



Genetic Characterization for Dominant, Additive and Epistatic Variations in *Gossypium Hirsutum* L.

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Abstract: The choice of an effective breeding procedure mainly depends upon the knowledge of genetic mechanism involved in the inheritance of different traits. The purpose of present research is to evaluate the quantitative traits gene action heritability in nine crosses developed by using six parents. Six generations ($BC_{1,2}$, P_1 , P_2 and F_1 , F_2) have been and subjected for generation mean analysis. Results of the study keep epistatic, additive and dominant gene effects were more important for plant height and ginning out turn while, gene additive effects found to be predominant for controlling inheritance number of sympodial branches per plant, cotton seed production in plants fiber fineness and length. In case of boll weight and number of bolls per plant additive as well as dominant gene effects were prevalent. In addition to this, low to high broad sense heritability estimates (30-93%) were found for all traits. Combining the information obtained by the generation mean analysis and heritability estimates, it is concluded that mostly traits were genetically determined and this genetic material could open the new avenue for cotton breeder to develop the elite cotton genotypes.

Keywords: Generation mean analysis, quantitative traits, broad sense heritability, genotypic variance, phenotypic variance, cotton

1.

INTRODUCTION

Generation mean analysis is a biometrical approach used for genetic studies and measurements of phenotypic performance for definite quantitative traits on as many as accessible plant stuffs in abecedarian experimental breeding generations (parental, filial, backcross and segregation generations) under conventional breeding methods (Spehar and Galwey, 1995). Genetic analysis of quantitative traits further aids to elucidate the genetic variation, nature and magnitude of exists in the population. The estimates of gene effects in a plant improvement programme have a direct bearing upon the choice of breeding procedure to be followed (Vijayarajan *et al.*, 2007). Such as additive gene effects are beneficial to evolve pure lines whereas dominance and epistatic effects can be helpful to tap hybrid vigour. Furthermore, different traits are improved depending upon existence of transferable or heritable variation that is measure of degree of genetics determination of traits and helps the selection process. Different degree of heritability ranged from low to high for various traits (Bahadar *et al.*, 1993). This technique has been used to interpret potential of plant material used in experiment to determine the breeding procedure in many crops like wheat, maize, cotton, etc.

Cotton (*Gossypium hirsutum* L.) has been playing a pivotal role in both agriculture as well as Pakistan's economy. Cotton fiber yield is of utmost importance and intricate trait owing to multigenes and markedly affected by environment (Song and Zhang, 2009). Many scientists have conducted a lot of research to find out gene effect,

nature and its magnitude in relation to inheritance of different quantitative parameters in upland cotton, and reported interrelation of non additive and additive effects of gene (Patel *et al.*, 2007). Even though gene action of morphological, yield contributing and fiber quality traits under study has been addressed earlier nevertheless the fluctuation in plant material with its environment. So that it is important to deduce gene action of quantitative traits before starting breeding program. This scenario envisages quantitative genetic analysis from a sample of cotton genotypes and their crosses using generation mean analysis help to elucidate magnitude, generation and its nature involved. Therefore current research was planned to work out the appropriate breeding strategy using generation mean analysis and heritability for the development of elite cotton genotypes.

2. **MATERIALS AND METHODS**

Plant materials

The experimental material was comprised of six genotypes of upland cotton *Gossypium hirsutum* L. having contrasting traits. Using six parental lines, nine F_1 hybrids were developed during 2007 (Table 1). The F_0 seed was sown in the field to grow F_1 generations and backcrosses were developed by crossing the both parent with F_1 in each cross during 2008. These genotypes were selfed for many years to ensure the purity and homozygosity.

Experimental layout

The seeds of each of six generations like BC_1 ($F_1 \times P_1$), BC_2 ($F_1 \times P_2$) and P_1 , P_2 , F_1 , F_2 , were raised in field at Cotton Research Station, Multan, Pakistan during mid-

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May of 2009 by Complete Randomized Block Design replicated thrice. The seeds were dibbled 2.5 cm deep having row to row and plant to plant distance 30 cm and 75 cm, respectively.

Data recording

At maturity, 10 guarded plants for P_1 , P_2 and F_1 , 30 for each of the backcrosses and 50 for F_2 generation were selected in each replication to record data of nine traits such as height of plant (cm), weight of boll (g), per plant production, and length of fiber (mm) on individual plant basis. After ginning of seed cotton the samples were tested for staple length and fiber fineness using instrument high volume (HVI), Spectrum 1, Uster made in America in the fibre testing lab, Cotton Research Station, Multan, Pakistan. The out turn of ginning was calculated with the help of formula:

$$\text{GOT (\%)} = \frac{\text{weight of lint in sample}}{\text{weight of seed cotton in sample}} \times 100$$

Genotypic variances, environmental variances, phenotypic variances and broad sense heritability estimates (H^2) were also determined (Falconer, 1981).

Statistical procedure

Mean of generation analysis was described and performed by Mather and Jinks (1982). Variances and Means of each population were analysed from single plant with replication. For calculating least square generation means method was used. Best model was chosen as the one which had non-significant chi-square value. For each trait the higher value parent was always taken as P_1 in the model fitting. Moreover, genetic, environmental and phenotypic variances, broad sense heritability (H^2) were determined using ANOVA mean squares for each trait.

3. RESULTS

The variance analysis exhibited pronounced differences among six generations, number of bolls, sympodial monopodial branches per plant and plant height, boll weight, cotton seed yield, ginning out turn percentage, fiber length and fiber fineness/micronaire (**Table 1**). Furthermore the mean squares of different generations indicated mainly due to first filial generation F_1 's, interaction components due to segregating generations F_2 's and back crosses (P_1 , F_1 vs F_2 , BC's) were highly significant among the traits except monopodial and sympodial branches per plant. Similarly, interaction components due to parents and (P vs F_1) and interaction components due to segregating generations (F_2 vs BC's) found to be significantly higher at ($P < 0.01$) in case of plant height, ginning out turn, fiber length and fiber fineness.

Generation mean analysis for morphological and fiber quality attributes

The result of generation mean analysis provided estimation to the effects of gene (Table 2). In case of sympodial branches, the additive (d) gene action type was observed in cross 2 (S-12 × MNH-554), cross 4 (ACALA-1517-C × LRA-5166), cross 7 (CIM-70 × LRA-5166) and cross 8 (CIM-70 × MNH-554). Similarly, for seed cotton yield per plant a simple model with two genetic parameters m, [d] in all crosses except cross 3 (S-12 × CIM-448) provided a good fit to the data. In the same way, for fiber length, a simple two parameters model m, [d] with additive type of gene action resulted ideal fit to the data in cross 3 (S-12 × CIM-448), cross 7 (CIM-70 × LRA-5166) and cross 9 (CIM-70 × CIM-448). Likewise, for fiber fineness in cross 1 (S-12 × LRA-5166), cross 7 (CIM-70 × LRA-5166) and cross 9 (CIM-70 × CIM-448) a simple additive model was found to be fit, showing the presence of additivity.

The results depicted low to high estimates of in broad sense for different traits in all crosses (Table 3). The values of broad sense heritability were higher for boll weight (52 – 90 %), plant height (52 – 90 %), number of bolls per plant (62 – 84 %), ginning outturn (60 – 91%), sympodial branches per plant (47 – 77 %) monopodial branches per plant (30 – 70 %), seed cotton yield per plant (42 – 93 %), staple length (50 – 82 %) and fiber fineness (43 – 72 %).

4. DISCUSSION

Generation mean analysis figured out additive gene effects of sympodial branches, seed cotton yield per plant, fiber idealness suggesting that the improvement of these traits would be effective useful during early segregating generations (Abbas *et al.*, 2008). Additive and dominant genes for bolls number, ball count and weight recommended in that the betterment of these traits need intensive selection following later generation (Bertini *et al.*, 2001). Additive, dominance and epistatic gene effects (additive × dominance) for plant height whereas additive, dominance and epistatic gene effect (dominance × dominance) for ginning outturn suggested delayed selection and intermating the segregants following recurrent selection to enhance the trait (Ramalingam & Sivasamy, 2002).

However, in some cases, different genetic models (additive, additive + dominance and epistatic) based on various combinations of crosses and traits could not suitably fit to the data. Thus, indicated more complex mechanisms of genetic control suggesting that improvement of traits would be more difficult. Such condition is not satisfactory for a breeder and it is wise to suggest revised breeding program. In addition to this further succeeding generations are required owing to the

gene effects complexity occurring in these generations. Therefore, there should be reasonable generations to recognize whether the reason for unfit model would be existence of higher order gene interaction or linkage gene effect (Dvojkojic *et al.*, 2010).

Furthermore, genetic and phenotypic variances for each parameter were estimated to construct a definite selection index (Soomro *et al.*, 2010). In addition to this, the total variance attributes helps to determine heredity of the population of genotypic variation. It also tells the extent to which individual phenotypes are estimated by their genotypes. In the current study, genotypic variances were higher than environmental variances. Consequently, moderately high to high broad sense heritability estimates revealed higher degree of genetic determination (Banumathy *et al.*, 2000). Hence there are better chances to improve all these traits in early generations by selection because high heritable characters are least affected by the environment (Soomro *et al.*, 2010).

5.

CONCLUSION

Additive as well as dominance forces seemed to play a major role in inheritance of characters studied. However, the nature and magnitude of gene effects varied from cross to cross and thus demanded specific handling for its full exploitation. The mean generation resulted into additive and dominance effects were useful from number of traits with minute gene interactions. Therefore, selection would be appropriate in early generations to enhance these characters through breeding strategy. In addition to this, moderately high to high broad sense heritability estimates for traits studied expressed that these traits are genetically determined providing sufficient scope for betterment of these traits genetically by means of selection and breeding because maximum portion of genetic variance is heritable. This information will be of great importance for cotton breeders to improve yield potential and develop an elite cotton genotype.

Table-1 Analysis of variances for traits measured in six generations of *Gossypium hirsutum* L. under field conditions

Source of variance	PH (cm)	NMB	NSB	BW (g)	NB	SCY	GOT (%)	FL (mm)	FF (µg/inch)
Replications	14.46 ^{NS}	0.159 ^{ns}	2.705 ^{NS}	0.003 ^{NS}	1.363 ^{NS}	3.348 ^{NS}	0.366 [*]	0.033 ^{NS}	0.000 ^{NS}
Generations	1213.887 ^{**}	0.287 ^{**}	7.33 ^{**}	0.575 ^{**}	88.345 ^{**}	1165.532 ^{**}	20.633 ^{**}	1.092 ^{**}	0.061 ^{**}
Parents	5361.386 ^{**}	1.258 ^{**}	34.62 ^{**}	0.826 ^{**}	249.669 ^{**}	3711.937 ^{**}	55.895 ^{**}	3.441 ^{**}	0.179 ^{**}
F ₁ 's	229.784 ^{**}	0.081 ^{NS}	0.890 ^{NS}	0.335 ^{**}	111.936 ^{**}	645.311 ^{**}	14.378 ^{**}	0.782 ^{**}	0.059 ^{**}
F ₂ 's	48.015 ^{**}	0.055 ^{NS}	2.378 ^{NS}	0.405 ^{**}	26.436 ^{**}	630.053 ^{**}	9.919 ^{**}	0.421 ^{**}	0.026 ^{**}
BC's	153.012 ^{**}	0.198 ^{**}	3.133 ^{**}	0.317 ^{**}	44.458 ^{**}	455.181 ^{**}	17.223 ^{**}	0.992 ^{**}	0.050 ^{**}
P vs F ₁	12553.23 ^{**}	0.53 ^{**}	42.94 ^{**}	7.84 ^{**}	482.67 ^{**}	10404.04 ^{**}	25.833 ^{**}	0.012 ^{NS}	0.034 ^{**}
F ₂ vs BC's	15.829 ^{**}	0.147 ^{NS}	2.206 ^{NS}	0.000 ^{NS}	7.413 [*]	28.235 [*]	21.969 ^{**}	0.4900 ^{**}	0.008 ^{**}
PF ₁ vs F ₂ BC ₂	5569.797 ^{**}	0.359 [*]	2.971 ^{NS}	0.305 ^{**}	20.976 ^{**}	846.464 ^{**}	31.48 ^{**}	0.567 ^{**}	0.040 ^{**}
Error	8.676	0.064	1.358	0.006	1.769	13.704	0.084		0.000 ^{**}

PH = Plant height, NMB = Number of monopodial branches per plant, NSB = No. of sympodia per plant, BW = Boll weight, NB = No. of bolls per plant, SCY = Seed cotton yield per plant, Ginning out turn, FL = Fiber length, FF = Fiber fineness, NS = Non significant, * = significant at 5 % level, ** = Significant at 1% level

Table-2 Estimate of the best fit model for generation mean parameters, mean (m), additive (d), dominance (h), additive × additive (I), additive × dominance (j) and dominance × dominance (l) about various plant traits in nine crosses.

Crosses	[m]	[d]	[h]	[i]	[j]	[l]	x ²	df
Plant height (cm)								
Cross 1	86.349 ± 3.961	35.796 ± 3.942	45.179 ± 9.296	-	-	-	7.1132 [*]	3
Cross 2	90.210 ± 3.326	46.439 ± 3.241	97.192 ± 10.29	-	-	49.059 ± 11.86	4.136 [*]	2
Cross 3	82.480 ± 3.093	38.653 ± 3.058	88.890 ± 10.06	-	-	54.664 ± 10.82	2.6355 [*]	2
Cross 5	124.97 ± 4.581	34.324 ± 3.524	-	39.822 ± 6.169	-	-	6.3045 [*]	3
Cross 6	128.15 ± 4.851	32.221 ± 2.350	-	42.757 ± 6.264	-	-	7.0351 [*]	3
Cross 7	95.172 ± 3.970	43.342 ± 4.074	31.234 ± 10.49	-	65.109 ± 13.89	-	2.8100 [*]	2
Cross 8	80.783 ± 3.506	42.777 ± 3.508	48.447 ± 10.46	-	-	-	6.2583 [*]	3
Cross 9	123.48 ± 6.580	34.113 ± 3.832	-	38.308 ± 8.046	-	-	5.7632 [*]	3
Number of monopodial branches per plant								
Cross 2	3.00 ± 0.318						2.122 [*]	5
Cross 7	2.423 ± 0.240						3.474 [*]	5
Cross 8	2.374 ± 0.263						4.464 [*]	5
Cross 9	2.316 ± 0.238						3.616 [*]	5
Number of sympodial branches per plant								
Cross 1	16.305 ± 0.920						5.367 [*]	5
Cross 9	14.677 ± 0.844						6.991 [*]	5
Boll weight (g)								
							494	
Cross 5	3.111 ± 0.130	0.773 ± 0.287	-	-	-	-	5.7093 [*]	4
Cross 6	3.461 ± 0.0999	0.326 ± 0.114	-	-	-	-	5.7122 [*]	4
Cross 8	2.676 ± 0.136	0.641 ± 0.136	0.798 ± 0.262	-	-	-	7.5970 [*]	3
Cross 9	2.902 ± 0.113	0.825 ± 0.114	0.693 ± 0.256	-	-	-	5.3952 [*]	3

Number of bolls per plant								
Cross 1	28.531 ± 1.826	10.44 ± 2.116	-	-	-	-	3.5914*	4
Cross 4	26.557 ± 2.169	7.060 ± 2.171	16.108 ± 4.235	-	-	-	2.790*	3
Cross 6	24.690 ± 1.909	4.588 ± 2.295	-	-	-	-	6.874*	4
Cross 7	28.055 ± 2.107	11.27 ± 2.501	-	-	-	-	3.613*	4
Cross 8	24.158 ± 2.009	5.000 ± 2.356	-	-	-	-	4.096*	4
Cross 9	22.824 ± 1.835	-	-	-	-	-	6.394*	5
Seed cotton yield per plant (gm)								
Cross 3	52.701 ± 4.599	28.409 ± 11.87	-	30.574 ± 12.99	-	-	4.284*	3
Ginning outturn (%)								
Cross 1	33.935 ± 0.368	-	-	-	-	-	4.656*	5
Cross 3	36.595 ± 0.452	2.4500 ± 0.465	3.065 ± 0.781	-4.210 ± 1.515	-	-	2.022*	2
Cross 4	34.284 ± 0.344	-	-	-	-	-	10.361*	5
Cross 6	37.277 ± 0.593	-	-	-	-	-	8.623*	5
Cross 9	36.098 ± 0.345	3.2200 ± 0.383	-	-	-	-	3.392*	4
Fiber length (mm)								
Cross 1	26.346 ± 0.374	1.355 ± 0.290	-	2.059 ± 0.552	-	-	4.402*	3
Cross 2	28.148 ± 0.290	0.843 ± 0.337	-	-	-	-	4.511*	4
Cross 4	27.358 ± 0.299	-	-	-	-	-	6.660*	5
Cross 8	28.485 ± 0.230	1.069 ± 0.393	-	-	3.041 ± 641	-	3.274*	3
Fiber fineness/micronaire (µg/inch)								
Cross 3	4.392 ± 0.039	0.117 ± 0.053	-	-	-	-	6.972*	4
Cross 4	4.454 ± 0.039	0.305 ± 0.068	-	-0.625 ± 0.13	-	-	2.461*	3
Cross 5	4.269 ± 0.057	0.235 ± 0.054	0.373 ± 0.114	-	-	-	3.146*	3
Cross 6	4.349 ± 0.031	0.159 ± 0.048	-	-	-	-	4.332*	4
Cross 8	4.349 ± 0.033	0.138 ± 0.053	-	-	-	-	8.188*	4

* Significant at 5 % level

Table-3 Estimate of genotypic and phenotypic of variances and broad-sense heritabilities in nine cotton crosses

Crosses	Variances			h ² B.S
	Genotypic	Environmental	Phenotypic	
Final height of main stem (cm)				
Cross 1 (S-12 × LRA-5166)	919.41	1.27	920.68	0.66
Cross 2 (S-12 × MNH-554)	1476.92	1.41	1478.33	0.52
Cross 3 (S-12 × CIM-448)	1046.6	2.15	1048.21	0.81
Cross 4 (ACALA-1517-C × LRA-5166)	972.71	5.17	977.88	0.87
Cross 5 (ACALA-1517-C × MNH-554)	943.43	1.42	948.86	0.78
Cross 6 (ACALA-1517-C × CIM-448)	837.58	3.41	840.99	0.90
Cross 7 (CIM-70 × LRA-5166)	904.01	1.15	905.16	0.78
Cross 8 (CIM-70 × MNH-554)	1293.83	3.04	1296.87	0.89
Cross 9 (CIM-70 × CIM-448)	871.65	2.38	874.04	0.77
No. of monopodial branches per plant				
Cross 1 (S-12 × LRA-5166)	0.08	0.01	0.094	0.70
Cross 2 (S-12 × MNH-554)	0.105	0.03	0.14	0.73
Cross 3 (S-12 × CIM-448)	0.03	0.02	0.05	0.69
Cross 4 (ACALA-1517-C × LRA-5166)	0.00093	0.01	0.014	0.57
Cross 5 (ACALA-1517-C × MNH-554)	0.037	0.009	0.046	0.62
Cross 6 (ACALA-1517-C × CIM-448)	0.019	0.006	0.024	0.59
Cross 7 (CIM-70 × LRA-5166)	0.20	0.02	0.22	0.43
Cross 8 (CIM-70 × MNH-554)	0.24	0.009	0.25	0.30
Cross 9 (CIM-70 × CIM-448)	0.236	0.01	0.249	0.56
Number of sympodial branches per plant				
Cross 1 (S-12 × LRA-5166)	3.56	0.111	3.68	0.47
Cross 2 (S-12 × MNH-554)	7.31	0.19	7.5	0.77
Cross 3 (S-12 × CIM-448)	2.56	0.36	2.92	0.69
Cross 4 (ACALA-1517-C × LRA-5166)	2.85	0.38	3.24	0.65
Cross 5 (ACALA-1517-C × MNH-554)	1.48	0.49	1.97	0.69
Cross 6 (ACALA-1517-C × CIM-448)	0.57	0.40	0.97	0.49
Cross 7 (CIM-70 × LRA-5166)	0.53	5.60	6.13	0.69
Cross 8 (CIM-70 × MNH-554)	5.87	0.09	5.95	0.67
Cross 9 (CIM-70 × CIM-448)	4.35	0.02	4.55	0.68
Number of bolls per plant				
Cross 1 (S-12 × LRA-5166)	65.75	0.47	66.23	0.84
Cross 2 (S-12 × MNH-554)	34.55	0.33	34.88	0.70
Cross 3 (S-12 × CIM-448)	53.91	0.577	54.49	0.82
Cross 4 (ACALA-1517-C × LRA-5166)	73.01	0.57	73.59	0.74
Cross 5 (ACALA-1517-C × MNH-554)	8.34	0.41	8.7	0.62
Cross 6 (ACALA-1517-C × CIM-448)	28.65	0.56	29.21	0.77

Cross 7 (CIM-70 × LRA-5166)	70.1	0.85	70.92	0.76
Cross 8 (CIM-70 × MNH-554)	27.52	0.40	27.92	0.78
Cross 9 (CIM-70 × CIM-448)	17.25	0.60	17.87	0.80
Boll weight (g)				
Cross 1 (S-12 × LRA-5166)	0.15	0.003	0.153	0.52
Cross 2 (S-12 × MNH-554)	0.17	0.0009	0.71	0.90
Cross 3 (S-12 × CIM-448)	0.29	0.003	0.296	0.67
Cross 4 (ACALA-1517-C × LRA-5166)	0.05	0.004	0.257	0.78
Cross 5 (ACALA-1517-C × MNH-554)	0.18	0.0005	0.18	0.59
Cross 6 (ACALA-1517-C × CIM-448)	0.19	0.0009	0.191	0.83
Cross 7 (CIM-70 × LRA-5166)	0.21	0.001	0.21	0.85
Cross 8 (CIM-70 × MNH-554)	0.41	0.001	0.41	0.87
Cross 9 (CIM-70 × CIM-448)	0.391	0.0006	0.392	0.77
Seed cotton yield per plant (g)				
Cross 1 (S-12 × LRA-5166)	865.37	17.85	883.22	0.88
Cross 2 (S-12 × MNH-554)	692.94	1.10	694.04	0.70
Cross 3 (S-12 × CIM-448)	1173.62	0.53	1174.15	0.42
Cross 4 (ACALA-1517-C × LRA-5166)	117.38	2.51	119.89	0.76
Cross 5 (ACALA-1517-C × MNH-554)	263.19	2.57	265.77	0.92
Cross 6 (ACALA-1517-C × CIM-448)	351.25	1.45	352.70	0.93
Cross 7 (CIM-70 × LRA-5166)	810.83	1.02	811.86	0.87
Cross 8 (CIM-70 × MNH-554)	644.50	0.74	645.23	0.61
Cross 9 (CIM-70 × CIM-448)	1034.85	0.66	1035.51	0.80
Ginning outturn (%)				
Cross 1 (S-12 × LRA-5166)	0.92	0.05	0.98	0.86
Cross 2 (S-12 × MNH-554)	7.45	0.009	7.46	0.60
Cross 3 (S-12 × CIM-448)	4.26	0.005	4.264	0.77
Cross 4 (ACALA-1517-C × LRA-5166)	1.74	0.008	1.75	0.71
Cross 5 (ACALA-1517-C × MNH-554)	8.76	0.02	8.79	0.91
Cross 6 (ACALA-1517-C × CIM-448)	3.91	0.035	3.94	0.78
Cross 7 (CIM-70 × LRA-5166)	2.99	0.026	3.02	0.85
Cross 8 (CIM-70 × MNH-554)	16.50	0.026	16.53	0.85
Cross 9 (CIM-70 × CIM-448)	12.94	0.03	12.97	0.60
Staple length (mm)				
Cross 1 (S-12 × LRA-5166)	0.73	0.01	0.75	0.82
Cross 2 (S-12 × MNH-554)	40.53	0.01	0.54	0.76
Cross 3 (S-12 × CIM-448)	0.46	0.01	0.47	0.65
Cross 4 (ACALA-1517-C × LRA-5166)	0.80	0.009	0.81	0.84
Cross 5 (ACALA-1517-C × MNH-554)	0.49	0.004	0.498	0.59
Cross 6 (ACALA-1517-C × CIM-448)	0.22	0.004	0.225	0.69
Cross 7 (CIM-70 × LRA-5166)	0.46	0.01	0.47	0.73
Cross 8 (CIM-70 × MNH-554)	0.54	0.007	0.55	0.78
Cross 9 (CIM-70 × CIM-448)	33.0	0.005	0.334	0.50
Fiber fineness (µg/inch)				
Cross 1 (S-12 × LRA-5166)	0.03	0.0002	0.032	0.54
Cross 2 (S-12 × MNH-554)	0.01	0.0001	0.01	0.54
Cross 3 (S-12 × CIM-448)	0.027	0.0001	0.027	0.64
Cross 4 (ACALA-1517-C × LRA-5166)	0.049	0.000	0.0495	0.43
Cross 5 (ACALA-1517-C × MNH-554)	0.021	0.0003	0.0215	0.49
Cross 6 (ACALA-1517-C × CIM-448)	0.01	0.0002	0.013	0.53
Cross 7 (CIM-70 × LRA-5166)	0.037	0.00006	0.0375	0.65
Cross 8 (CIM-70 × MNH-554)	0.018	0.0001	0.018	0.60
Cross 9 (CIM-70 × CIM-448)	0.018	0.0001	0.018	0.72

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