

Cultivar Development in Self Pollinated Crops

Suma Krishnappa¹, Satish Hosakoti², Arun Zacharia³ and Jwala Pranati^{4*}

¹PhD Scholar, Department of Genetics and Plant Breeding, UAS, GKVK, Bengaluru – 560065

²M.Sc Student, Department of Genetics and Plant Breeding, UAS, GKVK, Bengaluru – 560065

³BSc (Ag), College of Agriculture and Allied Sciences, Baramati – 413102

⁴PhD Scholar, Department of Genetics and Plant Breeding, PJTSAU- 500030

ARTICLE ID: 21

Introduction

As most of the food grain crops are predominantly self-pollinated, and with lack of pollination control systems like male sterility, affecting crosses is difficult in these crops. Hence, Pure-lines are the only best cultivar option for commercial production in self-pollinated crops. The recombinant inbred lines (RILs) which are better than the parents (Transgressive RILs) and existing cultivars developed through pedigree selection of different crosses could be used as pureline cultivars (Ashwini *et al.*, 2021). The plant breeders regularly develop a large number of crosses in turn large number of breeding populations (BPs) to implement pedigree selection to identify superior RILs. Handling of a large number of BPs is resource demanding, hence reduces the efficiency of plant breeding. The crosses made between parental combinations that fail to produce useful cultivars consume most of the resources (Witcombe *et al.*, 2013). Early generation selection in self-pollinated crops involves evaluation of F₂- or F₃- derived lines from the cross between two pure-lines. Early elimination of inferior crosses and allocation of resources only to large-sized BPs derived from a few promising crosses selected based on an objective criterion is expected to enhance the chance of identifying desirable RILs for use as pure-line cultivars and thus helps to enhance efficiency of plant breeding (Chahota *et al.*, 2007; Witcombe *et al.*, 2013; Bernardo, 2020).

Procedure to develop better pure lines/ transgressive RILs:

1. Selection of best parents

“Quantitative genetic theory” suggest that probability of development of transgressive RILs is maximum from crosses/breeding populations (BPs) emanating from high mid-parental value (Bernardo, 2020). Parents with higher mid parental value will give head start to the breeding programme, therefore breeder need to start with good parents. However, good × good crosses might not result in exploitable genetic variance and transgressive segregation (TS) if both the parents share same alleles. Hence, parents with high mid parental value and differing in the dispersion of number of favorable and unfavorable alleles controlling target traits should be selected to affect the crosses. Combining ability studies and diversity analysis will aid in choosing best parents.

2. Best breeding population

Best breeding population is the one with high breeding potential in terms of predicted genetic gain and predicted frequency of transgressive RILs, which differs across breeding populations. Breeding potential is the genetic worth of a population in terms of recovery of superior RILs in the advanced generations. Ideal segregating generation should have high mean and variance. High mean in the early segregating generations leads to high means of selected progeny and higher variance offers scope for selection of desirable combination of traits. Best RILs can be derived by assessing the relative potential of crosses by comparing means and variances in early segregating generations. Various statistical parameters will aid in selection of best breeding population.

Statistical parameters to decide upon the best breeding population

Higher the estimates of traits’ mean, absolute range (AR), standardized range (SR), transgressive segregation index (TSI), absolute phenotypic variance (σ_p^2), phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV) and usefulness index (U_I), better is the breeding potential of the crosses.

a. Transgressive segregation index

Transgressive segregation is the basis of plant breeding, as it stably passes to next generation in contrast to heterosis which is not stable across generations. Transgressive segregation index (TSI) indicates the proportion of phenotypic differences between both parents and the phenotypic range in the F_2 population. It takes into account absolute range in segregating population in relation to parental mean difference. It provides objective means to select segregating populations with better breeding potential (Koide *et al.*, 2019).

$$TSI = \frac{\text{Absolute range in } F_2 \text{ and } F_3 \text{ population}}{\text{Trait mean difference between parents}}$$

b. Usefulness index

Breeding potential of the crosses varies with the trait studied and with the statistic used. Hence, it is necessary to use a comprehensive statistic to assess breeding potential of crosses such as usefulness index (U_I), which is an objective tool for selecting early segregating population with better breeding potential to derive superior RILs for use as pure-line cultivars (Melchinger, 1987).

$$U_I = \text{Trait mean} + \left(k \times \frac{\sigma^2_A}{\sigma_P}\right)$$

Where, k =standardized selection differential at different selection intensities; $k=2.67$ and 2.06 at 1% and 5% selection intensities, respectively (Bernardo, 2020); σ^2_A = additive genotypic variance; σ_P =phenotypic standard deviation

c. Prediction of frequency of transgressive RILs

Frequency of transgressive RILs is calculated in early segregating generations such as $F_{2,3}$ by estimating the quantitative genetic parameters, like mid-parental value (m), additive gene effects [a] and additive variance (σ^2_A).

The above-mentioned descriptive statistics helps to decide upon the best breeding population. Cross with high quantitative traits means, absolute range, standardized range, phenotypic coefficient of variation (PCV), TSI and U_I and predicted frequency of transgressive RILs in early segregating generations was considered as the one with better breeding potential.

But there is ambiguity in the choice of best breeding population, since ranking of the crosses in terms of breeding population varies with the trait and statistics used. Among all the estimates, U_I provides most promising results in selection of best breeding population as it is a summary statistic that considers first order statistics (traits means, absolute range, and standardized range) and second order statistics such as absolute variance and PCV. These statistics helps in implementing selection among a large number of segregating populations developed in breeding programs and helps in forwarding only few crosses to the later generations there by leading to effective utilization of resources.

Conclusion

In self pollinated crops, where development of hybrids is costly and difficult, we can employ pure-lines as the best cultivar option. Selection of best parents and making best \times best crosses, selecting potential breeding population will increase the efficiency of breeding program. Statistics such as TSI and U_1 provides objective assessment and helps in isolating superior RILs which can be further employed as cultivars. The quantitative genetic parameters need to be used in combination to obtain best results. This strategy leads to focus-based breeding where poor/inferior crosses are discarded and focus will be laid on to the few best crosses. Thereby breeding will move from a trial-and-error method to strategy/planning-based phenomenon.

References

- Ashwini, K. V. R., Ramesh S. and Sunitha, N. C.(2021). Comparative BLUP, YREM-based performance and AMMI model-based stability of horse gram [*Macrotyloma uniflorum* (Lam.) Verdc.] genotypes differing in growth habit. Genetic Resources Crop Evolution, <https://doi.org/10.1007/s10722-020-01089-x>
- Bernardo, R.(2020). Breeding for quantitative traits in plants. Third Edition. *Stemma Press*. Woodbury, Minnesota, USA.
- Chahota, R. K., Kishore, N., Dhiman, K. C., Sharma, T. R. and Sharma S. K. (2007). Predicting transgressive segregates in early generation using single seed descent method-derived micro-macrosperma gene pool of lentil (*Lens culinaris* Medikus). *Euphytica*, **156**: 305-310.
- Koide, Y., Sakaguchi, S., Uchiyama, T., Ota, Y., Tezuka, A., Nagano, A. J., Ishiguro, S., Takamura, I. and Kishima, Y. (2019). Genetic Properties Responsible for the Transgressive Segregation of Days to Heading in Rice. *G3 Genes Genomes Genetics*, **9(5)**: 1655-1662.
- Melchinger, A. E.(1987). Expectation of means and variances of testcrosses produced from F_2 and backcross individuals and their selfed progenies. *Heredity*, **59**: 105-115.
- Witcombe, J. R., Gyawali, S., Subedi, M., Virk, D. S. and Joshi, K. D.(2013). Plant breeding can be made more efficient by having fewer, better crosses. *BMC Plant Biol.*, **13(1)**: 1-12.

