus takes place (Mackay *et al*., 2020). While LTL7 x S343 displayed higher TSI than AP x S343 and PDL1 x S343 for yield of marketable and consumable product (green fruit yield plant^{-1}) (Table 2 and fig.2). Shreya *et al.* (2017) in groundnut, Guindon *et al.* (2019) in pea and Chandana and Ramesh (2021) in Dolichos bean have also reported TS for economically important traits. According to theoretical research, the dispersion of advantageous complementing alleles across the parents from which the segregating population is formed causes TS (Bernardo, 2020 and Mackay *et al*., 2020).

In the present study, UI for selection intensities at 1 *per cent* was found to be higher than 5 *per cent* and at both intensities breeding population from the cross LTL7 x S343 was found to be highest (Table 2 and Fig. 3). Melchinger (1987) suggested utility of Schnell's (1983) concept of 'usefulness' as a valuable tool for determining the potential of breeding populations. Millicent *et al*. (2020) and Ongom *et al.* (2021) in cowpea, suggested that the use of UI aids in making informed decisions for selecting among the numerous breeding populations routinely developed in crop breeding programs. When choosing a cross with superior breeding potential, this introduces uncertainty. Therefore, in order to evaluate the breeding potential of crosses, a more thorough quantitative measure that successfully integrates various first- and second-degree data must be used. UI, a summary statistic that takes into account a trait's mean, variance, and heritability, can be used as an objective tool (Bernardo 2020, Chandana and Ramesh, 2021 and Bhat *et al*.,2024) to select the segregating populations with good breeding potential to derive superior RILs for use as parents in hybridization program.

Conclusion

Breeders often face resource constraints when managing numerous crosses or populations. In such cases, prioritizing potential crosses or derived populations over others can help isolate promising segregants. Consequently, early-generation identification of promising crosses is essential to address resource limitations effectively. From among three F_2 populations, breeding potential of (LTL7 × S343) F_2 population was better than that of other F_2 population for green fruit yield plant^{-1} based on higher

Descriptive Statistics, TSI and UI. Hence, potential productive populations can be further forwarded to recover the superior RILs.

Table 1: Estimates of first and second-degree statistics in F_2 populations for green fruit yield plant^{-1} in chilli

Crosses	**Mean**	**Absolute range (g)**	**Standardized range**	**PCV (%)**	**GCV (%)**	**Heritability**
AP × S343	319.73	629.7	1.96	42.50	41.27	94.31
PDL1 × S343	256.72	456.1	1.77	41.68	39.95	91.85
LTL7 × S343	358.38	1155.1	3.22	71.13	70.57	98.43

Table 2: Estimates of absolute phenotypic variance, TSI and UI for green fruit grain yield plant^1 in F_2 populations

Crosses	Absolute phenotypic variance (σ^2_p)	Levene's test statistic	p- value	TSI	UI	
					1%	5%
AP × S343	18470.48	12.56	1.1e-16 ***	8.20	661.98	583.79
PDL1 × S343	11454.49			7.17	519.22	459.25
LTL7 × S343	64995.62			9.98	1028.39	875.32

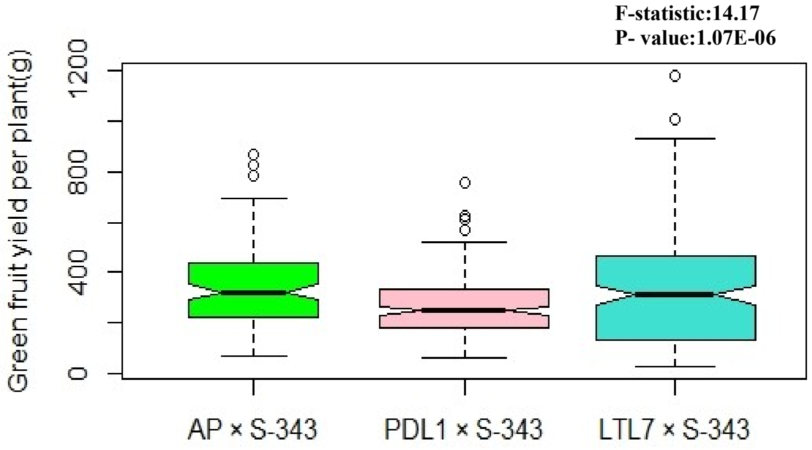

Fig. 1: Box-plot depicting means of green fruit yield plant^{-1} in F_2 population.

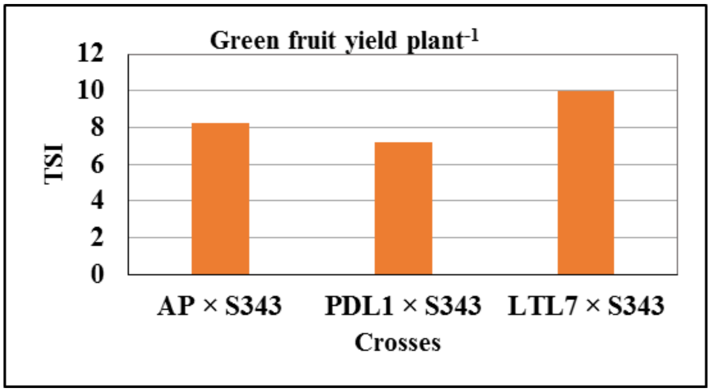

Fig.2: Bar graph depicting estimates of transgressive segregation index for green fruit yield plant^{-1} in F_2 population.

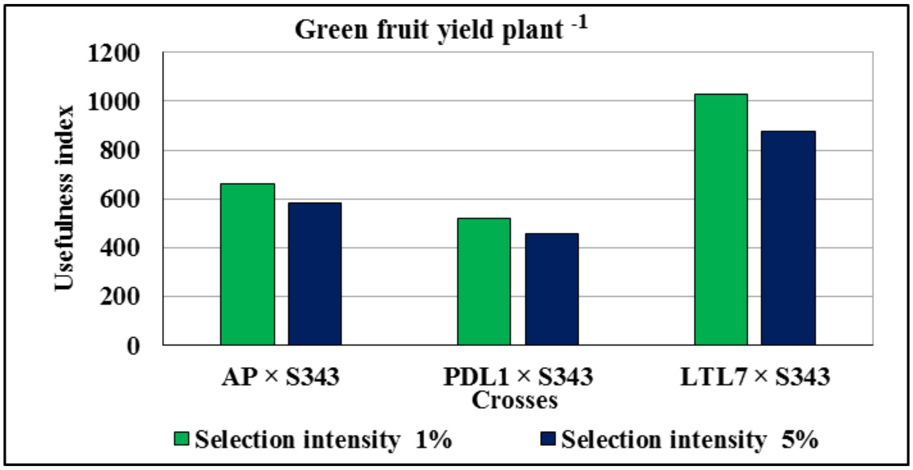

Fig. 3: Bar graph depicting estimates of usefulness index for green fruit yield plant^{-1} in F_2 population

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