

Performance of bi-clonal DxP planting material at United Plantations Berhad¹

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Abstract

A progeny testing trial was set up in October 1999 to evaluate the performance of 36 bi-clonal DxP progenies on coastal soils at Ulu Bernam Estate in Lower Perak Region. Results on ANOVA revealed that a highly significant difference among progenies for bunch number and average bunch weight ($P < 0.01$), while for ffb yield, it was only significantly different at $P < 0.05$. There was also a highly significant year and genotype \times year effects at $P < 0.01$ for all the yield and yield components traits. Results had shown that the mean ffb yield for 36 progenies was $183.6 \text{ kg p}^{-1} \text{ y}^{-1}$, with a range from $166.8 \text{ kg p}^{-1} \text{ y}^{-1}$ to $205.9 \text{ kg p}^{-1} \text{ y}^{-1}$.

Based on yearly performance, the mean ffb yield was lowest at 132.7 kg p^{-1} (range: 95.1 kg p^{-1} to 175.2 kg p^{-1}) in year 1, to the highest of 223.8 kg p^{-1} (range: 132.3 kg p^{-1} to 303.6 kg p^{-1}) in year 6 of recording.

Results on ANOVA for vegetative traits indicate significant difference ($p < 0.05$) among progenies for height increment and petiole cross section, but not for frond length. The mean height increment for progenies was 0.45 m y^{-1} with a range of 0.4 m y^{-1} to 0.5 m y^{-1} . The mean frond length was 5.9 m (range: 5.6 m to 6.2 m), while the mean for petiole cross section was 39.5 cm^2 (range: 34.4 cm^2 to 45.3 cm^2).

Results on ANOVA for bunch and fruit components had shown a highly significant difference ($p < 0.01$) among progenies for bunch weight, % kernel to bunch, fruit weight, % shell to fruit, % kernel to fruit, % mesocarp to fruit, % oil to mesocarp, % oil to dry mesocarp and % oil to fruit. The mean % oil to bunch for 36 progenies was 28.1% (24.0% OER) with a range of 25.9% to 29.7%.

Low phenotypic coefficients of variation (pcv) and genotypic coefficients of variation (gcv) values were recorded for ffb yield, palm height increment, frond length, petiole cross section, % oil to bunch, % fruit to bunch and fruit weight, less than 10%.

High broad sense heritability values was noted for bunch number, average bunch weight, % mesocarp to fruit and % shell to fruit, exceeding 80%.

High oil yield has shown to be obtained with planting bi-clonal DxP seeds with an estimated oil yield production of 6.5 t ha^{-1} over 6 years of harvesting.

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Introduction

The oil palm (*Elaeis guineensis*) being the major plantation crop in Malaysia had contributed a sum RM 49.6 billion (www.palmoilhq.com) to the export income for the country in 2010. In 2010, the country average oil yield ha⁻¹ was at 3.69 ton and average ffb yield ha⁻¹ of 18.03 ton (econ.mpob.gov.my). The constant demand for more oil with an ever increasing global population and restrictions on land space, strains the breeders and agronomists to find ways of increasing total output of oil per hectare. To date, one of the most effective methods has been the utilization of the high quality hybrid planting materials. One of the possible approaches is through cloning of parent palms using tissue culture techniques, with end products being dura and pisifera clones. These clones are then evaluated in trials and only the best performance palms are selected for crossing in production of clonal DxP seeds. The strategy to produce clonal seeds has been well explained by Jacquemard et al., (1999). The first paper on semi-clonal DxP was presented by P. Verappan et al., (2000) at the International ISP conference in Kuala Lumpur, highlighting the performance this material at Sime Darby Plantations. Based on this, it is possible to produce the planting material using the concept of cloning one or both parents for production clonal DxP seeds. At United Plantations Berhad (UPB), both bi-clonal and semi-clonal programmes were initiated in the 1980s, and have now been successfully produced clonal DxP seeds for commercial plantings. This paper aims to elaborate the performance of UPB's biclonal DxP planting materials tested on coastal soils.

Materials and Methods

Dura clones

The dura clones were derived by culturing dura mother palms which were used in commercial DxP seed production in 1988. A total of 3 dura clones (B24, B26 and B29) were derived from three different dura mother palms and field planted in 1993 at Jendarata Estate. The source of ortets for clones B26 and B29 was a combination of Ulu Remis and Banting deli dura of some Serdang Avenue genes (Rosenquist,1999), whereas for clone B24, it was a combination genes of Ulu Remis and Marihat Baris.

Pisifera clones

The pisifera clones were also cultured in 1988 and field planted in 1993 at Jendarata Estate. Two pisifera clones were created and coded as B25 and B27. The pisifera source is Yangambi origin for clone B25 and INEC-AVROS genes combination for clone B27.

Bi-clonal DxP progenies

A sample of 33 palms from 3 dura clones were crossed with four pisifera palms of two pisifera clones to form a group of 36 bi-clonal DxP progenies (Table 1) to use in this progeny testing trial.

Experimental design

The trial was set up in October 1999 at Ulu Bernam Estate at Lower Perak Region. The bi-clonal DxP progenies were arranged in Randomised Complete Block Design (RCBD) in three replications. Plot size was 16 palms plot⁻¹ and spaced at 29 feet in equilateral triangle to form a planting density of 148

palms ha⁻¹. The soil type of the trial area was of Bria Series, a variety of coastal soil commonly found in Peninsular Malaysia. Maintenance of the trial was as UPB estate practice.

Data collection

Fresh fruit bunch (ffb) yield and its components were recorded for a period of six years from 2002 to 2008. Vegetative palm data were collected once in 2011, when palms were at 12 years of age. Bunches from individual palms of each progeny were subjected to bunch analysis throughout the trial period from 2003 to 2008.

Data analysis

All data of yield, vegetative and bunch analysis were subjected to a statistical analysis using PROC GLM and PROC VARCOMP (SAS 9.1). Plot mean data was utilized in data analysis for yield and its components as well as vegetative traits. However, this was not possible for data of bunch analysis as there were insufficient samples collected from certain plots.

Estimation on phenotypic coefficients of variation (pcv) and genotypic coefficients of variation (gcv) were in accordance to methods suggested by Singh and Chaudhry (1977). As for estimation of phenotypic variance (σ^2_{ph}), genotypic variance (σ^2_G) and broad sense heritability (h^2_B) were calculated based on formula by Lukhele and Obilana (1984).

Results

FFB yield and yield components

Analysis of variance (ANOVA) in Table 2 revealed that a highly significant different among progenies for bunch number and average bunch weight at $P < 0.01$, whereas for ffb yield, it was only significant at $P < 0.05$. Highly significant year and genotype x year effects at $P < 0.01$ was also noted for all the yield traits.

Mean ffb yield for 36 progenies was 183.6 kg p⁻¹y⁻¹, with a range from 166.8 kg p⁻¹y⁻¹ to 205.9 kg p⁻¹y⁻¹ (Table 3). Estimated mean ffb yield for the six years of all progenies was 27.2t ha⁻¹ (range: 24.7t ha⁻¹ to 30.5t ha⁻¹). The mean bunch number was 19.4 p⁻¹, whereas mean for bunch weight was 10.7 kg (Table 3). It was also noted that both PCV and GCV for ffb yield was low (< 10%), whereas moderate PCV and GCV (< 18 %) was recorded by bunch number and bunch weight (Table 3).

Based on yearly performance, mean ffb yield was lowest at 132.7 kg p⁻¹ (range: 95.1 kg p⁻¹ to 175.2 kg p⁻¹) in year 1, to highest of 223.8 kg p⁻¹ (range: 132.3 kg p⁻¹ to 303.6 kg p⁻¹) in year 6 of recording (Table 4). A similar trend was also showed by average bunch weight. For bunch number, highest number (27.4) was recorded in year 2 and lowest (14.7) was in year 6 of production (Table 4).

Variance components analysis on ffb yield had shown a trend of decreasing order as year variance (σ^2_y) > error variance (σ^2_e) > genotype x year variance (σ^2_{gy}) > genotype x replicate variance (σ^2_{gr}) > genotype variance (σ^2_g) > replicate variance (σ^2_r). For bunch number, the order was year variance (σ^2_y) > genotype variance (σ^2_g) > error variance (σ^2_e) > genotype x year variance (σ^2_{gy}) > replicate variance (σ^2_r) > genotype x replicate variance (σ^2_{gr}). Whilst the order for average bunch weight was

year variance (σ^2_y) > genotype variance (σ^2_g) > error variance (σ^2_e) > genotype x replicate variance (σ^2_{gxr}) > genotype x year variance (σ^2_{gxy}) > replicate variance (σ^2_r) (Table 5).

It was noted that broad sense heritability estimates were in decreasing order as bunch number > average bunch weight > ffb yield (Table 6). The values were from 28.8% to 90.4%.

Height increment, frond length and petiole cross section

Results on analysis of variance for height increment, frond length and petiole cross section is shown in Table 7. Among progenies, a significant different at $p < 0.05$ was detected for height increment and petiole cross, but not for frond length.

Mean height increment for progenies was 0.45 m y^{-1} with a range of 0.4 m y^{-1} to 0.5 m y^{-1} . Mean frond length was 5.9 m with a range from 5.6 m to 6.2 m , whereas mean for petiole cross section was 39.5 cm^2 with a range from 34.4 cm^2 to 45.3 cm^2 (Table 8). Both PCV and GCV for all 3 vegetative traits were at low values with less than 10%.

Low genotypic variance has shown as compared to error variance for all 3 vegetative traits (Table 9). Moderate heritability values were recorded by all three traits with the order as petiole cross section > height increment > frond length.

Bunch and fruit components

Results on analysis of variance for bunch and fruit components are shown in Table 11. It was noted that a highly significant difference ($p < 0.01$) among progenies for bunch weight, % kernel to bunch, fruit weight, % shell to fruit, % kernel to fruit, % mesocarp to fruit, % oil to mesocarp, % oil to dry mesocarp and % oil to fruit, whereas % fruit to bunch and % oil to bunch recorded significantly different at $p < 0.05$.

Means, range, PCV and GCV for bunch and fruit components is shown in Table 12. For bunch components, it was shown that mean bunch weight was 14.3 kg (range: 10.5 kg to 17.8 kg), mean % fruit to bunch was 65.8% (range: 61.0% to 68.6%), mean % kernel to bunch was 5.0% (range: 4.1% to 6.1%) and mean % oil to bunch was 28.1% or 24% OER (range: 25.4% to 29.7%). For fruit components, it was indicated that mean fruit weight was 11.2 g (range: 9.5 g to 13.6 g), mean % mesocarp to fruit was 82.5% (range: 78.2% to 86.5%), mean % shell to fruit was 9.9% (range: 7.2% to 13.8%), mean kernel to fruit was 7.6% (range: 6.3% to 8.9%), mean % oil to mesocarp was 51.7% (range: 49.0% to 55.3%), mean % oil to dry mesocarp was 76.7% (range: 74.9% to 78.6%) and mean % oil to fruit was 42.7% (range: 39.7% to 45.1%). For PCV and GCV values, there were generally low with less than 10% for most of traits, except for bunch weight and % shell to fruit which was exceeding 10%.

Relatively low genotypic variance values were noted as compared to error variance for bunch weight, % fruit to bunch, % kernel to bunch, % oil to bunch, fruit weight, % kernel to fruit, % oil to mesocarp, % oil to dry mesocarp and % oil to fruit. Whereas moderate values were recorded for % mesocarp to fruit and % shell to fruit (Table 13).

High heritability values were indicated for % mesocarp to fruit (84.8%) and % shell to fruit (89.83%), and moderate heritability values were noted for bunch weight (69.41%), % kernel to bunch (60.94%), fruit weight (67.65%), % kernel to fruit (51.36%), % oil to mesocarp (67.82%), % oil to dry mesocarp

(65.21%) and % oil to fruit (57.48%). Low heritability values were recorded for % fruit to bunch (35.13%) and % oil to bunch (30.85%).

Discussion

The significant different among progenies for yield and yield components, petiole cross section, palm height increment and some bunch and fruit components traits, infer that the performance of progenies are not equal due to differences in genetic makeup of the progenies, as the materials were derived from combination genes of 3 dura and 2 pisifera clones.

The significant year and genotype x year effects on yield and yield components for the progenies indicated some degree of environment factors influencing the performance.

A similar finding was reported by Lee and Donough (1993) in their study on oil palm clones planted at different locations.

Relatively, a good first year yield performance with an estimated ffb yield of 19.6 t ha⁻¹ has been achieved, with an average yield of 27 t ha⁻¹ recorded over 6 years of yield recording. The 6th year of recording recorded the highest mean yield of 33 t ha⁻¹. The yield trend appeared to be similar as compared to the earlier yield pattern in DxP materials (Hartley, 1977), but the different was bi-clonal DxP recorded better yield performance.

Bi-clonal DxP progenies had shown a good oil to bunch (O/B) with a mean value of 28% which is 3% higher than the SIRIM Standard requirement of 25% for commercial DXP materials. Higher oil yield can be gained by planting bi-clonal DxP materials as produced by United Plantations Berhad. By calculation, the estimated oil yield production at yearly basis were in a range of 4.7 t ha⁻¹ to 7.9 t ha⁻¹, and its overall mean was at 6.5 t ha⁻¹. This oil yield production was 76.2% higher than the national average for oil yield production of 3.69 t ha⁻¹ as recorded in 2010 (econ.mpob.gov.my).

Low PCV and GCV values were recorded by most of traits such as ffb yield, height increment, frond length, petiole cross section, % oil to bunch, % fruit to bunch and fruit weight with value less than 10%. This indicates uniformity or less variability among the progenies. A similar result was obtained from Deli-AVROS material as reported by Musa (2004).

High broad sense heritability were recorded on bunch number, average bunch weight, % mesocarp to fruit and % shell to fruit. It revealed that these traits are less influenced by the changes of environment or strongly controlled by genetic factors rather than the environment. A similar finding was reported by Musa (2004)

Conclusion

High ffb yield and high oil extraction rate (oer) are shown to be obtained with planting of bi-clonal DxP. Mean oil yield of 36 progenies recorded an average 6.5 t ha⁻¹ over 6 years of recording. It was also noted that less variability as indicated by less PCV and GCV values (<10 %) for most of traits under assessment.

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Table 1: List of the bi-clonal DxP progenies planted in trial 29.48

Progeny code	Female	Male	Number planted
1.3-771	1551/B24/22.11	39-22/B25/20	48
1.3-788	1545/B24/22.11	39-22/B25/20	48
1.3-775	1551/B24/22.11	37-21/B27/20	48
1.3-767	34-17/B26/20	39-22/B25/20	48
1.3-768	27-7/B26/20	39-22/B25/20	48
1.3-769	17-4/B26/20	39-22/B25/20	48
1.3-770	19-11/B26/20	39-22/B25/20	48
1.3-773	1270/B26/22.11	39-22/B25/20	48
1.3-778	26-28/B26/20	39-22/B25/20	48
1.3-784	17-9/B26/20	39-22/B25/20	48
1.3-790	25-28/B26/20	39-22/B25/20	48

Table 1: List of the bi-clonal DxP progenies planted in trial 29.48 (cont'd)

Progeny code	Female	Male	Number planted
1.3-764	27-19/B26/20	37-20/B27/20	48
1.3-765	1274/B26/22.11	37-19/B27/20	48
1.3-766	34-17/B26/20	37-20/B27/20	48
1.3-772	20-4/B26/20	37-20/B27/20	48
1.3-774	25-7/B26/20	37-21/B27/20	48
1.3-776	27-7/B26/20	37-21/B27/20	48
1.3-777	17-9/B26/20	37-19/B27/20	48
1.3-779	17-11/B26/20	37-21/B27/20	48
1.3-780	19-11/B26/20	37-21/B27/20	48
1.3-781	17-4/B26/20	37-21/B27/20	48
1.3-782	19-10/B26/20	37-20/B27/20	48
1.3-783	35-9/B26/20	37-20/B27/20	48

Table 1: List of the bi-clonal DxP progenies planted in trial 29.48 (cont'd)

Progeny code	Female	Male	Number planted
1.3-786	17-25/B26/20	37-19/B27/20	48
1.3-787	20-25/B26/20	37-19/B27/20	48
1.3-789	25-28/B26/20	37-21/B27/20	48
1.3-797	37-3/B29/20	37-20/B27/20	48
1.3-785	292/B29/22.11	37-19/B27/20	48
1.3-791	21-6/B29/20	37-19/B27/20	48
1.3-792	22-13/B29/20	37-21/B27/20	48
1.3-793	37-11/B29/20	37-21/B27/20	48
1.3-794	22-13/B29/20	37-19/B27/20	48
1.3-795	301/B29/22.11	37-19/B27/20	48
1.3-796	301/B29/22.11	37-20/B27/20	48
1.3-798	37-3/B29/20	37-20/B27/20	48
1.3-799	301/B29/22.11	37-21/B27/20	48

Table 2: Mean squares on ANOVA for FFB yield and yield components of bi-clonal DxP progenies in trial 29.48

Source of variation	Df	FFB p ⁻¹ y ⁻¹ (kg)	BNO p ⁻¹ y ⁻¹	BWT (kg)	FFB ha ⁻¹ y ⁻¹ (t)
Replication (R)	2	2062.893 **	44.924 **	0.823 ns	45.475 **
Progeny (G)	35	2160.917 *	184.503 **	38.067 **	47.294 *
Year (Y)	5	112523.504 **	2960.494 **	1938.688 **	2464.428 **
G x R	70	989.851**	5.347*	4.195 **	21.726 **
G x Y	175	721.543**	5.598 **	2.364 **	15.809 **
Error	355	304.307	3.437	1.006	6.657

** and *: significant at $p < 0.01$ and $p < 0.05$, respectively

Table 3: Means, range, PCV and GCV for FFB yield and yield components of bi-clonal DxP progenies in trial 29.48

Trait	Mean	Range	PCV (%)	GCV (%)
FFB p ⁻¹ yr ⁻¹ (kg)	183.6	166.8 - 205.9	6.50	3.49
BNO p ⁻¹ yr ⁻¹	19.4	15.4 - 25.3	17.78	16.89
BWT (kg)	10.7	8.3 - 12.7	13.91	12.81
FFB ha ⁻¹ yr ⁻¹ (t)	27.2	24.7 - 30.5	6.49	3.48

PCV = Phenotypic coefficients of variation and GCV = Genotypic coefficients of variation

Table 4: Mean FFB yield and yield components of bi-clonal DxP progenies from year 1 to year 6 in trial 29.48

Year	FFB p ⁻¹ y ⁻¹ (kg)	Range	BNO p ⁻¹ y ⁻¹	Range	BWT (kg)	Range	FFB ha ⁻¹ y ⁻¹ (t)	Range
1	132.7 f	95.1-175.2	23.9 b	15.7 - 35.5	5.6 f	4.1-7.5	19.6 f	14.1-25.9
2	176.1 d	128.2-227.2	27.4 a	20.6 - 35.6	6.6 e	4.4-9.0	26.1 d	19.0-33.6
3	169.9 e	120.5-216.2	19.6 c	12.0 - 28.5	8.9 d	6.3-12.2	25.1 e	17.8-32.0
4	184.9 c	134.8-253.2	15.9 d	10.3 - 24.8	12.1 c	8.7-16.3	27.4 c	19.9-37.5
5	213.8 b	142.1-294.3	14.7 e	9.0 - 20.3	15.2 b	9.9-20.3	31.6 b	21.0-43.6
6	223.8 a	132.3-303.6	14.7 e	10.1 - 21.5	15.6 a	9.8-21.3	33.1 a	19.6-44.9

Means with the same letter are not significantly different at $p < 0.05$

Table 5: Estimation of variance components for FFB yield and yield components of bi-clonal DxP progenies in trial 29.48

Components	FFB p ⁻¹ y ⁻¹ (kg)	BNO p ⁻¹ y ⁻¹	BWT (kg)	FFB ha ⁻¹ y ⁻¹ (t)
σ_y^2	1067.80	27.896	18.461	23.387
σ_r^2	0.00	0.349	0.00	0.00
σ_g^2	41.229	10.748	1.879	0.896
σ_{gr}^2	124.109	0.322	0.559	2.727
σ_{gy}^2	141.116	0.731	0.459	3.095
σ_e^2	304.307	3.438	1.006	6.657

σ_y^2 = Year variance, σ_r^2 = Replicate variance, σ_g^2 = Genotype variance, σ_{gr}^2 = Genotype x replicate variance, σ_{gy}^2 = Genotype x year variance and σ_e^2 = Error variance

Table 6: Phenotypic variance, genotypic variance and broad sense heritability for FFB yield and yield components of bi-clonal DxP progenies in Trial 29.48

Trait	σ_{ph}^2	σ_g^2	h_B^2 (%)
FFB $p^{-1} y^{-1}$ (kg)	142.665	41.229	28.89
BNO $p^{-1} y^{-1}$	11.894	10.748	90.36
BWT (kg)	2.214	1.879	84.86
FFB $ha^{-1} y^{-1}$ (t)	3.115	0.896	28.76

σ_{ph}^2 = Phenotypic variance, σ_g^2 = Genotypic variance and h_B^2 = Broad sense heritability

Table 7: Mean squares on ANOVA for height increment, frond length and petiole cross section of bi-clonal DxP progenies in trial 29.48

Source of variation	df	Height increment (m y ⁻¹)	Fond length (m)	Petiole cross section (cm ²)
Replication (R)	2	0.0006 ns	0.123 ns	271.951 **
Progeny (G)	35	0.004 *	0.074 ns	30.106 *
Error	70	0.002	0.048	16.714

** and *: significant at $p < 0.01$ and $p < 0.05$, respectively

Table 8: Means, range, PCV and GCV for height increment, frond length and petiole cross section of bi-clonal DxP progenies in trial 29.48

Trait	Mean	Range	PCV (%)	GCV (%)
Height increment (m y ⁻¹)	0.45	0.40 - 0.50	7.03	4.44
Fond length (m)	5.9	5.6 - 6.2	2.63	1.52
Petiole cross section (cm ²)	39.5	34.4 - 45.3	8.02	5.35

PCV = Phenotypic coefficients of variation and GCV = Genotypic coefficients of variation

Table 9: Estimation of variance components for height increment, frond length and petiole cross section of bi-clonal DxP progenies in trial 29.48

Components	Height increment (m y ⁻¹)	Fond length (m)	Petiole cross section (cm ²)
σ_r^2	0.000	0.002	7.089
σ_g^2	0.0004	0.008	4.464
σ_e^2	0.002	0.048	16.713

σ_r^2 = Replicate variance, σ_g^2 = Genotype variance and σ_e^2 = Error variance

Table 10: Phenotypic variance, genotypic variance and broad sense heritability for height increment, frond length and petiole cross section of bi-clonal DxP progenies in Trial 29.48

Trait	σ_{ph}^2	σ_g^2	h_B^2 (%)
Height increment (m y ⁻¹)	0.001	0.0004	40.0
Fond length (m)	0.024	0.008	33.3
Petiole cross section (cm ²)	10.035	4.464	44.5

σ_{ph}^2 = Phenotypic variance, σ_g^2 = Genotypic variance and h_B^2 = Broad sense heritability

Table 11: Mean squares on ANOVA for bunch and fruit components of bi-clonal DxP progenies in trial 29.48

Source of variation	df	BWT (kg)	% F/B	% K/B	% O/B	FWT (g)	% S/F	% K/F	% M/F	% O/WM	% O/DM	% O/F
Progeny (G)	35	82.679 **	50.254 *	4.872 **	19.094 *	16.201 **	75.842 **	7.696 **	110.007 **	48.184 **	22.057 **	41.507 **
Error	718	25.291	32.591	1.905	13.197	5.239	7.714	3.742	16.721	15.517	7.682	17.598

** and *: significant at $p < 0.01$ and $p < 0.05$, respectively

Table 12: Means, range, PCV and GCV for bunch and fruit components of bi-clonal DxP progenies in trial 29.48

Trait	Mean	Range	PCV (%)	GCV (%)
BWT (kg)	14.3	10.5 - 17.8	13.91	11.59
% F/B	65.8	61.0 - 68.6	2.36	1.39
% K/B	5.0	4.1 - 6.1	9.65	7.54
% O/B	28.1	25.4 - 29.7	3.40	1.89
FWT (g)	11.2	9.5 - 13.6	7.86	6.47
% M/F	82.5	78.2 - 86.5	2.78	2.56
% S/F	9.9	7.2 - 13.8	19.24	18.24
% K/F	7.6	6.3 - 8.9	7.98	5.72
% O/WM	51.7	49.0 - 55.3	2.94	2.42
% O/DM	76.7	74.9 - 78.6	1.34	1.08
% O/F	42.7	39.7 - 45.1	3.30	2.50

PCV = Phenotypic coefficients of variation and GCV = Genotypic coefficients of variation

Table 13: Estimation of variance components for bunch and fruit components of bi-clonal DxP progenies in trial 29.48

Components	BWT (kg)	% F/B	% K/B	% O/B	FWT (g)	% M/F	% S/F	% K/F	% O/WM	% O/DM	% O/F
σ_g^2	2.746	0.845	0.142	0.282	0.525	4.465	3.261	0.189	1.564	0.688	1.144
σ_e^2	25.291	32.591	1.905	13.197	5.239	16.721	7.714	3.742	15.517	7.682	17.598

σ_g^2 = Genotype variance and σ_e^2 = Error variance

Table 14: Phenotypic variance, genotypic variance and broad sense heritability for bunch and fruit components of Bi-clonal DxP progenies in Trial 29.48

Trait	σ_{ph}^2	σ_g^2	h_B^2 (%)
BWT (kg)	3.956	2.746	69.41
% F/B	2.405	0.845	35.13
% K/B	0.233	0.142	60.94
% O/B	0.914	0.282	30.85
FWT (g)	0.776	0.525	67.65
% M/F	5.265	4.465	84.80
% S/F	3.630	3.261	89.83
% K/F	0.368	0.189	51.36
% O/WM	2.306	1.564	67.82
% O/DM	1.055	0.688	65.21
% O/F	1.990	1.144	57.48

σ_{ph}^2 = Phenotypic variance, σ_g^2 = Genotypic variance and h_B^2 = Broad sense heritability