

**IMPROVEMENT OF YELLOW PASSION FRUIT (*Passiflora edulis* F. *flavicarpa*) THROUGH RECURRENT SELECTION**

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**ABSTRACT**

A study was carried out to develop a series of improved yellow passion fruit selections by recurrent selection. In the first phase, genetic parameters of 62 clones selected from seven orchards were estimated in a randomized complete block design with two replications. Genetic variation among clones was indicated by high broad sense heritability for yield and fruit weight. By selection of 18 highest yielding clones, a genetic gain of +35.2% was expected for total yield with minor changes in average fruit weight, soluble solids and percent pulp. In the second phase, eighteen half-sib progenies originating from the recombination of 18 selected clones were evaluated in a randomized complete block design with two replications and five plants per plot. Estimates of the genetic parameters and correlations as well as the genetic gains observed allowed the selection of 13 superior progenies of passion fruit. Selection among and within half sib families has been adopted. This strategy constitutes an alternative of accumulating genetic gains in yellow passion fruit and increasing the efficiency of the selective process.

**Key words:** Yellow passion fruit, Genetic gain, Recurrent selection, Heritability

**INTRODUCTION**

The passion fruit is a member of the family Passifloraceae which contains 12 different genera and approximately 500 species (Marte, 1991). The majority of *Passiflora* species are indigenous to the tropical and sub-tropical regions of South America and Brazil is the centre of diversity of the Passifloraceae (Cunha, 1996). Of the known species of *Passiflora* about 50 or 60 bear edible fruits. The main economically important species are *Passiflora edulis* F. *Flavicarpa*, the yellow passion fruit and *Passiflora edulis* F. *Eduilis*, and the purple passion fruit.

The yellow passion fruit *P. Edulis* is widely cultivated in Sri Lanka. The average annual production of the country is 500 mt and the productivity is very low being around 3-4 mt/ha. Some of the barriers to crop expansion are lack of high yielding and high quality lines and an absence of a verifiable source of quality seed material which is uniform and exhibiting some level of tolerance to pests and diseases. The genetic improvement becomes essential to overcome the limiting factors, such as the low productivity.

Self-incompatibility of yellow passion fruit hinders the selection of a single high yielding variety. However exploiting the self-compatibility was thought to be a useful approach, but, did not produce useful types (Menzel *et al.*, 1989). Passion fruit breeding can be done by methods that increase the favourable alleles through selection procedures such as mass selection, selection with progeny testing, but, also by heterosis enhancement with hybrids, synthetic or composite varieties (De Lira *et al.*, 2016).

Some studies that have been developed until now have focused on selection alternatives (Gonçalves *et al.*, 2007) and genetic parameters (Moraes *et al.*, 2005; Viana *et al.*, 2003; 2004). Recently, systematic breeding programmes resulted in the development of highly productive cultivars (synthetic populations) to fulfil the needs of the Brazilian juice industry. Thus, the work of Maulf *et al.* (1989) resulted in the selection of a highly productive synthetic population with large fruits and pulp content of about 45%. Melletti *et al.* (2000) obtained a series of improved yellow passion fruit selections by recurrent selection. The Ministry of Agriculture (MOA), IICA and CARDI in Dominica developed a composite (M-I-C Selection) with high yields seed and Juice quality for farmers in 1989 (Bridgemohan, 1993).

The breeding program of passion fruit at the Fruit Research and Development Institute, Horana (FRDI), Sri Lanka began in 2008 with the collection of various genotypes from larger commercial cultivations from the Low Country Wet Zone (LCWZ) in Sri Lanka. The variability observed in the cultivations which associated with seed multiplication and open pollination were allowed very gentle mass selection in the field. Mass selection, based on the visual observation of the plant phenotype, allows identifying potentially

interesting individuals for an improvement program. It has been widely used as a source of commercially desirable genes, including by some producers, who develop their own selections (Oliveira, 1980). Thus, the pioneer research work was based on clonal selection. Further, recurrent selection was performed based on the results obtained by different passion fruit improvement programmes (Goncalves *et al.*, 2005; Silva *et al.*, 2009; Maluf *et al.*, 1989). This method improves the population performance continuously and progressively, by increasing the frequency of favourable alleles of the traits under selection, maintaining the genetic variability that allows genetic gains in subsequent cycles.

## MATERIALS AND METHODS

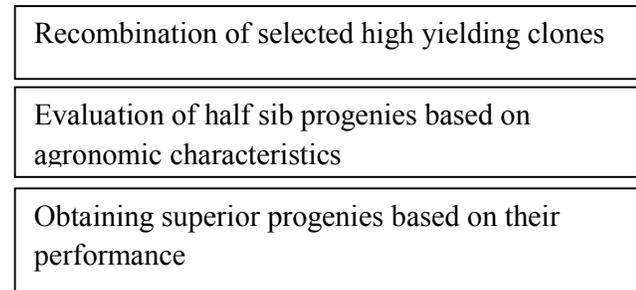
The experiment was conducted at the FRDI, Horana. In the first phase of the experiment, genetic variability of 62 clones were assessed to study the inheritance of characters which allow the prediction of gains obtained with the selection based on an assessment of breeding value. In the second phase half-sib progenies originating from the recombination of selected clones were evaluated to estimate the genetic parameters and correlations as well as the genetic gains to select superior progenies of passion fruit. The two phases of the experiment series were discussed separately. The Figure 1 shows the experimental series of yellow passion fruit improvement programme adopted in this study.

### Phase 1

Base population of large number of clones
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Mass selection of high yielding clones
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## Phase 2



**Figure 1. Experiment series of yellow passion fruit improvement programme.**

## Phase 1: Base population

The base populations for individual plant selections belonged to commercial orchards located in the LCWZ of Sri Lanka where the majority of passion fruit cultivations are distributed. Seven orchards were sampled varying in size from 200 plants to 1,500 plants each. The total number of plants in these seven orchards was estimated to be 8,000. All populations were subjected to mass selection and a total of 62 plants were selected on the basis of phenotypic superiority relative to the orchard mean as observed on the day of sampling. Stem cuttings of selected plants were taken and propagated at the FRDI.

## Mass selection

Rooted cuttings were transplanted in the field in a randomized complete block design with 62 treatments and 2 replications. Spacing was 2m between rows, with 4.5 m between plants within a row. Each plot comprised five plants of same clone. Recommendations of the Department of Agriculture were practiced and irrigation was supplied whenever necessary.

## Data collection

Data were collected during a period of one year from the first harvest starting in October 2009 to November 2010. Number of fruits and total yield (kg) were recorded on a plant basis at each harvest. The average fruit weight per plant was calculated as the ratio between total yield and the total number of fruits. Percent soluble solids and percent pulp were measured on a fruit basis

### **Estimation of variance components**

The genotypic ( $V_G$ ) and environmental ( $V_E$ ) components of variance were estimated by equating the mean squares of variation in the ANOVA table to their respective expected mean squares, as described by Becker (1984). These estimates of  $V_G$  and  $V_E$  were used in the estimation of broad sense heritabilities both on a single-plant basis ( $H^2$ ) and on a clonal mean basis ( $H^2_m$ ). The standard errors associated with the estimates of  $V_G$ ,  $V_E$ ,  $H^2$  and  $H^2_m$  were estimated according to Hallauer and Miranda (1981). Genetic coefficients of variation ( $CV_G$ ) were calculated as the ratio between the genotypic standard deviation and the mean of all clones. Genetic gains obtained by selection of the 20 highest yielding clones were calculated by the Formulas

$$\text{GAIN} = (Y_{18} - Y_{\text{all}}) \times H^2_m$$

Where

$Y_{\text{all}}$  = average of all clones

$Y_{18}$  = average of the 18 high yielding clones

$H^2_m$  = broad sense heritability on a clonal mean

Genotypic correlations among the traits under consideration were estimated as indicated by Hallauer and Miranda (1981).

### **Phase II: Recombination and progeny testing**

Eighteen progenies of half-siblings from the recombination of the clones selected during 2010 were evaluated in the design of Comstock & Robinson (1948). This recombination was done using maternal half-siblings, where the mother was the own progeny selected and the father was the pollen mixture of all the selected progenies. Thus, the progenies evaluated represent the work population for the conduction of the second selection cycle. 18 progenies were evaluated in the randomized complete block design with two replications and five plants per plot. Spacing was 2m between rows, with 4.5 m between plants within a row. Recommendations of Department of Agriculture were practiced and irrigation was supplied whenever necessary.

The progenies were evaluated from March 2011 to April 2012, measuring the following characteristics: early yield (EY) , evaluated from the first harvest to 10 weeks, average number of fruits per plant (NF), evaluated by the visual count of the number of fruits per plant, from the first harvest, average weight of fruits in grams (FW), obtained by digital weighing, sampling fifteen fruits per plant; average length of fruits in centimetres (FL), obtained by measurements of the longitudinal dimensions of fruits with vernier calliper, sampling fifteen fruits per plant; Average fruit width in centimeters (FWT), obtained through cross-sectional measurements of fruits with vernier calliper, sampling fifteen fruits per plant; Average thickness of peel in millimetres (PT), obtained by means of four points of the outer shell in the median portion of the fruits with vernier calliper, sampling fifteen fruits per plot.

To verify the existence of genetic variability among the progenies studied, a variance analysis was performed and the genetic parameters of the population were estimated. For such procedures, the Genes computational program (Cruz, 2006) was used. The statistical model used was  $Y_{ij} = m + g_i + b_j + \varepsilon_{ij}$ , where  $Y_{ij}$  = observation regarding the progeny  $i$  in block  $j$ ,  $m$  = general mean,  $g_i$  = effect of progeny  $i$ ,  $b_j$  = effect of block  $j$  and  $\varepsilon_{ij}$  = error associated with observation.

To calculate the correlation coefficients between pairs of characteristics the expressions as Cruz & Regazzi (2001) were used where  $r_f = \text{COV}_{F(X, Y)} / \sigma_{FX} \sigma_{FY} = \text{VOC}_{G(X, Y)} / \sigma_{GX} \sigma_{GY}$  where:  $\text{COV}_{F(X, Y)}$  and  $\text{VOC}_{G(X, Y)}$  correspond respectively to the phenotypic and genotypic covariance between  $x$  and  $Y$  characteristics;  $\sigma_{FX}$  and  $\sigma_{GX}$  correspond to the standard deviation phenotypic and genotypic characteristic  $x$ ;  $\sigma_{FY}$  and  $\sigma_{GY}$  correspond to the standard deviation phenotypic and genotypic feature  $Y$ .

For the estimation of the predicted genetic gains, the selection index of Mulamba & Mock (1978) was used in addition to the direct selection in the evaluated characteristics. This index consists of progenies rank in relation to each of the characteristics in order to improve favourable, so the orders

regarding the characteristics are added to each progeny obtaining the sum of ranks. Thus, the lower the value obtained, the better the performance of a progeny in relation to the various characteristics studied (Cruz & Regazzi, 2001).

## RESULTS AND DISCUSSION

### Phase 1

The estimates of values of genotypic ( $V_G$ ) and environmental ( $V_E$ ) variances, broad sense heritability, and genotypic coefficient of variation for the traits under study are shown in table 1. The selected 18 clones have considerable genetic variation for total yield, number of fruits per vine and average fruit weight, as indicated by the significant estimates of  $V_G$  obtained.

**Table 1. Variance components, broad sense heritability and genetic coefficient of variation of selected traits in passion fruit.**

Trait	Variance components		Broad sense heritability		Genetic co-efficient of variation
	$V_G$	$V_E$	$H^2$	$H^2_m$	
Total yield (kg/ha)	23.542	14.342	0.723	0.812	97.6%
Number of fruits/vine	25.76	19.57	0.465	0.492	43.7%
Average fruit weight (g)	415.27	46.34	0.921	0.986	29.5%
Brix%	1.6843	1.5642	0.598	0.612	10.6%
Pulp%	55.678	142.132	0.421	0.497	11.9%

Broad sense heritability both at the single plant ( $H^2$ ) and clonal mean ( $H^2_m$ ) levels, and genetic coefficient of variation were high for yield and average fruit weight, indicating a favourable condition for selection for these traits. Total yield and average fruit weight proved to be highly heritable trait

with broad sense heritability estimates higher than 0.8. Direct selection for these traits should result in rapid genetic progress.

Total yield showed a significant positive correlation ( $r=0.65$ ) with average fruit weight followed by number of fruits/vine. (Table 2). Selection for larger fruits would also increase total yield. Genotypic correlation between total yield and fruit length, fruit width, percent pulp and brix% were generally low indicating that genetic gains in yield can be achieved without major changes in the other traits.

**Table 2. Genotypic correlation between economic traits in passion fruit.**

Character	TY	NF	FW	FL	FWT	BX%
NF	0.4567					
FW	0.6574**	0.3176				
FL	0.1323	0.2362	0.5432*			
FWT	0.1654	0.3244	0.4521	0.2354		
BX%	0.1291	0.0546	0.0643	0.0124	0.008	
PU%	0.1456	-0.1234	0.0567*	0.435*	0.3256	-.0432

Note: TY- Total yield (kg/vine), NF- Number of fruits/vine. FW-Average fruit weight (g), FL- Fruit Length (cm), FWT (Fruit width) and BX% (brix%) and PU%- Pulp%; \* and \*\* significant at 5% and 1%, respectively.

Table 3 indicates the expected genetic gains obtained by direct selection of the 24 highest yielding clones and the indirect genetic gains obtained for average fruit weight, total soluble solid sand percent pulp. A considerable genetic gain of +35.2% is estimated for total yield. Average fruit weight, total soluble solids and percent pulp remained essentially unchanged. The genetic gain anticipated by selection and direct utilization of 24 clones was 29% for yield and 89% for early yield (Maulf *et al.*, 1989)

### Phase 11

The mean squares showed significant genetic variability by the F test for early yield and average fruit weight at 1% probability and 5% probability for number of fruits per vine, fruit length, fruit width, and pulp % indicating the possibility of selection of superior progenies (Table 4). The experimental

precision, evaluated through the coefficient of variation (CV), ranged from 4.5% to 18.3% and are in agreement with the values obtained by Gonçalves *et al.* (2007), Moraes *et al.* (2005) and Viana *et al.* (2004).

**Table 3. Genetic gain for total yield obtained by selection of the 13 highest yielding passion fruit clones.**

Character	Population mean	Mean of the 13 highest yielding clones	Selection differential	Genetic gain	% genetic gain
Total yield (t/ha)	16.6	23.8	6.2	+5.03	35.2
Number of fruits/vine	148	176	28	+13.78	9.3
Average fruit weight (g)	112.7	135.5	22.8	+22.4	19.9
Brix%	16.7	17.2	0.5	+0.306	1.8
Pulp%	50.4	54.8	4.4	+2.18	4.32

**Table 4. Variance analysis for agronomic characteristics of yellow passion fruit and some important genetic parameters associated.**

Source of variation	DF	Early yield kg/vine	Mean squares				Pulp %
			Number of fruits/vine	Average fruit weight (g)	Fruit length (cm)	Fruit width (cm)	
Blocks	1	453781	398765	47685	28743	1786	1284
Progenies	18	234156**	156438*	654387**	21768*	13268*	19643*
Residue	25	126543	108634	167954	10532	5643	4532
Average		15.3	76.54	164.3	6.9	6.6	51.8
CV%		18.3	14.8	10.7	8.5	6.6	4.5
H <sup>2</sup>		72.6	54.3	78.9	62.1	67.3	48.7

Note: \* Significant at 5% level    \*\* Significant at 1% level

Estimates of the coefficients of heritability presented values from 48.7% to 78.9%. For all characteristics, the values found are in accordance with those observed in other studies (Gonçalves *et al.*, 2007; Moraes *et al.*, 2005; Viana *et al.*, 2004) and indicate the possibility of selecting genetically superior progenies. The knowledge of the correlation between two characters is of fundamental importance in the improvement of any culture, since it facilitates the selection process in characters those are difficult to measure and identify or that have low heritability (Cruz & Regazzi, 2001).

**Table 5. Estimates of the phenotypic ( $r_f$ ) and genetic ( $r_g$ ) correlation coefficients between characteristics of passion fruit.**

Character		Correlations					
		NF	FW	FL	FWD	PT	PU%
EY	$r_f$	0.6675**	0.7234**	0.1765	0.2341	0.2111	0.2317
	$r_g$	0.6435*	0.7128*	0.1265	0.1998	0.1275	0.1476
NF	$r_f$		-0.2134	-0.1765	-0.1657	0.0932	0.1537
	$r_g$		-0.1276	-0.0987	-0.1254	0.0876	-0.1327
FW	$r_f$			0.8254**	0.8769**	0.6345*	0.9345**
	$r_g$			0.7982**	0.9012**	0.5498*	0.8465*
FL	$r_f$				0.6394*	-0.1654	0.8732**
	$r_g$				0.5437*	-0.1543	0.7932**
FWD	$r_f$					0.0432	0.6754*
	$r_g$					0.3253	0.7832*
PT	$r_f$						-0.4536
	$r_g$						-0.5436

Note: EY- Early yield (kg/vine), NF- Number of fruits/vine. FW-Average fruit weight (g), FL- Fruit Length (cm), FWT (Fruit width) and PU%- Pulp%; \* Significant at 5% level; \*\* Significant at 1% level.

Table 5 shows the estimates of coefficients of genetic and phenotypic correlations among the pairs of characteristics studied. The genetic correlation between early yield and average fruit weight was significant and high (0.71) followed by number of fruits per vine (0.64). Viana *et al.* (2003) found a positive correlation between number of fruits and average fruit weight for the Campos environment. According to Table 5, positive correlations were found between fruit weight and other characters indicating that progenies with higher

fruit weight tend to have larger fruits with higher pulp content. Table 6 shows the estimates of genetic gains predicted by means of the truncated selection and the use of selection index, considering two gain simulations. Five superior families were selected by the index GS<sub>1</sub> and another (GS<sub>2</sub>) selected 13 superior individuals.

It can be observed that the direct gains for each individual characteristic were higher than those obtained by the selection index. The predicted genetic gains are directly proportional to the selection differential that is, the lower the selection differential, the lower the genetic gain, since the number of selected is increased, contributing to the decrease of the mean value. Thus, both direct and index-based gains are greater when one considers the selection of the top five families.

**Table 6. Estimates of predicted genetic gains for 18 progenies of half sibs in yellow passion fruit.**

Character	Direct selection		Selection index	
	GS <sub>1</sub>	GS <sub>2</sub>	GS <sub>1</sub>	GS <sub>2</sub>
Early yield	3.56	2.59	3.21	2.31
Number of fruits/vine	3.02	2.78	2.93	2.18
Fruit weight (g)	5.67	3.68	3.78	3.01
Fruit length (cm)	1.85	0.95	1.13	0.67
Fruit width (cm)	2.03	1.83	1.96	0.74
Peel thickness (mm)	1.05	0.78	0.95	0.32
Pulp%	2.84	1.27	2.42	1.05

GS<sub>1</sub> and GS<sub>2</sub> selection gain in percentage, considering of 5 and 13 families respectively

It was verified that, for the selection of the 13 progenies, the index-based genetic gains were close to the direct selection, except for peel thickness, where the gains were smaller (table 6). Silva *et al.* (2009) found that for the selection of eight progenies the index based genetic gains were close to the direct selection except for fruit length and the peel thickness. When the selection of the 13 best performing materials was considered, the objective was the continuity of the recurrent selection program. Seeds from the 13 best individuals obtained from the best families are used in the second cycle.

## CONCLUSIONS

Genetic variability of 62 clones selected from seven orchards revealed a high level of heritability for early yield and fruit weight of passion fruits. By selection of 18 high yielding clones, a genetic gain of +35.2% was achieved for total yield with minor changes in average fruit weight, soluble solids and percent pulp. In the second phase, the genetic parameters and correlations as well as the genetic gains were estimated in 18 half sib families. Thirteen best families were selected according to both direct and index-based genetic gains.

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